PERSPECTIVES on Science and Christian Faith

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In This Issue …

"The fear of the Lord
is the beginning of Wisdom."
Psalm 111:10

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Perspectives on Science and Christian Faith

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Editorial

Happy Anniversary!


James C. Peterson

The American Scientific Affiliation, the Canadian Scientific and Christian Affiliation, and Christians in Science will soon be gathering together in Canada for a joint meeting this July 25–28. It is particularly fitting then to wish here a hearty congratulations to the CSCA on the 40th anniversary of its founding.

Forty years ago was a time of rapid change in Canada. Canada had just celebrated its centennial and repatriated its constitution from Britain. There was a sense of joining the world stage as its own country. That impetus was spurred further by new laws in Canada that donations would only be recognized for income tax reduction if they were to a Canadian organization. Canadian members of the American Scientific Affiliation worked with the ASA to establish the Canadian Scientific and Christian Affiliation as a unique voice alongside the ASA. The ASA could not have been more gracious ever since in sharing expertise, publications, and people with its continental ally.

The USA and Canada are distinct from each other, yet have much in common. Canadians remember that armed forces have invaded from the United States as recently as 1866, yet despite more stringent controls of late for security on the American side and taxes on the Canadian side, the border remains the world's longest boundary without military defense. Both are geographic giants. When the CSCA council meets by Skype, it is over eight time zones from the president Arnold Sikkema in Vancouver PST to the early career representative, Bethany Sollereder on Greenwich Mean Time at the University of Exeter, England. The two countries occupy an almost identical number of square miles, but Canada has one-tenth the population. Both nations are increasingly urban, but Canada's cities have more open space between them. Both are democracies, but one has a queen. Both work in dollars, but one shows a portrait of Lincoln on the five and the other has a game of pond hockey. We build and drive the same cars, but in kilometers and miles. There are identical Thanksgiving Day feasts of turkey and apple pie, but one is celebrated in October and the other in November.

Only the most experienced Europeans can distinguish us North Americans from each other, yet we are different enough that we can complement each other and serve better for it. For example, Canada has a geography and history that lends itself to bringing together for this year's annual meeting the sibling associations of Christians in the sciences from the neighboring colossi of the US and the UK. As with the ASA, the CSCA has been about people learning with each other, enjoying each other, struggling with each other, working alongside each other, in a remarkably diverse yet common service to one Lord. There has been much challenge, dialogue, and insight.

Forty years. A biblical generation. That is long enough to be clear that no one individual has carried the CSCA. The only persons who have been at the center all the way through have been the Father, Son, and Holy Spirit. For our Lord's calling, work, and encouragement to that work, we are thankful. May the next forty be as collegial, fruitful, and enduring for the CSCA as the last.

With deepest appreciation to all those who have made and continue to make the service of the CSCA possible, moving forward in common cause and fellowship with the ASA,

Grace and peace,

James C. Peterson, *Editor*

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"All things hold together in Christ"
Colossians 1:17

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Article

Keith B. Miller

The Fossil Record of the Cambrian “Explosion”: Resolving the Tree of Life[1]

Keith B. Miller

The Cambrian “explosion” has been the focus of extensive scientific study, discussion, and debate for decades. It has also received considerable attention by evolution critics as posing challenges to evolution.

In the last number of years, fossil discoveries from around the world, and particularly in China, have enabled the reconstruction of many of the deep branches within the invertebrate animal tree of life. Fossils representing “sister groups” and “stem groups” for living phyla have been recognized within the latest Precambrian (Neoproterozoic) and Cambrian. Important transitional steps between living phyla and their common ancestors are preserved. These include the rise of mollusks from their common ancestor with the annelids, the evolution of arthropods from lobopods and priapulid worms, the likely evolution of brachiopods from tommotiids, and the rise of chordates and echinoderms from early deuterostomes.

With continued new discoveries, the early evolutionary record of the animal phyla is becoming ever better resolved. The tree of life as a model for the diversification of life over time remains robust, and strongly supported by the Neoproterozoic and Cambrian fossil record.

The most fundamental claim of biological evolution is that all living organisms represent the outer tips of a diversifying, upward-branching tree of life. The “Tree of Life” is an extremely powerful metaphor that captures the essence of evolution. Like the branches of a tree, as we trace individual lines of descent (lineages) back into the past (down the tree), they converge with other lineages toward their common ancestors. Similarly, these ancient lineages themselves converge with others back in time. Thus, all organisms, both living and extinct, are ultimately connected by an unbroken chain of descent with modification to a common ancestral trunk among single-celled organisms in the distant past.

This tree metaphor applies as much to the emergence of the first representatives of the major groups of living invertebrates (such as snails, crabs, or sea urchins) as it does to the first appearance and diversification of dinosaurs, birds, or mammals. This early diversification of invertebrates apparently occurred around the time of the Precambrian/Cambrian boundary over a time interval of a few tens of millions of years. This period of rapid evolutionary diversification has been called the “Cambrian Explosion.”

The Cambrian explosion has been the focus of extensive scientific study, discussion, and debate for decades, and is increasingly receiving attention in the popular media. It has also received considerable recent attention by evolution

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critics as posing challenges to evolution. These critics argue that the expected transitions between major invertebrate groups (phyla) are absent, and that the suddenness of their appearance in the fossil record demonstrates that evolutionary explanations are not viable.

What are some of the arguments of the evolution critics? John Morris of the Institute for Creation Research writes,

> If evolution is correct, the first life was quite simple, evolving more complexity over time. Yet the Cambrian Explosion of Life has revealed life's complexity from the start, giving evolution a black eye. The vast array of complex life that appears in the lowest (or oldest) stratigraphic layer of rock, with no apparent ancestors, goes hard against evolutionary dogma. Evolution's desperate attempt to fill this gap with more simple ancestral fossils has added more injury ... Think of the magnitude of this problem from an evolutionary perspective. Many and varied forms of complex multi-celled life suddenly sprang into existence without any trace of less complex predecessors. There are numerous single-celled forms at lower stratigraphic levels, but these offer scant help in solving the mystery. Not one basic type or phyla [sic] of marine invertebrate is supported by an ancestral line between single-celled life and the participants in the Cambrian Explosion, nor are the basic phyla related to one another. How did evolution ever get started?[2]

Intelligent design advocate Stephen Meyer and others have written:

> To say that the fauna of the Cambrian period appeared in a geologically sudden manner also implies the absence of clear transitional intermediates connecting the complex Cambrian animals with those simpler living forms found in lower strata. Indeed, in almost all cases, the body plans and structures present in Cambrian period animals have no clear morphological antecedents in earlier strata.[3]

And

> A third feature of the Cambrian explosion (as well as the subsequent fossil record) bears mentioning. The major body plans that arise in the Cambrian period exhibit considerable morphological isolation from one another (or "disparity") and then subsequent "stasis." Though all Cambrian and subsequent animals fall clearly within one of a limited number of basic body plans, each of these body plans exhibits clear morphological differences (and thus disparity) from the others. The animal body plans (as represented in the fossil record) do not grade imperceptibly one into another, either at a specific time in geological history or over the course of geological history. Instead, the body plans of the animals characterizing the separate phyla maintain their distinctive morphological and organizational features and thus their isolation from one another, over time.[4]

Are these critiques warranted? To what extent is the Cambrian explosion really problematic for the evolutionary picture of an unbroken tree of life extending back to the earliest life on Earth?

Defining the Cambrian "Explosion"

The relative rapidity of the diversification of invertebrates during the Cambrian "explosion" is set against the backdrop of the earth's geologic and biologic history. Geologic time is unfamiliar to most people, and its shear vastness is difficult to grasp.

Two lines of evidence impact our understanding of the duration of the animal diversification that led to the appearance of the major groups of living invertebrates. The first is the dating of critical levels within the geological timeline such as the Precambrian-Cambrian boundary and various important fossil-bearing horizons. The second is the time of appearance of the first widely recognized fossil representatives of the major living groups (phyla) of invertebrate animals. The latter is in considerable flux as new fossil discoveries are made.

Originally, the base of the Cambrian had been set at the earliest appearance of organisms with mineralized skeletons—particularly trilobites. However, a diverse collection of tiny mineralized plates, tubes, and scales was discovered to lie below the earliest trilobites.[5] This interval of "small shelly fossils" was designated the Tommotian. Because of the presence of even earlier tiny mineralized tubes and simple burrows, there was no internationally accepted definition for the boundary until 1994. At that time, the base of the Cambrian was placed at the first appearance of a particular collection of small fossil burrows characterized by *Treptichnus pedum*.[6]

Until the early 1990s, the age of the Precambrian-Cambrian boundary was not tightly constrained, and was estimated to be about 575 million years ago. However, in 1993, new radiometric dates from close to the accepted Precambrian-Cambrian boundary revealed that it was significantly younger—about 544 million years.[7] A more precise date of 542 ± 0.3 million years has recently been formally accepted by the International Commission on Stratigraphy. The basis for this date was the discovery that a sharp worldwide fall (or negative spike) in the abundance of the isotope carbon-13 was coincident with the Cambrian boundary as previously defined. In Oman, this isotopic marker also coincides with a volcanic ash layer that yielded the 542-million-year date using uranium/lead radiometric methods.[8] This horizon also marks the last occurrence of several fossils characteristic of the underlying late Precambrian Ediacaran Period.[9] Such extinction events are commonly used to subdivide the geologic time scale.

The earliest diverse fossil invertebrate communities of the Cambrian are represented by the Chengjiang, in China. These deposits are dated at 525–520 million years. The famous Burgess Shale is considerably younger, dating at about 505 million years, and the end of the Cambrian Period is set at 490 million years. The Cambrian Period thus lasted for 52 million years, and the Early Cambrian alone was an extended period of time lasting 32 million years.[10] To put this in perspective, the time elapsed from the extinction of the dinosaurs at the end of the Cretaceous to the present has been 65 million years. The Cambrian was a very long period of time (see fig. 1).

If the Cambrian "explosion" is understood to comprise the time from the base of the Cambrian to the Chengjiang fossil beds, then this period of diversification in animal body plans appears to have lasted about 20 million years. However, not all living animal phyla with a fossil record first appear within this time window. The colonial skeleton-bearing bryozoans, for example, are not known from the fossil record until near the end of the Cambrian around 491 million years ago.[11] In addition, most of the Early Cambrian fossils recognized as related to modern phyla are actually intermediates or stem groups (see discussion below). Furthermore, recent refined dating of first appearances of the Early Cambrian stem groups has indicated that even the "explosive" start of the Cambrian diversification was more gradual and episodic than previous thought.[12]

Defining the Cambrian "explosion" is not as straightforward as it might seem. Although there was clearly a major burst of evolutionary innovation and diversification in the first 20 million years or so of the Cambrian, this was preceded by an extended period of about 40 million years during which metazoans arose and attained critical levels of anatomical complexity. Significantly, several living invertebrate phyla have a fossil record that extends into the late Neoproterozoic before the Cambrian. Sponges have been recognized as early as 580 million years, cnidarians (the group including jellyfish and anemones) are present among the Ediacaran animals at around 555 million years, and the stem groups for some other phyla were also likely part of the Ediacaran communities. The Ediacaran saw the appearance of organisms with the fundamental features that would characterize the later Cambrian organisms (such as three tissue layers, and bilaterally symmetric bodies with a mouth and anus), as well as the first representatives of modern phyla. The base of the Cambrian is not marked by a sharp dramatic appearance of living phyla without Precambrian roots. It is a subjectively defined point in a continuum.

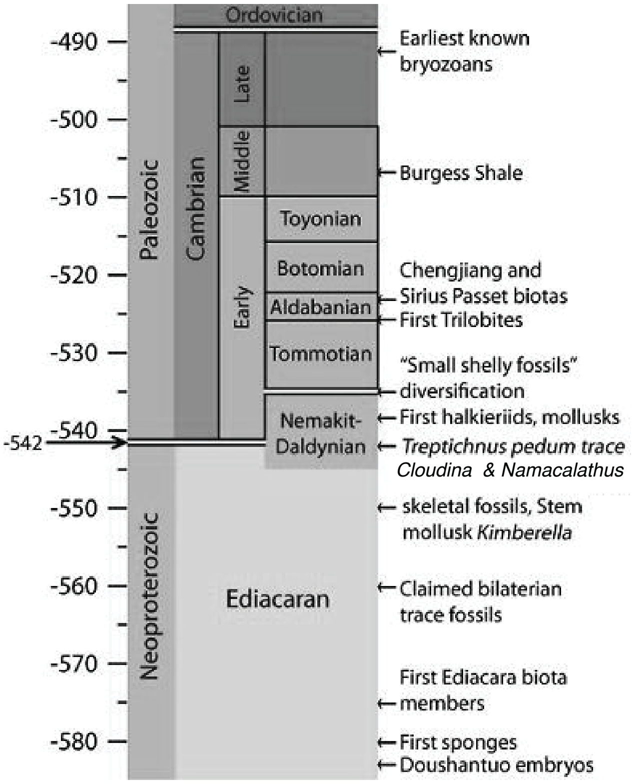

Figure 1. Timeline showing the interval from the late Neoproterozoic (Ediacaran) through the Cambrian. Marked on the timeline are the positions in time of some of the more important fossil localities, and the time of first appearances of selected metazoan groups.

Drawing Trees and Assigning Names

The procedure of classifying organisms is called taxonomy, and the general name for individual groups is "taxa." The first question that needs to be addressed is "What is a phylum?" A phylum is often identified as a group of organisms sharing a basic "body plan" or a group united by a common organization of the body. However, phyla can be understood fundamentally, like all other taxonomic categories, as groupings of taxa that are more closely related to each other than to any other group.

The most widely accepted method for grouping organisms today is called cladistics.[13] In cladistics, all taxonomic groups are monophyletic, that is, all of the members of the group are descended from a common ancestor that is the founding member of that taxon. A branch of the tree of life whose members all share the same ancestor is called a "clade"—thus the term "cladistics." A taxon or taxonomic group that is the closest relative of another group, and that shares the same common ancestor, is called a "sister taxon" or "sister group." The early representatives of two sister groups commonly resemble each other more than the descendant relatives resemble the ancestors of their clade. As a result, placing these organisms into their correct monophyletic groups can be very difficult. Thus, primitive organisms within a given phylum may bear close similarities to those from another closely related sister phylum. In fact, the assignment of a given organism or fossil specimen to a phylum can be just as problematic as assignments to lower-ranked taxa such as classes, orders, families, and so forth.[14] This fact alone indicates that biological diversity is more a continuum than a collection of discrete groups.

Further complicating the assignment of fossil organisms to phyla is that the anatomical characteristics that are used to define living phyla did not appear simultaneously, but were added over time. This has resulted in the distinction between "crown groups" and "stem groups" in the scientific literature[15] (fig. 2). This terminology can be applied to any level of the taxonomic hierarchy. A crown group phylum is composed of all the living organisms assigned to that phylum, plus all the extinct organisms that were descended from the common ancestor of those living organisms. The stem group is composed of extinct organisms more closely related to one particular living phylum than to any other, but that were not descended from the common ancestor of the living representatives of that phylum. Stem groups typically do not possess all of the defining characters of the crown group of that phylum. It turns out that the organisms appearing in the Early Cambrian are, with few exceptions, not crown groups but stem groups. That is, the complete suite of characters defining the living phyla had not yet appeared. Many crown groups do not appear in the fossil record until well after the Cambrian.[16]

The existence of stem groups provides a way to understand how the basic body plan of a living invertebrate could have been built up in steps. The major invertebrate groups are often portrayed by evolution critics as possessing anatomies that are both irreducible in organization and separated from other groups by unbridgeable gaps. However, the identification of stem and sister groups explicitly recognizes the existence of fossil taxa that possess transitional morphologies between recognized modern taxonomic groups (including phyla).

Some critics of evolution make much of the "top-down" versus the "bottom-up" pattern of appearance of higher taxa. That is, phylum-level diversity reaches its peak in the fossil record before class-level diversity, and the class-level diversity before that of orders, and so forth. These critics interpret this apparent "top-down" pattern as contrary to expectations from evolutionary theory. For example, Stephen Meyer and others have argued:

> Instead of showing a gradual bottom-up origin of the basic body plans, where smaller-scale diversification or speciation precedes the advent of large-scale morphological disparity, disparity precedes diversity. Indeed, the fossil record shows a "top-down" pattern in which morphological disparity between many separate body plans emerges suddenly and prior to the occurrence of species-level (or higher) diversification on those basic themes.[17]

However, this pattern is an artifact, being generated by the way in which species are assigned to higher taxa. The classification system is hierarchical with species being grouped into ever larger and more inclusive categories. When this classification hierarchy is applied to a diversifying evolutionary tree, a "top-down" pattern will automatically result. Consider species belonging to a single evolving line of descent given genus-level status. This genus is then grouped with other closely related lines of descent into a family. The common ancestors of these genera are by definition included within that family. Those ancestors must logically be older than any of the other species within the family. Thus the family-level taxon would appear in the fossil record before most of the genera included within it. Another way of looking at this is the fact that the first appearance of any higher taxon will be the same as the first appearance of the oldest lower taxon within the group. For example, a phylum must be as old as the oldest class it contains. Most phyla contain multiple classes, which in turn include multiple orders, and so forth. Thus, each higher taxon will appear as early as the first of the included lower taxa. The "top-down" pattern of taxa appearance is therefore entirely consistent with a branching tree of life.

There is one last bias in our reconstruction of the past that is generated by the process of assigning organisms to a particular phylum. Because phyla are defined by particular anatomical character traits, they cannot be recognized in the fossil record until after those specific characters evolve. However, the splitting of the branch of the tree of life to which

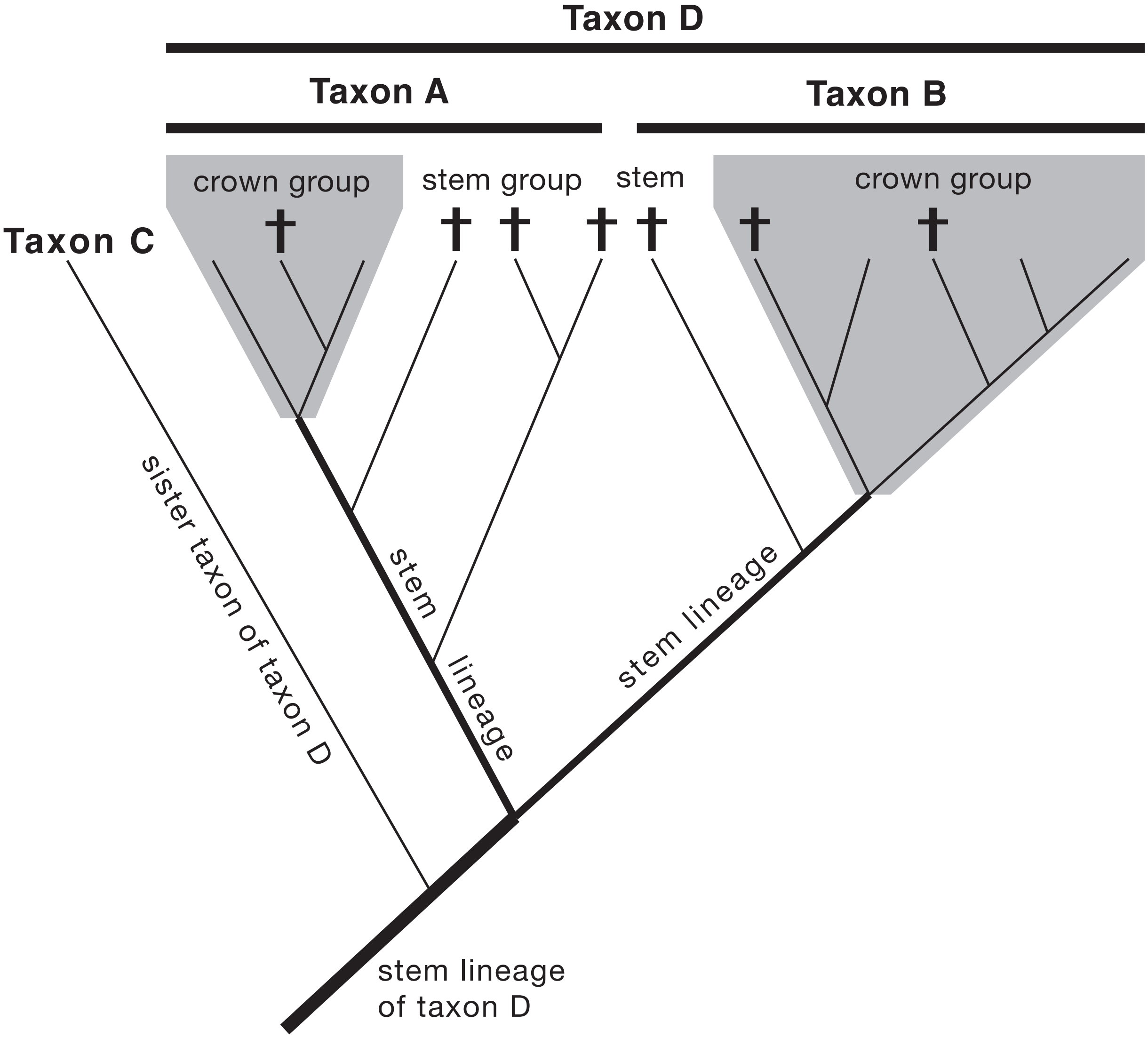

Figure 2. Diagram illustrating the difference between stem and crown groups. The crown group includes the living organisms that possess the characters used to define a modern taxonomic group, and all of the extinct fossil organisms that were descended from the last common ancestor of all members of the crown group. The extinct fossil organisms of the stem group possess some, but not all, of the characters diagnostic of the crown group, and are more closely related to the crown group than any other organisms. A sister group includes those organisms that are more closely related to the total group (crown and stem group) than to any other group of organisms. In this diagram, taxon A and taxon B are sister groups, and taxon C is a sister group to the more inclusive taxon D. (This diagram was modified from the Palaeos website, http://www.palaeos.org/Crown_group.)

a phylum belongs may have occurred many millions of years previous to the evolution of those characters. The characters that we use to define a phylum very likely do not correspond to the characters that actually marked the initial separation of that evolutionary lineage from its closest relative. The actual first appearance of a fossil assignable to a particular phylum thus would likely occur after significant anatomical evolution has occurred along that particular branch of the tree. Branching points in the tree of life will always be older than the named taxa.[18]

The Completeness of the Fossil Record

There are two opposite errors which need to be countered about the fossil record: (1) that it is so incomplete as to be of no value in interpreting patterns and trends in the history of life, and (2) that it is so good that we should expect a relatively complete record of the details of evolutionary transitions within all or most lineages.

What then is the quality of the fossil record? It can be confidently stated that only a very small fraction of the species that once lived on Earth have been preserved in the rock record and subsequently discovered and described by science.[19]

There is an entire field of scientific research referred to as "taphonomy"—literally, "the study of death." Taphonomic research includes investigating those processes active from the time of death of an organism until its final burial by sediment. These processes include decomposition, scavenging, mechanical destruction, transportation, and chemical dissolution and alteration. The ways in which the remains of organisms are subsequently mechanically and chemically altered after burial are also examined—including the various processes of fossilization. Burial and "fossilization" of an organism's remains in no way guarantees its ultimate preservation as a fossil. Processes such as dissolution and recrystallization can remove all record of fossils from the rock. What we collect as fossils are thus the "lucky" organisms that have avoided the wide spectrum of destructive pre- and post-depositional processes arrayed against them.

Soft-bodied organisms and organisms with non-mineralized skeletons have very little chance of preservation under most environmental conditions. Until the Cambrian, nearly all organisms were soft bodied, and even today the majority of species in marine communities are soft bodied. The discovery of new soft-bodied fossil localities is always met with great enthusiasm. These localities typically turn up new species with unusual morphologies, and new higher taxa can be erected on the basis of a few specimens! Such localities are also erratically and widely spaced geographically and in geologic time.

Even those organisms with preservable hard parts are unlikely to be preserved under "normal" conditions. Studies of the fate of clam shells in shallow coastal waters reveal that shells are rapidly destroyed by scavenging, boring, chemical dissolution, and breakage. Environments with high sedimentation rates, or those with occasional rapid sedimentation during major storm events, tend to favor the incorporation of shells into the sedimentary record, and their ultimate preservation as fossils.[20]

The potential for fossil preservation varies dramatically from environment to environment. Preservation is enhanced under conditions that limit destructive physical and biological processes. Thus marine and fresh water environments with low oxygen levels, high salinities, or relatively high rates of sediment deposition favor preservation. Similarly, in some environments biochemical conditions can favor the early mineralization of skeletons and even soft tissues by a variety of compounds (e.g., carbonate, silica, pyrite, phosphate). The likelihood of preservation is thus highly variable. As a result, the fossil record is biased toward sampling the biota of certain types of environments, and against sampling the biota of others.

In addition to these preservational biases, the erosion, deformation, and metamorphism of originally fossiliferous sedimentary rock have eliminated significant portions of the fossil record over geologic time. Furthermore, much of the fossil-bearing sedimentary record is hidden in the subsurface, or located in poorly accessible or little studied geographic areas. For these reasons, of those once-living species actually preserved in the fossil record, only a small portion have been discovered and described by science. However, there is also the promise, and reality, of continued new and important discovery as new sedimentary units are examined, and new techniques are applied. The rapidity with which new fossil discoveries are being made within Neoproterozoic and Cambrian strata is actually quite remarkable.[21]

The forces arrayed against fossil preservation also guarantee that the earliest fossils known for a given animal group will always date to some time after that group first evolved. The fossil record always provides only minimum ages for the first appearance of organisms.

Because of the biases of the fossil record, the most abundant and geographically widespread species of hardpart-bearing organisms would tend to be best represented. Also, short-lived species that belonged to rapidly evolving lines of descent are less likely to be preserved than long-lived stable species. Because evolutionary change is probably most rapid within small isolated populations, a detailed species-by-species record of such evolutionary transitions is unlikely to be preserved. Furthermore, capturing such evolutionary events in the fossil record requires the fortuitous sampling of the particular geographic locality where the changes occurred.

Using the model of a branching tree of life, the expectation is for the preservation of isolated branches on an originally very bushy evolutionary tree. A few of these branches (lines of descent) would be fairly complete, while most are reconstructed with only fragmentary evidence. As a result, the large-scale patterns of evolutionary history can generally be better discerned than species-by-species transitions. Evolutionary trends over longer periods of time and across greater anatomical transitions can be followed by reconstructing the sequences in which anatomical features were acquired within an evolving branch of the tree of life.

The Precambrian Fossil Record

A very important concern is what organisms existed before the Cambrian "explosion." Were there Precambrian precursors, or did the Cambrian "explosion" really happen in a biological vacuum? Many critics of evolution claim that the Precambrian is devoid of fossils that could represent body plans ancestral to those of the Cambrian invertebrates.

The words of Darwin are often cited as evidence of the seriousness of the problem for evolution.

> There is another and allied difficulty, which is much more serious. I allude to the manner in which species belonging to several of the main divisions of the animal kingdom suddenly appear in the lowest known fossiliferous rocks. Most of the arguments which have convinced me that all the existing species of the same group are descended from a single progenitor, apply with equal force to the earliest known species.[22]

When Darwin published his model of descent with modification by means of natural selection, knowledge of the fossil record was in its infancy. In particular, the Precambrian and Early Cambrian fossil record was virtually unknown. Even the fossils of the now famous Burgess Shale and similar units were as yet undiscovered. After nearly a century and a half of paleontological work, the situation has changed dramatically. In keeping with evolutionary expectations, fossils are now known from the late Precambrian and early Cambrian that record several dramatic transitions in the history of life.

The presence of Late Precambrian animals was recognized in the 1950s and became widely publicized by the early 1970s. These are the famous Ediacaran fossils named for fossil-rich beds in the Ediacara Hills of South Australia and now recognized at sites throughout the world. These organisms are typically preserved as impressions in sandstones and siltstones. Associated with these fossils are trails and simple burrows of organisms that show a limited increase in complexity and diversity toward the Cambrian.

The record of life actually extends far beyond the Ediacaran fossils (~575–542 My) into the deep geologic past. Fossils of algae, protists, and bacteria are present throughout much of the Precambrian. The earliest convincing fossils of bacteria are recognized in rocks 3.5 billion years old, and chemical signatures point to the presence of life even earlier. Finely layered mounds (called stromatolites) produced by the activity of mat-building bacteria and algae appear at about this time and become relatively abundant by around 2.7 billion years ago. Evidence of eukaryotic algae, possessing membrane-bounded nuclei and internal organelles, dates to about 1500 million years ago, or earlier if chemical evidence is accepted. Multicellularity had appeared by 1000 million years ago in the form of diverse and relatively advanced seaweeds.[23] The earliest fossils of metazoans (multicelled animals) may be represented by simple disk-shaped fossils found in rocks 610–600 million years old.[24]

The earliest unambiguous indication of the rise of metazoan life is preserved in the spectacular phosphorite deposits of the Doushantuo Formation of China dating to at least 580 million years ago. Phosphate can preserve organisms and tissues in such great detail that individual cells can often be recognized. Where environmental conditions are ideal for this type of preservation, extraordinary fossil deposits may result. In the case of the Doushantuo, phosphatization has preserved not only a variety of algal remains, but also the cellular tissues and spicules of sponges.[25] These sponges appear to belong to the class Demospongia. However, even more spectacular within the Doushantuo phosphorites is the preservation of metazoan eggs and early embryos. These embryos are of uncertain affinities, but they may represent stem cnidarians (the phylum including "jellyfish," anemones, and corals) or even bilaterians (animals with bilateral symmetry).[26] Recently described millimeter-sized phosphatic tubes with internal chambers and apical budding also suggest a cnidarian affinity.[27]

The Ediacaran biota provide the next window into the rise of metazoans. These fossil-bearing units span from about 575 million years to the base of the Cambrian (an interval of ~33 million years), and are found in south Australia, Namibia, the White Sea coast of Russia, and Newfoundland. The enigmatic soft-bodied organisms were preserved as impressions, or molds, on the surfaces of sandstone and siltstone layers. These sediment layers accumulated in shallow-marine environments where the seafloor was covered by firm microbial algal mats. The microbial mats covering the seafloor appear to have been important in determining the lifestyles of the Ediacaran organisms, as well as their unique mode of preservation.[28]

Most soft-bodied impressions of the Ediacaran can roughly be placed into three general groups—disks; fronds; and flat-bodied, bilaterally-symmetric forms. The biological affinity of these fossils is very difficult to determine and highly debated.[29] Disks are the earliest appearing, and most common, Ediacaran fossils. A few disk-shaped fossils are fossil impressions of sponges. One such form appears to be a sponge that might be assignable to the modern class of Hexactinellida.[30]

Many disk-shaped impressions have often been identified as medusoids ("jellyfish") but many appear to have been attached to the bottom, and none bear clear structures that would place them in a living group. Some do clearly possess tentacles around their margins, suggesting a stem or sister group relationship to the cnidarians. Furthermore, recent descriptions of very small phosphatized fossils that predate the Cambrian by 25 million years or more have demonstrated the presence of cnidarians that might even be stem anthozoans (the cnidarian class that includes anemones and corals).[31]

The frond-shaped forms include organisms that were attached to the bottom by a stalk, and others that appear to have been free lying. These fossils have also been assigned by some workers to a group of modern cnidarians (the "sea pens") or to ctenophores. However, like the disks, the fronds are fairly diverse and some may be unrelated to living phyla.[32] Others, although likely not able to be placed into a living cnidarian group, may be stem cnidarians, or even stem anthozoans. The discovery of better preserved fronds in the Cambrian that closely resemble some of the Ediacaran fossils would seem to support this interpretation.[33]

The bilaterally symmetric forms of the Ediacaran are the most diverse and most enigmatic fossils of the late Precambrian. Some of these fossils may represent early experiments on the pathway to the living phyla.[34] For example, *Dickinsonia* and the similar *Yorgia* are fairly large flat highly segmented forms that some workers have interpreted as annelids or stem annelids, while others have seen resemblances to other worm phyla or even chordates. These organisms do appear to have been able to move about the bottom as seen by associated crawling and resting traces. Even if not members of a living phylum, these organisms appear to at least be mobile bilateral metazoans (or bilaterians).

Another bilateral form that has been the subject of much recent attention is the 555-million-year-old mollusk-like *Kimberella* (see fig. 3). This organism appears to have lacked several features characteristic of modern mollusks and thus has been interpreted as a stem mollusk.[35] Scratch marks found associated with *Kimberella* indicate that it had some form of feeding structure (though probably not a true mollusk radula) that enabled it to graze the abundant algal mats.

An important, but less attention-getting, component of the Ediacaran fossil record is the presence of trace fossils such as trails, burrows, and feeding traces.

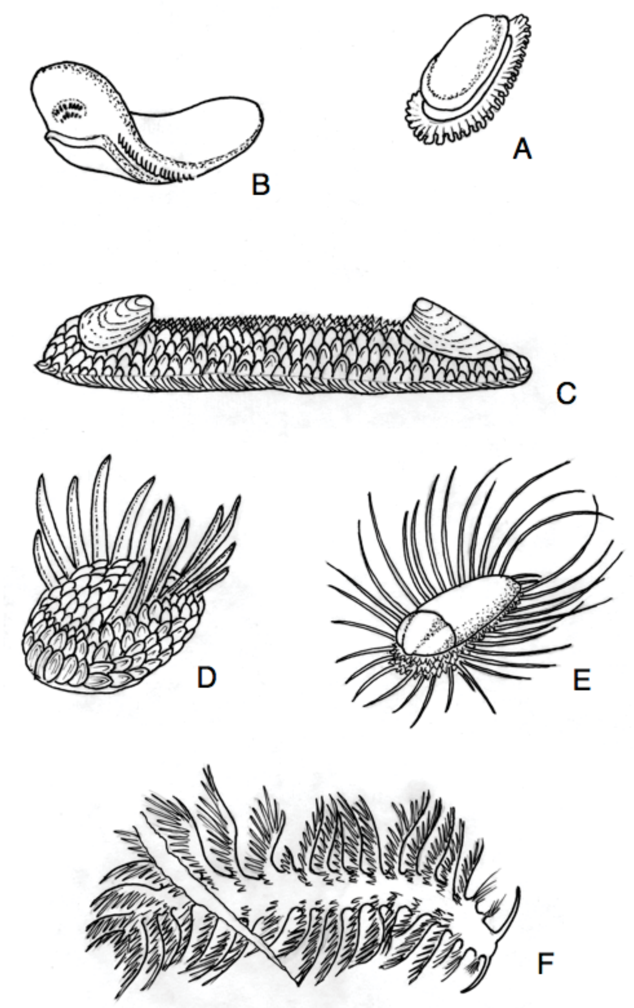

Figure 3. Examples of stem mollusks and annelids, and of halwaxiids, a possible sister group of the annelids, include (A) the probable stem mollusk *Kimberella* from the Ediacaran; (B) the Cambrian stem mollusk *Odontogriphus*; (C) the early Cambrian halwaxiid *Halkieria* with mineralized sclerites covering the body, and anterior and posterior mollusk-like shells; (D) the early Cambrian halwaxiid *Wiwaxia* covered in unmineralized chitinous sclerites similar to the setae of annelids, and possessing long ribbed spines; (E) the recently described middle Cambrian halwaxiid *Orthozanclus* with slender unmineralized chitinous spines and a single anterior mollusk-like shell; and (F) the middle Cambrian stem annelid *Canadia* with rigid setae extending from lateral outgrowths of the body. (A is modified from reconstruction by M. A. Fedonkin and B. M. Waggoner, “The Late Precambrian Fossil *Kimberella* Is a Mollusc-like Bilaterian Organism,” *Nature* 388 [1997]: 868–71. B is redrawn from reconstruction in J. B. Caron, A. Scheltema, C. Schander, and D. Rudkin, “A Soft-Bodied Mollusc with Radula from the Middle Cambrian Burgess Shale,” *Nature* 442 [2006]: 159–63. C is based on the illustration in Susannah Porter’s website http://www.geol.ucsb.edu/faculty/porter/Early_Animals.html by Jennifer Osborne. D is based on the illustration at the website of the Burgess Shale Geoscience Foundation http://www.burgess-shale.bc.ca/discover-burgess-shale/ancient-creatures/wiwaxia. E is redrawn from S. Conway Morris and J. B. Caron, “Halwaxiids and the Early Evolution of the Lophotrochozoans,” *Science* 315 [2007]: 1255–8. F is drawn based on specimen shown at the Royal Ontario Museum website, http://burgess-shale.rom.on.ca/en/fossil-gallery/list-species.php.)

Except in the few cases mentioned above, there are no body fossils preserved of the organisms that made these traces. These traces tend to be small unbranched sediment-filled burrows that run horizontally along the sediment surface or under the microbial algal mats. Somewhat more complex burrows appear toward the base of the Cambrian, including irregularly branching burrows and shallow vertical burrows.[36] These traces are important because they point to the existence of small worm-like organisms that were probably feeding on and in the algal mats that covered extensive areas of the seafloor. The biological identity of these burrowing organisms is unknown, although they were clearly bilaterian.

There is one more set of fossils that are known from the late Ediacaran (550–543 million years) that reveal yet another aspect of the metazoan diversity before the Cambrian. These fossils include tiny calcified or phosphatized tubes, cones, and goblet-shaped structures that record the presence of animals capable of producing mineralized skeletons. They are commonly embedded within algal buildups that formed reef-like structures, and are locally quite abundant.[37] These algal-metazoan reefs foreshadow the later algal reefs of the Cambrian. The very peculiar cm-sized goblet-shaped *Namacalathus* (found as calcified fossils) lived attached to the algal mounds by stalks. Although the preserved shape of these fossils is consistent with that of cnidarians, their biology is uncertain. The tiny partitioned and budded tubes of *Sinocyclocyclicus* bear a strong resemblance to the skeletons of some primitive corals.[38] The cone-in-cone structures of *Cloudina*, and the more tubular *Sinotubulites* could have been produced by various types of worms such as serpulids. However, as with the trace fossils, the identity of the actual tube formers remains unknown. A significant observation of the *Cloudina* fossils is that many of them are perforated by borings. These borings provide the first clear evidence of predation before the Cambrian.

It is clear from the above discussion of the latest Precambrian, that the Cambrian “explosion” did not occur in a biological vacuum. Although many of the fossil specimens are enigmatic and difficult to classify, they nonetheless show significant biological diversity. Furthermore, at least a few living phyla had already appeared by the beginning of the Cambrian, and other forms likely represented sister groups or stem groups related to later-evolving phyla.

The Cambrian Record of Evolutionary Transitions

One of the most important features of the Cambrian "explosion" was the rapid diversification of organisms with shells, plates, and various other types of hard parts. A wide variety of soft-bodied organisms are also known from the Cambrian. Although some fossils can be assigned to living phyla, there are also specimens that appear to represent stem groups or intermediates between modern phyla, as well as specimens of unknown relationship. Representatives of several living classes and other lower taxonomic categories also appear in the Cambrian. A few deposits with exceptionally good preservation of fossils, such as the Burgess Shale in Canada, contribute to the wide range of taxa known from the Cambrian. Such deposits with exceptional preservation are known as Konservat-Lagerstätten (from the German "conservation deposits"). Similar deposits have since been found around the world in the Early to Middle Cambrian, notably the Early Cambrian Chengjiang fauna of China. Additionally, trace fossils become much more varied, complex, and abundant in the Cambrian, suggesting a newly widened range of animal activity.

As stated earlier, the first appearance of the burrow *Treptichnus pedum* defines the base of the Cambrian. The organisms forming those burrows were likely priapulid worms, a worm phylum that is well represented among the Chengjiang and Burgess fossils.[39] Significantly, the early Cambrian is marked by a significant increase in the diversity of burrows associated with the onset of vertical mixing of the sediment by organisms, and the destruction and loss of the algal mat-grounds that characterized the Ediacaran. This "substrate revolution" from stable firm ocean floors to soft, muddy, turbid ones, had a major impact on the bottom-dwelling organisms of the Cambrian.[40] Organisms responded by becoming more mobile, and by moving below the sediment surface and into the overlying water column.

Some of the very first fossils to appear near the base of the Cambrian are tiny skeletal plates, spines, tubes, and cap-shaped shells that have been called the "small shelly fossils."[41] Among these are the spicules of different groups of sponges and the shells of the earliest known "crown group" mollusks and brachiopods. However, the biological identities of many of these tiny skeletal elements were completely unknown until fairly recently. Well-preserved complete fossils in the Chengjiang, and other fossil lagerstätten around the world, have revealed that many of these small shelly fossils were actually the spines and "armoring" of larger metazoans. More detailed analysis of other fossils has revealed that they may represent the stem groups of living phyla rather than evolutionary dead ends.

The discovery of complete specimens from later in the early Cambrian has revealed that a variety of scales, plates, and spines found among the "small shelly fossils" actually fit together and overlapped to cover the bodies of slug-like organisms.[42] These organisms are the halkieriids and wiwaxiids (fig. 3). The halkieriids bore conical mollusk-like shells as well as calcareous structures similar to the chitinous bristles typical of polychaete annelid worms. The slightly younger *Wiwaxia* was covered in scale-like and spine-like structures even closer to those of the polychaetes, and also possessed a radula diagnostic of mollusks. These various unusual organisms bear resemblances to both mollusks and polychaete annelid worms, which are closely related phyla.[43] Thus these organisms would appear to be positioned somewhere on the evolutionary tree near the branching point of the mollusks with the annelids. Stem group polychaete annelid worms also appear in the early Cambrian.[44]

The first likely "crown group" mollusks appear in the earliest Cambrian as part of the small shellys. While recognizable as mollusks, many of these fossils belong either to sister groups or to stem groups of living classes. Cap-shaped fossils called helcionelloids are interpreted as monoplacophoran-like crown group mollusks. There is good fossil evidence of the transition from these primitive cap-shaped helcionelloids to the first bivalves by way of the extinct group of rostroconchs. The hinged valves of clams appear to have evolved by the lateral compression of cap-shaped shells and then the thinning and loss of shell material along the hinge line.[45] There are also likely fossil transitions from coiled helcionelloids to the first gastropods.

Another important group of organisms represented by small plates in the early Cambrian are the lobopods. Lobopodians, until very recently an enigmatic group of strange fossils, were "caterpillar-like" organisms with fleshy lobed limbs and mineralized plates or spines running along their backs. They are similar to the living Onychophora, or velvet worms, but are considered a distinct group.[46] The oldest known lobopodian bears certain similarities to a distinctive group of worms called the palaeoscolecid priapulids that also bore small plates or tubercles along their bodies.[47] Lobopods may have been derived from these worms that also have an early Cambrian fossil record. Furthermore, the lobopods have become recognized as the critical link in reconstructing the assembly of the arthropod body plan. They have anatomical features in common with the arthropods, particularly with peculiar Cambrian stem arthropods such as *Opabinia* and *Anomalocaris* that are preserved in the younger Chengjiang and Burgess fossil beds. These later organisms possessed lobopod limbs but also had gill flaps along their bodies and jointed feeding appendages. Intermediates between lobopodians and the early stem group arthropods have also been discovered that possessed gills.[48] Of even greater interest is the evidence available from the extraordinary preservation of muscle tissue in a few of these transitional organisms. These specimens suggest a progression of steps in the transformation of internal anatomy from lobopodians to true arthropods.[49]

The tommotiids, a group of tiny roughly conical-shaped shells composed of calcium phosphate, have been, until recently, one of the most enigmatic of the small shelly fossils. However, new discoveries of articulated specimens have shown that pairs of symmetrical skeletal elements fit together to form an open cone that was attached to the seafloor at the base. An opening at the base indicates the presence of a muscular attachment structure likely similar to the pedicle of brachiopods. The paired shells also have features similar to the tiny paterinids, crown group brachipods with calcium phosphate shells that also appear in the early Cambrian.[50] These fossils therefore appear to represent stem brachiopods that were themselves derived from armored tubular filter feeders attached to the seafloor (fig. 4).

The living phoronid worms are a phylum closely related to the brachiopods. Like the brachiopods, they are filter-feeders using a ring of ciliated tentacles called a lophophore. However, unlike brachiopods, they are not enclosed within paired shells but construct chitinous tubes. The recent description of an early Cambrian unmineralized, "soft-shelled" lingulid brachiopod strongly suggests that phoronids evolved from crown-group brachiopods by the loss of a mineralized shell.[51] This transitional form also provides evidence for the transformation of the musculature from that typical of shelled brachiopods to the longitudinal arrangement of phoronids. These "soft-shelled" brachiopods are likely stem-phoronids.

Following the appearance of the small shelly fossils, the diverse metazoan fossil communities of the Chengjiang in China are dated at around 525– 520 million years, 20 million years after the beginning of the Cambrian. The exceptional preservation in these fossil beds is similar to that of the Burgess Shale deposits that are dated around 515–505 million years.

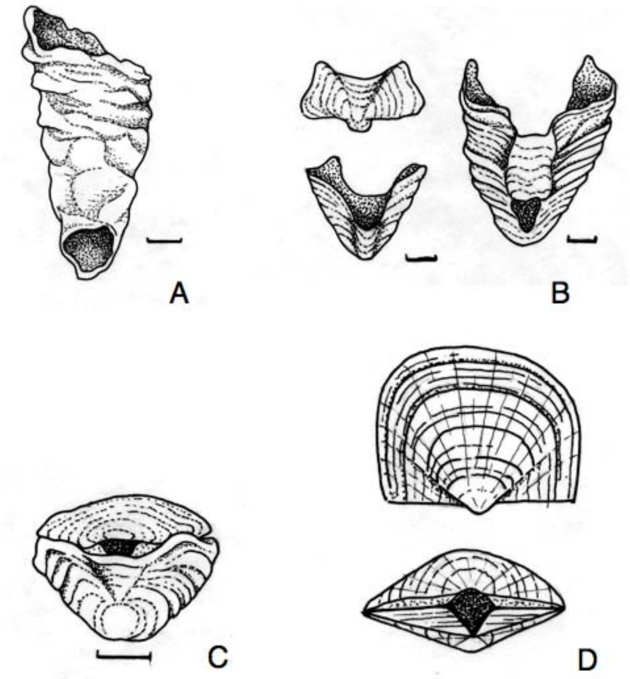

Figure 4. These fossils illustrate the transition from tommotiids to brachiopods: (A) the conical phosphatic shell of the tommotiid *Eccentrotheca* with an opening at the apex (scale bar 0.5mm); (B) the tommotiid and stem brachiopod *Paterimitra* with a conical shell of articulated phosphatic sclerites, a "pedicle tube" for attachment, and an upper valve (scale bar 0.2mm); (C) the bivalved *Micrina*, the most brachiopod-like tommotid yet known (scale bar 0.5m); and (D) the early Cambrian crown group brachiopod *Psiloria* (shell about 1 cm across). (A is drawn from an image in C. B. Skovsted, G. A. Brock, J. R. Paterson, L. E. Holmer, and G. E. Budd, "The Scleritome of *Eccentrotheca* from the Lower Cambrian of South Australia: Lophophorate Affinities and Implications for Tommotiid Phylogeny," *Geology* 36 [2008]: 171–4. B is drawn from an illustration in C. B. Skovsted, L. E. Holmer, C. M. Larsson, A. E. S. Högström, G. A. Brock, T. P. Topper, U. Balthasar, S. P. Stolk, and J. R. Paterson, "The Scleritome of *Paterimitra*: An Early Cambrian Stem Group Brachiopod from South Australia," *Proceedings of the Royal Society B* 276 [2009]: 1651–6. C is drawn from L. E. Holmer, C. B. Skovsted, G. A. Brock, J. L. Valentine, and J. R. Paterson, "The Early Cambrian Tommotiid *Micrina*, A Sessile Bivalved Stem Group Brachiopod," *Biology Letters* 4 [2008]: 724–8. D is drawn from an illustration at the website http://www.museumwales.ac.uk/en/1625/.)

These extraordinary fossil sites give us our best views into the composition of marine biological communities from these times, preserving both soft-bodied organisms and those with mineralized skeletons.[52] These beds contain abundant and diverse sponges and cnidarians, as well as priapulid worms, annelid worms, lobopods, stem mollusks such as *Wiwaxia*, and brachiopods. However, probably the most dramatic characteristic of the Chengjiang- and Burgess Shale-type deposits is the abundance and diversity of arthropods.

Arthropods comprise 50% or more of all of the fossil specimens collected from these beds. These fossils include stem arthropods such as the anomalocarids, trilobites which came to dominate the Paleozoic, and some species that appear to be crustaceans and chelicerates. However, most of the fossils belong to primitive stem groups that likely represent evolutionary dead ends after the appearance of true arthropods but before the rise of most living arthropod groups. In the Burgess Shale, one such primitive species (*Marrella*) alone comprises a third of all fossil specimens. These fossils show unusual arrangements, and types, of appendages.

The chordates (that include vertebrates), hemichordates (that include the living "acorn worms"), and echinoderms (that include the living starfish and echinoids) are all deuterostomes and have the same pattern of early embryo development. Although the modern representatives of these phyla appear extremely different, they are actually closely related branches on the tree of life, and are understood to have evolved from a common ancestor. Some rare, but very significant, specimens in the Chengjiang seem to be stem chordates and stem echinoderms, as well as specimens that have been interpreted as organisms close to the common ancestors of chordates and echinoderms. These rather simple Cambrian organisms possess the anatomical characteristics that would be expected in organisms that had acquired some, but not all, of the distinctive features of chordates or echinoderms.

A newly described group of primitive soft-bodied deuterostomes, called vetulocystids, bears similarities to some of the bizarre early echinoderms. These organisms rested on the bottom and possessed echinoderm-like respiratory openings and two ribbed cones that likely represented the mouth and anus. Unlike all living echinoderms, however, they lacked any calcite skeletal plates.[53] They may represent organisms that belonged to a sister group ancestral to the first stem-group echinoderms. The most primitive echinoderms were characterized by flattened, nearly bilaterally symmetrical forms. The earliest stage of echinoderm evolution is represented by *Ctenoimbricata* from the early middle Cambrian. These flattened stem echinoderms were completely covered on their lower side by calcite plates, but were largely uncalcified on their upper (dorsal) sides.[54] The ctenocystoids and cinctans were similar stem echinoderms that show increasing coverage of their dorsal sides by interlocking calcite plates (fig. 5).

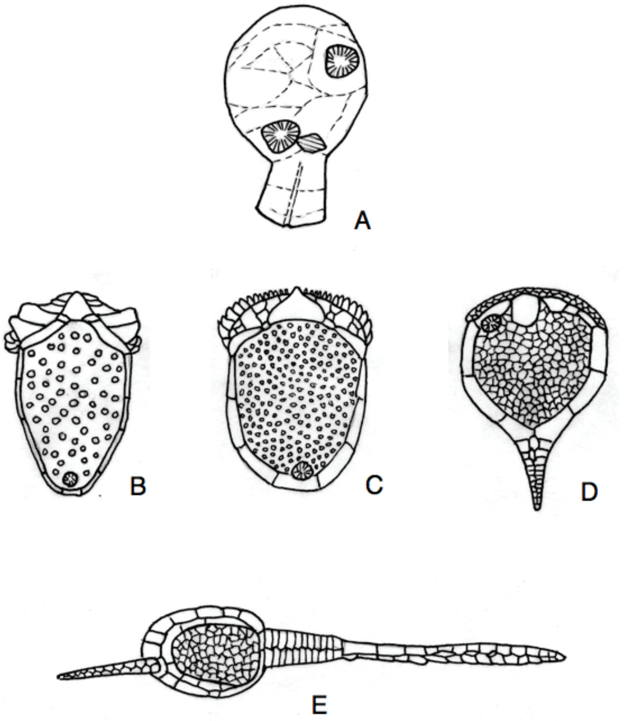

Figure 5. Stem echinoderms and the early evolution of the Echinodermata as illustrated by (A) the soft-bodied ventulocystid *Ventulocystis*, a primitive deuterostome, possibly a sister group to the stem echinoderms; (B) *Ctenoimbricata* is the most primitive known stem echinoderm with only scattered calcified elements on the dorsal side; (C) the ctenocystid *Courtessolea*, a slightly more derived stem echinoderm; (D) the cinctan *Sotocinctus*, a stem echinoderm with a body completely covered by calcite plates and a "tail" appendage; and (E) the stem group solute *Syringocrinus* with a "tail" and feeding arm appendage. (A is drawn from an illustration in D-G. Shu, S. Conway Morris, J. Han, Z-F. Zhang, and J-N. Liu, "Ancestral Echinoderms from the Chengjiang Deposits of China," *Nature* 430 [2002]: 422–8. B, C, and D are redrawn from S. Zamora, I. A. Rahman, and A. B. Smith, "Plated Cambrian Bilaterians Reveal the Earliest Stages of Echinoderm Evolution," *PLoS ONE* 7, no. 6 [2012], e38296. doi:10.1371. E is redrawn from the Palaeos website http://palaeos.com/metazoa/deuterostomia/homalozoa/soluta.html.)

Another very primitive stem group of deuterostomes, called ventulicolians, has also recently been described that might represent the anatomy of organisms near the base of the deuterostome evolutionary branch that were ancestral to both the chordates and echinoderms. These soft-bodied organisms possessed segmentation and oval structures interpreted as gill slits, and a terminal mouth.[55] The most primitive group of chordates are the urochordates, or tunicates, that have a sack-like adult body that filters seawater through pharyngeal slits. In their tadpole-like larval form, they possess stiff notochords (a structure diagnostic of chordates) that is lost in the adult form. A likely tunicate has been described from the Chengjiang.[56] Another group of primitive chordates are the cephalochordates (represented today by the lancelets) that possess a notochord as adults, pharyngeal slits, and muscles arranged in parallel bundles. Some fossils have been interpreted as stem cephalochordates.[57] Lastly, and of particular interest, is a fossil that may be a stem vertebrate.[58] *Myllokunmingia*, in addition to a notochord, gill pouches and muscle bundles, also appears to have had some structures characteristic of vertebrates. These vertebrate features include a cavity surrounding the heart, a dorsal fin, and cartilage around the head and as a series of elements along the notochord. The Chengjiang thus includes fossil specimens that occupy several significant transitional stages from primitive deuterostomes to stem echinoderms and stem chordates (fig. 6).

Conclusions

Given our current, and continually growing, knowledge of the deep past, it is increasingly clear that the rise of multicellular animals is not an impenetrable mystery. While there is much that is not known, and some that will never be known, there is also much that has been discovered, and much excitement for what will yet be learned. New discoveries and analyses are continually adding to our knowledge of evolutionary transitions in the latest Precambrian and Cambrian.

The Cambrian "explosion" was a time of great evolutionary significance, as it established the anatomical templates for much of the diversification to come. It was also extraordinary in that it was a time of accelerated evolutionary change for marine organisms across the animal kingdom. However, despite its relative rapidity, the time during which the rise of modern animal phyla occurred was still a lengthy interval, with the Early Cambrian alone lasting 32 million years. Furthermore, critical evolutionary innovations were established in the 40 million years of the Ediacaran preceding the Cambrian.

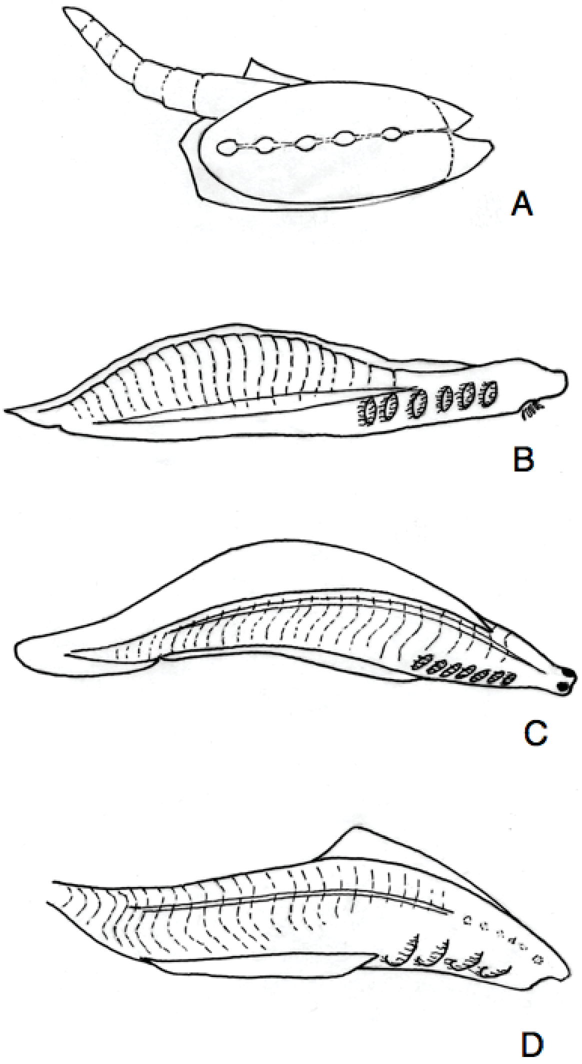

Figure 6. The evolution of chordates from primitive deuterostomes as illustrated by (A) the vetulicolian *Vetulicola* interpreted as a stem deuterostome with some features suggestive of chordates; (B) the lancelet-like stem chordate *Haikouella* (about 3cm long); (C) *Haikouichthys*, another likely stem chordate (about 2.5cm long); and (D) *Myllokunmingia*, is a possible stem vertebrate (about 3cm long). (A is drawn from an illustration in D-G. Shu, S. Conway Morris, J. Han, L. Chen, X-L. Zhang, Z-F. Zhang, H-Q. Liu, Y. Li, and J-N. Liu, "Primitive Deuterstomes from the Chengjiang Lagerstätte (Lower Cambrian, China)," *Nature* 414 [2001]: 419–24. B is redrawn from J-Y. Chen, D-Y. Huang, and C-W. Li, "An Early Cambrian Craniate-Like Chordate," *Nature* 402 [1999]: 518–22. C is modified from a reconstruction in X-G. Zhang and X-G. Hou, "Evidence for a Single Median Fin-Fold and Tail in the Lower Cambrian Vertebrate, *Haikouichthys ercaicunensis*," *Journal of Evolutionary Biology* 17, no. 5 [2004]: 1162–6. D is drawn from an illustration in D-G. Shu, H-L. Luo, S. Conway Morris, X-L. Zhang, S-X. Hu, L. Chen, J. Han, M. Zhu, Y. Li, and L-Z. Chen, "Lower Cambrian Vertebrates from South China," *Nature* 402 [1999]: 42–6.)

The animals of the Cambrian did not appear in all their modern complexity out of a void, but rather they provide pointers to their common ancestry. Despite the claims of evolution skeptics, the fossil record provides multiple examples of organisms displaying transitional anatomies. As we have seen, these fossil organisms were largely representative of stem groups that possessed some, but not all, of the diagnostic features that define the major groups of living organisms. The anatomical characters that define the body plans of the major living animal phyla can be seen to have been acquired piecemeal during the early evolution of the metazoans. Just as with all other taxonomic groups (e.g., classes, orders, families, genera, species), the divisions between phyla break down as we move closer to their times of origin from common ancestors. While the picture is incomplete, recent spectacular fossil discoveries strongly support the conclusion that the major branches of the animal tree of life are joined to a common metazoan trunk. The tree of life continues to stand tall.

Acknowledgments

I would like to thank the editors at BioLogos for initially encouraging me to write a blog series on the Cambrian explosion. Those essays formed the foundation for this article. I also greatly appreciate the very thorough and constructive comments by an anonymous *PSCF* reviewer. Any errors of fact or interpretation are mine alone.

Notes

[1] Some material in this article appeared earlier in the six-part blog series "The Cambrian 'Explosion,' Transitional Forms, and the Tree of Life" on The BioLogos Forum, December 2010 to March 2011, http://biologos.org/.

[2] J. D. Morris, "The Burgess Shale and Complex Life," *Acts & Facts* 37, no.10 (2008): 13.

[3] S. C. Meyer, M. Ross, P. Nelson, and P. Chien, "The Cambrian Explosion: Biology's Big Bang," in *Darwinism, Design and Public Education*, ed. J. A. Campbell and S. C. Meyer (Lansing, MI: Michigan State University Press, 2003), 326.

[4] Ibid., 333.

[5] A. Y. Rozanov, "The Precambrian-Cambrian Boundary in Siberia," *Episodes* 7 (1984): 20–4; A. Y. Rozanov and A. Y. Zhuravlev, "The Lower Cambrian Fossil Record of the Soviet Union," in *Origin and Early Evolution of the Metazoa*, ed. J. H. Lipps and P. W. Signor (New York: Plenum Press, 1992), 205–82.

[6] E. Landing, "Precambrian-Cambrian Boundary Global Stratotype Ratified and a New Perspective of Cambrian Time," *Geology* 22, no. 2 (1994): 179–82.

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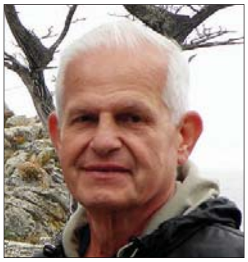
David L. Wilcox

Our Genetic Prehistory: Did Genes Make Us Human?

David L. Wilcox

Despite our close genetic match with the chimpanzee, the human genome is radically different in its expression and radically different in its outcome. Though we share 98.7% of the same protein-coding sequences,[1] the difference between our species is not in the 1.5% of the genome that codes for proteins, but rather in the 98.5% that controls their production. No other lineage has evolved as fast as ours, at least within the last 1.5 million years. The changes which differentiate us are primarily due to rapid changes in genetic control sequences.[2] These changes involve every known class of control element, with the most profound changes found in the noncoding control elements shaping our neural system, especially the frontal cortex of the cerebrum. Further, the speed of the change is in large part due to the unique action of retrotransposons acting as "genetic engineers," providing the raw genetic material selected in support of our cultural explosion. Although these are "natural" forces which we in part can understand, as Christians we should remember that they reveal what God ordained in eternity and realized through providence.

The discovery that chimpanzees are our closest genetic relatives is one of the most controversial new ideas of the last few decades. What is the source of that counterintuitive idea? How should we react? First, keep in mind that science works by predicting patterns of data based on our understanding of the shape of reality. Thus, let us begin with prediction. Based on known morphological data, what would be the expected (i.e., predicted) pattern of difference in genetic sequences between the various species of primates—assuming common descent versus assuming separate creations?

In the 1960s (before the genetic revolution), the accepted anthropological evaluation of human/ape morphological differences grouped chimpanzees with gorillas, and both with orangutans, as pongids—a separate evolutionary clade from humans. The pongid clade and the hominoid clade were thought to be descended, respectively, from the two extinct ape species *Dryopithecus* and *Ramapithecus*. The anthropological expectation was therefore that molecular distances (immune, protein, or nucleic acid) would be proportional to the perceived physical divergence in lineages. It has been an ongoing and progressive shock to find out how wrong that prediction was.[3]

The logical prediction from separate creations (the baramin paradigm of Wayne Frair and Kurt Wise) paralleled the anthropological expectation. They placed gorillas and chimpanzees within the same "holobaramin," meaning that they shared descent from the same directly created ancestral species. In contrast, humans only resembled apes due to shared common ideas in God's mind—thus humans and apes are within a shared "apobaramin."[4]

In both schools of thought, despite their different background beliefs, the accepted prediction was that the molecular distances would reflect morphological distances.

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They thus shared a common theory, but for different reasons—with different specifying assumptions. However, the predictions of both schools of thought were wrong. Chimpanzee DNA is closer to human DNA than to gorilla DNA. And, gorilla DNA is closer to human DNA than to orangutan DNA. What should be our reaction to this discovery? Should we conclude that human beings are not truly unique image-bearers of God? Of course not, but we should carefully evaluate the data from the creation before we react.

As a heuristic process, science alters its theories as it discovers new patterns in the data—as it should, if the Creator God is the source of those patterns. For the non-Christian who yet believes in a real world, authority is in the data. Likewise, for the Christian, data are authoritative because God created a real world. So, if we truly trust God to be faithful, we should carefully and prayerfully accept corrections to our previous theories. But as Jitse van der Meer has pointed out, that does not mean that we must alter our background beliefs.[5] Rather, we must examine the specifying assumptions by which we have linked those beliefs to our expectations (our theoretical predictions)—and change them when we are mistaken. Genetic anthropology has done so, and we likewise need to evaluate what is legitimate for Christian thought. But first, we should evaluate whether such a change is justified by the data from genetics. That is not easy. The complexity of the discipline has grown exponentially over the last half century.

Starting with the simple Mendelian definition of genes as the determiners of traits (genotype → phenotype), genetics progressed to identifying proteins as agents of traits, and then to DNA as the genetic material which spelled out proteins (through the genetic code, using the mechanisms of replication, transcription, and translation). This was followed by Operon theory, the realization that some DNA sequences are recognized as control elements by proteins, and further, that this recognition allows control proteins to tie the genes into logic circuits. It also became clear that eukaryotic genomes were far more complex than bacterial genomes, both in control structure and in the processing of transcripts (due to the splicing out of introns and the fusing of exons—thus the entire RNA transcript of a locus was not translated). The Human Genome Project which followed showed that there are not enough protein-coding genes (ORFs—open reading frames) to specify known phenotypic complexity. However, alternate transcript splicing increases the transcriptome (effectively, giving more proteins). And now the ENCODE project has suggested that massive amounts of noncoding transcriptions (ncRNAs), including anti-codes, introns, micro-RNAs, long noncoding transcripts (lncRNAs—over two hundred nucleotides), and transposon transcripts act in the control of genetic expression. And of all things, that ultimate genomic parasite, the transposon or jumping gene, looks like an agent of genomic engineering.

What we want to find out is whether all the new genetic information shows us to be an upgraded species of chimpanzee or truly a "new" thing. In what sense have these multiple classes of altered genetic controls produced human uniqueness? And how did it occur? Was it gradual or sudden? According to Britten, if any species looks as if it has developed by "punctuated" evolution, it is ours. That, he says, is the implication of the evolution of human cognition within a few million years—a span of time in which typical mammal species remain unchanged.[6]

Cognition is about the brain, and humans do have more neurons than chimps, but not as many as you would think. The real difference is in their neuropil—that is, the white matter connecting the neurons. Humans' neurons have an order of magnitude more neural connections than chimps, longer axons with more branches, increased long connectivity (connections between distant parts of the brain), increased local modularization (local cerebral centers), and dramatically delayed synaptic maturation (increased neural reorganization).[7] There are thousands of unique human genetic changes altering cell proliferation and differentiation, tissue organization, the growth of long axons and dendrites, the amount of axonal branching and connectivity, the timing and degree of synaptic plasticity, and so on.[8] And it is not just the neurons which are different—humans also have a unique class of neuroglial (the astrocytes) which are now known to modulate synaptic activity—the human forms have ten times as many processes and faster calcium waves than the chimpanzee versions.[9]

Direct comparisons of the human nuclear genome with those of the two species of chimpanzees do indeed indicate that we share about 98.7% of our genetic sequence/genome with each of them.[10] But then, if there is such a close genetic match, why are human brains so different from those of chimps?

Both human and chimp genomes have been fully sequenced and placed in the public domain, and powerful comparative algorithms have been developed. But despite truly significant morphological differences,[11] the total sequence difference is only 2% to 4%, and little of that difference (only 1.5%) is between coding sequences. However, 5.5% of the human genome has undergone purifying selection (the removal of alternate sequences), and is therefore composed of significantly different functional sequences. It follows that the most obvious place to look for significant differences are noncoding control sites. Of the long lists of significantly different coding genes and control sequences which have been identified, two-thirds are in noncoding control sequences for the amount, timing, and location of expression of coding genes.[12]

So, human-chimpanzee differences are apparently due to human-specific changes in gene expression rather than changes in protein sequences. In fact, the genes coding for protein sequences expressed in chimpanzee brains may actually have changed their sequences (by mutation) more rapidly than have their human counterparts.[13] But as a general rule, genetic changes of morphology are instead due to modified transcriptional regulators. This makes sense, since morphologies are products of complex genetic programs encoded through a hierarchy of genetic feedback loops. Likewise, alterations in neural complexity are products of complex genetic hierarchies, and occur mainly via noncoding regulatory changes. In contrast, altered physiological traits are due to altered proteins such as channel proteins, transporters, receptors, and enzymes.[14] Tissue-specific changes such as alterations to immunity, olfaction or male reproduction are mostly due to genetic protein-coding changes and show significant pleiotropic inhibition (since proteins can have multiple effects). In contrast, noncoding changes typically do not show pleiotropic constraints.[15] Thus, it makes sense that rodent genomes have higher levels of conservation for regulatory elements than do hominid genomes. This might imply less effective selection, but it more likely indicates higher selection for new adaptive changes such as those in hominid neural systems.[16]

If regulatory mutants are more likely to produce subtle changes than altered proteins, there should be evidence for such noncoding regulators. Apparently most of the transcripts which are copied from DNA do not code for proteins. And a wide variety of these ncRNA (noncoding RNA) transcripts are being recognized as regulators of transcription, particularly through various interactions with transcription proteins. The list of ncRNA effects includes gene silencing, position effect, hybrid dysgenesis, chromosome dosage compensation, imprinting, allelic exclusion, transvection, transduction, paramutation, and altered chromatin modifying complexes. To explain all of these would need a rather large book. However, RNA transcripts are particularly active in tissue differentiation and regulation—and notably, ncRNAs are enriched in specific areas of the central nervous system. Such ncRNAs are sensors of neural stress, influence synaptic plasticity, and are implicated in several neural diseases. Yan et al. identified 82 novel intermediate (50–500b) ncRNA transcripts, many particular to the human fetal brain, with different area-specific expression levels.[17] These ncRNAs regulate protein production and increase the transcriptome (the locally expressed array of proteins). The absence of some of them is correlated to brain tumors.[18] Mattick terms such ncRNAs "environmentally sensitive epigenetic regulators," which allow RNA editing in response to environmental signals—especially in the brain.[19]

There are some significant changes in uniquely human proteins, although the majority of identified highly selected human genes do not yet have defined functions. However, more than four hundred are involved with immunity (such as the HLA antigen series), around 130 with sensory perception, one hundred with the brain and another one hundred with gametogenesis.[20] In some cases, significant neural genes have been altered. The most familiar is FOX-P2 which has been implicated in language deficits. FOX-P2 increases axon growth in the striatum of the basal ganglia, resulting in improvements in the learning of motor skills.[21] Likewise, the genes ASPM and MCPH1 are implicated in the size of the brain, as well as PDYN, GLUD2, COX8, and CMAH which may change brain regulation, cerebral metabolism, and so forth.[22] Or, M003-A06, a zinc finger gene with a human-specific allele, controls brain (head) size.[23] And, the highly conserved neuropeptide PACAP which regulates neurogenesis and neuronal signal transduction has eleven amino acid changes, a rate of mutational substitution in humans seven times faster than observed in other mammals—a signal of very strong selection.[24]

A recent scan for newly evolved genes in humans (meaning, genes absent in mice) found 198 genes unique to apes and humans which are specifically upregulated in the fetal prefrontal cortex at a fourfold higher rate than that of other tissues. Fifty-four of these genes are unique to humans. An additional 72 of these genes we share with chimpanzees alone, and the remaining 72 with both chimps and orangutans. As a general rule, human brain development genes are upregulated and their transcription factors are enriched. Although new genes may arise by different mechanisms, they show the same expression bias. Also, young genes show faster protein sequence evolution than co-expressed older genes. All of this indicates that positive selection for increased brain function acted in their origin and modification.[25]

Alternate exon splicing of the transcripts of human protein-coding genes (open reading frames—ORFs) increases the transcriptome, compensating for the unexpectedly low level of ORFs, and for the lower mutation level in neural loci. The rate of such alternate transcript splicing differs across taxa, but is highest in primates—and among primates, highest in humans, and in human tissues, especially high in the brain. Such widespread human-specific alternative splicing in neural tissues makes clear its importance in the evolution of neuronal gene regulation and function.[26] Further, even the neural somatic genome itself is altered, with 13% of all neurons having copy number variations in their chromosomes.[27]

However, the most significant changes do seem to be regulatory mutations' controlling of the timing and quantity of the gene products, especially in sites close to developmentally active genes.[28] The most rapidly evolving human locus yet identified, HAR-1, is such a control site, producing a lncRNA expressed in the Cajal-Retzius neurons of the neocortex—at the time those neurons are being specified and positioned into the six-layered human cortex.[29] The unique human HAR-1 transcript contains eighteen substitutions (since its divergence from the chimp version) which alter the form of the RNA transcript from a hairpin to a clover-leaf.[30]

In another paper evaluating the recent selection on gene networks contributing to cognitive function, Shulha et al. mapped the genome-wide distribution of histone H3 trimethylated at lysine 4 (H3K4me3), an epigenetic mark sharply regulated at TSS (transcription start sites).[31] They identified 471 sequences with human-specific enrichment or depletion. Thirty-three methylated loci show modern human-specific nucleotide substitutions and regulatory motifs with particularly strong enrichment in prefrontal cortex neurons. One specific locus with strong regulatory selection in neural tissues is prodynorphin, an opioid precursor leading to changes in behavior, perception, and memory.[32]

Nowhere are the chimp/human differences clearer than in the postnatal expression of genes involved with brain development. In a comparison of humans, chimpanzees, and macaques, simple changes in gene expression levels—cis-regulatory changes—accumulated at similar rates. This highlights the striking differences in the timing and shape of human developmental expression patterns which are due to trans-regulatory changes. (cis-regulatory sites are close to specific loci; trans-regulatory sites are distant signaling sites.) Four times as many human-specific genes show altered developmental expression as do chimpanzee-specific genes, again, particularly in the prefrontal cortex.[33] This remarkable developmental remodeling of the human cortex is controlled by the expression of hundreds of genes, but the process is likely driven by alterations in the expression of a few key regulators, such as the microRNAs (which are transcription regulators) preferentially associated with neural activity. Certain specific miRNAs, as well as their target genes, show some of the most rapid rates of human-specific evolutionary change—notably, miR-92a, miR-454, and miR-320b.[34]

Such miRNAs modulate gene expression post-transcriptionally, again increasing the transcriptome (increasing protein diversity). Iwama et al. evaluated 1433 miRNAs in humans, and identified two major retained peaks of miRNA introduction. Of these, 28% are from the period of the early eutherian radiation and 53% arose during the evolution of the simian lineage into the hominoid lineage. Approximately 28% of the latter group of miRNAs appeared within hominid lineage itself.[35] One example, miRNA-941, expressed in pluripotent cells, acts on human-specific genes involved in neurotransmitter signaling. The deletion of the miR-941 precursor disrupts language/speech. This locus shows a decreasing copy number with the move out of Africa; it (speculatively) has been suggested that it is involved in longer life spans and higher cancer rates.[36] Such significant differences in miRNA expression between human populations probably are involved with local adaptations, for instance, the "rheostat" control by miR-155 of melanin production gene TYRP1.[37]

Long noncoding RNA transcripts are also involved in the epigenetic regulation of gene expression. A major mechanism of lncRNAs seems to be to tie chromatin (chromosome sections) together into functional locations.[38] On the average, about ten different lncRNA are produced for every coding locus, using alternative reading frames overlapping the locus—including transposons, templating of the noncoding side, and so forth. Long noncoding RNA transcripts are also involved in the epigenetic regulation of gene expression. They are involved in genomic imprinting (and not just the imprinting of alleles). They are activators, regulators—both cis and trans acting—cis-tethers, cis-targeting, trans-targeting, enhancers, decoys, scaffolding, allosteric modifiers, co-activators, and co-repressors (details are beyond the scope of this paper).[39] Ng et al. identified four (of 35) lncRNAs specifically required in neurogenesis and brain development which regulate nuclear proteins and cytoplasmic miRNAs, and induce neural pluripotency in embryonic cells.[40] In addition, lncRNAs sometimes are converted into new protein-coding loci, and the majority of those are expressed in the cerebral cortex.[41]

Of course, there are similar sites in the genome which affect other parts of the body. For instance, a decrease in the rate of apoptosis (programmed cell death) in human brain tissue may have been selected by the pressure to increase brain tissue—but this altered rate is expressed all over the body, which may be the reason humans have more cancer than chimps.[42] Or, the noncoding (control) sequence HACNS1 has evolved very rapidly in humans. In genetically modified mice, the human form of HACNC1 is expressed in the thumb, whereas the chimpanzee form is not. Thus, the modified HACNS1 is probably involved in the altered shape of the human thumb.[43]

Gene expression can also be modified by gene duplication. Genetic loci have been duplicated multiple times in the human lineage (some very recently). Multiple copies of alleles increase the amount of gene product without changing the sequence itself.[44] For instance, AMY1 (an amylase gene) is present in extra copies in populations with high-starch diets,[45] and humans have multiple copies (200+) of the gene DUF1220. The loci produce a protein of unknown function, but it is one highly expressed in neuronal dendrites in those parts of the brain involved with higher cognitive function[46]—and dendrites have just been identified as "micro-processors," significantly increasing the brain's complexity.[47] There is good evidence that such changes in the expression of specific proteins at synaptic junctions are a major cause for advanced neural function.[48]

And it is not just comparisons with the chimpanzee genome which show significant genetic changes—the Neanderthal and Denisovan genomes are also available. But just how different were they? High resolution genome scans of the archaics (the Neanderthals and Denisovans) make it possible to zero in on specific loci which are different in modern humans. Of course, most loci are the same. For instance, the site HAR1 (human accelerated region 1) mentioned above, the most rapidly evolving site on the human genome, is the same in both modern humans and archaic humans.

However, the initial Denisovan study did identify a number of unique "modern" protein loci.[49] These are sites highly conserved in primates, but changed in the modern human lineage *after* separation from the archaics. Of the twenty-three most conserved positions with significant amino acid changes, eight affect nervous system genes in function or development—NOVA1, SLITRK1, KATNA1, LUZP1, ARHGAP32, ADSL, HTR2B, and CNTNAP2. Of these, SLITRK1 and KATNA1 control axonal and dendritic growth, ARHGAP32 and HTR2B are involved in synaptic transmission, and ADSL and CNTNAP2 are implicated in autism. CNTNAP2 is regulated by FOXP2 and is associated with speech problems. NOVA1 is a neuron-specific RNA binding protein, and LUZP1 is a leucine zipper (control) protein active in neural tube development. Both of those loci are subject to alternative splicing. The researchers also located four altered loci affecting the skin and six affecting the eye.

Another locus which seems to have been selected after the human lineages diverged is MEF2A, a locus which delays synaptic development, allowing longer plasticity in brain development.[50] In chimps, the expression of this locus peaks before one year, but in humans, it peaks at around five years. Linkage data indicates that the selective sweep for the modern allele of this gene postdates the split from the archaic lineages, a finding which matches physical data from tooth growth, showing that the Neanderthals matured more rapidly than modern people.[51] There also is skeletal evidence for a different trajectory of cranial growth likewise supporting a difference in genetic expression during brain development. The rounded modern cranium is due to a unique globularization growth phase occurring during the first year, growth which did not occur in Neanderthals.[52] Such changes likely reflect an altered brain and mind—and require alterations in the control sequences of the genome.

But regulatory changes can be quite subtle. A good deal has been made of the fact that FOX-P2, the "speech" gene, is the same in modern humans and the archaics. However, there is a significant difference in the modern FOX-P2 locus. The eighth intron has an altered recognition site for the control protein POU3F2 which decreases the level of expression of FOX-P2, a change in modern people which may lengthen the time available for altering neural hard-wiring.[53]

What is truly mind-boggling is that this explosion of diversity in functional RNA/DNA controls is being driven by jumping genes known as retrotransposons. Retrotransposons, or "short interspersed repeated sequences" (SINEs) are related to retroviruses such as HIV, and they litter the human genome. The most common of these elements in humans, the Alu's, number about 1.1 million copies and compose around 10% of our genome. Alu's have long been considered junk DNA. However, these mobile elements are transcribed, both as distinct RNA polymerase III transcripts and as a part of RNA polymerase II transcripts. (And Pol III transcripts can interact with Pol II to block mRNA transcription.) So, Alu transcripts potentially can have important regulatory functions. And indeed, they have been shown to control mRNA processing at several levels, through complex regulatory functions such as mRNA transcriptional repression or the modulation of alternative splicing, and they are implicated in many genetic diseases. Further, Alu RNAs which are embedded in Pol II transcripts can promote proteome evolution and diversity.[54] By such insertion, transposable elements (TEs) can add, control, or become part of genetic regulatory sequences.

In general, genes with associated Alu's show higher levels of editing in humans, especially if the genes enhance neural complexity. Many specific Alu inserts are of interest—for instance, 57% of the neurally active microcephalin locus is composed of TEs found in the introns. Control areas showing significantly different expression also have a great many differences in INDELs (insertion/deletion mutations) due to retrotransposon activity. Alteration by moving TEs therefore seems likely to have been a major factor in the changes in human gene functions which produced the major morphological and functional changes in the human lineage.[55] That sounds like saying that many derived human characteristics are a matter of "untraceable" genetic "engineering" (mutations) for novel genetic combinations rather than due to the environmental selection of small variants. But of course, selection is also involved in the survival of transposon induced changes. The issue is the high rate of new coding being made available by transposons for selective "evaluation." If selection is the engine of change, new variation is its fuel.

Since Alu's are retroposons, they are transcribed, but only if they are not repressed by methylation, a process controlled by miRNAs. If transcribed, their transcripts can fold into potentially active RNA hairpins, as well as being randomly reverse-transcribed back into the genome, particularly at sites where the DNA is most active. But transposon transcripts do not have a free ride. Piwi interacting RNAs (piRNA 24–30 nt) repress specific TEs by cleaving their transcripts. These small piRNA elements are also under strong selective constraints (based on data from African populations), and there is a strong correlation between the age of the TE family and the number of associated piRNAs. Note, however, that humans have an abnormally low level of those particular piRNAs which specifically deactivate Line 1 reverse transcriptase. (L1—long interspersed repeated sequence 1—codes for those reverse transcriptase enzymes which make DNA copies from specific TE transcripts, the copies which can then be inserted back into the chromosomes.) This human exception suggests that the L1 reverse transcriptase enzyme supports a specific important human function, namely, the continuing insertion of new Alu's.[56]

Of course, such new Alu insertions do cause cancers and other genetic defects—but that is far from the whole story. Alu's are involved in all known classes of regulatory elements, from new exon formation and alternative splicing to gene silencing, from INDEL formation to the regulation of the lncRNAs which organize chromatin loops into functional areas. Jacques et al. published a paper in 2013 titled "The

Majority of Primate-Specific Regulatory Sequences Are Derived from Transposable Elements."[57] They point out that TEs have contributed nearly half of the regulatory elements of the human genome. In mammalian genomes, 44% of the open (active) chromatin is in TE-rich regions, hence with transposon-driven regulatory elements. In primate-specific regions, the figure is 68%. Hundreds of thousands of TE sites in the human genome are highly conserved and enriched with binding sites. Such conserved TEs located within genes frequently act as cis-regulatory elements modulating the expression of their "host" genes.

Controlling transcripts of Alu's are also edited by ADAR (Adenosine Deaminase Acting on RNA) enzymes. Such adenosine to indosine editing forms a significant alternate information mechanism, forming a binary A/I combinatorial code editor expanding the transcriptome and used to refine somatic cellular differentiation. Correlated editing is observed for pairs and triplets of specific adenosines along the Alu sequences. Such A to I editing of Alu transcripts by ADAR1 enzyme is especially high in neural stem cells and is widely involved in the differentiation of human embryonic stem cells, especially in neural cell lines (30 genes).[58] Alu editing modifies the transcriptome at a much higher level in humans than in chimps, particularly in neuronal loci, even where the genomic Alu structure is unmodified.[59]

Transposable elements such as Alu's are common in loci involved with DNA damage and repair, and are notably active in tissue (cell-type) differentiation. TEs play roles in inflammation, immune function, embryogenesis, cellular response to external stimuli, and in hormonal responses.[60] They are activated not only in embryonic cells and cancer cells, but also in some active somatic cells, notably in the brain—as many as 13,692 Alu's and 1,350 SVAs. TEs mobilize protein-coding genes, which are actively expressed in neural cells during development, producing a somatic mosaicism (cells with different nuclear DNA), particularly in the hippocampus and caudate nucleus.[61] This implantation of new TEs continues throughout life in active neural tissue (such as the hippocampus) in which they may be involved in memory formation. Producing further diversity, there are thousands of Alu inserts which vary between populations. Notably, probably due to their longer history, African populations have numerous intermediate frequency inserts which are absent in non-Africans. However, few of these population-specific insertions are in exons, since exonic interruptions are rapidly removed by selection.[62]

Also, most of the extensive INDEL variation (insertion/deletion mutations) between chimps and humans (26,509 sites) is due to Alu insertions in the human lineage, insertions which correlate with significant differences in gene expression and with large INDEL variation close to coding loci. Seventy-seven percent of chimp-human INDEL variants are associated with retrotransposons, and two-thirds of them are in humans. In humans, INDELs are mostly insertions, in chimps they are evenly split between insertions and deletions. There is substantial evidence that INDELs caused by TEs have produced significant adaptive changes in gene regulation in multiple human tissues.[63]

Transposons are also shown to modify and control lncRNAs. As stated, lncRNA transcripts organize chromatin into functional locations, and there are at least five to ten thousand lncRNAs in the genome. TEs specifically signal for the biogenesis of many lncRNAs, including 30,000 unique sites for transcription initiation, splicing, or polyadenylation in humans. Thirty-five thousand of these TEs marked as open chromatin are located within 10 kb upstream of lncRNA genes.[64]

But not all TEs involved in regulation are Alu's. Other ancient DNA transposons, such as the zinc finger ZBED proteins, have also been utilized as regulatory proteins for controlling a variety of "host" functions. ZBEDs originate from hAT transposons, which have contributed modular DNA and protein interacting domains to vertebrate regulatory innovation in lineages from zebra fish to humans.[65]

Further, although genetic stasis is typically maintained by blocking TE mobilization (by DNA methylation and histone modification), physical stress due to climate change, and other things, may disrupt such epigenetic regulation and release the TEs. The epi-transposon hypothesis proposes that TEs can cause a punctuated pattern of evolution due to such alterations in their epigenetic regulation. Methylated (deactivated) Alu sites are frequently reactivated (demethylated) under stress, thus allowing an explosion of new diversification, possibly punctuated change, driving new adaptive evolution. Also note that the effective epigenetic silencing of retained transposons in eukaryotes not only blocks their activation—it also blocks their selective removal.[66] Such blocking allows further transposon accumulation, which potentiates still higher levels of cleavage and DNA resection, thus increased sequence variation and genome rearrangement. Then, in theory, when some form of shock reactivates blocked TEs by removing their epigenetic constraints, it can allow punctuated bursts of innovation. Such nonadaptive evolution could escape adaptive peaks, disrupt genetic stasis, restructure the genome, and increase genetic innovation and diversification.

Transposable elements move and spread in genomes in a lineage-specific fashion—which is particularly true in humans. Specifically, Alu's are unique to primates and apparently have been involved in their evolution for 55 million years, with new bursts of Alu's appearing at bifurcations of the lineage (for instance, at the time of primate emergence 74K/98K years ago, or at other primate branch points such as 65M, 45M, 30M in old world monkeys, the expansion of ALUY in apes, or the rapid expansion of the ALUYa5 and ALUYb8 families in humans at 2.5–3.5 mya).[67] Britten considers transposing elements to be major actors in the rapid evolutionary alterations which have produced humanity. He ties the uniquely rapid evolution of the human lineage for the last 1.5 million years specifically to Alu activation, showing that TEs continue to actively generate effective genetic alterations at the present.[68] Notably, humans have seven new families of Alu's not present in chimpanzees. In particular, humans have a unique highly active class of Alu's—ALUYa5s—with an Alu insertion rate twice as high as any found in chimpanzees. In further evidence of recent activity, 655 perfect Alu copies have been reported in humans—that is, copies which are so recent that they have not accumulated any mutations.

But what a paradox—a uniquely high level of essentially unpredictable inputs from a genetic cut-and-paste mechanism has apparently produced the most remarkable species on the planet! This, of course, does not deny the action of natural selection in vetting these new variants. What is remarkable is not their survival, but their mode of arrival. One hint may be that TE insertions tend to target active genes; thus, higher levels of activity in neural genes might potentiate the production of higher diversity at those loci—at exactly that time when the demand for more neural processing power and plasticity was heating up, producing a snowballing increase in neural capacity.

So, what insights might the knowledge of the unique nature of human genetics yield to a Christian view of humanity? We must not change our background principles—God has made us in God's image. But how should we alter our "specifying assumptions" to connect these data with those background principles? The long discussion of the *imago dei* has centered on several concepts—notably, reason, righteousness, relationship, and rule—or culture, character, community, and commission.[69] And scientific descriptions of human origins do indeed have some relationship to these foci. The rational capability of the human mind is a product of a myriad of genetic alterations to neural loci. Questions of morality and community—as in "theory of mind" studies—are considered key elements of the functional purpose human rationality has played in survival (selective regime). The extended plasticity of human neural development and the recursive nature of human language make possible the growth and retention of culture. And all of these unique human features give us the power, for better or worse, to shape our environment toward our goals. Of course, this no more means that the image of God is "nothing but" a product of our biology, than that a Beethoven concerto is "nothing but" the product of microscopic pits on a plastic disk.

There are really two questions to ask in relating the genetic evidence to the nature of humanity: what has been done, and how was it done? One thing that the data make clear is that the unique character of the human mind is not due to a "magic bullet"; it is not a matter of just a few major alterations to an existing pattern, that is, it is not the injection of a "new" set of control genes. Rather, it involves the wholesale alteration of the entire hominine genetic package. Every known type of regulatory component which acts to shape the brain has been altered. It seems a selecting regime has indeed been at work, drawing the entire genetic system toward the human state. But, speaking of a selective regime is not an explanation—it is simply a description of the exterior pressures implied by the interior change.

Whether or not one wishes to invoke only "natural" causes, the acceptance of providence as a specifying assumption demands that what we see in nature be viewed as the action of the creative hand of God.

That alters the meaning of "natural cause," of course, making it different from the assumptions of a materialist. But "providence" does not necessarily mean that God acted by altering the direction of causation—not if the entire creation has been directed toward this end from its beginning (not that we have arrived yet). The creation is the product of the command of God spoken in eternity; it is shaped by the Word of his power, that Word that has echoed down through all of space and time from its end to its beginning, drawing all things toward the parousia, the final goal—a "holo-teleology." If God ordains the effects (the end point), then that necessitates their causes, and that ordaining occurs in eternity. But for observers within time, those effects simply flow from their causes "naturally."

In terms of the question of how this change was brought about, clearly transposons were a central factor. Alu's in particular have been particularly active in altering the human genome. Does the use of such a uniquely high level of transposon activity in the production of the modern human genome militate against viewing human evolution as a providentially guided process? After all, transposon movement/insertion appears to be a matter of pure "chance," unaffected by the "needs" of an organism. Does this make humanity a happenstance, the product of the biggest engine of chance in the animal kingdom? Or are we seeing the providential hand of God who is the Lord of "chance"? Or both? The evidence of "random" events does not exclude providence—in fact, the meaning can be viewed as quite the opposite. Our origin does not look like "business as usual" in the ecosystem, even if we can explain what happened. This judgment, I would suggest, can be viewed as a valid perception of "design" if one wishes to, but what can be seen is the design of the whole, not the designing of its parts. However, such perception requires the acceptance of the specifying assumption that God governs natural events (the doctrine of providence). Thus, it is rational to hold this view, but it is not necessarily statistically demonstrable to those who cannot perceive it. I do not know what new data will turn up in the next few years, but in my opinion, I do not think that we are irrational in holding that there was a highly directed process involved in the making of humanity.

Return for a moment to the question of how we should react to our kinship with the chimpanzees. Yes, our genetic likeness indicates that we are their closest relatives. But the data surveyed in this paper show that the human race has been made truly different. We are not simply the third chimpanzee species. Our reaction as Christians to all of this should simply be to stand in awe and wonderment at the complex methods which God used to mold us into his image—and to be thankful that he has allowed us to discover so much, to be allowed to look over his shoulder as he created us.

One final question: if God made us through evolution, are we still evolving? It depends on what you mean. There are indications that different human populations have become adapted to changes in their environment or culture through selected genomic changes. For instance, African populations have had an almost complete selective sweep of the FAD gene complex. Their allele freed them from dependence on marine omega 3 oils, and allowed them to move into the interior from the coastal regions. The FAD complex allows us to convert small fatty acids to the long chain versions necessary for brain development.[70] The less efficient, but original, allele is found in the chimp and in both Neanderthals and Denisovians.[71] The more efficient allele is specific to modern humans and arose after the lineages split, with a level of haplotypic diversity which indicates an origin at about 300,000 years. (The haplotypic diversity surrounding the original allele reflects an origin at around 600,000 years.)

This is interesting in light of one proposal, that modern humans evolved from an archaic population in the Levant around 300,000 years ago due to dietary pressures for the high fat intake needed to support their large brains.[72] Individuals with the less efficient allele need high levels of dietary omega 3 and omega 6 oils, which probably tied early members of the species either to marine habitats or to large animal predation. Individuals homozygous for that older allele must take care to breast-feed to support brain development. Individuals homozygous for the efficient allele should avoid overloading with long chain fatty acids to avoid inflammatory diseases.[73] Non-African populations have diversity at the locus; European, about three-quarters the efficient allele; far Asian, about one-half efficient; and Native American, almost entirely nonefficient.[74] Assuming that the African population of 60,000 years ago was mixed, the emigrants apparently took with them both alleles. Either drift or selection seems to have eliminated the efficient allele on the way to America, perhaps due to a primarily marine diet of the migrants moving through arctic Beringia.

There are plenty of other examples. Agricultural populations have accumulated multiple copies of the amylase gene to digest their bread. Dairying populations have preserved regulatory changes (lactase persistence) which allow them to digest the milk of their cows. High latitude populations have conserved mutations that modulated the production of melanin which was blocking the ultraviolet rays that they needed for vitamin D/calcium metabolism. High altitude populations have adaptive changes to their respiratory and circulatory systems.[75] So yes, local populations are still changing under local selective regimes. But I know of no evidence that the core genes of our neural systems are being selected for different responses in different parts of the world. We would not expect that to be the case, if they have been shaped to allow us the neural flexibility to produce culture. And we are a young species, for all of that. We still have more genetic similarities, though we come from the ends of the earth, than two chimpanzees living 500 miles apart in the African forest. So no, we show no signs of splitting into multiple species. We remain brothers and sisters, one flesh.

Notes

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ASA/CSCA/CiS 2014 Annual Meeting

Pre-Meeting Workshops

McMaster University, Hamilton, Ontario
July 25, 2014
8:30am–4:30pm

ORIGINS TODAY: GENESIS THROUGH ANCIENT EYES

Leader: *John Walton, Wheaton College*

The rift between faith and science in Christian circles today often results in the marginalization of Christians engaged in the sciences, impediments to evangelism, and the attrition of young believers who are told that Christianity is incompatible with the acceptance of evolution or an old earth. This presentation on Genesis 1–3 offers a fresh perspective on this complex issue by seeking to understand the message of scripture within its ancient context. Attendees will receive a free copy of John Walton's DVD on the same topic.

John H. Walton, professor of Old Testament at Wheaton College, specializes in the ancient Near Eastern backgrounds of the Old Testament, and specifically in Genesis. In recent years, he has focused attention on the issue of origins in books such as Lost World of Genesis One *(IVP) and* Genesis 1 as Ancient Cosmology *(Eisenbrauns). He has also contributed to two recent discussion books,* Reading Genesis 1–2: An Evangelical Conversation *(Hendrickson) and* Four Views of Historical Adam *(Zondervan).*

PROGRESS AND CHALLENGES IN UNDERSTANDING LIFE'S ORIGINS

Leader: *Stephen Freeland, U Maryland Baltimore County*

The origin of life on Earth remains one of science's biggest mysteries. On the one hand, there is little agreement about exactly how, when, and where this took place. On the other, there have been remarkable advances on related fronts—from evolutionary biologists using DNA to look back ever further in time to geophysicists detecting life's presence in Earth's oldest rocks; from astronomers discovering ever more-habitable environments within our own solar system and countless solar systems separate from our own to chemists understanding how crucial building blocks may have arisen. This workshop will present an overview of these topics.

Stephen Freeland is an evolutionary biologist who studies how and why life on our planet evolved a system of genetic encoding. He is director of Interdisciplinary Studies at the University of Maryland Baltimore County (UMBC). He received a PhD from Cambridge University's Department of Genetics before crossing the Atlantic to pursue a scientific career in the USA.

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Clayton D. Carlson

Transgenerational Epigenetic Inheritance

Clayton D. Carlson

Recent findings in the emerging field of transgenerational epigenetic inheritance suggest that the lifestyle choices and experiences of an individual have biological implications for offspring not yet conceived. Studies show that diet, drugs, and even social experiences can lead to life-long changes in gene expression. Some changes in gene expression are passed down to future generations. These conclusions deserve careful analysis from Christians trained in science who should teach freedom from epigenetic determinism, the fallenness and blessing displayed in the results, and the limits of the new field. Christian communities generally should show special grace to those that are epigenetically burdened, work to liberate victims from destructive epigenetic cycles, and prepare a healthful epigenetic inheritance for their children.

New revelations from the rapidly expanding field of epigenetics show that lifestyle decisions made by individuals could have biological consequences for future generations. Epigenetics studies chemical modifications to the chromatin of our genome that influence gene expression. These modifications are established by the cellular or organismal environment and are passed down during cell division in order to maintain cellular identity. Transgenerational epigenetic inheritance is the handing down of these epigenetic marks across generations resulting in changes in gene expression.

The purpose of this article is to explain the basic science of transgenerational epigenetic inheritance, highlighting particularly intriguing examples from human beings and rodent models, and to suggest that these discoveries require appropriate responses from Christian educators in science and from Christian communities in general.

Genetics and Epigenetics

In 1809, Jean Baptiste de Lamarck published his theory that changes acquired over a lifetime's effort can be passed on to successive generations.[1] His example explaining the development of the giraffe's long neck through generations of giraffes stretching for the highest leaves is still shared and corrected in numerous introductory-level biology textbooks.[2] His theory lacks a mechanism that would explain the inheritance of these earned traits. The later theory of evolution by natural selection proposed by Charles Darwin and Alfred Wallace rejected the concept of use versus disuse. Their theory, combined with genetics in the modern synthesis, provides a better understanding of how genes are passed from parent to offspring.

As an example of the modern explanation of inheritance, consider the mutation of a gene that codes for a protein responsible for regulating gene expression. If this mutation led to a slight change in the affinity of this protein for its typical

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binding partners in the cell, it could orchestrate a broad change in gene expression in the organism. If the mutation in a certain environment is detrimental to survival or procreation, perhaps by leading to severe cognitive defects, then this mutation would be less common in the next generation than it is in the current. On the other hand, if the mutation were beneficial, perhaps by leading to an ability to better tolerate cold temperatures, and thereby increasing the probability of having children, the mutation would be expected to be more common in the next generation than the current.

The genetic code of higher organisms is written in chromosomes made up of DNA wound around histone proteins in the form of nucleosomes. Each nucleosome contains two copies of four different histone proteins (H2A, H2B, H3, and H4) as well as around 141 base pairs of DNA.[3] Each histone protein has flexible tails that extend out past the wrapped DNA. These tails are made of amino acids that are able to accept numerous chemical modifications. Histone tails can be methylated, acetylated, phosphorylated, and much more. These modifications help regulate the expression of genes wrapped on the nucleosome. Histone modifications can precondition the DNA to be very easily read into RNA or, conversely, they can effectively shut down gene expression. Histone modifications are required for a cell to maintain its identity.[4] Epigenetic marks such as histone modifications will prevent heart-specific genes from being expressed in the liver or retina-specific genes from being read in bone. For the integrity of the tissues, these marks are passed down during mitotic cell division. The epi-genetic inheritance of a daughter cell prepares it for the kinds of gene expression that will be needed in its cellular environment.

There are many types of epigenetic modifications. Acetylation of lysines of the histone tails often correlates with increased levels of gene expression, and the enzymes that add these modifications are often found bound to DNA with the machinery responsible for reading DNA into RNA.[5] Removal of these acetyl groups can lead to inhibition of gene expression. Methylation of histone tails can have varying effects, depending on the level of methylation (single, double, or triple) and on which lysine is being methylated.[6] Another important epigenetic modification is methylation of the DNA itself. DNA methyltransferases can add a methyl group to the nucleotide cytosine. The methylation typically occurs in the context of the short DNA sequence cytosine-guanine or CG. This sequence is a palindrome in DNA and will read CG on both strands (because C binds with G and G binds with C). The cytosines on both strands will be methylated. DNA methylation can inhibit transcription in a number of ways.[7] It can prevent appropriate binding of a transcriptional activator that promotes gene expression. It can recruit proteins that specifically bind methylated DNA and then actively inhibit gene expression. Some methyl DNA-binding proteins will recruit enzymes that remove the acetyl groups of histones in the region, further suppressing gene expression.

Maintenance of Epigenetic Marks

The maintenance of these modifications during DNA replication and cell division is not yet fully understood. An overview of the current understanding is as follows.[8] During DNA replication, the nucleosomes are unwound and partially disassembled. Each daughter strand of DNA, after replication, will be rewound on nucleosomes made of some recycled histone proteins from the DNA mother strand and of histones that are freshly made. Since reused histones are thought to be incorporated into new DNA within just hundreds of base pairs of their original location, the inherited histones will include the modifications that are relevant for the current stretch of DNA.[9] The freshly produced histone proteins will require appropriate modification.

As for the inheritance of DNA methylation, the processes of semiconservative DNA replication will produce two daughter strands of DNA that will each be hemimethylated, with the inherited strand methylated and the recently synthesized strands unmethylated. Cells contain regulatory proteins that identify hemimethylated DNA and recruit the DNA methyltransferases that will methylate the other strand, restoring the parental methylation state.[10]

Transmission of epigenetic information across generations is even less well understood. At or just after conception, DNA methylation is dramatically reduced. Early in development, the few cells of an organism require the flexibility to express genes appropriate for whatever kinds of tissue they differentiate into. These early cells have much less DNA fully shut down from gene expression than do mature tissues. Therefore, only very few DNA methylation patterns are passed directly from one generation to the next. Similarly, during formation of mature sperm cells, more than 85% of the histone proteins are removed, and DNA is compacted by forming a complex with proteins called protamines. The small number of histones donated to the offspring could carry some epigenetic information, but this may not be the dominant means of conveying this regulatory information.[11]

Another possible way that epigenetic information could be passed down across generations is in the form of regulatory RNA. Regulatory RNAs are known to have roles in controlling the epigenetic landscape of the genome.[12] Regulatory RNA is required for proper maintenance of DNA methylation and some histone modifications. Additionally, both male and female sex cells carry active RNA molecules. The RNA packaged with a sex cell will have developmental, and potentially epigenetic, consequences, some of which may be passed on to generations yet to come.

Transgenerational Epigenetic Inheritance

In the winter of 1944–1945, the Western Netherlands experienced a season of extreme cold, devastation from years of war, and a food embargo enforced by German forces still in control of the area.[13] The resulting famine, called the Dutch Hunger Winter, decreased average caloric intake for residents to a low of about five hundred Calories a day and killed an estimated twenty thousand people. The human tragedy created a group of survivors that, because of the organized and meticulous records of the Dutch medical system, could be studied for effects on later generations. Females that experienced the famine in the earliest stages of fetal development were born at average birth weights; however, *their* offspring have a higher-than-average birth weight. Additionally, victims of the famine that were in the first weeks of fetal development during the famine had changes in the DNA methylation patterns of a gene, IGF2, even six decades after the Dutch Hunger Winter.

Famines experienced at other stages of development beyond birth also have transgenerational epigenetic consequences. Marcus Pembrey and others have studied the historical records, including harvest records and food prices, of the remote Swedish community of Överkalix.[14] They find that food supply during the slow growth period of late childhood has biological consequences for future generations. Intriguingly, the effect is strongest for the grandparent on the father's side that shares the same sex as the grandchild. For example, low food availability during the slow growth period in a female leads to a statistically significant decrease in the mortality rate of her son's female offspring. Likewise, abundant food availability during the slow growth period in a male correlates with increased mortality in his son's male offspring. These results, and others like it,[15] that show a clear transgenerational effect through the male lineage, offer clues as to the mechanism of how this occurs, but currently the exact answers are not yet known.

The effects of parental diet on future generations can be more carefully studied in rodents. A study published in *Nature* in 2010 determined the effect of a paternal high-fat diet on the regulation of gene expression in the pancreases of their offspring.[16] The male rats with this high-fat diet showed an increase in body weight and body fat, and showed symptoms of diabetes, including decreased glucose tolerance and insulin insensitivity. Although these male rats were almost identical genetically to the control males that were fed a standard diet, their daughters showed a significant difference in the expression of hundreds of genes in the cells responsible for regulating glucose. Of the hundreds of genes that showed a significant change in gene expression dependent on the diet of the father, the gene most disturbed (*Il13r*a2, 1.75-fold increase in expression) had less DNA methylation, which could explain the increase in gene expression. In human beings, paternal diabetes increases the risk of diabetes in offspring.[17] While this increased risk could certainly be genetically and/or environmentally transmitted, this study in rodents indicates that transgenerational epigenetic inheritance may also be involved.

Another study, published in *Cell* that same year, reports the effect on offspring of feeding male mice a low-protein diet.[18] This group found hundreds of genes involved in lipid and cholesterol synthesis with changed levels of expression in the next generation. Numerous genes in the offspring, which were fed a standard diet, showed slight changes in the level of DNA methylation, including the regulatory region of one of the key genes that oversees the lipid biosynthesis (*Ppar*). Interestingly, the sperm showed normal methylation levels in this gene, ruling out a direct transmission of the methylation pattern but leaving room for transmission of the signal via an RNA molecule.

Other reports indicate that parental diet or caloric restriction at specific times in development, from embryo to adolescent, may have ties to heart disease, psychological disorders, and more.[19] Though the mechanisms are not yet fully understood, the dietary choices of one generation seem to have potential lifelong consequences for the next and perhaps even for generations yet to come.

Unfortunately, there is also evidence that some molecules and environmental toxins can cause epigenetic changes. The most widely reported example comes from the fungicide vinclozolin.[20] Vinclozolin is a hormone disrupter that is able to decrease sperm production, reduce sperm motility, and increase cell death in the testes of male rodents whose mothers were exposed to the molecule. In the key study, pregnant rats were injected with high doses (100mg/kg/day) of the fungicide throughout pregnancy. In addition to affecting fertility of the male rats exposed in utero, *their* male offspring also showed reduced fertility through four generations.[21] These descendants also showed changes in DNA methylation patterns in fifty-two different genes.[22]

A human example showing the potential consequence of transgenerational inheritance of environmentally induced epigenetic changes comes from the drug diethylstilbestrol (DES), once given to prevent miscarriage. DES is an estrogen disrupter that is able to cross the placenta and cause developmental changes in the fetus. Now known to cause birth defects and to increase the risk of cancer of the reproductive system in those exposed in utero, it is possible that even granddaughters of women that took this drug may pay a biological price for this decision. In mice fed doses of DES similar to what was given to pregnant women, granddaughters of mice given the molecule still show increased rates of uterine cancer when compared to a control group.[23] The mechanism of this transmission is not yet known, but changes in DNA methylation patterns of important estrogen-dependent genes have been reported in response to DES treatment.[24]

There is evidence that not only diet and toxins, but also social experiences, can cause epigenetic changes that are passed on to future generations. Signs of good mothering in rats include licking, grooming, and arched-back nursing. Rats that receive this caring nurture in their first weeks of infancy are less fearful as adults and have a more moderate hormonal response to stress.[25] Michael Meaney and others reported a possible epigenetic explanation for this result in 2004.[26] They found that mice which are raised by mothers that provide attentive licking, grooming, and arched-back nursing have decreased methylation patterns in the regulatory region of the glucocorticoid receptor in the hippocampus of the brain. Methylation of this region was later shown to disrupt an interaction between the regulatory DNA of the glucocorticoid receptor gene and a protein that controls transcription of the gene.[27] Decreased methylation permits increased expression of the receptor and could explain the lifelong decrease in stress response these rats experience. These experiments indicate that, in rats, the attentiveness given by a mother in the first weeks of her offspring's life leads to a permanent change in how that youth will respond to stress throughout its life.

Conversely, the data also suggest that harsh treatment in early infancy has lifelong and even transgenerational consequences. A study published in *Biological Psychiatry* in 2010 showed that newborn mice exposed to chronic unpredictable maternal separation for the first two weeks of life show depressive-like behaviors and have a reduced response to novel environments as adults.[28] Offspring of males that experienced this maternal separation show the same psychological consequences as their fathers. This is a complex behavior and could have many explanations, but the researchers did find changes in DNA methylation patterns that affected gene expression in the deprived males and their offspring. Another study exposed rats in infancy to caregivers that were under substantial stress.[29] These rat pups experienced "significant amounts of abusive maternal behaviors." Victims of this abuse showed DNA methylation and reduced expression of the gene *BDNF* in the prefrontal cortex of the brain. Additionally, offspring of females that experienced the abuse also show these changes in gene expression in the brain. Female mice that suffered abuse as pups were more likely to treat their own offspring abusively, explaining some of the transgenerational response. However, even if young rats were removed from the abused mother at birth and given nurturing, adoptive mothers, they still showed some of the changes in *BDNF* methylation and gene expression.

Whether these results directly transfer to human beings is not yet understood, but there is evidence that human child abuse causes epigenetic changes in the brain. Michael Meaney and others compared DNA methylation patterns and gene expression of the glucocorticoid receptor in brains of suicide victims who had suffered abuse as children, and compared them to other suicide victims who had not been abused.[30] They found increased methylation and decreased gene expression, which may have caused an increased stress response in suicide victims who had been abused. While this is a complicated study, it at least suggests that some of what has been learned about the transgenerational epigenetic inheritance of traits acquired by the social experiences in rodents may be true in humans as well. The social choices and experiences of one generation have biological consequences for the next generation and potentially for generations yet to come.

Christian Responsibilities

Christian Educators in Science

The provocative conclusions coming from this field have ramifications for Christian educators of science. Scientists should emphasize that there is freedom from epigenetic determinism.[31] A simple reading of the work summarized above may suggest that how an individual responds to stressful situations and to sugars may already be determined by the DNA and histone methylation patterns that they inherited. That deterministic understanding could lead to incredibly damaging decisions. Students with anger issues could feel that their outbursts were justified and feel no need to change because their response is predetermined by how they were raised as infants. Overweight students may feel no personal responsibility for their health because they are already predetermined to suffer from diabetes due to their father's dietary choices. Educators in science should remind students of their relative autonomy as adults, of the probabilistic nature of genetics generally and epigenetics specifically, and of their freedom in Christ. DNA methylation patterns may increase the likelihood of contracting a certain disease or responding in a certain way, but persons are still responsible for their own actions. We are to remind them that while they may be predisposed to alcoholism, no histone modification makes anyone open an alcoholic beverage. We are to show them that while their probability of struggling with diabetes may be higher than the student in the next row, it is the responsibility of each of us to eat well and exercise. Human health is a complex outcome of environment, genetics, sociology, psychology, faith, and epigenetics.[32] By the grace of God, each of us can overcome epigenetic burdens that would predispose us toward crime, sickness, or sin.

Another responsibility of Christian educators in science is to highlight not just the fallenness revealed in this new field, but the grace it shows as well. The examples discussed above, particularly regarding the epigenetic inheritance of poor parenting and violent behavior that could be a factor in generational cycles of abuse, clearly demonstrate the fallenness of transgenerational epigenetic inheritance. But I would like to suggest that this is only a twisted version of how good, or even holy, transgenerational epigenetic inheritance can be. Transgenerational epigenetic inheritance is a mechanism by which wisdom from one generation can have positive implications for the next. There are undoubtedly numerous examples of inheritance of DNA methylation patterns that are beneficial for the offspring. One example from plants bears mentioning. *Campanulastrum americanum* is a small plant that produces lovely purple flowers. It grows both in the deep shade of forests and in broken light under thinner tree growth. A study published in *Science* in 2007 shows that, even for genetically identical plants, seeds that land in the same light conditions as their parent have 3.4 times greater fitness than those that are moved to different light conditions.[33] What this means is that the experience of the paternal generation, the gene expression decisions that a certain plant finds are most successful for the environment in which it lives, can be shared with its offspring. If this is true in humans, then by God's grace, children have an opportunity to learn from their parents even if the children and their parents had never met.

Further, Christian educators in science should teach students the limits of this work. The study of transgenerational epigenetic inheritance is still a very new field. There is certainly a chance that many of the modifications to DNA and histones that have been discussed here are effects instead of causes. It may be that proteins that regulate gene expression determine the biological response of a cell (or an organism) to a certain environment. The epigenetic marks could be put in place once the cellular response has already begun. While the results that have been discovered so far are exciting, huge numbers of experiments have been disappointing. One researcher, Steve Cole, who studied changes in human epigenetic marks in response to socio-economic status, is reported to have said, "Lots of people have spent lots of time and money and are now a little grumpy about this."[34]

Which choices, experiences, or molecules lead to an epigenetic response are not yet known. There is certainly no reason to avoid any medication, food, or experience until it has been proven to cause detrimental epigenetic consequences. The exact means of transmission of epigenetic marks is not yet understood, and until it is, it will remain difficult to make predictions about transmission. The conditions that maintain or disrupt inherited epigenetic marks are also not yet known, which means that it is still impossible to predict gene expression in the offspring even if the epigenetic landscape of the parent is fully known. With the incredible amount of work being done in this area, answers to these questions are likely to be the headlines of scientific articles in the near future. In the meantime, Christian educators should highlight the exciting conclusions this field is producing while explaining the limits of what is, so far, known.

Christian Communities Generally

One responsibility for followers of Christ in light of the findings in epigenetics is to show special grace to those who might be biologically disadvantaged in their struggles against sin and disease. While on Earth, our King showed special grace, love, and respect to someone caught in adultery and to others sick or impoverished. As followers of Christ, we are expected to show love and grace to those whose decisions lead to destruction and sin. Of course, as modern readers, we know nothing of the circumstances that led to these displays of brokenness and, as yet, there is no definitive evidence that a cycle of broken relationships will result in epigenetic changes that are able to perpetuate the destructive cycle. However, I suspect that, knowing that there is a possibility that poor decisions regarding relationships, drugs, or health may be made as a product of the cycle of brokenness and epigenetic consequences, this knowledge could offer some comfort for those left in the destruction of a loved one's choices. As it is easier to show patience and grace in the face of the difficulties in learning to read when we know the student struggles with dyslexia (which may have a genetic component[35]), so perhaps we can better love like our Lord when we understand that a potential epigenetic change has occurred in a person's brain that could make it biologically more difficult to make good decisions. Dyslexia and a predisposition toward poor decisions can be overcome, but it may take grace, love, and assistance from a community.

Another obligation of Christian communities that deserves emphasis, given what epigenetics is suggesting, is that we are called to liberate people from destructive cycles. As mentioned above, some part of the destruction caused by cycles of poverty, violence, or abuse could come from epigenetic changes in the brains of those raised within the cycle. Fortunately, the field of epigenetics has provided evidence that breaking the destructive cycle can also have lasting consequences for generations. James Curley and others published a study in 2009 that analyzed maternal BALB/c mice.[36] The BALB/c mouse strain displays significant deficiencies in social interactions including parenting.[37] The 2009 study found that the BALB/c mothers who raise their pups in isolation show increased levels of aggression (such as biting) and reduced displays of maternal care (such as licking, grooming, or arched-back nursing). However, they found that when BALB/c mice with brand new pups raise their young in community, they display reduced stress response, reduced aggressive behaviors, and increases in maternal care. The pups (which still bear the BALB/c genetics that predispose them to antisocial behavior), once grown, show many of these same increases in maternal care to their offspring even if they raise them in isolation. These changes may be explained by changes in gene expression in the brains of these mice as a result of the nurturing parenting they received as pups. Some of the beneficial physiological and social consequences were still present when the granddaughters of the females that had reared their young in community became mothers themselves. These results imply that, at least in this example from rodents, epigenetic changes that result from positive social experiences can break a cycle of abusive parenting.

Even the possibility that such results could occur in humans demands that followers of Christ begin to break these destructive cycles. This could mean that cycles of alcoholism, abuse, sexual sin, poverty, or poor decisions in relationships could be broken in ways that change the brain chemistry of not only those freed from the cycle, but also of their children and their children's children. Churches and Christian communities can help those trapped in destructive cycles to find freedom in the body of Christ. By teaching one young mother how to care for her daughter with love and compassion, we may be influencing the hardwiring of her daughter to be a better mother herself one day.

Another responsibility of Christian communities is to foster lives that provide a healthful epigenetic inheritance. In addition to breaking cycles of abuse, Christian communities should encourage those within and around their community to make epigenetically healthful decisions regarding food and relationships. The effects of male rats' diet on the insulin response of their daughters should demand that we are conscious of the epigenetic legacy we will pass on to our children. If a young father made a habit of filling bottles for his six-month-old daughter with cola, a mentor could teach, in love, the possible detrimental health consequences that that decision could have for his daughter. Perhaps we should make similar interventions to young men (and women) who will one day be parents. If a young person is making poor decisions about friends or romantic interests, a loving member of their Christian community could try to help them learn to make God-honoring decisions. Perhaps we should actively train young parents in what God-honoring relationships look like in order to change the environment (and possibly the epigenetic state) of their children. Most Christian communities take leaving a healthy spiritual legacy for the next generation very seriously. I suggest that we should also work to leave a healthy epigenetic inheritance for them as well.

The discoveries being made in epigenetics suggest a new and exciting meaning to the question asked by the righteous in Matthew 25:37.

> *Lord, when did we see you hungry and feed you, or thirsty and give you something to drink? When did we see you a stranger and invite you in, or needing clothes and clothe you? When did we see you sick or in prison and go to visit you?*

We know that when we do these things for the least among us, we do it for Christ. However, we now know that when we care for the least among us, we are not only helping them and honoring our Savior, we may also be helping their children down through the generations.

Conclusions

Like so much else in our time between Calvary and the new creation, transgenerational epigenetic inheritance shows evidence of the brokenness of our world while still displaying the overwhelming goodness of God's creation. Transgenerational epigenetic inheritance could increase an infant's risks for disease, sin, and death in response to decisions, actions, foods, chemicals, and experiences from earlier generations. However, transgenerational epigenetic inheritance also gives us another way to prepare our offspring to thrive in the world, even if we never meet one another. While we wait and see what this exciting field will finally offer, I suggest that we seek transgenerational justice, love epigenetic mercy, and walk humbly in our God's creation. ❧

Notes

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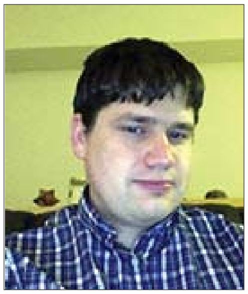
Article

A Mono-Theism Theorem: Gödelian Consistency in the Hierarchy of Inference

Winston Ewert and Robert J. Marks II



Winston Ewert

Robert J. Marks II

Logic is foundational in the assessment of philosophy and the validation of theology. In 1931 Kurt Gödel derailed Russell and Whitehead's Principia Mathematica *by showing logically that any set of consistent axioms will eventually yield unknowable propositions. Gödel did so by showing that, otherwise, the formal system would be inconsistent. Turing, in the first celebrated application of Gödelian ideas, demonstrated the impossibility of writing a computer program capable of examining another arbitrary program and announcing whether or not that program would halt or run forever. He did so by showing that the existence of a halting program can lead to self-refuting propositions. We propose that, through application of Gödelian reasoning, there can be, at most, one being in the universe omniscient over all other beings. This Supreme Being must by necessity exist or have existed outside of time and space. The conclusion results simply from the requirement of a logical consistency of one being having the ability to answer questions about another. The existence of any question that generates a self-refuting response is assumed to invalidate the ability of a being to be all-knowing about the being who was the subject of the question.*

Can the necessity of, at most, a single Supreme Being be deduced from logic applied to the definition of universal omniscience? Based on Gödelian reasoning and a need for logical consistency, we make a case that it can.

Alfred North Whitehead and Bertrand Russell's three-volume tome, *Principia Mathematica*,[1] has been called "the most influential book never read."[2] Whitehead and Russell's quest was to describe a set of axioms and inference rules in symbolic logic from which all mathematical truth could be proven.[3] Their quest was shown to be futile by a beautiful theory crafted by Kurt Gödel. Gödel used a self-referencing proposition to show that whatever system resulted from Whitehead and Russell's theory would either be incomplete, in the sense that there would remain unanswerable truths, or be inconsistent, such as showing that $1+1=2$ and $1+1=3$. Here is a simplified explanation. Gödel's incompleteness theorem says that at some point Whitehead and Russell would encounter a proposition something akin to

Theorem X: Theorem X cannot be proved.

If Theorem X can be proved, then the mathematical system is inconsistent. You have proven something that you have claimed cannot be proven. If you cannot prove Theorem X, then your system is incomplete. There are propositions you cannot prove. An assumption of consistency therefore dictates incompleteness, and the conclusion is that there are truths that cannot be proven.[4]

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Strange Loops

Theorem X is an example of a self-refuting statement, the most famous of which is the paradox spoken by the Cretan Epimenides.[5] We paraphrase:

> "Everything I say is a lie."

If true, then Epimenides has just told a lie; in which case, he is telling the truth. But if he is telling the truth, he just lied. Self-reference has created an unresolvable contradiction.

Hofstadter refers to such recursive flip-flops in logic as "strange loops" and notes their occurrence in drawings and music.[6] The art of M. C. Escher shows ever-ascending staircases that seem to magically loop to the bottom of the stairs with no appearance of descending. In music, the downward Shepard-Risset glissando seems to ever decrease in pitch while, in reality, the music is a repetitive strange loop akin to Escher's looping stairs.[7] Likewise, there are rhythms that seem ever to accelerate while, in reality, the beats per second remain the same.[8]

Strange loops do not exist in reality. Ascending stairs that repeatedly loop back to the base of the stairs are not possible. Escher's art is an optical illusion. A musical pitch that decreases forever also does not exist. The Shepard-Risset glissando is an audio illusion.

In mathematics, Penrose points out that Theorem X in context is not a strange loop.[9] If the originating foundational axioms are consistent, Theorem X is, rather, true: a truth that cannot be proven on the foundation of the axioms on which the theory is built. Gregory Chaitin, a father of algorithmic information theory, takes us even further. There are things that are true, like Theorem X, which can be proved not to be provable. Chaitin says that most truths cannot be proven from foundational axioms. Most things, rather, are true simply because they are true.[10]

More on Cretans or Moron Cretans?

What of Cretans who only tell lies? Can they exist? Here is the reality. If a man walks into my office and proclaims, "Everything I say is a lie!" I would not spend time logically analyzing him. If I were not a psychiatrist interested in curing his mental disease, I would feel that this wacko was wasting my time.

The Apostle Paul confirms the dishonesty of Cretans when he refers to Epimenides and writes,

> "One of themselves, a prophet of their own, said,
> 'Cretans are always liars …' This testimony is true"
> (Titus 1:12–13a, edited).

There are no strange loops here.

1. Since Paul is not a Cretan, there is no self-reference and therefore no ambiguity nor contradiction in his statement.
2. Saying "Cretans are always liars" is not the same as saying "Everything a Cretan says is a lie." Paul is simply saying that Cretans are not to be trusted. Sometimes they lie and sometimes they do not. Curiously, a strange loop only occurs if a Cretan says something like "Everything I say is a lie," and you trust him!

Strange Loops in Reality

The bottom line is this: Requiring the universe to be logically consistent requires the avoidance of all universal strange loops.

Contradictions arising from self-reference at first can appear to be nothing more than recreational word play. But the contradictions can be, in fact, deadly serious. Alan Turing, the father of computer science, used Gödelian self-reference to prove the *halting problem*: It is not possible to write a computer program that can examine any arbitrary computer program to see whether the program will eventually stop or run forever.[11] Turing proved the halting problem by assuming that a halting program existed and by submitting the augmented halting program for analysis to another copy of the halting program. In Turing's analysis, the halting program is therefore examining a version of itself. The unresolvable contradictions arising from such an exercise reveal that halting programs cannot be written. Today the halting problem is part of most undergraduate computer science curricula.

Halting programs do not exist in reality because they invoke a strange loop, and strange loops do not exist in reality. Omniscience, though, is not constrained by strange loops within a closed system. Certainly an omniscient God can tell us whether or not any computer program will halt. A computer cannot.

Gödelian Omniscience

We are now ready to begin development of our main result: Gödelian reasoning applied to omniscience implies that there can be but one being who is omniscient over all others. By necessity, this being must exist or have existed external to time and space. The basics of the idea are from an intriguing paper by Wolpert.[12]

Unanswerable Questions

Prophets of the Old Testament were infallible. They conversed with God and were able to accurately forecast events. If a prophet was shown to give false prophesy, the prophet was executed by stoning. To reach retirement, career prophets could therefore make no falsifiable prophesies. Close to the idea of a prophet is an *oracle*. Like prophets, oracles can predict the future. Prophets basically work for free. Oracles, on the other hand, are typically thought of as sources of truth that require payment. Ask an oracle a question, slip him a twenty dollar bill, and you get an answer. More generally, an oracle is a device or entity that performs observation, prediction, or recollection. A more formal name for the oracle is a *physical inference device*.[13]

Oracles are all-knowing (omniscient) in certain areas of knowledge. By omniscient, we mean that the oracle is able to answer any question accurately. In principle, we could consider an oracle which knows the answer, but is unable to communicate it. However, we do not consider that to be true full omniscience. We use the terms *inference device* and *oracle* (subsequently, the term *node*) interchangeably. Individuals (or beings) involved with prophecy will be called *agents*. An agent may or may not be an oracle. The God of the Bible is certainly greater than a prophet or an oracle. But we can agree that anything done by an oracle or a prophet can be done by God.

Let's introduce the idea of a *binary oracle*. You can ask the binary oracle any "yes" or "no" question, and the oracle will respond with either a "yes" or a "no" answer. Attention is restricted to oracles that make prophecies about another agent. Questions proposed to an oracle are restricted. We will exclude *subjective questions* such as "Will Agent 89 be more beautiful than Agent 86 tomorrow?" Answers that are a matter of opinion rather than fact have no place in being laid at the feet of an oracle. There are also many *stupid questions* such as "Will Agent 23 ever weigh more than love?" or "Is Agent 007 leafy?" Stupid questions are usually based on faulty presuppositions. Love does not have mass, and people are not "leafy."

Gödel based his transformative theory on strange loops emerging from self-reference. So let's ask a binary oracle named Bob a simple statement about himself:

> Question 1 to Bob: *Will you respond "yes" to this question?*

There are only two answers Bob can give: "yes" and "no." If Bob says "yes," his single response serves two purposes. First, "yes" is Bob's next response. Second, it is an answer to Question 1. Since both are "yes," Question 1 has been answered clearly and without ambiguity. A response of "no" is also a good answer.

Here is another question for Bob that is even more curious.

> Question 2 to Bob: *Will you respond "no" to this question?*

Note that Question 2 is neither subjective nor stupid. Let's look at the two responses Bob can give and the logical consequences of each. If Bob says "yes," his next response is "yes" even though he is also saying his next response will be "no." We have an unresolvable contradiction. We also get a contradiction when Bob says "no." His response is "no" even though he said it would not be. We have a strange loop.

What are we to make of Question 2? Since the question is neither stupid nor subjective, we need to create a new category. Let's call such questions *unanswerable*. Unanswerable questions expose a limitation of the binary oracle. Bob has limited power. There are some questions he is unable to answer while maintaining consistency. Note that while Bob cannot answer the question, at least in principle another agent could. Using another agent removes self-reference.

There are statements about God that look as if they land in the category of unanswerable. Consider the statement:

> "With God all things are possible" (Matthew 19:36b).

If true, then it is possible for God to create something impossible for God to do! Have we discovered a limitation to God through this strange loop?

No, there is no inconsistency. There is, rather, incomplete context in the statement. Scripture reveals that God cannot do, or more properly chooses not to do, actions that are contrary to his nature. God is just and righteous. He therefore cannot do anything against his nature of justness or righteousness. To include this context, we might rewrite the statement as "With God all things are possible that are consistent with his nature." In this case, an unanswerable question can be made resolvable by the introduction of additional context.

Restricting his actions to his chosen nature allows God to be logically consistent. He is immune from the logical quagmire of statements that appear on the surface to be self-refuting. But are we then to conclude that these restrictions impose limitations on God? To the extent that God cannot be contrary to his nature, the answer is an obvious yes. God has self-imposed limitations. Perfection is limited to be perfect. More on this later.

Let's return to our talk about binary oracles. We see that with a single binary oracle, there are self-referential unanswerable questions that invoke contradictory strange loops. Does this extend to two binary oracles each making a prediction about the other? As you might expect, things get a bit more complex to analyze.

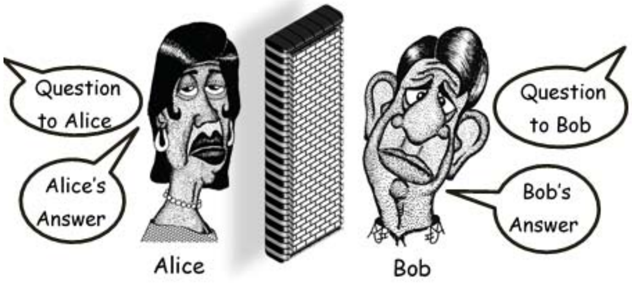

Figure 1

Suppose we have the two binary oracles shown in Figure 1: a male binary oracle named Bob and a female binary oracle named Alice. In isolation relative to each other, each answers "yes" and "no" questions posed to them. Because of the possible strange loops associated with self-referential questions, we will not allow Alice to ask a question about herself nor Bob a question about himself. But Bob can be asked a question about Alice and Alice a question about Bob.

Here is the first pair of questions asked simultaneously:

Pair #1.

- Question to Alice: *Is Bob's next response "yes"?*
- Question to Bob: *Is Alice's next response "yes"?*

There are two ways Bob and Alice can respond correctly. Truth and consistency prevail if both Bob and Alice answer "yes." This is in fact the most obvious answer. Another correct response is for both Bob and Alice to say "no." So the possible answers are:

- o Both Bob and Alice say "yes," or
- o Both Bob and Alice say "no."

Let's try a second pair of questions.

Pair #2.

- Question to Alice: *Is Bob's next response "no"?*
- Question to Bob: *Is Alice's next response "no"?*

Let's think this out. Suppose that Alice answers "yes" and Bob answers "no." Does this work? Alice is saying, "Yes, Bob's next answer is 'no,'" which is correct. And Bob is saying, "No, Alice's next response *will not* be 'no,'" which is also correct. So, Alice responding "yes" and Bob "no" give a valid and consistent response. If we switch Alice to "no" and Bob to "yes," it also works. So the possible valid responses to Pair #2 are

- o Alice says "yes" and Bob says "no," or
- o Alice says "no" and Bob says "yes."

Here is an even more curious pair of questions to Bob and Alice that results in a strange loop.

Pair #3.

- Question to Alice: *Is Bob's next response "no"?*
- Question to Bob: *Is Alice's next response "yes"?*

Although probably not initially apparent, these two questions are unanswerable, just as when Bob was asked "Will you respond 'no' to this question?" This is tricky for two agents, so let's walk through the self-contradictory logic:

- ✓ If Alice answers "yes," she is saying that Bob will predict that she will say "no," which is contradictory.
- ✓ If Alice answers "no," she is saying that Bob will reply "yes," thus predicting that Alice will respond "yes"—but she did not, thus producing another contradiction.

So whatever Alice says, she will be wrong. The two questions posed are therefore unanswerable.

The exchange of two binary oracles is akin to the single oracle being asked to predict the opposite of what his next response will be. So like the single oracle, there is a limitation on what a pair of binary oracles can predict about each other. Omniscience cannot make allowance for the possibility of unanswerable questions.

One way to resolve this limitation is to use arrows pointing only one way. This is illustrated in Figure 2 with the introduction of a third agent named Edgar. Alice can make predictions about Bob and Edgar. And Bob can make predictions about Edgar. But that is it. If an arrow pointed from either Bob or Edgar to Alice, we would introduce the possibility of unanswerable questions. An additional arrow from Edgar to Bob also would allow the asking of unanswerable questions. These strange loops are *feedback loops*. In our oracle analysis, feedback loops are strange loops. To avoid unanswerable questions, feedback loops among oracles must be avoided.

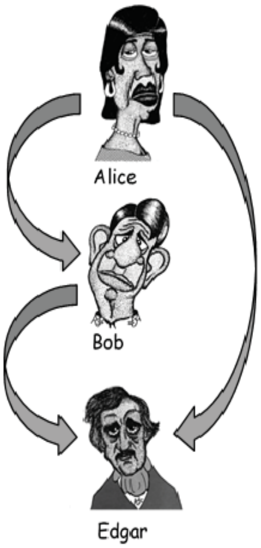

Figure 2

Feedback loops are not allowed at any level—not even for one oracle. Remember “Question 2 to Bob: Will you respond ‘no’ to this question?” The question can be viewed as a reference of Bob to himself—a kind of auto feedback loop as is shown in Figure 3. A two-oracle loop example is one arrow pointing from Bob to Alice and another arrow pointing from Alice to Bob. Feedback loops in both cases can lead to the asking of unanswerable inference questions. And Hofstadter is right. These loops are indeed strange.

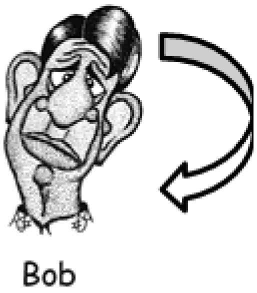

Figure 3

A feedback loop can be indirect as illustrated in Figure 4. It looks like Figure 2 except that the arrow connecting Edgar to Alice has been reversed and we have feedback. Each of the three agents can make predictions only about the agents to which their arrow points.

With this configuration, there are valid cross referential inferences that can be made. An obvious example is the following.

Triple-header questions #1.

- Question to Alice: *Is Bob’s next response “yes”?*
- Question to Bob: *Is Edgar’s next response “yes”?*
- Question to Edgar: *Is Alice’s next response “yes”?*

All three binary oracles answer “yes,” and everybody’s happy. Our goal, however, is to avoid any possibility of asking unanswerable questions. So here is a series of questions that is unanswerable even though the feedback loop in the logic is indirect.

Triple-header questions #2.

- Question to Alice: *Is Bob’s next response “yes”?*
- Question to Bob: *Is Edgar’s next response “yes”?*
- Question to Edgar: *Is Alice’s next response “no”?*

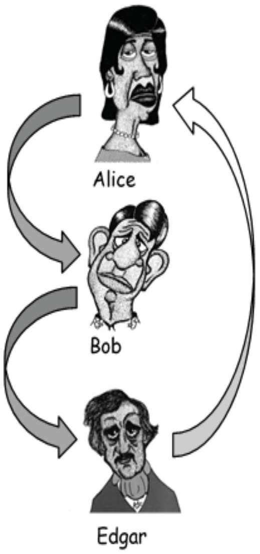

Figure 4

Let’s unpack this. There are a lot of mental gymnastics needed to analyze this simple problem, so understanding will take some head scratching. The conclusion is that Alice can neither answer “yes” nor “no” without subsequent contradiction.

1. Alice answers “yes.”

- If Alice answers “yes” to the question asked her, she is saying that Bob will say “yes” (and Bob *must* then say “yes,” according to the rules).
- If Bob says “yes” in answer to the question asked him, in effect he is stating that “Yes, Edgar’s next response will be ‘yes.’”
- Edgar must say “yes” in answer to the question asked him, thereby affirming that “Alice‘s next response will be ‘no.’”
- But Alice’s response had been “yes”—and this is a contradiction.

2. Alice answers "no." (The double negatives make this next analysis even harder.)
    - If Alice answers "no," she is saying that Bob's next response will "not be 'yes.'" Thus, Bob will answer "no" to the next question put to him.
    - Bob must say "no" in answer to the question asked him, in effect stating that "No, Edgar's next response will not be 'yes.'" Therefore Edgar must answer the next question put to him with "no."
    - Edgar must say "no" in answer to the question asked him, in effect stating that "No, Alice's next response will not be 'no.'" This means that Alice's next response will be "yes."
    - But Alice answered with "no"—a contradiction.

Triple-header questions #2 are therefore unanswerable.

Here is a shorthand version of the two possibilities we just discussed about the triple-header question.

1. A+ → B+ → E+ → Ao
2. Ao → Bo → Eo → A+

where A = Alice, B = Bob, E = Edgar, + = "yes," o = "no," and implication is denoted by the arrow "→". In both of these statements, the last entry is in direct opposition to the first.

A Consistent Inference Hierarchy and Spatial Omniscience

In general, unanswerable questions in an inference structure can be avoided if there are no feedback loops. Here is a way that this can be guaranteed. Assume that we have nine agents as shown in Figure 5. Instead of giving the agents human names, let's simply number them one to nine. *Any arrangement that connects an agent to one or more agents with only higher numbers is guaranteed to have no feedback loops*.[14] A connection geometry obeying this simple rule is said to be a *feedforward directed graph*.[15]

In Figure 5, for example, agent ❷ can infer things about agents ❺, ❻, and ❼. That is why the arrows pointing from agent ❷ point to the larger numbered agents ❺, ❻, and ❼. But agent ❽ is not allowed to infer anything about the lower numbered agent ❶ less we encounter undesirable feedback loops that can result in possibly unanswerable questions. (If ❽ connected ❶, for example, we would have feedback loops ❶❹❽❶ and ❶❺❽❶.)

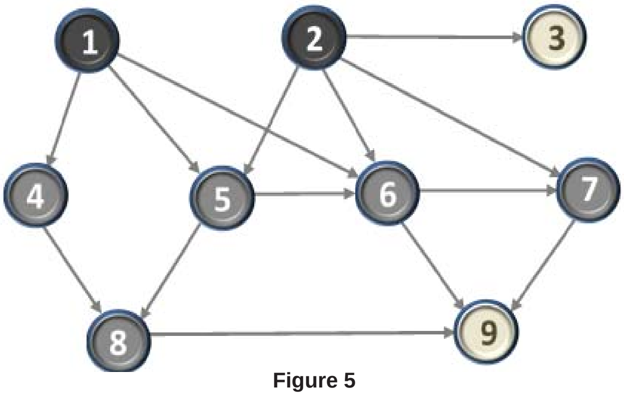

Figure 5

In graph theory, each agent in the group of nine is dubbed a *node*. We will henceforth interchangeably use the terms *node* and *agent*. There are three classes of nodes. We assume that each node has, at minimum, one arrow pointing to it or one arrow pointing from it.

1. *Source nodes*. These nodes only have arrows coming from them and no arrows pointing to them. In Figure 5, ❶ and ❷ are source nodes. The source nodes infer, but no one infers them.
2. *Sink nodes*. These are nodes that have only incoming arrows. There are no outgoing arrows. One or more oracles infer things about sink nodes, but sink nodes do no inferring themselves. Nodes ❸ and ❾ in Figure 5 are sink nodes. If you follow the flow of arrows in a graph and end up at a sink node, there is no escape. You have to stay there.
3. The third class consists of all nodes that are neither source nodes nor sink nodes.

In a graph that allows no unanswerable questions, an additional oracle can always be added that can make inferences about all the oracles directly. We will call the new oracle the *omniscient oracle*. It will have to be numbered lower than all of the other oracles, so we will assign it the number zero. Figure 6 shows the graph in Figure 5 addended by an omniscient oracle ⓿. The omniscient oracle can make inferences about all other oracles in the universe of agents and oracles without introducing any feedback loops and therefore any unanswerable questions.

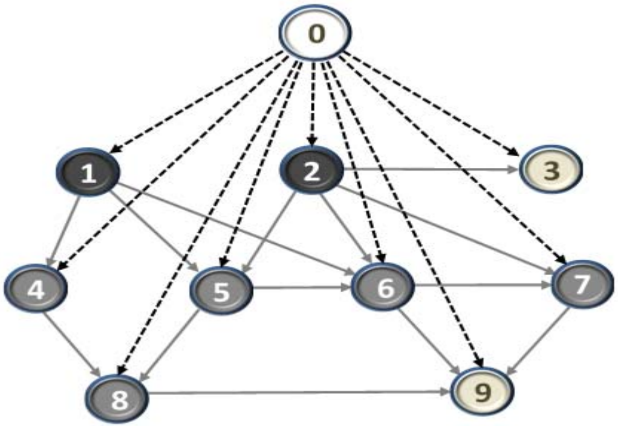

Figure 6

But *there can be only one universally omniscient oracle*. The universally omniscient oracle is always a source node and the only source node in the graph. An additional omniscient inference device can always be added. We can, for example, add a source node numbered (-1) to the graph and draw arrows from it to all of the other nodes. The (-1) node then replaces the ⓿ node as the omniscient inference device. Doing so robs ⓿ the status of a source node. The (-1) node becomes the omniscient oracle and is now the sole source node in the graph.

We can construct an additional node to be omniscient over (-1) and then one omniscient over that. This regress seems silly, however. The Bible indicates that, in the context of our analysis, there is a stopping point and there is an inference device superior to all other oracles who is the "Oracle above all other oracles." Such omniscience about Israel would be characteristic of the "LORD God of gods":

> "The LORD God of gods, he knoweth, …"
> (Joshua 22:22a).

Temporal Omniscience

Omniscience, as we have defined it, can be both spatial and temporal. Thus far, only spatial omniscience has been considered. The graphs of the numbered nodes with arrows, such as in Figure 5, depict a single snapshot in time. The physical inference devices that we dub oracles also exist in the flow of time. Oracles can die and can be born. There is nothing in our development that prohibits the inference graph from changing from time to time. A graph without loops need not even contain an omniscient inference device at some point in time.

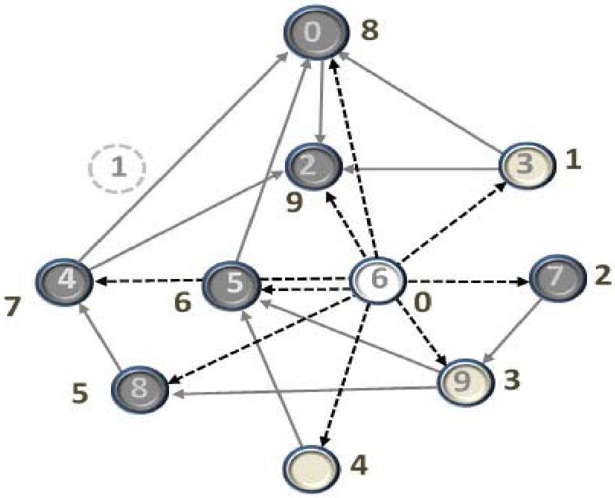

Figure 7

The graph in Figure 6 can, a few minutes later, become the graph in Figure 7. Comparing the two, we see that agent ❶ has died and a new agent numbered **4** has been born. The positions of the remaining agents are the same, but the arrows have changed. Previously, the former node ❻ was not a very exciting node. Now it is the omniscient inference node! It has oversight of all other nodes. The node is still labeled ❻ in Figure 7, but we have written the number **0** beside the circle to show the node's new omniscient status. All of the other nodes also have new numbers written beside them. In the new graph, as before, an arrow emerging from a node can only point to a node with a higher number. This avoids feedback loops and therefore unanswerable questions.

The model of the omniscience thus far presented is a necessary, though not sufficient, model of the universal omniscience of the God of the Bible. In our exercise to describe the characteristics of a universal omniscient God, however, the possibility of temporal shifting of omniscience from one time to the next is troubling. The possibility of losing omniscience for intervals of time is also troubling. We can, though, further sharpen our model and address these concerns through an appeal to biblical references to creation and to the Big Bang as modeled by astrophysics.

Time, like space, is just another dimension. It differs only in the property that it can flow only one way. One can pace back and forth across the floor. One cannot travel back and forth in time. To continue the discussion about temporal omniscience, consider

Figure 8 where our old friend Bob the binary oracle flows through time. We have in the flow of time "Young Bob" in the past and "Old Bob" of the future. What can either infer about the other? The relationship does not seem symmetric. Old Bob, for example, knows what Young Bob said and did in the past. Because of time's unidirectional flow, the converse is not true. We will see, interestingly, the one-way flow of time does not make a difference in avoiding the feedback loops and the corresponding troubling unanswerable questions.

We begin by posing a pair of questions to Young Bob and Old Bob.

Pair #4.

- Question to Young Bob: *Will Old Bob's response be "no"?*
- Question to Old Bob: *Was Young Bob's response "yes"?*

No matter what Young Bob answers, Old Bob is stumped. As is usually the case in unwrapping the paradoxes of self-reference, the analysis at first seems like double talk. Closer inspection reveals that, indeed, Question Pair #4 is an unanswerable strange loop. Here we go.

- o If Young Bob replies, "Yes! I predict Old Bob will say No," then what can Old Bob say to answer the question?
  - ✓ If Old Bob says, "yes," then Young Bob was wrong.
  - ✓ If Old Bob says, "No. Young Bob's response was No (not Yes)," then he is telling an untruth about what Young Bob said.
- o If Young Bob replies, "No! I predict Old Bob will *not* say No (i.e., Old Bob will say Yes)," can Old Bob accurately respond?
  - ✓ If Old Bob says "yes," then he is saying "Young Bob's response was Yes." But Young Bob's response was "no."
  - ✓ If Old Bob says "no," then Young Bob was wrong. Young Bob said that Old Bob would say "yes," but he said "no."

Question Pair #4 is thus unanswerable. Therefore neither foresight nor hindsight can extinguish the possibility of strange feedback loops across time and the possibility of unanswerable questions. As in the spatial case, no feedback loops can exist in time between an oracle and itself. Generalizing, no feedback loops among several oracles in time can exist if we require avoidance of unanswerable questions.

From Question Pair #4 about Young Bob and Old Bob, we see that a feedback loop across time is not permissible. Young Bob can make inferences about Old Bob and Old Bob about Young Bob. But both cannot make an inference about each other simultaneously if we require eradication of the possibility of all unanswerable questions. In other words, feedback loops cannot exist across time. As before, feedback loops can be avoided by lexicographically ordering all inference devices at every point in time and, to avoid feedback, by never allowing a node to point to another node of lower number.

Prohibiting feedback loops across space and time is illustrated in Figure 9. There are nodes illustrated at two points in time: the *past* and the *future*. Each of the nodes is numbered. Some nodes exist in both points of time. Node ❷ in the past is node ❸ in the future. Some agents, such as ❺, die. Others, such as ❻, are born. Inference arrows, even across time, are prohibited from pointing to a node of lower (or equal) number. Node ❷ can make an inference about itself in the future as node ❸. But to avoid a feedback loop, node ❸ is not allowed to simultane-

Figure 8

ously make an inference about node ❷.[16] Likewise, node ❼ is allowed to make an inference about itself in the past when it was node ❽.

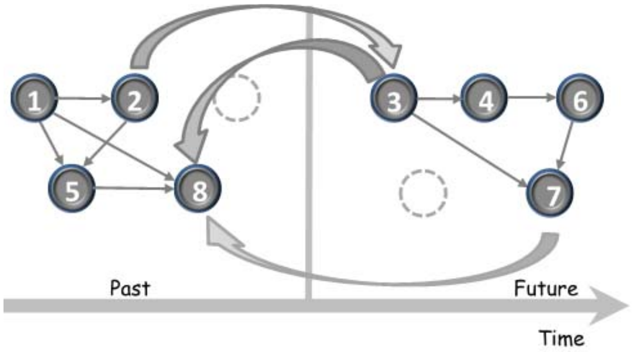

Figure 9

Omniscience across Time and Space

What about omniscience in the flow of time? In the past in Figure 9, node ❶ was universally omniscient for an instant of time. In the future, no node is universally omniscient over all other nodes.

How can there be universal omniscience when inference devices are spread out in both space and time? The key is that the omniscient oracle lies outside of both space and time. Both scripture and cosmology indicate that God lives outside of time and space. Consider the following description of creation from the perspective of the Big Bang.

> It's common to picture the universe before the Big Bang [a]s a large black void empty space. No. This is a flawed image. Before the Big Bang there was *nothing*. A large black void empty space is something. So space must be purged from our visualization. Our next impulse is then, mistakenly, to say, "There was nothing. Then, all of a sudden …" No. That doesn't work either. "All of a sudden" presupposes there was time and modern cosmology says that time in our universe was also created at the Big Bang. The concept of *nothing* must exclude conditions involving time and space. *Nothing* is conceptually difficult because the idea is so divorced from our experience and familiarity zones. [17]

If God created both space and time, he lies outside of space and time or he did. The first words in both Genesis and the Gospel of John are "In the beginning …" Other more explicit supporting verses include

- "the beginning of time'' in John 9:32, AMP; Titus 1:2, NIV; and 2 Timothy 1:9, NIV;
- "from the birth of time'' in Proverbs 8:23, BEB;
- "before time began" in 1 Corinthians 2:7, NIV; and
- "before time was" in Psalm 90:2, BEB.[18]

God's universal omniscient character, therefore, is allowed to exist outside of time and space, and we can fill in an eternal universally omniscient oracle in Figure 9 as shown in Figure 10. The omniscient oracle by necessity exists or has existed outside of time and space. Hugh Ross contends that God exists outside of time, and he explains God's view of time as akin to seeing both the beginning, middle, and end of a movie on a celluloid film reel unwound and laid on the floor.[19] William Lane Craig, on the other hand, argues that God existed outside of time and, after creation, chose to flow with time.[20] Since God's temporal omniscience prior to creation would still be intact after the transition was made, the interpretations of both Ross and Craig are consistent with our model.

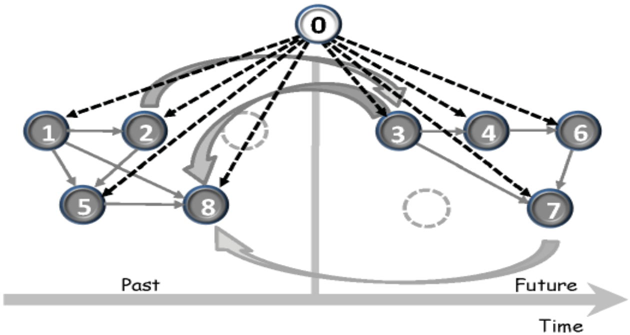

Figure 10

We return to our discussion of Figure 10. As was the case in space only, if the numbering and the labeling of the graph is such that no feedback loops are present, inclusion of the universally omniscient node ⓿ will introduce no feedback loops and the universe of inference devices can never ask any unanswerable questions.

The existence of the omniscient node outside of time and space resolves what initially appears as an unanswerable question not yet addressed. We have seen that an oracle cannot ask itself, "Will you respond 'no' to this question?" Does this strange loop still apply to the omniscient oracle and invalidate the principle of omniscience? No. The question contains an erroneous presupposition. The question assumes a future and therefore the flow of time. There can be no future if there is no time. Because this self-referential prophecy contains a faulty presupposition, it is a faulty question and is therefore disqualified from consideration. The omniscient oracle outside of time and space contains no strange loops and therefore remains consistent.

From Figure 10, we see that there can be, at most, only one universally omniscient oracle. There can be only one omniscient entity, and it will be the only source node in the universe (or multiverse). The characteristic of universal omniscience can therefore be assigned to only one God.

Conclusion

Self-refuting statements are powerful tools to demonstrate the invalidity of flawed propositions. Strange loops that result from such consideration do not exist. By avoiding strange loops in questions proposed by one agent about another, we have argued that there can exist, at most, a single Omniscient Being and that this being must exist by necessity outside of both time and space. This exercise neither proves the existence of God nor refutes atheism. It also does not exclude the possibility of multiple nonomniscient gods. It does, however, demonstrate logical consistency of biblical claims concerning monotheism and timeless omniscience.

Note also that the model does not imply that God is unknowable. In the graphs, arrows representing *some* knowledge of other agents can point in many directions, including to the omniscient being. Arrows representing all-knowing omniscience, however, are more restrictive and indicate that there can be, at most, one omniscient being.

Acknowledgments

The authors are indebted to the reviewers for insightful comments concerning the first draft of the manuscript. We also appreciate the useful comments of George Montañez and Matthew Beauregard on earlier versions of this paper.

Notes

[1] Alfred North Whitehead and Bertrand Russell, *Principia Mathematica*, 3 vols. (Cambridge: Cambridge University Press, 1910, 1912, and 1913).

[2] John Cassidy, "The Most Influential Book Never Read," *New Yorker* 75, no. 13 (May 1999): 32.

[3] Kurt Gödel, "Über formal unentscheidbare Sätze der *Principia Mathematica* und verwandter Systeme, I" [On Formally Undecidable Propositions of *Principia Mathematica* and Related Systems, I] (1931) in Solomon Feferman, ed., *Kurt Gödel Collected Works*, vol. 1 (Oxford: Oxford University Press, 1986), 144–95.

[4] Roger Penrose, *The Emperor's New Mind: Concerning Computers, Minds, and The Laws of Physics* (Oxford: Oxford University Press, 1989).

[5] Douglas R. Hofstadter, *Gödel, Escher, Bach: An Eternal Golden Braid* (New York: Random House, 1979).

[6] Ibid.

[7] Roger N. Shepard, "Circularity in Judgements of Relative Pitch," *Journal of the Acoustical Society of America* 36, no. 12 (1964): 2346–53, doi:10.1121/1.1919362.

[8] J. C. Risset, "Pitch and Rhythm Paradoxes: Comments on 'Auditory Paradox Based on Fractal Waveform,'" *Journal of the Acoustical Society of America* 80, no. 3 (1986): 961–2. Examples of pitch and rhythm strange loops can be heard at http://en.wikipedia.org/wiki/Jean-Claude_Risset.

[9] Penrose, *The Emperor's New Mind.*

[10] G. J. Chaitin, *Conversations with a Mathematician* (New York: Springer-Verlag, 2002).

[11] G. J. Chaitin, *Thinking about Gödel and Turing: Essays on Complexity, 1970–2007* (Singapore: World Scientific Publishing, 2007).

[12] David H. Wolpert, "Physical Limits of Inference," *Physica D: Nonlinear Phenomena* 237, no. 9 (2008): 1257–81.

[13] Ibid.

[14] Whitehead and Russell, *Principia Mathematica,* used a similar hierarchical theory of types to avoid the strange loop arising from Russell's paradox. See, for example, Hofstadter, *Gödel, Escher, Bach.*

[15] Russell D. Reed and R. J. Marks II, *Neural Smithing: Supervised Learning in Feedforward Artificial Neural Networks* (Cambridge, MA: MIT Press, 1999).

[16] Using the word "simultaneously" to describe inferences at two different points in time, although a curious word choice, is clear in the context used.

[17] William A. Dembski and Robert Jackson Marks, "Bernoulli's Principle of Insufficient Reason and Conservation of Information in Computer Search,'' in *Proceedings of the 2009 IEEE International Conference on Systems, Man, and Cybernetics* (San Antonio, TX: Institute of Electrical and Electronics Engineers, 2009), 2647–52.

[18] We will leave the deeper meaning of these verses to study by Bible scholars. A literal interpretation of these passages, though, establishes scriptural and cosmological consistency concerning the creation of time.

[19] Hugh Norman Ross, *The Fingerprint of God: Recent Scientific Discoveries Reveal the Unmistakable Identity of the Creator* (Columbia, TN: Promise Publishing, 1991); and Hugh Ross, *The Creator and the Cosmos: How the Greatest Scientific Discoveries of the Century Reveal God* (Colorado Springs, CO: NavPress, 1993).

[20] William Lane Craig, *Time and Eternity: Exploring God's Relationship to Time* (Wheaton, IL: Crossway, 2001).

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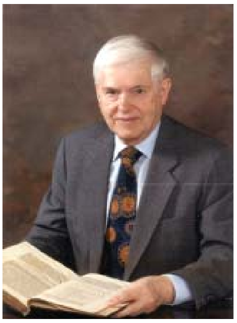
Photo courtesy: Bachrach

Owen Gingerich

Do the Heavens Declare the Glory of God?

Owen Gingerich

Do the heavens declare the glory of God?[1] Does the firmament show forth his handiwork? I am sure this congregation would be shocked if I simply said "yes" and sat down. On the other hand, you would all be even more stunned if I said, "No, the heavens do not declare the glory of God," and sat down. So, I think you can safely deduce that there is something more to be said about the psalmist's ancient declaration.

Back in my office, I have a considerable collection of early astronomy textbooks, mostly small and inexpensively printed. What was then the recent invention of letterpress printing made it possible for university students to have their very own copies of the textbook. This was particularly true at Martin Luther's university in Wittenberg, where the cheap, small textbooks were essentially invented around 1530. So it is inspiring to have a shelfful of astronomy books written by authors who knew Martin Luther personally.

In these books, I have placed my own bookplate, which includes the motto *Coeli enarrant gloriam Dei*—"The heavens are telling the glory of God" (as translated in Haydn's glorious *Creation* oratorio). It is appropriate for my bookplate to be in Latin, since virtually all of the astronomy books from that period are written in Latin.

When those authors looked up at the nighttime sky, they were perceiving a far-different universe than we know today. They saw the moon and the stars that God had ordained. They knew the moon was thirty earth diameters away, actually a pretty good reckoning, and they thought that the sun was twenty times farther and therefore twenty times larger than the moon (since they both have the same apparent size during a total solar eclipse). Actually the sun is four hundred times farther and therefore sixty-four million times larger in volume than the moon.

Hell, deep inside the earth, was no doubt pretty much layered as Dante had described it, and as for hell fire, there was evidence for that any time a volcano erupted. As for heaven itself, it lay just beyond the shell of stars that enclosed the planetary system. It was the "habitacle of the blessed" as the English astronomer Thomas Digges would describe it later in the century. So altogether it was a pretty cozy universe.

When a Wittenberg astronomer looked up at the majestic Milky Way spanning the sky on a clear, dark night, the sight was awesome, indeed glorious, and God was not so far away. His view and his appreciation were not all that different from the ancient Psalmist himself.

Owen Gingerich, *an ASA Fellow and long-time contributor to PSCF, is Professor Emeritus of Astronomy and History of Science at the Harvard-Smithsonian Center for Astrophysics in Cambridge, Massachusetts. In addition to two hundred technical or research articles and three hundred reviews, he has written more than 250 educational, encyclopedia, or popular articles. His role in the science-religion dialogue was well established with the first Dwight Lecture at the University of Pennsylvania, "Let there be Light: Modern Cosmogony and Biblical Creation," later given in forty venues, many under ASA sponsorship. His William Belden Noble Lectures at Harvard's Memorial Church have been published as* God's Universe. *In October 2013 at Gordon College, he gave the Robert Herrmann Lectures, which will be published this September by Harvard University Press under the title* God's Planet, *which will pair with his earlier book. He has given two advent sermons at the National Cathedral, and is an active member of the Mennonite Congregation of Boston.*

I, too, have witnessed the dazzling spangle of the Milky Way from the land of the Psalmist. I vividly remember the vista from a dark setting east of the Dead Sea, where I could almost reach up and pluck a star of my own. And besides the brilliance of the Milky Way, there was a much less common sight, the pyramid of a fainter glow in the west, the so-called zodiacal light, which I recognized as dust grains in the solar system, reflecting the light of the sun. And to the east was the faint fuzzy patch of the Andromeda galaxy, an island universe two million light years away. It was the same sky the Psalmist saw, or Martin Luther saw, but in my twentieth-century understanding, the heavens were far vaster than either of them could have imagined. In both space and time in my mind's eye, my universe was overwhelmingly different from the heavens they saw and envisioned.

It was a long time ago that I was on the West Bank, seeing that star-filled sky, and we then did not know whether the universe stretched to a distant horizon ten billion or twenty billion light years away. Today we would put the horizon 13.7 billion light years away, and with the Hubble Space Telescope, we can record galaxies in their infancy, nearly that old, born of the Big Bang cataclysm that started it all in an inconceivably immense split-second blast of energy. It was an event that Martin Luther's astronomers could barely have imagined. And so, asking the question "Do the heavens declare the glory of God?" today is not the same question *"Enarrantne coeli gloriam Dei?"* that Martin Luther could have considered back in the days of Columbus, Leonardo Da Vinci, or Copernicus.

We are no longer in ecstasy about the beauty of creation, but we are instead crushed down by our insignificance in the vastness of the universe. Rather than Psalm 19, we turn to Psalm 8:3–4a.

> When I consider thy heavens,
>   the work of thy fingers,
> the moon and the stars
>   which thou hast ordained;
> What is man that thou art mindful of him?

Where do we fit in as little specks in such an immense and ancient universe?

More than once I have been asked, "Why does the universe have to be so big and so old?" My answer is that I suppose the almighty Creator could have made the universe in many different ways, and our challenge as scientists is to discern how God did it. The mere fact that we creatures can ask this question tells us that there is some special relationship between ourselves as an intelligent species and the universe itself. Of the millions of species that have been or are now on the earth, we uniquely have the ability to ask this question, of how the universe and we ourselves in it have come to be. The mere fact that such a question can be asked in itself gives us some hint that a creative intelligence lies behind this universe. As Genesis 1:27 says, "God created man in his own image, male and female created he them." That is undoubtedly the most important verse in the whole first chapter of the Bible. God as Creator has endowed us with creativity in his own image, the ability to research, to imagine, to discover many fascinating details about the nature and origin of the universe.

So what is the consequence of a universe being so old? Our universe is made of many different things—atoms, dark matter, and dark energy—and most of these we barely understand apart from their being significant in the large-scale structure of the universe. But we know that we would not be here without atoms, and, in particular, we need oxygen and carbon, the basis of organic chemistry. In the Big Bang, when pure energy was being turned into matter, huge amounts of the simplest atom, hydrogen, were produced. That happened in the first three minutes. But carbon and oxygen were not made, so these and other atoms required for life were lacking. These critical elements came along much later, through nuclear reactions in the hot interiors of evolving giant stars, and they came about much, much more slowly.

Sunday morning is probably not the best time for a lecture on nuclear physics, but there is one detail of the story that is really quite astonishing, the reason there was not any carbon in the initial brew. In principle, elements could be made by sticking the simple hydrogen atoms together and going up the ladder to form heavier and heavier atoms. If basic hydrogen atoms have a mass of one unit, stick two together and you get heavy hydrogen of mass 2, stick another onto that and get mass 3, and another for mass 4, which turns out to be a helium atom, and so on up the ladder to 12, which is a carbon atom. The problem is that mass 5 is not stable. It almost always falls apart in a split second before another hydrogen can be added, so the process simply did not climb the ladder. In those first few minutes, the universe was cooling down so rapidly that the Big Bang was over before the heavier atoms had a chance to be formed.

To get around this obstacle requires lots more time, like billions of years. That is why we need a very old universe, to get the building blocks for life.

In the 1950s, the maverick British astronomer Fred Hoyle made some calculations about how much time it would take to cook up these critical elements in the cores of giant stars, and found that with ordinary structures in the nuclei of carbon and oxygen atoms, ten billion years still would not be enough time to make significant quantities of these important elements. The missing mass 5 was a serious obstacle. But because we do have carbon and oxygen, there had to be something else going on, some undiscovered feature in the structure of the carbon nucleus that raised the probability of its being formed, and Hoyle made a prediction of what it would be. There had to be what is called a resonance at a precise energy level in the carbon atom. Hoyle was at that moment on leave in Pasadena, California, so he went to physicist Willy Fowler, who had access to an atom-smashing accelerator that could probe the nuclear resonance levels. Fowler thought it was kind of crazy that this visiting Englishman believed he could predict the inner structure of the carbon nucleus, but he agreed to try, and there it was. Not only was it there, but at precisely the right energy level. Four percent lower, and there would be essentially no carbon.

Long ago I had heard rumors that nothing had shaken Hoyle's atheism as much as this discovery. From time to time, I had occasion to discuss one thing or another with him, but I never had quite enough nerve to say, "Fred, is it really true that the resonance level in the carbon atom has shaken your atheism? Do you believe that the heavens declare the glory of God?"

But an answer of sorts came when he wrote about his discovery in the Cal Tech alumni magazine as follows:

> Would you not say to yourself, "Some supercalculating intellect must have designed the properties of the carbon atom, otherwise the chance of my finding such an atom through the blind forces of nature would be utterly minuscule." Of course you would … A commonsense interpretation of the facts suggests that a superintellect has monkeyed with physics, as well as with chemistry and biology, and that there are no blind forces worth speaking about in nature. The numbers one calculates from the facts seem to me so overwhelming as to put this conclusion almost beyond question.[2]

That is a truly remarkable quotation, especially considering the fact that Hoyle already had a reputation as a public skeptic. The numbers do give us some pause. If they had only slightly different values, we would not be here. And these are not the only physical settings that are so subtly configured. The British Astronomer Royal, Martin Rees, has written a book entitled *Just Six Numbers*. In it, he points out six numbers that describe our physical world whose precise values are essential for a life-bearing universe. Tweak them only slightly and our universe would be devoid of life. These and other very sensitively set numbers are what we refer to as fine tuning.

We have to be very pleased about this situation, since our existence depends on it. Is the universe declaring something? That makes many of my physicist friends very nervous. They do not like the idea of a supercalculating intellect tinkering with the universe. That would not be natural, the universe would not be entirely subject to physical laws they could discover. It would be *super*natural, and that would be superstitious.

When Isaac Newton described the role of gravity in keeping our moon in tow, the French scientists cried, "Superstitious!" How could the earth affect the moon if nothing was touching it? It was the same when Kepler proposed that the moon controlled the tides. Galileo declared, "I am surprised that the most astute Kepler gives ear to such superstitions."[3]

It does not disturb me that the universe could be designed for life, superstitious as that might be. I must warn you that I am psychologically incapable of believing that the universe is purposeless. I like the analogy that the distinguished physicist John Wheeler proposed. He likened the universe to a giant plant whose purpose was ultimately to bring forth one small, delicate flower. Wheeler suggested that we are that one small flower of the universe, and that our destiny and purpose is to understand the universe. Perhaps the universe is designed to be understandable, and we as human beings are at work trying to understand the universe and its laws. The human brain is the single most complex thing that we know about in the entire universe. What better instrument to contemplate the universe? Ironically, our brains are even complex enough to contemplate the possibility that our brains might not be the most complex things in the universe!

But if our purpose in this universe is to understand God through the majesty of this universe, I have a problem. This opens us to a God of very large numbers. The energy required for the Big Bang is incomprehensibly large. As the physics is calculated back in time, the universe gets hotter and hotter, the elapsed time to the beginning of time itself becomes smaller and smaller, but the number gets huge in its tininess, 10^{-43} second before which the physics no longer works. And the time back to the beginning, nearly 14 billion years, is staggering. If you want to count to just one billion, a number every second, counting day and night, would take you thirty-one years.

A God of very large numbers is impressive, but it is not a God we would choose to worship—a God of incomprehensible majesty, yes. However, trying to understand a God of very large numbers is like a puppy trying to understand Isaac Newton. Is it just wishful thinking when we say that the heavens declare the glory of God?

But wait a minute! A God of such magnificence and wisdom could well have power to limit itself, to wear a mask of himself or herself in order to relate to its creatures. And notice that word "creatures." In itself, it carries the idea of our being created, created creatures who have the power to think—to think theologically, to think inspired thoughts.

If we regard God's world as a site of purpose and intention and accept that we, as contemplative surveyors of the universe, are included in that intention, then the vision is incomplete without a role for divine communication, a place for God both as Creator-Sustainer and as Redeemer, a powerful transcendence that not only can be a *something* but also can take on the mask of a *someone*; a *which* that can connect with us as a *who*. Such communication will be best expressed through personal relationships, through wise voices and prophets in many times and places. The divine communication will carry a moral dimension, only dimly perceived in the grandeur of creation, yet present through the self-limitation of the Creator who has given both natural laws and freedom within its structure. Here, implications for human morality are discernible, for this view implies a self-renunciatory ethic. As Jesus said to Pilate, "My kingdom is not of this world; if my kingdom were of this world, then my followers would fight."[4]

Within the framework of Christianity, Jesus is the supreme example of personal communication from God, an exemplary life of service, of forgiveness, of sacrifice. When the apostle Philip requested, "Show us the Father," Jesus responded, "Anyone who has seen me has seen the Father."[5] When Jesus, hanging on the cross and slowly suffocating, cried out, "My God, my God, why hast thou forsaken me?"[6] the nature of God's self-limited world became excruciatingly clear. God acts within the world, but not always in the ways most obvious to our blinkered vision.

This view of the central message of the biblical story is not closely tied to the heavens declaring the glory of God. Still, I cannot help but remember the thrill I had, as a ten-year-old, when I was able to see the rings of Saturn with a simple telescope my father helped to build, and the excitement of sharing that view with my fourth-grade teacher. Likewise, a year later, when I saw a stunning view of the moon with the 60-inch reflector on Mount Wilson, I had to be impressed with God's glory. But it was not just when I was a kid. Watching the eclipsing moon slowly move across the disk of the sun, and then suddenly, like a light switch turning off the light, the darkness and the eclipsed sun, which you can admire directly without a dark filter, like a sparkling jeweled ring on black velvet—it is enough to raise the pulse even of a skeptic.

We know that we are living at a very special time in the history of the universe, when apparent size of the moon just covers the sun. In the far future, it will not be like this, but, for now, it is one of the most breathtaking views from or on our planet. Yet I doubt that this is enough to sway a skeptic. And perhaps that is how it should be. There is a telling passage in First Kings:

> And, behold, the Lord passed by, and a great and strong wind rent the mountains, and brake in pieces the rocks before the Lord; but the Lord was not in the wind: and after the wind an earthquake; but the Lord was not in the earthquake: And after the earthquake a fire; but the Lord was not in the fire: and after the fire a still small voice.[7]

The message is in a still, small voice, God's inspiration, literally the bringing in of the spirit. The glory of the heavens does not knock the skeptic from his perch. It is in the eye of the beholder. For me, the glory of the heavens inspires me to understand the handiwork of the Lord. However, it does not work for everyone.

But let me quote from Fred Hoyle, a public skeptic, in a little-known passage made toward the end of his life:

> The issue of whether the universe is purposive is an ultimate question that is at the back of everybody's mind … And Dr. Anshen has now just raised exactly the same question as to whether the universe is a product of thought. And I have to say that that is also my personal opinion, but I cannot back it up by too much of precise argument. There are very many aspects of the universe where you either have to say there have been monstrous coincidences, which there might have been, or, alternatively, there is a purposive scenario to which the universe conforms.[8]

As I said earlier, I am psychologically incapable of believing the universe is purposeless. So, unlike Fred Hoyle, I am not sitting on the fence. Let me simply say that the sheer beauty of the heavens declares the glory of God! ❧

Notes

[1] A sermon given by Owen Gingerich at the First United Methodist Church in Henderson, Kentucky, on April 21, 2013.

[2] Fred Hoyle, "The Universe: Past and Present Reflections," *Engineering and Science* 45, no. 2 (November 1981): 8–12, esp. 12.

[3] Paraphrased translation from Galileo Galilei, *Dialogo … sopra i due massimi sistemi del mondo* (Florence, 1632), 456.

[4] John 18:36.

[5] John 14:8, 9.

[6] Matt. 27:46.

[7] 1 Kings 19:11–12.

[8] Fred Hoyle, *The Origin of the Universe and the Origin of Religion* (Wakefield, RI: Moyer Bell, 1993), 83.

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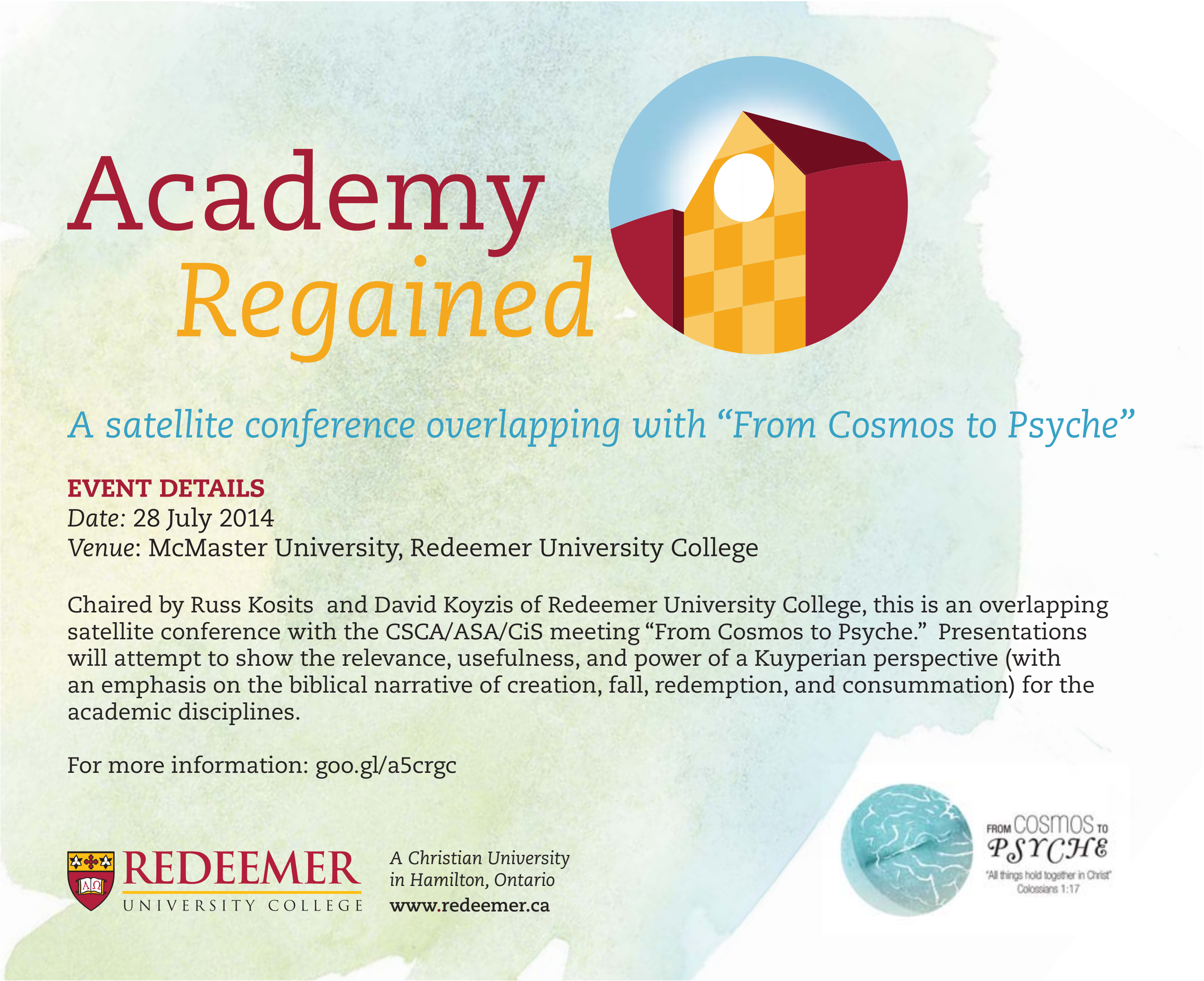

GENERAL SCIENCES

WEIRD LIFE: The Search for Life That Is Very, Very Different from Our Own by David Toomey. New York: W.W. Norton and Company, 2013. 221 pages, endnotes, works cited, index. Hardcover; $25.95. ISBN: 9780393071580.

Weird Life by David Toomey is a wide-ranging exploration of what defines life as we know it and as we don't know it. Life as we don't know it is "weird" by Toomey's definition, and he takes the reader on a fascinating journey starting with extreme environments on Earth as studied by microbiologists and ending with mind-bending multiverses as theorized by astrophysicists. In between the two extremes, Toomey treats the reader to some history of science, the basic chemistry of life, possible alternatives to life as we know it, artificial intelligence, quantum mechanics, and a comprehensive look at life as portrayed in science fiction. His speculations are well researched, and he manages to ask some fundamental questions about the nature of life along the way. By delighting his audience with life at the extremes, Toomey leads the reader to ponder about all of God's creations, not just those normally within our thoughts.

Toomey sets the groundwork for his discussion of "weirdness" by outlining the parameters defining the carbon-based, water soluble life that we find on Earth. He makes the process easy by introducing the reader to the biologists who have studied life on earth in extreme environments (hot, under pressure at the bottom of the ocean, or both). He gives the reader enough historical background to understand how revolutionary the discoveries of life at the extremes were in their time. To keep his narrative dynamic and exciting, Toomey jumps from the present to 1977 to 1922 to 1830 to 1957 to 1964 and back to the present. Rather than simply presenting dry facts, he puts the information in interesting context and introduces the scientists in a personal fashion as he makes the case for weird life on Earth.

Since Toomey's weirdness is "life that is very, very different than our own," he next sets out to define what chemistries are essential to our life so that he can explore the possibilities of life based on alternative life chemistries. We learn about solvents, stability, and substitutions in the macromolecules that make up not only familiar life but also what we might encounter in weird life. Perhaps, he opines, the accidental chirality of our macromolecules "set the stage" for life as we know it, and alternate forms of life could easily exist.

Throughout the book, readers are asked whether we would recognize weird life if we encountered it, describing in great detail vignettes from over more than 50 years of NASA's experiments and explorations from Viking to Voyager to SETI. His thesis is that weird life is not likely to be the English-speaking stranger from science fiction, but rather more likely either some rudimentary life form based on an alternate chemistry or sophisticated machinery left by a long-gone society.

Given that some of his speculations sound like science fiction, Toomey acknowledges and embraces this, sprinkling science fiction references throughout the book and devoting an entire chapter to how various authors' imaginations have shaped our view of hypothetical life. Even nonscience fiction buffs will enjoy his witty analysis of the life forms dreamed up by literary giants and should appreciate the science on which these fictional characters are (or are not) based.

The latter part of Toomey's book is devoted to quantum mechanics and the multiverse, subjects a bit less accessible to most biologists. He explains them in a straightforward way, interweaving the science with personal stories in an interesting manner. Toomey is of the opinion that it is the astrophysicists, those who don't really know as much about life here on Earth, who can best imagine alternatives to life as we know it, weird life.

Weird Life is well researched, well documented, and compelling to read. By exploring all of God's creation, it can start a conversation on the creation mandate, humanity's call to care for all creation. It is a synthesis of scientific reporting and speculation that draws the reader in with its clear conversational style. I highly recommend this book to high school students, college students, grown-ups, and anyone interested in science.

Reviewed by Monica Lee Tischler, Professor of Biology, Benedictine University, Lisle, IL 60532.

THE FOREST UNSEEN: A Year's Watch in Nature by David George Haskell. New York: Viking, 2012. 288 pages, bibliographical references, and index. Paperback; $16.00. ISBN: 9780143122944.

In his first book, *The Forest Unseen*, David Haskell begins every chapter in exactly the same spot, but takes you on a flight with his words. The entire "story," as it were, takes place in a mandala-sized patch of old-growth forest in Tennessee. But during each of his regular visits to the mandala—three or four recorded dates each month for a year—he looks anew at this space. He sees not only what is before him, but also reaches out across space and time to make connections to everything from the strands of fungi in the soil to the fungi in the gut of a ruminating deer, from bees visiting flowers in the early spring to the migrating birds visiting in the fall.

Reading this award-winning text (finalist for the 2013 Pulitzer Prize in General Nonfiction, winner of the 2013 Reed Environmental Writing Award, winner of the 2012 National Outdoor Book Award for Natural History Literature), you will be transported from the central US into the past, when giant ground sloths and woodland musk oxen grazed in the forest, then to the present, where you will view the forest from the viewpoint of a bee or a caterpillar or a maple tree or even a shrew (at which point Haskell reminds us that the earliest mammals on Earth were shrew-like, drawing connections to our own everyday existence in a jest). You will get caught up in Haskell's creeping and crawling on the forest floor, getting closer looks at tiny mosses, fragile spring flowers, and the "bestiary" in the soil. You will worry as you read about his short experiment with experiencing the January cold as animals do (minus a coat and boots, and, well, more than enough to worry an empathic reader) or as he mentions, briefly, a trip to the hospital where he receives aspirin (derived from the bark of willow trees and meadowsweet leaves) and digitalis (derived from the leaves of foxglove) that leave him looking around at the forest and noticing the potential for pharmacology therein.

The Forest Unseen is arranged in forty-three chapters, each with a date (from January 1 to December 31) and a one- or few-word title that gives a good clue about the focus: Salamander is on February 28, Chainsaw on April 2 (spoiler: fortunately, found in the golf course that looks over the forest, and not the forest itself), and Sharp-shinned Hawk for November 15. Each chapter is under ten pages long, making this an easy book to read in pieces. In fact, one or two short chapters at a time may be the best way to approach *The Forest Unseen*, as Haskell fills the pages with enough natural history and ideas to make it well worth taking time to consider them before moving on to the next section.

The text includes a bibliography that is not meant to be exhaustive but will allow readers to find more information on any topic they find interesting. Many of the entries are scientific journal articles, but there are books and textbooks and even literary references, indicative of the breadth of the ideas in this book. Citations are not included in the text itself; this seems appropriate, as the writing is more contemplative than technical in most places.

Like Thoreau or Muir or other master nature writers, Haskell will take you into the forest and show you the world that is hidden there, just beyond your view. Anyone interested in the natural world will find jewels in this worthy and well-written book. Just be sure to make time to go outside after you've read it, so that you can experience the world in your backyard anew.

Reviewed by Cheryl Heinz, Associate Professor of Biological Sciences, Benedictine University, Lisle, IL 60532.

HISTORY OF SCIENCE

THE LIFE OF DAVID LACK: Father of Evolutionary Ecology by Ted R. Anderson. New York: Oxford University Press, 2013. x + 246 pages, index. Hardcover; $59.00. ISBN: 9780199922642.

Reviewing a *festschrift* for the Oxford University entomologist E. B. Ford, Harvard geneticist Dick Lewontin notoriously wrote that many British scientists come "from the fascination with birds and gardens, butterflies and snails which was characteristic of the prewar upper middle class." David Lack could have been the sort of person Lewontin had in mind. Born in 1910 to a London surgeon and the daughter of an Indian Army officer, he was educated at a private school and at Cambridge University. There is no doubt that he had a fascination with birds from an early age. He wrote three ornithological papers in the year he went to university to read zoology. During and after completing his undergraduate degree in 1933, he took part in several ornithological expeditions; he became a schoolmaster; he next enjoyed a career-changing four months on the Galapagos Islands in 1938–1939, writing a much-quoted book on *Darwin's Finches* from his work there. After military service, he became Director of the Edward Grey Institute of Field Ornithology in Oxford in 1945, remaining in that post until his premature death from lymphoma at the age of 62.

Lack's biography has been written by Ted Anderson, himself a distinguished ornithologist. It is a very readable account of a family man with limited social skills who made some of the most significant discoveries about natural populations of animals in the twentieth century, particularly the factors affecting reproduction rates, based on his extensive studies and knowledge of birds in many parts of the world. (His last—posthumous—book was *Island Biology Illustrated by the Land Birds of Jamaica*, prompted by Lack's skepticism about some of the conclusions of MacArthur and Wilson's *Theory of Island Biogeography*.) Anderson's work is structured around the thirteen books authored by Lack.

The reason that David Lack is relevant for readers of *PSCF* is that one of the thirteen books was *Evolutionary Theory and Christian Belief*, published in 1957. Lack was raised in a nominally Christian home, but he enjoyed singing and regularly attended chapel in his Cambridge college. However, he claimed to be an agnostic until 1948, when Armstrong records that he was converted under the influence of friends from his school-teaching days. He was confirmed in the Church of England in 1949. Anderson does not tell us much about the details or development of Lack's faith, but he must have been known as a Christian because, in 1953, he was invited to contribute to a lecture series on "Theology and the Future of Science." Encouraged by Nobel Laureate Peter Medawar, he expanded his lecture into *Evolutionary Theory and Christian Belief*.

Lack was conscious of his loneliness as both a Christian and an evolutionary biologist and was nervous about the reception of the book. In its preface, he records that he sent his manuscript to no fewer than nine friends, "Roman Catholic, Anglican, Quaker, and agnostic, biologist, philosopher, priest and layman." His Royal Society obituarist, W. H. Thorpe, a Gifford Lecturer, pioneer ethologist, and Quaker (and one of Lack's nine friends), wrote that I "discussed [the book] extensively with him since I am one of a considerable number of biologists who are convinced that religion and science (especially biology) can and must be brought together in one harmonious scheme of thought." Thorpe continued, "David ... seemed somehow able to embrace simultaneously both evolutionary theory and a conservative and somewhat limiting interpretation of what he regarded as orthodox Christianity."

Lack's book is a key building block in the modern phase of the Christianity and evolution debate, a debate which still rumbles on more than half a century later. Its significance is that it was probably the first account of the debate from a scientist of his calibre and concentrates on scientific rather than sociological questions. Thorpe notes that "there is no doubt that the work served a valuable function in clearing the air and bringing what some feel to be basic differences into broad daylight." Lack's own conclusion is worth repeating:

> All should accept the findings of science … On the other hand, it is important that the claims made by scientists in the name of science should relate to genuinely scientific matters, and that when they really refer to philosophical problems, those should be made clear. In particular the claim that man has evolved wholly by natural means is philosophical and not scientific.

Anderson suggests that Lack "seemed to hold a dualist view, accepting the fundamental contradictions between the conceptions of man inherent in evolutionary biology and in Christianity, but asserting that both have great value in our attempts to understand our lives and our place in the universe" (p. 126). Many still wrestle with the same dualism.

Lack produced a second edition of his book in 1961, reporting on new findings of fossil hominids and reacting (unfavorably) to Teilhard de Chardin's *Phenomenon of Man*. He returned to the question of human nature in the context of T. H. Huxley's views in a volume of collected essays (*Enjoying Ornithology*) published in 1965, but died before publishing any development of his ideas. There is much one would like to know. Was Lack influenced by the mathematician Charles Coulson, an Oxford colleague and contributor with Lack to the "Theology and the Future of Science" series? Coulson was well known at the time as the author of several influential works (*Christianity in an Age of Science*, 1953; *Science and Christian Belief*, 1955; *Science, Technology and the Christian*, 1960). Anderson tells us that Lack had "difficulties in understanding the place of miracles in a scientifically informed world view." How did he regard the Resurrection, the supreme miracle?

Anderson has written an entertaining and informative account of one of the leading biologists of the twentieth century; it will undoubtedly be read widely by ornithologists and animal ecologists whose science was significantly influenced by the middle-class Englishman who was fascinated by birds. The biography is not an analysis of the beliefs of that biologist, but Lack's faith was obviously important to him and is clearly proclaimed in the book. We should all be encouraged that such a man was an unashamed Christian.

Reviewed by R. J. (Sam) Berry, University College, London WC1E 6BT, UK.

MEDICINE

THE HEALING GODS: Complementary and Alternative Medicine in Christian America by Candy Gunther Brown. New York: Oxford University Press, 2013. xii + 336 pages. Hardcover; $29.95. ISBN: 9780199985784.

This book has been published at the right juncture in time as people in the United States debate upcoming changes in national healthcare policy. Complementary and alternative medicine (CAM) has emerged as a prevalent alternative treatment option for many individuals. In 2007, the National Health Interview Survey from the National Institutes of Health found that 38% of adults and 12% of children in the United States used some form of CAM.[1] The high prevalence of CAM use suggests that we need to define more adequately what major CAM categories exist in the United States, especially in regard to clinical efficacy (or lack of), and what background framing such techniques (including spiritual concepts) is involved. Brown's book, *The Healing Gods*, appears to fit the bill.

The book is organized into eight chapters followed by a lengthy conclusion. One of the main aspects of the book is a concentration on the rather recent incorporation of CAM into the culture of evangelical Christianity. In particular, many of the metaphysical aspects of CAM that come from other religions (such as Hinduism) have been co-opted by Christians. The book begins by discussing the potential religious connotations of CAM. Brown rightly points out that many practitioners of CAM define its use as spiritual, as opposed to religious, in order to provide a marketing basis for Christians. CAM practitioners also can describe what they do as scientific, as opposed to religious, in order to appeal to non-Christian entities such as hospitals.

Yoga, in particular, is reviewed extensively as an example of how CAM practices can be co-opted by Christians. The history of yoga is described in very good detail as an expression of Hinduism that started as early as 800 BCE. A significant debate exists in evangelical Christian circles as to whether yoga should be practiced, due to its non-Christian historical roots. The book provides a good discussion regarding the controversy of using yoga, including Pilates, in the Christian community. Brown then continues to give an objective discussion of the pros and cons of Christian CAM use. As I read through this section, I felt the book provided a good understanding of the concerns expressed by Christian leaders regarding CAM. As an example, one issue concerning which Christian churches and leaders express consternation is a "… lack of scientific evidence that CAM is effective or works through scientifically plausible mechanisms" (p. 75).

Other important chapters discuss specific subjects, including chiropractic (chap. 4), acupuncture (chap. 6), and energy medicine (chap. 8). As a physician, I found these chapters to be most helpful since patients will often advocate for these specific CAM uses in conjunction with standard medical care. Healthcare providers should know how these ideas are being utilized. Again, it is made clear in these chapters that such concepts do not have a Christian origin. For example, chiropractic founders such as B. J. Palmer proposed that this form of CAM is a form of religion that is separate from Christianity. I was happy to see Brown point out that up to fifty percent of chiropractors do not accept vaccinations as valid. It should be made quite clear that the anti-vaccination line of thinking is extremely dangerous. In a similar manner, Brown reviews energy medicine techniques, such as Reiki and therapeutic touch, which also have non-Christian origins and have been marketed to be, at various times, Christian or part of mainstream medicine.

Brown is effective in explaining why CAM continues to have pervasive use despite the practice of evidence-based medicine, which has led modern medical advances over the past 100 years (chap. 5). She discusses in appropriate detail concepts that non-medically trained people should be aware of, including defining Cochrane reviews, reviewing aspects of a good clinical trial, and describing what makes an appropriate journal publication. However, the best part of the book is the thirty-page conclusion entitled "Why Does It Matter If CAM Is Religious (and Not Christian)—Even If It Works?" This section alone is worth the book's price. Significant discussion is spent on informed consent, the lack of disclosure by some CAM providers about care that might go against a patient's belief system, and the very real concern that engaging in certain CAM practices may lead to changing a patient's religious belief system without providing appropriate informed consent.

The use of CAM by medical providers and hospital systems is a tricky issue. Unlike standard medical care, there is often a lack of standardization and research to back up the success claims offered by some CAM providers. For example, herbal supplements sold in North America have been shown to have poor quality control and high rates of contamination.[2] However, patients may prefer to have certain CAM aspects available for their outpatient and inpatient care, and medical models continue to be developed to bring such therapy to hospital-based care.[3] The only criticism of this book is that more information should have been made available regarding the unscientific and unethical anti-vaccination theories that have been propagated by some CAM providers. Indeed, a large percentage of unvaccinated Americans have "philosophical objections" to vaccination, which include some church groups who have strong anti-vaccination beliefs.[4] I am hopeful that future editions of this book can include a discussion of this important issue.

I highly recommend this book to medical providers who wish to know what aspects of CAM are used by their patients, and to individuals with no medical training who are considering CAM as part of their medical regimen.

Notes

[1] P. M. Barnes, B. Bloom, and R. L. Nahin, "Complementary and Alternative Medicine Use among Adults and Children: United States, 2007," *Natl Health Stat Report* 12 (2008): 1–23.

[2] S. G. Newmaster et al., "DNA Barcoding Detects Contamination and Substitution in North American Herbal Products," *BMC Med* 11 (2013): 222.

[3] L. Knutson et al., "Development of a Hospital-Based Integrative Healthcare Program," *J Nurs Adm* 43 (2013): 101–7.

[4] *Los Angeles Times*, http://articles.latimes.com/2013/sep/12/science/la-sci-sn-cdc-measles-vaccines-20130912.

Reviewed by John F. Pohl, MD, Professor of Pediatrics, University of Utah, Salt Lake City, UT 84113.

ORIGINS & COSMOLOGY

THE THREE FAILURES OF CREATIONISM: Logic, Rhetoric and Science by Walter M. Fitch. Berkeley, CA: University of California Press, 2012. 194 pages, index. Paperback; $26.95. ISBN: 9780520270534.

Walter Fitch was a professor of ecology and evolutionary biology at University of California, Irvine until his death in 2011, shortly before the publication of this concise book. The author describes his target audience as advanced high school or early college students, "who have no irrevocable position on at least some of the differences of opinion between creationists and evolutionists," and who are presumably Christians. The title of the book is therefore appropriate in that the target audience is made up of those who would be intrigued by it rather than those who would be offended.

Fitch's identification with materialistic methods and evolutionary theory and his belief that opposition to them is illogical is clear throughout. Those who are not particularly interested in logic as the ultimate authority on this matter likely will not find his arguments compelling. I believe he is mostly successful at pitching his content at the target level throughout the book. Extensive science background on the reader's part is not necessary, though acquaintance with genetics and fossil basics will be helpful.

The book comprises 150 pages of text divided into four chapters: (1) an introduction to logic and rhetoric; (2) "the basics"—categories of knowledge and belief; (3) math and statistics relevant to genetics, dating and other methods used in scientific study of genetics and fossils; (4) arguments put forth by young earth creationists (YEC) for their position and against evolutionary biology. The chapters are further divided into as many as twenty sections of varying lengths, an organizational style that gives the book an unwieldy feel, like an outline of a book rather than of a fully realized work. These lists of ideas, especially in the final two chapters, cover a large amount of ground, some of it rather shallowly with few references. The interested reader/student might therefore use this book as a jumping-off point for further research, rather than using it as the final word on any given subject. The end matter includes a generous glossary for those unfamiliar with the genetics terminology presented, references, and an index.

The first two chapters set the stage by presenting the logical framework and definition of terms the author will use throughout the book to meet his goal as stated at the beginning of the first chapter:

> to establish what science is and how biological evolution is a scientific study … even if Darwinian evolution itself should be proven wrong. In contrast, creationism, intelligent design, and irreducible complexity are not scientific, even if their conclusions … were shown to be all correct. (p. 2)

Chapter one is an introduction to logical methods and logical fallacies, and the author uses this framework to explain several arguments used by YEC advocates against biological evolution in this and subsequent chapters. While this chapter can be a bit tedious for the casual reader, it is essential to the author's purpose and is a unique aspect of this book. Examples are presented, and the writing is clear and easy to understand.

In chapter two, a great variety of terms are defined, again as groundwork for later chapters: seven ways of knowing, four mutually exclusive areas of knowledge, types of creationist beliefs, a definition of science, definitions of the terms "definitions," "facts," and "theory," and finally an explanation of why biological evolution should be understood to be a "fact." Most of these sections include a discussion of common issues between creationists and evolutionists (logical issues with social Darwinism, what creationists and evolutionists mean when they refer to evolution as a "theory," etc.).

Chapter three, entitled "Some Simple Math and Statistics," presents the way scientists see the age of the earth and how it came to be populated with species. Sections on the scientific method, methods of dating fossils and the earth itself, the gaps in the fossil record, and natural selection are presented from a naturalistic point of view, and occasionally points on which this view differs from YEC arguments are also discussed. The author is more at home with the materialist side of the arguments, and aims only to illustrate that YEC arguments are unscientific. Discussions of these points of contention may not be convincing or satisfying for readers who take issue with the accuracy of the methods presented or do not believe that scientific reasoning is the highest standard of truth. Fitch uses Occam's razor liberally as the arbiter of truth in illustrating how data and statistics should be interpreted by scientists. How young earth creationists might incorporate such science into their worldview alongside their faith is not discussed. Students will emerge from this chapter, however, with a better understanding of what "truth" means to a scientist, and the ever-present statistical uncertainty that necessarily remains in the interpretation of any given set of data.

In the final chapter, Fitch presents a long list of YEC arguments both for their beliefs and against evolution. The author rebuts several of these, including literal interpretation of Genesis 1 and 2, intelligent design, irreducible complexity, and gaps in the fossil record. It is here that the primary goal of the book, to show that creationism is unscientific, is achieved. Students who are curious about what a scientist thinks about creationist beliefs will find ideas that they can explore further. The tone of the writing is mostly even-handed, but the arguments may still be difficult for a nonscientist who has strong creationist beliefs to swallow. However, the author believes that even such Christians should at least consider these questions: the epilogue is a quotation from St. Augustine's *The Literal Meaning of Genesis* in which the great bishop suggests that Christians would do well to refrain from talking nonsensically about science to nonbelievers who know it well, as this may convince those nonbelievers that the Bible itself is likewise untrustworthy. While it is unclear whether the author is himself a Christian, I believe he does a good job of attempting to come alongside the Christian reader.

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RELIGION & SCIENCE

GOD IN PROOF: The Story of a Search from the Ancients to the Internet by Nathan Schneider. Berkeley, CA: University of California Press, 2013. 272 pages. Hardcover; $34.95. ISBN: 9780520269071.

> I think there is no suffering greater than what is caused by the doubts of those who want to believe … A faith that just accepts is a child's faith and all right for children, but eventually you have to grow religiously as every other way, though some never do … It is much harder to believe than not to believe. If you feel you can't believe, you must at least do this: keep an open mind. Keep it open toward faith, keep wanting it, keep asking for it, and leave the rest to God. (Flannery O'Connor, *The Habit of Being: Letters of Flannery O'Connor*)

God in Proof is a fascinating book about that experience of doubting, wanting to believe, wanting not to believe, believing, and not believing. Specifically, it is an historical survey of the search for proofs of God's existence, but such a description by itself might make the book sound like an academic yawner, good only for those studying historical apologetics or the philosophy of religion. It is anything but. Schneider is a very young journalist (only twenty-nine at time of publication), editor at KillingTheBuddha.com and WagingNonviolence.org, author of articles on faith and culture in popular magazines and of *Thank You, Anarchy: Notes from the Occupy Apocalypse* (published only three months after this book by the same press). That kind of résumé might lead one to the opposite conclusion—that, instead of being an academic yawner, the book is a shallow and trivial treatment of a longstanding and complex topic. Again, it is anything but.

What Schneider has produced is better than either of those options. First, the book is erudite; he is remarkably well acquainted with the topic, from the writings of the ancient Greeks to the arguments of medieval Arab philosophers, from the skeptics of the Enlightenment era to the champions of a vigorous theism among twenty-first-century evangelicalism. At times the book reads like a collection of conversations from late-night talk shows, as he brings one thinker after another to the forefront and gently, respectfully engages their ideas before moving on. When he discusses contemporary thinkers, he is more than likely to include personal details—what they were wearing when he interviewed them, what they say about each other, what they like to eat or drink when talking philosophy, religion, or both.

One puts the book down with a sense of the personality of William Lane Craig or Richard Dawkins, not just their ideas.

But the personality that pervades the entire text is the author's own. And this is what turns a good book into an absorbing and compelling tale of personal faith, for Schneider intersperses his historical narrative with the story of his own faith journey, including his conversion to Catholicism and his continuing, lingering questions even as a person of faith. The autobiographical content is, like the historical narrative, respectful of the reader. Schneider's approach strays from the self-indulgent; these are not Facebook posts of "why I believe and you must also." There seems to be little in the way of overt agenda; the book is not written to convince anyone of belief or unbelief. If anything, the intent may be to assist those who have drawn battle lines on this issue to understand each other better, to regard each other with more generosity of spirit and to offer each other more hospitality in the debate over ideas.

The book has its oddities. The slightly off-beat index at the back of the book (arranged chronologically, not alphabetically) lists nearly one hundred individuals who have "proffered proofs about the existence of God" and who are discussed in the book (complete with page numbers). It is an impressive and eclectic list that includes Plato, Ibn Rushd, Maimonides, Aquinas, Spinoza, Pascal, Voltaire, Hume, Kierkegaard, Kurt Gödel, Bertrand Russell, C. S. Lewis, Henry Morris, Alvin Plantinga, Richard Swinburne, John Polkinghorne, William Dembski, Richard Dawkins, William Lane Craig, Bill O'Reilly, and Kirk Cameron, among others. Inexplicably missing, however, are several significant individuals familiar to readers of *PSCF*, such as Francis Collins (former head of the Human Genome Project), Owen Gingerich (former professor of astronomy at Harvard) and even Alister McGrath (scientist, turned noted theologian).

He redeems these absences with a very handy "table of proofs" for and against the existence of God, divided into eight categories (cosmological, dialectical, historical, ontological, phenomenological, sociological, teleological, and transcendental), each with its own subset (e.g., teleological includes "from fine tuning," "from intelligent design," "from language," "from providence," and "from unintelligent design"), and each subsection includes a brief summary and the relevant page numbers from the text. It is both handy and helpful.

After discussing mostly ideas for 230 pages, Schneider closes the book by reminding us that this topic is about more than that in the end. Ultimately, there is a deep mystery at work whenever one attempts to know about God, much less know God, and it is obvious that Schneider's faith is not merely intellectual assent to the idea of God. He has what Michael Polanyi called "personal knowledge." He has had experience with this deep mystery, and there is a knowing in such experience that can be understood only by others who have gone there themselves. Schneider thus concludes by offering his own proof, or something less than a proof but perhaps the best that can be done by finite, imperfect humans contemplating Infinite Perfection—that knowing God is a special kind of sight, a gift even. "The proofs can be explained and taught and respected from a distance, yet there still remains the fact that you either grok it or you don't, and that's that" (p. 229). And that is not terribly far removed from the admonition given by Flannery O'Connor: "Keep asking for it, and leave the rest to God."

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SCIENCE & BIBLICAL STUDIES

READING GENESIS 1–2: An Evangelical Conversation by J. Daryl Charles, ed. Peabody, MA: Hendrickson, 2013. xxi + 240, with scripture index. Paperback; $24.95. ISBN: 9781598568882.

Origins questions continue to generate controversy today, particularly among conservative evangelical Christians. Unfortunately, an adequate understanding of the interpretive issues involved in reading the early chapters of Genesis rarely informs popular debates. Reading *Genesis 1–2: An Evangelical Conversation* brings careful, deeply informed, and leading biblical scholarship to bear on identifying and analyzing such issues, and is thus a welcome contribution.

The book presents five views on interpreting Genesis 1–2, each of which receives a chapter-length treatment written by a representative Old Testament scholar followed by brief (typically 2–4 pages) critical responses from the other four scholars.

Richard A. Averbeck presents the first view, which he calls the "literary day, inter-textual, and contextual reading." His view is "literary" because it seeks to pay close attention to literary features such as grammar, genre, and discourse; it is "inter-textual" because it seeks to read the creation account in light of the entire canon (he devotes considerable space to reading Psalm 104 and the days of Genesis 1 in light of each other); and it is "contextual" because it seeks to account for the ancient near eastern (ANE) historical context within and against which God spoke. Averbeck's overarching view is that Genesis 1–2 describes the actual creation of the cosmos *expressed analogically*. Genesis 1 focuses on the universe as a whole and describes the creation of its parts phenomenologically in terms that ancient people could observe and understand. Its purpose is to teach the people of Israel to understand their lives as framed by the God who created and ordered the world. Genesis 2 then provides a more standard literary narrative which, unlike Genesis 1, contains recognizable historical markers (e.g., the Tigris and Euphrates rivers; Adam and Eve as historical individuals).

The second view is a "literal approach" endorsed by Todd S. Beall, which interprets Genesis 1–2 as a historical account of God creating the world in six literal twenty-four-hour days. Beall argues, first, that we should not use two different hermeneutics for reading Genesis (chaps. 1–11 vs. chaps. 12–50), but employ one hermeneutic consistently (he does not recognize that one consistent hermeneutic can identify various forms of literature in Genesis). Second, we should not separate the first two chapters of Genesis; both are narrative accounts, not poetry (the respondents point out that narratives can be fictional yet true, e.g., parables). Third, Genesis 1 does not represent an ANE worldview and admitting otherwise would compromise the uniqueness of scripture as God's Word. Fourth, the New Testament writers refer to Genesis as a literal account of actual history. Finally, nonliteral views are motivated by a desire to capitulate to modern scientific theories. Beall fears that figurative approaches initiate a slippery slope of reinterpreting the Bible in light of modern biases.

The third view, presented by C. John Collins, seeks to read Genesis 1–2 "with the grain" and accordingly treats the six days of creation as *analogical days*. Collins reads Genesis 1–11 as "prehistory," which involves recognizing historical features of the text but "without undue literalism." Genesis 1:1–2:3 forms a preface to the book written as "exalted prose narrative." Its chief (but not sole) observation is that GOD made us all! Specifically, God made all things: (a) from nothing; (b) by the word of his power; (c) in the space of "six days" (representing the pattern of a human work week); (d) very good; (e) so that creation bears God's imprint; and (f) as the right kind of place in which we live out our story as human beings and as God's people. Collins argues that we should read Genesis 1–2 together and presents evidence that the two accounts are coherently linked (citing the immediate context, rabbinic tradition, and the broader biblical canon).

In his chapter, entitled "What Genesis 1–2 Teaches (and What It Doesn't)," Tremper Longman III offers the view that "the main purpose of Genesis 1–2 is to proclaim in the midst of contemporary counterclaims that Yahweh the God of Israel was the creator of everything and everyone." Further, the Bible does not intend to explain *how* God created the cosmos or human beings (the Old Testament presents multiple, differing descriptions of creation). Longman suggests that Genesis 1–2 is "theological history" written as "high style literary prose narrative." For example, it teaches that the Lord of Israel is the GOD who created all things; that God is other than, yet involved with, creation; and that human beings are a part of creation, yet also have a special relationship with God and serve as God's representatives. Longman also offers very helpful theological reflections on the relationship between science and exegesis, the doctrines of the perspicuity and sufficiency of scripture, and how to interpret Adam and Eve in light of modern science (biblical inerrancy does not require the affirmation of a historical Adam).

John H. Walton presents the fifth and final view, which reads Genesis 1 as ancient cosmology. He begins with some comments about what it means to read the Bible competently, ethically, and virtuously. He then proceeds with his thesis that Genesis, being an ANE text sharing an ANE cosmological worldview, should be interpreted in light of a functional rather than a material ontology (in a functional ontology, "to be" is to have a function and place in an ordered cosmos). In light of this reading, days 1–3 of creation record God creating the basis for the functions of time, weather, and food; days 4–6 describe God establishing functionaries to rule over or govern the functions created in days 1–3. Genesis 1 is a temple text, culminating with day 7, and thus the cosmos is a temple in which God "rests" (indwells and rules). Genesis 2 should also be interpreted functionally. The point of the story is not to record the material creation of Adam and Eve, but to depict their function in the cosmos with respect to God, each other, and the world. Thus, the story is archetypal rather than literal—which is not to say nonhistorical (Walton affirms Adam and Eve as historical individuals).

Among the five contributors, Beall is unique in rejecting the significance of the ANE context, excluding modern science from having any bearing on reading the text, and denying figurative features of the narrative. The other four authors hold much in common, but have different perspectives on how to use ANE literature, the relation of Genesis 1:1 to 1:2, the precise meaning and function of *bara'* (create) and *'asah* (make/do), whether to harmonize Genesis 1 and 2 (all agree on the unity of Genesis 1–2), and the significance of a historical Adam to the theological teaching of scripture.

Reading Genesis 1–2 is an excellent book. Each author treats his subject matter with care and detail and the book's general tone is congenial and constructive. My one disappointment was with the final reflection chapter written by Jud Davis, which seems overly dismissive of the significance of current scientific consensus and its relevance for biblical interpretation. It would have been more fitting to conclude a volume of this kind with a summary and constructive analysis of the key issues. That aside, readers of *PSCF* will find the book helpful for clarifying their own understanding of Genesis, as they seek to maintain faithfulness to the Bible *and* integrity in their scientific work.

Reviewed by Patrick S. Franklin, Providence University College and Theological Seminary, Otterburne, MB R0A 1G0.

THEOLOGY

MODELS OF ATONEMENT: Speaking about Salvation in a Scientific World by George L. Murphy. Minneapolis, MN: Lutheran University Press, 2013. 145 pages. Paperback; $18.00. ISBN: 9781932688856.

George Murphy ought to be no stranger to those who have been working at the theology and science interface for any length of time. With a Johns Hopkins PhD in physics and ordination as a Lutheran pastor, he has authored at least four other books at this crossroad. The present work builds on his *The Cosmos in the Light of the Cross* (T&T Clark, 2003), especially the theology of the cross motif central to the Lutheran theological tradition.

Whereas until relatively recently much of the Christian theological work written in the religion and science arena involved more generically Christian perspectives, more confessional or tradition-specific approaches are appearing, including specifically Orthodox, Wesleyan, and even Pentecostal contributions, to name some. Murphy is one of a few in the Lutheran tradition who has engaged in these matters by drawing deeply from the wellsprings of his own ecclesial resources, especially Martin Luther's theology of the cross theme. If "the cross tests everything," as Luther insisted, then theological reconstruction in a scientifically explicated world also ought to run the gauntlet of this cruciform criterion. Five middle chapters of this volume thus reconsider classical theological loci—including theological anthropology (human nature), the traditional doctrine of the Fall (the present sinful human condition or the creational problem), the drama of redemption (involving the renewal or reorientation of creation from its misdirectedness), the Christ-event (incarnation and passion, especially), and the doctrine of salvation (soteriology, especially justification, regeneration, and sanctification)—all in the light of the cross of Christ. The cross and resurrection thus, for instance, are understood as exerting *fiduciary influence*—not merely moral influence, as one particularly prominent strand of atonement theory avers—even for contemporary human beings, in generating the faithful response required for experiencing divine redemption in a world gone wrong. This is consistent, of course, with the Protestant emphasis on salvation by grace through faith, albeit inflected, in the Lutheran tradition, through emphasis on the centrality of the cross.

Murphy helpfully and clearly indicates that his goal is not specifically a scientific theology, as if traditional formulations would be revised utilizing scientific categories, but a restatement of biblical and historic Christian orthodoxy for twenty-first-century scientifically informed faithful. As such, he works diligently with both biblical and historical material, careful to clarify what carries over and how it carries over in the contemporary context. More precisely, as the title of the book indicates, Murphy is motivated to render coherent Christian understandings of salvation in a time when science has been understood by many to be salvific in its own right. The result is a primarily theological, even soteriological, work, not exactly a work in theology and science.

Yet scientifically literate believers wanting substantive theological reflection will find this book helpful and rewarding. The decision to publish this volume with Lutheran University Press is certainly understandable, although the importance of the cross for Christian faith in general means that the book's treatments of these historic Christian commitments ought to be of concern for those across the evangelical, ecumenical, and catholic (universal, that is) spectrum. As a book of relatively modest size covering as many central Christian doctrines as it does, no doubt some readers will want more extended discussions about this or that topic, even as those more to the "right" or "left" of the "great tradition" of Christian orthodoxy will also be dissatisfied that some moves are too "liberal" or too "conservative." But those desiring some guidance about how to make sense of Christian faith "in a scientific world" will not come away disappointed.

Reviewed by Amos Yong, J. Rodman Williams Professor of Theology and Dean, Regent University School of Divinity, Virginia Beach, VA 23464.

Letters

A Response to the Review of *Cleansing the Cosmos: A Biblical Model for Conceptualizing and Counteracting Evil*

I would like to thank Gregory Boyd for his review and critique of my book, *Cleansing the Cosmos: A Biblical Model for Conceptualizing and Counteracting Evil* (*PSCF* 66, no. 1 [2014]: 57–9). As I mention in the book, there is much I admire about his work on evil, and indeed our theologies have much in common. However, I do have a few points of clarification. First, with respect to my understanding of warfare models, I claim that warfare imagery only implies or suggests a view of equal and opposite forces (pp. 24, 125, 213), and I am clear that proponents of warfare models do not endorse a metaphysical dualism or believe that "spiritual warfare" occurs between equal forces (p. 24).

Second, with respect to metaphors, I maintain that Boyd's use of the concept of God at War is not well developed, although his response seems to indicate another point of agreement between us. Linguistic treatments of evil are seldom mentioned in works that affirm the reality of the demonic world; this led me to conclude that proponents of "spiritual warfare" models fail to appreciate the metaphorical nature of biblical references. This lack often leads to a focus on only a few biblical texts (Boyd's work being an exception).

Third, ontology is a secondary theme of my work, and although I attempt to use linguistic avenues rather than philosophical ones, I very much agree with Boyd that metaphorical and metaphysical truth can be difficult to extricate and explicate (this is evident in science as well). I suspect his difficulty in getting "clear what these descriptors mean" is a reflection of the very problem I address: the nature of evil spirits is nebulous. This is why I suggest that using multiple metaphors (not limiting ourselves to warfare ones) may enhance our understanding. Interestingly, Boyd's contention that "nothingness" is "a domain of possibilities that becomes actualized only when free agents, human or angelic, choose to do so against God's will" is a point I make several times, albeit with different language (pp. 116–7, 227, 250, 270, 273–6). In fact, I disagree with Barth that evil is not allowed ontological status; I suggest that it becomes real when humans open a doorway to the demonic through sin.

To further clarify, although I suggest that my spatial model has many advantages over a warfare model, I admit that my model could, in fact, incorporate warfare metaphors (pp. 126, 286). Ultimately, my conclusion is more modest: a spatial/boundaries model offers a viable alternative to a "spiritual warfare" one (pp. 126, 213, 285).

E. Janet Warren
CSCA Member

Microscopic and Macroscopic Quantum Realms

The quantum mechanical description of reality and its relevance and implications for the Christian faith plays a central role in the physics theme of the March 2014 issue of *PSCF*. Mann correlates the recent progress in physics with Christian theology by considering typicality, plurality, reduction, quantization, and eternity.[1] Faries emphasizes the challenge of chance and quantum physics to a theological worldview.[2] Carlson and Hine consider the question on how to integrate randomness in the physical world with our theological thinking.[3]

Quantum entanglement lies at the foundation of quantum mechanics. Witness Schrödinger highlighting entanglement with his puzzling cat thought experiment and Einstein deriding it as "spooky action at a distance."[4] Nonetheless, quantum entanglement has been verified experimentally and is essential for quantum information and quantum computing. The quantum superposition principle, together with entanglement, dramatically contrasts the quantum from the classical description of reality. This issue of *PSCF* helps integrate physical reality with a Christian worldview.

The question of the interpretation and the measurement problem in quantum mechanics is important since it clarifies and gives us an insight on how to reconcile physical reality with our Christian faith.5 Van Kampen has written extensively on how quantum mechanics successfully explains macroscopic, objective, recorded phenomena.6 The latter are the experimental data one obtains for microscopic objects that interact with a macroscopic measuring apparatus prepared in a metastable state, for example, the Wilson cloud chamber and the Geiger counter. Van Kampen emphasizes that the wave function ψ, which obeys the Schrödinger equation, is not observed directly. For instance, in the diffraction of a beam of electrons passing through a crystal, ψ for a single electron is calculated but the physically observed quantity is N|ψ|2, where N is the number of electrons in the beam.[7] It is, in this sense, that quantum mechanics provides a complete and adequate description of the observed physical phenomena on the atomic scale.

Van Kampen argues against various interpretations of quantum mechanics, for example, Bohm's hidden variables, de Broglie's pilot wave function, a nonlinear interaction with our consciousness, stochastic, and Everett's many-world interpretations.[8] Van Kampen agrees with Bohr on how to understand the formalism of quantum mechanics but differs from Bohr's theory of measurements and so also differs with what is commonly known as the Copenhagen interpretation. Van Kampen makes it clear how macroscopic observations can be recorded objectively, independently of the observation and the observer, and may be the object of scientific studies.[9]

The meaning of a macroscopic object (e.g., as a certain amount of a gas, a crystal, a pointer on a volt meter, a cat, human beings) is crucial since it makes it clear that although also governed by quantum mechanics, nonetheless, the combination of the enormous number of quantum states in the macroscopic object eliminates the quantum interference between macroscopic states, say, two human beings. Accordingly, macroscopic objects deal with probabilities rather than probability amplitudes, namely, a classical description by a density matrix rather than a wave function.[10]

Einstein refused to believe in the notion of the entanglement of two far-apart electrons.[11] This is a consequence of thinking of an electron as a localized particle rather than as a manifestation of a wave function. In fact, the universe is made of quantized fields, not particles, which implies, nonetheless, that fields exhibit many particle-like aspects. Clauser first established experimentally the discreteness of photons in 1974 by results that contradict the predictions by any classical or semiclassical theory.[12]

Notes

[1] R. B. Mann, "Physics at the Theological Frontiers," *Perspectives on Science and Christian Faith* 66, no. 1 (2014): 2–12.

[2] D. W. Faries, "A Personal God, Chance, and Randomness in Quantum Physics," *Perspectives on Science and Christian Faith* 66, no. 1 (2014): 13–22.

[3] R. F. Carlson and J. N. Hine, "Two Interlocking Stories: Job and Natural Evil and Modern Science and Randomness," *Perspectives on Science and Christian Faith* 66, no. 1 (2014): 23–34.

[4] Mann, "Physics at the Theological Frontiers," 12.

[5] Faries, "A Personal God, Chance, and Randomness."

[6] N.G. Van Kampen, "Ten Theorems about Quantum Mechanical Measurements," *Physica A* 153 (1988): 97–113; ____, "The Scandal of Quantum Mechanics," *American Journal of Physics* 76, no. 11 (2008): 989–90.

[7] Van Kampen, "Ten Theorems about Quantum Mechanical Measurements."

[8] Van Kampen, "The Scandal of Quantum Mechanics."

[9] Van Kampen, "Ten Theorems about Quantum Mechanical Measurements."

[10] Ibid.

[11] Mann, "Physics at the Theological Frontiers," 12; Faries, "A Personal God, Chance, and Randomness."

[12] J. F. Clauser, "Experimental Distinction between the Quantum and Classical Field-Theoretic Predictions for the Photoelectric Effect," *Physical Review D* 9, no. 4 (1974): 853–60.

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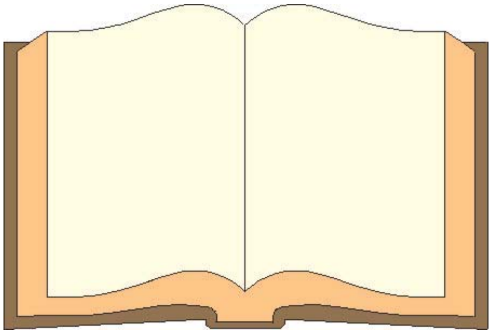

In addition to their other contributions, many members of ASA and CSCA publish important works. As space permits, *PSCF* plans to list recently published books and peer-reviewed articles related to science and Christian faith that are written by our members and brought to our attention.

To let us know of such works, please write to patrick.franklin@prov.ca.

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An individual wishing to participate in the ASA without joining as a member or giving assent to our statement of faith may become a **Friend** of the ASA. Friends receive all member benefits and publications and take part in all the affairs of the ASA except voting and holding office.

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