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Articles

- Flood Geology of the Crimean Peninsula 118
Part I: Tavrick Formation
Alexander V. Lalomov
- A Model for the Variation of the Fermi Constant 127
with Time
Eugene F. Chaffin
- The Molecular Biology of Genetic Transposition 139
Jerry Bergman
- Evolution Is Lethal Antiscience 151
Joseph Mastropaolo

Notes from the Panorama of Science

- The Growth Rate of *Muhlenbergia torreyi* 159
(Ring Muhly Grass) Colonies in Central Arizona
Van Andel Creation Research Field Study Note
George F. Howe and John R. Meyer
- Joseph B. Prestwich: Uniformitarianism and 162
Catastrophism
William Weston

Departments

- Editor's Comments 117
- Book Reviews
- $E=mc^2$ by David Bodanis 117
- God: The Evidence* by Patrick Glynn 124
- Darwin's God* by Cornelius Hunter 125
- Signs of Intelligence—Understanding intelligent design* by W.A. Dembski and J.M. Kushiner, editors 126
- Origins: Linking Science and Scripture* by Ariel A. Roth 138
- Big God vs. Big Science* by Bill Sardi 158
- Erratum 150
- Letters to the Editor 164
- Instructions for Authors 169
- Membership/Subscription Application 171
- Order Blank for Past Issues 172

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Haec Credimus

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

Editor's Comments

Creationist geologist Alexander Lalomov has begun to study the strata of the Crimean Peninsula from a Flood perspective. In his article in this issue, he discusses the Tavrick Formation. This type of investigation needs to be done all over the world by creationists. Gene Chaffin continues his work on the possibility that the so-called constants in physics could have been different in the past. The goal of this study is to produce a theoretical model for rapid nuclear decay at the beginning of the universe. Jerry Bergman presents a case for design when examining genetic transposition.

Dr. Mastropaolo views the concept of evolution as lethal antiscience. The theory, touted as the greatest idea of modern man, is in actuality an unreasonable religion that is destroying the field of science and, if followed to its logical consequences, will be destructive to the human race.

George Howe and John Meyer give the second report on ring muhly grass, an interesting species that grows at our Arizona research center. Very little has been written on the grass, so that this original study is likely the first of its kind on the growth habits of the plant.

I hope that you have had a fruitful year and that 2002 will be a successful year for you in the service of the Creator. Much work needs to be done by creationists. The re-interpretation of all areas of science into a creationist framework is a must. Consider using your talents for this effort. May I thank all of you who have supported the work of the Society for many years. We could not function without your help.

Emmett Williams
Editor

Book Review

E=mc² by David Bodanis

Walker and Company, New York. 2000, 337 pages, \$25

This book is subtitled "A biography of the world's most famous equation." There is much unusual, personal information on the pioneers of modern physics. These include Einstein, Marie Curie, Werner Heisenberg, and Lise Meitner.

Special attention is given to creation scientist Michael Faraday. Author Bodanis suggests that Faraday's biblical worldview guided his science insights (p. 15). Faraday often talked about the circular nature of the local church family whereby one person helps the next, and that person helps another, and so on until the circle is complete. Continuing this theme in the laboratory, he then described invisible circular lines of magnetism and electricity today known as *fields*. Faraday also saw the importance of the conservation of energy for apologetics (p. 20). Energy conservation shows that the world is dependable, because God has established basic laws. This understanding of the laws of nature provides a strong, credible alternative to random evolution.

There are few weaknesses in the book. Indian astronomer Subrahmanyan Chandrasekhar (1919-1995) is

wrongly credited with originating the concept of black holes (p. 199). Black hole theory actually was explained by creation scientist John Mitchell as early as 1783. Author Bodanis discusses the many contributions of Jewish physicists. However, he does not discuss why the Jewish faith and culture has dominated modern physics. The book speculates wildly on the distant future of the universe. Thus 10¹⁰⁰ years from now, there will exist only a dark mist of elementary particles (p. 200). According to Scripture, however, the Creator has far different plans for the future.

The book gives clear descriptions of nuclear energy and the Manhattan Project. It is recommended to all who are intrigued by the world's most famous equation, where mass is shown to be a form of "frozen energy."

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Flood Geology of the Crimean Peninsula Part I: Tavrick Formation

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Abstract

Sedimentary formations of the Crimean peninsula (southeast Europe, Black Sea coast) provide evidence of catastrophic deposition in a hydraulic cataclysm. In spite of this evidence, uniformitarian geologists of the former USSR described these Crimean sedimentary formations in terms of gradualism. This article is the first attempt to reinterpret the geology of Crimea in a creationist framework. Research of the overall Crimean sedimentary sequence provides evidence of catastrophic sedimentation in the basin. The first stage of this research reconstructs sedimentary conditions for the lower part of the sequence—the

Tavrick Formation. Investigation of the Crimean sedimentary sequence illustrates principles of Flood sedimentation which can then be correlated to strata in similar foldbelts in other regions. In the description of the geological structure of Crimea, I use the prevalent terms of the uniformitarian geological column, such as “Triassic,” “Jurassic,” and “Cretaceous.” This dating is based upon the biostratigraphic assumption that strata around the globe which contain the same fossils are of the same age. Inasmuch as the synchronous nature of such strata is questionable, the absolute dating of these strata is rejected.

Introduction

The Crimean Peninsula is located in southeastern Europe on the northern coast of the Black Sea (Figure 1). Its major geomorphic features include a plain in the north and mountains in the south. The mountains, part of the Alpine fold system, extend 200 km from southwest to northeast and reach an altitude of 1500 m. The peninsula has long been a popular site for geological field schools for many European Russian Universities.

The Crimean Peninsula has a very complex geological structure. Figure 2 shows a generalized cross section of the Crimean anticline from northwest to southeast. For easier visualization the cross-section is drawn with significant vertical exaggeration. The anticline is bounded by faulting to the southeast and folded strata to the northwest.

The basement of the sedimentary sequence is not seen in outcrop at the surface. In the northern part of the peninsula, deformed, high-grade metamorphic shales with diabase dikes and highly metamorphosed limestone are revealed by drill holes ranging in depth from 500 to 2000



Figure 1. Location of Crimean Peninsula.

meters (Sidorenko, 1969). The shales and limestones are assigned to the Precambrian and Paleozoic erathems, respectively.

Basement rocks are overlain by sandstones and shales of the Tavrick Formation, conventionally assigned to the Triassic System. The Tavrick Formation is also known by its informal, but widespread name—the “flysch formation”¹. The flysch formation is separated from the basement rocks by an apparent unconformity. Another formation, exhibit-

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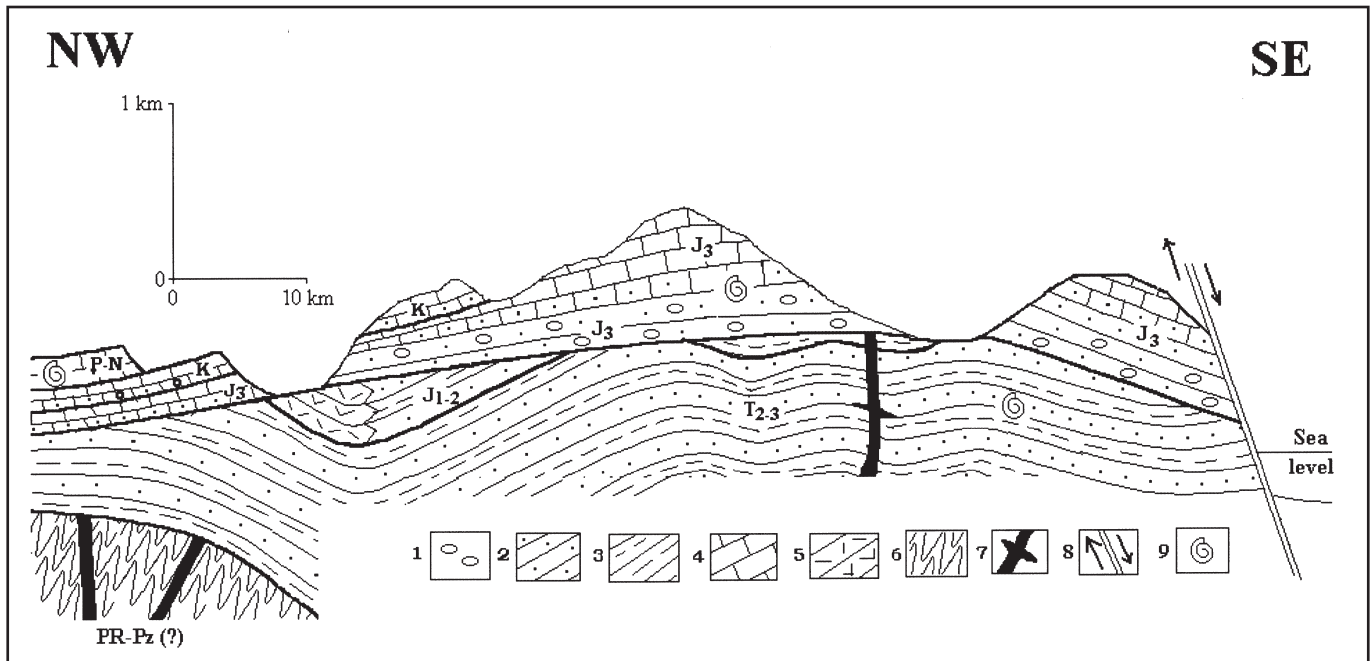


Figure 2. Schematic cross-section of Crimea anticline. Legend: 1. Conglomerate, 2. Sandstone, 3. Shale, 4. Limestone, 5. Volcanic rocks, 6. Metamorphosed shales and limestones, 7. Diabase dikes, 8. Fault and direction of the block movement, 9. Fossils, PR-Pz(?): "Proterozoic" and "Paleozoic" strata; T₂₋₃: "Middle and Upper Triassic" strata; J₁₋₂: "Lower and Middle Jurassic" strata; J₃: "Upper Jurassic" strata; K: "Cretaceous" strata; N-P: "Neogene" and "Paleogene" strata.

ing flysch-like layering of shales and sandstones with interlayers of gravel, tuff and volcanic rocks, is conventionally assigned to the lower and middle Jurassic series. It overlies the Tavrick Formation without an angular unconformity. In some outcrops, the transition from the Tavrick Formation to overlying "Jurassic" deposits is gradational. The formal name of the "Jurassic" strata is the Eksiordian Formation. The Tavrick and Eksiordian Formations form a second structural floor of the Crimean mountains. The strata of this structural floor are deformed by folding (Figure 2).

Conglomerate, gravel and sandstones assigned to Upper Jurassic series (Callovian and Oxfordian stages) overlie the Tavrick and Eksiordian rocks across an angular unconformity (Figure 2). The erosion surface is mechanical only; there is no evidence of chemical weathering, fossil soils, or a long hiatus of sedimentation. Limestones of Kimmeridgian and Tithonian stages of the Upper Jurassic series conformably overlie (and sometimes juxtapose) the conglomerates and sandstones. Both the "Upper Jurassic" conglomerates and limestones are tectonically tilted. They form the highest mountains of the Crimean ridge. Far to the northwest they are overlain by Cretaceous, Paleogene and Neogene limestones and marls.

Under the Soviet regime, all geological interpretation was performed under the principle of uniformitarianism. Catastrophic approaches were largely unknown or ridiculed. However, at the Crimean Peninsula, there are clear

field evidences of catastrophic geologic action that have been interpreted within the framework of uniformitarianism in spite of the evidence. A clear example of this is found in the Tavrick Formation. All of the scientific papers and monographs about the geology of Crimea, and the Tavrick Formation in particular, demonstrate a uniformitarian bias. One of the most complete investigations of the Tavrick was performed by noted Russian sedimentologist, Professor, and Doctor of Science Nicholas Logvinenko—my teacher and former Chair of Sedimentology (1968–1992) in the Geology Department of Saint Petersburg State University. Although his conclusions were colored by his uniformitarian perspective, his descriptions of the flysch formation are valuable.

Austin (1994) demonstrated that a catastrophist interpretation can be made for geologic features long interpreted in the light of uniformitarianism. In a similar fashion, I propose, on the basis of extensive field research, that the flysch formation of the Crimean Peninsula yields significant evidence of catastrophic deposition.

¹"Flysch" is an older geological term, popular in Europe, for alternating sand, silt, and shale sequences purportedly deposited in deep-water conditions. They are roughly the same as those defined by the term, "turbidite" in North America.

Sedimentological Features of the Tavrick Formation

The oldest rocks of the Crimean sedimentary sequence exposed in outcrop are those of the Tavrick, or flysch formation. It is exposed in the central part of the Crimean anticline and on the south coast of the peninsula. The formation is composed of rhythmically alternating sandstones, siltstones, and shales (Figure 3). Limestone layers are also present, but only in the upper part of the formation. In spite of large numbers of trace fossils, the flysch formation contains few body fossils. Only in the upper part of the strata are *Halobia* fossils observed.

There have been several stratigraphic interpretations of this formation by different authors. All of these interpretations are based upon uniformitarian assumption of continuity of the strata, which in one part is based on the assumption of the simultaneous deposition of each layer in the entire sedimentary basin. The most detailed classification was made by Logvinenko (1961) on the basis of his rhythmostratigraphical method. He distinguished five members (from bottom to the top): (1) Normal Flysch, (2) Normal Flysch with Quartzite Sandstones, (3) Lower Shale Flysch, (4) Sandstone Flysch (Inter Shale Member) and (5) Upper Shale Flysch. The first three members were assigned to the Middle Triassic Series, the last two members to Upper Triassic Series. These members are not homogeneous; both lateral lithology changes and local unconformities between the members are present.

The rhythmostratigraphical method is based upon the detailed measurement of all flysch layers. The ratio of thickness of sandstone to shale layers is assumed to be unique for each flysch member. Inasmuch as there is no one continuous outcrop of the flysch formation from bottom to the top, the local lithostratigraphic column is derived by correlating various sections. However, even this lithostratigraphic column is suspect; uniformitarian geologists themselves recognize that the character of flysch can change laterally very abruptly (Sidorenko, 1969). Also, the flysch formation appears to have been deposited from moving horizontal currents (as will be shown later), not evenly over a widespread area, increasing uncertainty in interpretation (Berthault, 2000). Hence, we can speak with confidence only about the predominance of shale flysch in the upper part of the formation. Therefore I propose to divide the Tavrick into two members, typical of many flysch sequences, which represent a transgressive series. The boundary between these members is not always obvious.

- The lower member, or “Normal Flysch”, with roughly equal thicknesses of sandstone or siltstone, and shale layers. The thickness of each layer varies with clast size: coarse-grained sand beds are between 40–200 cm thick; medium-grained sand beds, 10–50 cm; and fine-grained sands, 2–20 cm. The total thickness of the normal flysch



Figure 3. Lower member of Flysch Formation (normal flysch), showing alternation of sandstones, siltstones, and shales.

member is unknown. Drilling data shows that it is at least 2000 m, although visible thickness in outcrop is no more than 800 m.

- The upper member, or “Shale Flysch”, which is dominated by shales—up to 80–90 % of the member’s thickness. Sandstone or siltstone layers are up to 50 cm in thickness. The Shale Flysch member is 700–800 m thick.

The flysch formation is deformed by folding into a series of synclines and anticlines. The amplitude of folding ranges from several meters to kilometers. Small folds occur as a result of the slumping of unconsolidated deposits, whereas large ones are associated with large-scale tectonic movements, accompanied by faulting and intrusion of igneous dikes (Figure 2).

The flysch formation has many interesting sedimentary features, such as dragging grooves, erosion grooves, cross beds, and trace fossils, which aid interpretation of its origin.

Dragging grooves (or their casts) formed from dragging trees or stones over the sediment-water interface by the current (Figure 4). These have widths between 1 and 2 cm, lengths between 50 and 100 cm, and penetration into the rock between 0.5 and 1 cm. These marks are evidence of deposition of stratified sediments under conditions of high current velocity. Preservation of these marks is also evidence of rapid burial.

Erosion groove has been defined as “a sedimentary structure formed by closely spaced lines of straight-sided scour marks. The scouring may be initially concentrated by a pre-existing groove.” (Bates and Jackson, 1987, p. 227). These structures (or their casts) are common on the surface of the sandstone and siltstone beds (Figure 5). They reach 10 – 20 cm in width, 50 – 100 cm in length, and 5 – 10 cm penetration into the rock. Another evidence of vigorous erosion is the absence of part of the upper (shale) beds in the flysch sequence in the older normal flysch member. The presence of erosion grooves strongly



Figure 4. Dragging grooves on the surface of this layer is evidence of a vigorous water current during sedimentation.

suggests that these strata were deposited under conditions of vigorous water current (Dzulinski and Sanders, 1962). These marks also enable researchers to determine the direction and velocity of the paleocurrent. Erosion grooves demonstrate that the paleocurrent velocity exceeded the initial erosion threshold for clay particles (Potter and Pettijohn, 1963). Erosion grooves are commonly formed on the sediment surface during brief bursts of abrasion under fast-flowing water conditions (Allen, 1984). Thus, it is possible to estimate the paleocurrent velocity from the Hjulström diagram (Hjulström, 1935). For clay particles the paleocurrent velocity probably exceeded 1.0 m/s. Mapping of erosion and dragging grooves' orientations show a unidirectional paleocurrent from northwest to southeast during deposition of the flysch formation.

Cross beds are distinctly inclined thin layers of sand within thick sandstone stratum. The cross beds are observed in the sandstone layers of flysch. Shales are always flat-bedded (Figure 6). This is similar to what was observed by Julien, Lan and Raslan during laboratory flume experiments on stratification of heterogeneous sand mixtures in current conditions. They noted that:

...particle segregation mechanism is at the origin of stratification structure in which a cross-laminated deposit of mostly coarse particles lies between two near-parallel laminated deposits (Julien et al., 1998, p. 221).

Thus I propose that these structure were formed in similar current conditions, not as a result of continuous slow sedimentation in a low-energy basin.

The cross beds are generated as a result of the sand moving as waves. The thickness of the cross beds is up to 0.8 m. Because erosion has removed the top of each sand wave, the true height of each sand wave could have been double the present cross bed thickness (Austin, 1994, p. 34). Inasmuch as the sand-wave height is approximately one-fifth of the water depth (Austin, 1994, p. 34), the depth of the sedi-



Figure 5. Erosion grooves allow determination of both velocity and direction of the current.

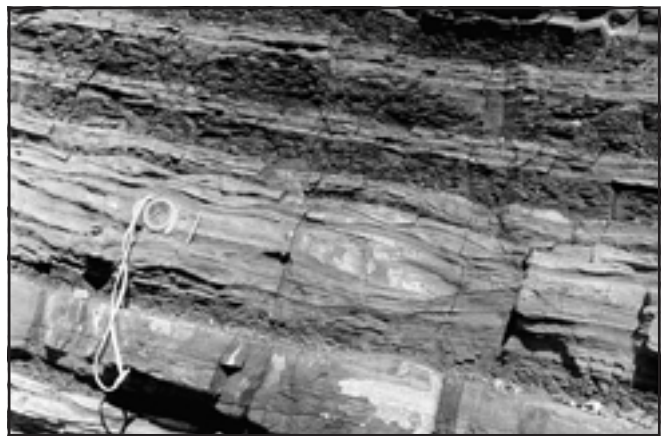


Figure 6. Cross bedded sandstones within flat bedded shales. This type of layering of coarse-grained and fine-grained particles was observed in flume experiments on stratification using heterogeneous sand mixtures.

mentary basin that time may be estimated as not more than 10 m. Using the Rubin and McCulloch diagram (Rubin and McCulloch, 1980, p. 214), the velocity of the paleocurrent may be estimated between 0.8–1.2 m/s.

Trackways of crawling worms and burrows of marine organisms are also observed in the flysch formation (Figure 7). More specific identification of the ichnofauna has not been made. There are both surficial and tunnelling crawling traces on the upper bedding plane of the shale layers. Usually we see only casts of these traces on the lower bedding plane of the superposed sandstone layers. Tunnels filled with sand which were later cemented. Very short fossil tracks (not longer than 0.5–1 m) are evidence of short time between sedimentation superposed strata.

Folds also reveal information about the geological history of the flysch formation. Detailed observation of small folds indicates that there was not a long period of time between deposition and folding. It appears that sedimentary beds were soft and plastic during folding (Figure 8); therefore deposition of strata and folding probably occurred



Figure 7. Trackways of crawling worms. Very short fossil tracks are evidence of short time between sedimentation of superposed strata.

within a short time of each other, not over a long geological time span.

Compositional similarity across all the flysch strata suggests that during flysch deposition there was only one source of clastic material for the entire basin. Moreover, the adjoining coal-bearing sedimentary sequence in the Donetsk Basin (300–400 km to the northeast) assigned to the Carboniferous System (Mississippian and Pennsylvanian) has a similar mineralogical composition (Logvinenko and Karpova, 1961, p. 262, table 63). Compositional similarities over such a broad area strongly suggests that all of these formations had one common source of sediment and were generated almost simultaneously by widespread and powerful depositional processes.

Origin of Flysch Formation

These data support several important conclusions:

- Deposition of the Tavrick Formation occurred under widespread catastrophic paleocurrent conditions with velocities up to 1.2 m/s, not in a low-energy marine basin. These high current velocities are seldom observed over large areas of the modern open ocean (Austin, 1994, p. 35; Hamilton, Sommerville and Stanford, 1980). Therefore, conditions during deposition of the Tavrick were probably significantly different from modern analogs.
- Constancy of the mineral association both within the Crimean sequence and between it and those in the Donetsk Basin is evidence of a consistent source relatively distant from the Crimean strata.
- Preservation of dragging and erosion grooves also strongly suggests rapid sedimentation under high current conditions. At the same time, trace fossil trackways are short, suggesting short time spans between deposition of successive layers.

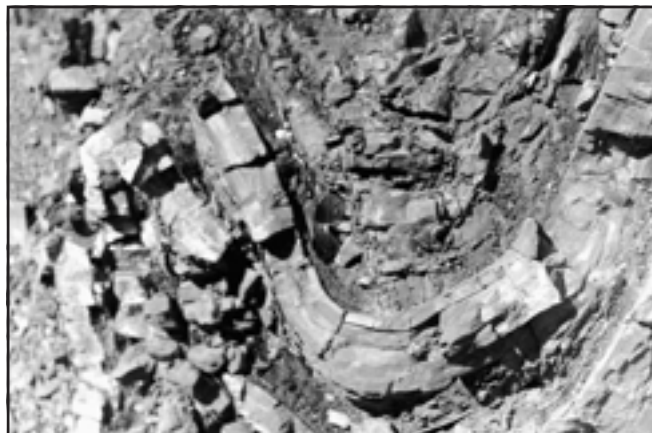


Figure 8. Folds in Flysch Formation showing plastic deformation of unconsolidated sediments during folding.

- The presence of erosion surfaces on the beds are not a result of long periods of time of quiescence, but are characteristic of deposition under high current velocity conditions.
- The period of time between deposition and folding of the strata was very short.

In summary, these features of the Crimean flysch formation clearly confirm the superiority of a catastrophic interpretive framework.

What does the relevant uniformitarian literature report? These papers described all of the features listed above in great detail. They were written by experienced and observant specialists such as Nicolas Logvinenko. However, the uniformitarian framework apparently prevented the proper inference of a catastrophic origin for the observed sedimentary features of the Tavrick Formation. Logvinenko wrote about the conditions of deposition for these strata:

The presence of dragging grooves with lengths more than 50–100 cm, widths 1–2 cm, depths 0.5–1 cm and erosion grooves with lengths up to 50 cm, widths 10–15 cm and depths up to 5 cm, often S-shaped, bear witness to high-velocity, turbulent currents (Logvinenko, 1961, translated from Russian by author).

The preservation of mechanically generated textures such as erosion grooves and ripple marks is evidence of considerable rate of sedimentation (Logvinenko and Karpova, 1961, p. 27, translated from Russian by author).

Invariability of the mineral associations is evidence of a single and complex source of detritus for all of the Crimean peninsula and adjacent territories during flysch deposition (Logvinenko and Karpova, 1961, p. 134, translated from Russian by author).

The S-shaped form of sills with thickness up to 10 m is evidence of a pre-fold age of intrusives. Penetration of these sills into non-solidified sediments has

been confirmed by the inviolate character of contacts and alteration of plagioclase near the contacts by steam (Logvinenko and Karpova, 1961, p. 199, translated from Russian by author).

Sedimentation occurred under conditions of high hydrodynamic activity and instability of the sediment... Conditions for the existence of marine organisms were unfavorable (Logvinenko and Karpova, 1961, p. 258, translated from Russian by author).

The amount of arriving detritus was tremendous: there was much mud not only near the shoreline, but also very far from the coast... The black color of the flysch rocks is evidence of a large amount of plant detritus and organic material arriving into the sedimentary basin (Logvinenko and Karpova, 1961, p. 260, translated from Russian by author).

What else is needed to draw a conclusion that the flysch formation was generated under catastrophic conditions of sedimentation? Thus it is interesting to note the conclusion of the uniformitarian, Logvinenko:

The formation of flysch occurred in marine basins bordering mountain systems similar to the present day Black Sea, under conditions of small oscillatory tectonic motions (Logvinenko, 1974, p. 237, translated from Russian by author).

This is an excellent example of the uniformitarian bias. Belief in an old age of the Earth and slow processes of sedimentation seems to preclude obvious inferences from field data.

Out-of-Order Limestones Associated with the Flysch Formation

There is another interesting feature of the geology of Crimea that appears to confound uniformitarian doctrine. This is the existence of a few large (up to hundreds of meters) blocks of limestone assigned to the Carboniferous System by paleontological dating within and above the flysch strata (Triassic System). Several uniformitarian geologists have described this feature. The many attempts to explain this paradoxical relationship include that of Nicolas Logvinenko:

One of the features of the Main Ridge of the Crimean Mountains is the inclusion within Triassic strata of more ancient Carboniferous strata. The genesis of this phenomenon is not clear. It is supposed that these blocks were located in central parts of Triassic folds and slumped down the slopes that consisted of clay deposits (Logvinenko, 1998, p. 6, translated from Russian by author).

Once again, the bias of uniformitarianism prevents these authors from drawing the more obvious conclusion that the dating method, and hence, biostratigraphy, might be false.

Conclusion

It is clear that a conceptual framework influences the interpretation of geologic features to a great extent. This is why researchers with similar qualifications and ability can draw radically different conclusions from the same data. Numerous investigations confirm this viewpoint. Valid interpretations have been performed based on a catastrophist framework at the Grand Canyon (Austin, 1994, pp. 21–56). Similarly, the age of submarine placer deposits in north-eastern Russia has been shown to lie in a range between 2000 and 5500 years, rather than the 40 million years estimated by uniformitarians (Lalomov and Tabolitch, 1996) and the age of associated alluvial placer deposits has been shown to be less than 2000 years—hundreds of times less than what uniformitarian geologists believe (Lalomov and Tabolitch, 1999).

In the same fashion, the flysch formation in Crimea can easily be interpreted within a creationist framework. Its rocks yield many evidences of rapid, catastrophic deposition. In spite of these, uniformitarians continue to assert that the strata were deposited over a long time span (about 30 million years) in a low-energy marine basin bordered by mountains with small oscillatory tectonic activity (Logvinenko, 1974). It is possible that uniformitarian interpretations of the Crimea were forced by the political situation of the USSR in the past. I hope that Russian scientists will reject the doctrine of uniformitarianism and consider the creationist alternative.

There are many difficult and unsolved problems in geology that require careful research and investigation. The data present challenges for both the uniformitarian and catastrophist frameworks. But in numerous cases, the principles of Flood stratigraphy and a recent creation can be successfully applied to interpretations of field data such as the Tavrick Formation of the Crimean Peninsula. Ongoing work there will address other features of the area within the creationist framework.

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Book Reviews

God: The Evidence by Patrick Glynn

Prima Publishing Co., Rocklin, CA. 1999, 216 pages, \$14.00

Patrick Glynn has made a remarkable transition from agnostic to believer, based on evidence from creation and conscience, the transition every intellectually honest seeker ought to make. Because of this, the book is valuable in helping others of similar bent to see the case for faith. In another sense, perhaps Mr. Glynn wrote the book too soon, because he shows signs of theological naivety that put him—and his readers—in danger of falling into a syncretistic or pantheistic version of the gospel.

In his personal search for truth, Mr. Glynn discovered that his tool of choice—reason—leads to some absurdities. For instance, a firm basis for morality is lost when the atheistic intellectual line is reeled out to the end, yet morality is absolutely necessary for society and individuals to survive. This was the dilemma of Socrates whose students apparently took the implications of the teaching a bit further than their teacher had hoped and thus he was charged with corrupting the youth of Athens. It is really a shame that the corruptors of our age do not take their crimes as seriously as the ancients apparently did.

Early in the book, the only sign of a problem is a compromise common to many believers, that of accepting evolution or at least long ages (p. 34). Most who take that position have not really thought through its implications for the authority of Scripture. In fact, if there were death long before human sin, even before human existence, then the Bible is misleading not only in its historical assertions, but also in key elements of the gospel, including the meaning of Christ's atonement as the defeat of that enemy death which entered creation because of human disobedience. Otherwise, death is just part of God's plan for creation.

Glynn goes on to delineate the evidence of God from design, including not only the complexity of living things, but also the way in which even the physical constants of the universe, the whole way in which matter and energy behave, seem designed in a way that makes life possible. He shows the silliness of some of the usual explanations of this "anthropic principle," such as the existence of infinite parallel universes of which ours is just one of those that

supports life. He also points to the research on the positive effect of faith on physical and mental health. (He draws heavily on the extensive work of David Larson and the National Institute for Healthcare Research.) Glynn wonders if it makes sense to think that we would literally thrive in what the critics call a fantasy world, or if this is actually an indicator that it is our design and our destiny to live in fellowship with our Creator.

In accepting the increasing evidence of a common and somewhat stereotypical “near death experience,” he finds in this a rational case for the existence of the soul. Because the counter-explanations (of metabolic disturbances, low oxygen, high carbon dioxide, delirium, hallucinations, endorphin release, birth memory or temporal lobe seizures) all fail to explain the data and because the person having the experience sometimes has knowledge of things going on while they were apparently unconscious and at a distance from the perceived events, there seems to be strong evidence for life outside the body and the existence of a spiritual realm.

Because there is not always a difference between the near-death experiences of Christians and non-Christians, Glynn leans towards a more inclusive theology. He notes that people come back from these near-death experiences as more loving and compassionate people. From this, Glynn concludes that the purpose of life on earth is to love—which is surely part but not all of the truth.

The history of spiritism, often neglected or even completely discredited in western society, ought to alert us that those who contact the supernatural realm may indeed touch on things that are real, although the admixture of charlatanism makes it easy for the scoffers to dismiss the whole thing. But, what they hear and see may not be the truth, for that spiritual realm contains clever and powerful deceivers who do not wish us well.

Unfortunately, Mr. Glynn proceeds from acceptance of the near-death experiences to a revision of Scripture and falls smack dab in the middle of the theologically liberal camp. For example, the God of the Old Testament is described as “culturally determined” or “tribal” (p. 150) The Scriptures containing the views of the apostle Paul are said to be inferior to Jesus’ teachings. (pp. 151 - 152) Witch burning is said to be like the crucifixion of Christ. (p. 150).

The founders of the United States are said to have not been religious but rather “not anti-religious. (p. 160) At least, compared to most secular writers, Glynn acknowledges that early America was “steeped in religion” but falls short of noting that the whole structure of the Republic is based on a Biblical world view.

In summary, Glynn has done a brave thing for an intellectual in documenting a path from the materialistic view of life to faith in the Creator, Who became our Savior, Who is also the Righteous Judge. Although his ideas contain the seeds that might germinate into heresy and apostasy, they are a good start for serious discussions with skeptics and atheists whose false sense of security needs to be challenged. It must be noted that others who seemed to have begun well, such as Elisabeth Kubler-Ross and M. Scott Peck, both moved from their early insights concerning the reality of a spiritual realm into a later pantheistic “New Age” view of that reality which carries them far from the gospel message of sin and salvation. A step in the right direction is a good idea but the spiritual journey potentially has many wrong turns.

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***Darwin's God* by Cornelius Hunter**
Brazos Press, Grand Rapids. 2001, 192 pages. \$17.99.

Author Cornelius Hunter was a successful high tech manager and is now completing a Ph. D. in biophysics at the University of Illinois. His thesis in *Darwin's God* is that evolution was developed as a *theodicy*, an explanation for the problem of evil. The problem is the existence of evil in a world created by a good God. Hunter gives many quotes to show that Darwin struggled deeply with this issue. In Hunter's view, Darwin's final solution was “to separate God from the world in order to explain its inefficiencies and quandries” (p. 165).

With a philosophical scapel, Hunter shows that evolution is a metaphysical system based on a faulty view of God. One hears evidence of this from creation critics who claim that “God would not have done it this way” (eye design,

panda's thumb, junk DNA, etc). Hunter is well aware of the weakness of evolution evidences. He concludes that there is some data supporting evolution, but also “a substantial body” of data in opposition (p. 170). Hunter reviews the theistic evolution position of Theodosius Dobzhansky, Terry Gray, Howard Van Till, and Kenneth Miller (pp. 166-170). This compromise position is shown to fail logically. The common view here is that God has no active role in nature. Thus God is not responsible for predation, struggle, or death. At the same time, the design and ultimate creation of species are seen as God's handiwork. However, “one cannot simultaneously hold that God would not have created the particulars (imperfections)...and that God did create the particulars (design) of this world (p.170).

If Hunter's thesis is correct, most creation compromises today begin with an attempt to rationalize evil in the world. And this is a theological problem which requires a theological solution. A consistent, heart-searching view of the curse leads to a creation position, not to compromise. Author Hunter concurs with this conclusion. His book is de-

lightful reading for anyone who wants to think deeply concerning the motives behind belief systems.

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***Signs of Intelligence — Understanding intelligent design* by W.A. Dembski and J.M. Kushiner, editors
Brazos Press, Grand Rapids. 2001, 224 pages, \$8.75**

This is one of several new books published by the Intelligent Design (ID) movement. The book introduces the reader with little previous acquaintance with ID to a wide range of topics by 15 authors.

William Dembski tackles the pseudo-issue of "non optimal design" that evolutionists surprisingly use as a "proof" against design. Examples of non optimal design that come to mind are the eye and the panda's thumb. A number of creationists have previously pointed out the lack of logic in this "proof." Later on in the book, Dembski summarizes his work on a quantitative method of determining intelligent design.

In his characteristic lucid style, Phillip Johnson provides an update on the naturalistic hold of science, pointing out examples of propaganda. Nancy Pearcey, Jay Wesley Richards, John West and Patrick Henry Reardon provide information on the importance of ID for life, culture, and apologetics. John Mark Reynolds tackles the logical inconsistencies of theistic naturalism - the secular temptation that many Christians have adopted.

Michael Behe gives an introduction to his book on irreducibly complex systems. Behe still seems to illogically cling to evolution, possibly because the hierarchy of the Catholic Church mostly believes in evolution.

Stephen Meyer's contribution is an update on the origin of life issue - a strong argument in favor of creation. Jonathan Wells delves into the intriguing possibility that more than genes control embryonic development. Since neo-Darwinism postulates that gene mutations are the mechanism for providing variety in evolution, this information would greatly weaken their theory. Paul Nelson provides new information that natural selection is a tautology and explains nothing. Robert DeHaan and John

Wiester show how the Cambrian explosion is powerful evidence against evolution and in favor of intelligent design.

Walter Bradley takes off on the anthropic principle, demonstrating how the universe is extremely fine tuned for life. At one point he interjects the big bang theory into the discussion, stating that the process of the big bang must have been fine-tuned to the nth degree. But it is unnecessary to borrow a naturalistic theory when simple creation can explain the anthropic principle.

Bruce Gordon ends the book with a case for the scientific validity of ID. He also makes a curious statement that creation science (belief in the young earth and global Flood) are falsifiable and in his opinion have been falsified. It seems that many Christian intellectuals believe the same. This is likely the reason ID is more appealing to them than young earth creationism. It would have been proper for Gordon to have provided documentation for this assertion. In my opinion, many of these intellectuals have not analyzed the evidence for the young earth and the global Flood in depth and have believed too easily in naturalistic interpretations and in some cases theory-tainted data. Gordon's assertion without documentation is a major flaw in an otherwise excellent book.

Those in the intelligent design movement desire to press the issue of design versus chance as a wedge into the naturalistic stronghold of science. They are optimistic that ID will become a serious subject of research and discussion in the academic world. I am totally in favor of this strategy and I wish them the best. Phillip Johnson and others emphasize that they will discuss other issues, such as the age of the earth, when ID becomes more or less mainstream. I hope the end of the age does not come first before we can enjoy discussing other issues with the ID community.

"The Modern Synthesis is a remarkable achievement. However, starting in the 1970s, many biologists began questioning its adequacy in explaining evolution. Genetics might be adequate for explaining microevolution, but microevolutionary changes in gene frequency were not seen as able to turn a reptile into a mammal or to convert a fish into an amphibian. Microevolution looks at adaptations that concern only the survival of the fittest, not the arrival of the fittest. As Goodwin (1995) points out, "the origin of species—Darwin's problem—remains unsolved."

Scott Gilbert, John Opitz, and Rudolf Raff (1996)
"Resynthesizing Evolutionary and Developmental Biology"
Developmental Biology 173, Article No. 0032, 1996, p. 361

A Model for the Variation of the Fermi Constant with Time

Eugene F. Chaffin*

Abstract

Genesis, chapter one, is discussed in terms of whether half lives could have been smaller early in creation week. Radioactive equilibrium of uranium is discussed in terms of such a scenario, along with U-235 and Pu-244 abundances. The discussion is related to evolutionary thoughts about ele-

ment production in stars. I discuss the possibility of variation of coupling constants and particle masses within modern string theory. Finally, a concrete, numerical approach is given for the possible variation of the Fermi constant over the history of the earth.

Introduction

Modern physics involves more abstraction than the physics of even 20 years ago. Hence, it becomes an endeavor which may lead researchers into false starts and/or require us to solve the same problem in several different ways. However, it appears that physics research needs to involve different approaches in order to succeed. Kaluza-Klein theories, which were previously discussed in this journal (Chaffin, 2000a), have developed in recent years into multidimensional string theory. These theories attempt to explain the existence of electromagnetic, gravitational, weak nuclear and strong nuclear forces within a single theoretical framework. The development of string theory provides many examples of false starts. However, new understandings of mathematics and physics have enabled reasons and explanations to be given in particle physics which had not been previously possible. Attempting to take advantage of these new descriptive capabilities, I will consider the possibility that string theory may be relevant to the age of the earth question.

In particular, I consider the subject of *accelerated* radioactive decay, which is the study of the possibility that radioactive half lives had smaller magnitudes earlier in history than today. I will consider how scriptural evidence can best be interpreted, in terms of a young-earth model. I will discuss isotopic abundances of uranium and a few other elements, as indicative of the types of data we would like to be able to explain. Then I will progress to some modern particle physics, in a search for possible mechanisms for changing half lives. In particular, I will give a model for variation of the Fermi constant, which is the number in beta decay

theory which most directly fixes the rate of nuclear decay by transmutations of neutrons to protons and vice versa.

If the age of the earth is measured in thousands rather than billions of years, then how do I explain the isotopic abundances of, for example, uranium, as found in geological samples? If half lives have varied over earth history, then nuclear physics must be altered in some way, and the altered theories could lead to new explanations for the isotopic abundance variations with time. If there has been accelerated decay at some points in earth history, it will be impossible to successfully explain the data without recognizing and modeling this fact. Examples of “constants” which are no longer considered to have remained constant over the history of the universe are found in great quantity in recent physics literature. A common denominator of many of these examples is multidimensional string theory. Hence, I will discuss some examples which are directly related to nuclear decay rates.

The work in this paper will begin with a short discussion of biblical interpretation as it relates to the sequence of events during creation week. Is accelerated radioactive decay, with the associated large radiation densities, consistent with the Genesis account? From there I will move to the interpretation of some uranium isotopic abundances and their explanation in terms of a young-earth model. This will be related to recent evolutionary ideas about the production of nuclei in stars and possible creation alternatives. Then I discuss some ideas about multidimensional topology and how this relates to the quantities in physics which most directly determine decay rates, the so-called “coupling constants.” I consider their allowed variability according to modern theories, principally relying upon some work of Weinberg (1983) and then progressing to a somewhat different approach starting with the paper by Nath and Yamaguchi (1999).

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Genesis Interpretation

The Genesis account, when taken straightforwardly, seems to imply an age of the universe of thousands rather than millions of years. In some early CRSQ articles, John Whitcomb, Jr., offered evidence in terms of the meanings of the original Hebrew language of Genesis one (Whitcomb, 1965; 1967). Many Christians, especially some from the earlier generations of the 1900's, advocated the view that an extensive time gap of millions of years existed between the first two verses of Genesis. To address these concerns, Whitcomb discussed the meanings of the original language, suggesting that Genesis 1:2, should read essentially the way it has been traditionally translated.

For example, the King James Version translation of Genesis 1:1–2 is:

1 ¶ In the beginning God created the heaven and the earth.

2 And the earth was without form, and void; and darkness was upon the face of the deep. And the Spirit of God moved upon the face of the waters.

The “was without form and void” in verse two is correctly translated according to Whitcomb. The contrary view is that the verb “was” should be translated “became,” implying that some pre-Adamic judgment destroyed the original perfection of God’s creation. Other biblical creationists have also expressed similar opinions to that of Whitcomb. Robert L. Reymond (1967; 1998) advocated the same view of *ex nihilo* creation, the historicity of the universal deluge, the tower of Babel incident, God’s covenant arrangement with Adam, the resultant effects on the race of Adam’s fall, and the decrease in longevity of the patriarchs following the Flood. Fields (1973; 1994) wrote a Master of Divinity thesis on this and related questions which later became a book. B. K. Waltke (1975a, b, c, d; 1976) wrote a series of articles in *Bibliotheca Sacra* discussing the cultural background of the Genesis account, the meanings of the original words, etc., and arrived at a view of creation very close to that of these other conservative scholars.

In an earlier article (Chaffin, 2000a), I gave a model in which accelerated radioactive decay occurred early in creation week, before the creation of man. This avoids abnormal radiation doses which living things would receive from an accelerated decay episode. In private discussions, some have expressed reservations about whether radioactive decay could have occurred before the fall of man (Genesis 3), since God’s creation was then “very good.” As a rebuttal to this view, one might note that radioactive decay is simply the emission of particles by nuclei, with some particles changing into other types of particles. It does not necessarily follow that this could not occur before the Fall. Also, the creation as described in Genesis is not an instantaneous one, but a stepwise process of six days. Hence,

although a creation with an inordinate amount of radioactive decay would certainly not be “very good,” it still may have occurred as a part of this stepwise creation in the first two and one-half days, before creation of life.

The authorities cited above have commented on the stepwise nature of the Genesis creation. Reymond (1998, p. 391), in discussing the meaning of Genesis 1: 1–3, offered what he thought was the best meaning. He has God creating a “well-ordered universe” in verse one. Then verse two begins the chronological sequence of telling how God did it, with the earth being empty and formless at first. Reymond wrote (p. 391):

Some object that this construction has God originally creating a “chaos”—an ascription insulting, it is said, to the divine nature. But such an objection is based on an unwarranted *a priori* perception of what God should or should not do in keeping with the perfections of his nature. The objection presumes that an originally unformed earth as a first creative act on his part is unbecoming to his character. But this cannot be demonstrated and therefore must not be assumed.

Whitcomb (1967, p. 71) commented on the state of the earth at the point of verse 2:

The crust, however, had no significant features, such as continents, mountains, and ocean basins, for these were formed on the third day. . . . As a planet, it [the earth] was perfect in every way, but at this stage of creation week it was not yet an appropriate home for man. It was “without form and void” (*tohu wabohu*).

Fields (1973, pp. 128–129) describes and agrees with the views of Calvin, Luther, and others that “the step in Genesis 1:2, was merely a step in the process of creation.”

After an extensive discussion of the gap theory and variations of the gap theory, Waltke concluded (1975c, p. 226):

...verse 1 [Genesis 1:1] is a summary statement, or formal introduction, which is exegeted in the rest of the narrative. It appears to this author that this is the only viewpoint that completely satisfies the demands of Hebrew grammar.

Thus, regarding these subjects, these authors, who have graduate training in bible fields, seem to express a consistent opinion, which opinion will be adopted in this work.

Isotopic Distributions of Uranium

Uranium isotopes U-238, U-235, and U-234 occur in the per cent abundances 99.27, 0.72, and 0.0055%, with other isotopes only occurring in trace amounts. The half lives of these isotopes are 4.47×10^9 years for U-238, 7.04×10^8 years for U-235, and 2.47×10^5 years for U-234. A condition known as *radioactive equilibrium* occurs when the activi-

ties of successive members of a decay chain are equal. The activity is defined as the decay constant (which is the natural logarithm of two divided by the half-life) times the number of atoms in the sample.

Figure 1 shows an analogy between fluid flow and the decay of the atoms in the U-238 to U-234 series. The level of the fluid in a bucket is a balance between the rate of inflow and the rate of outflow. For a given level of fluid in the bucket, a proportional amount of pressure is produced at the bottom of the bucket, where the valves are located. This is analogous to the amounts of radioactive parent atom present. However, the rate of decay also depends on how wide open the valve is, which is analogous to the half life. The most probable decay mode of U-238 is alpha decay, which produces Th-234. Thorium-234 undergoes beta minus decay with a half life of 24.1 days, producing Protactinium-234. Pa-234 then also undergoes beta minus decay with a half life of 6.69 hours producing Uranium-234. Thus U-234 is in the decay chain of U-238, and radioactive equilibrium does exist because 0.0055 times the decay constant of U-234 is the same as 99.27 times the decay constant of U-238. Departures from radioactive equilibrium exist in some samples (Chalov and Merkulova, 1966; 1968; Chalov, Merkulova, and Tuzova, 1966; Thurber, 1962) but the departures are relatively small.

The variations may possibly be explained in terms of the difference in relative solubility of U-234 and U-238 starting from hexavalent and tetravalent uranium in compounds and their decomposition products (Chalov and Merkulova, 1966; 1968). Thus, a fraction of the U-234 atoms present in a mineral lattice will have formed by radioactive decay starting from U-238. Due to the recoil of a nucleus during alpha decay, a significant number of daughter nuclei will lose their former link with the mineral lattice. These daughter U-234 nuclei will as a result be, on the average, found in different linkages as compared to the U-238 nuclei. This was Chalov and Merkulova's explanation for why they found different rates of dissolution of U-234 and U-238 in their laboratory experiments. Working together with T.Z. Tuzova, Chalov and Merkulova attempted to use this difference in solubility to obtain an age of the Aral Sea (southern Kazakhstan and northern Uzbekistan). Their result was 150 ± 30 thousand years. However, some fragile assumptions were needed to arrive at this number, and such ages are not well accepted even among evolutionists.

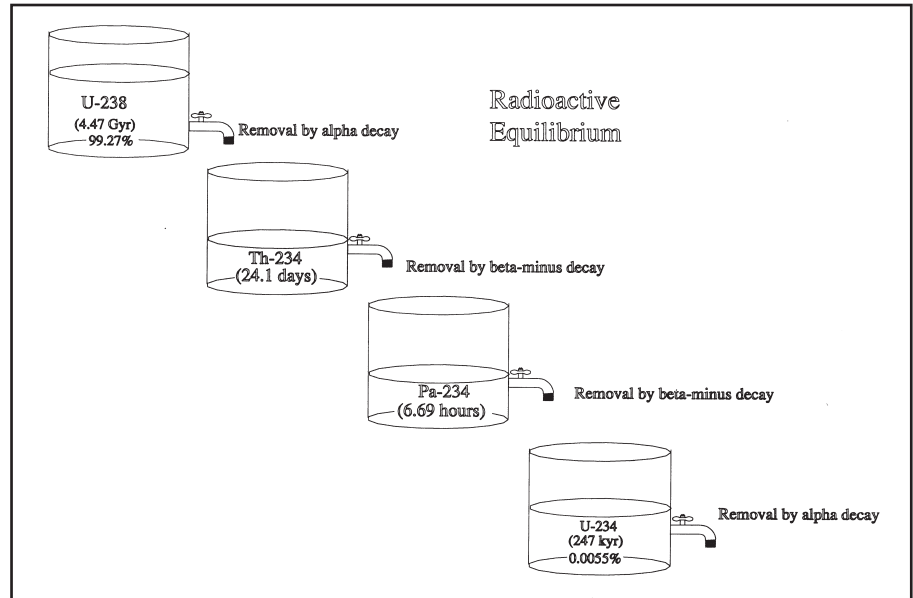


Figure 1. An analogy between fluid flow and the decay of the atoms in the U-238 to U-234 series.

From a young-earth viewpoint, it is easy to point to these fragile assumptions to invalidate age determinations such as those just mentioned. However, with an earth of only some thousands of years old, it is difficult to explain the bulk of the approximately equal ratios without an episode of accelerated decay. Starting from an arbitrary initial state, it takes more than one half life of U-234 to establish equilibrium, implying an age of the samples very much larger than straightforward Biblical interpretation would indicate. Figure 2 shows the graph of the U-234 abundance versus time, assuming the U-234 starts with a 100% abundance, or was equal in abundance to that of U-238. One sees that, for this starting assumption, and assuming no accelerated decay, an age of the earth of at least four million years is implied. A possible alternative assumption is to assume that there was no U-234 at all at the start. Figure 3 shows the result of that calculation. Assuming no accel-

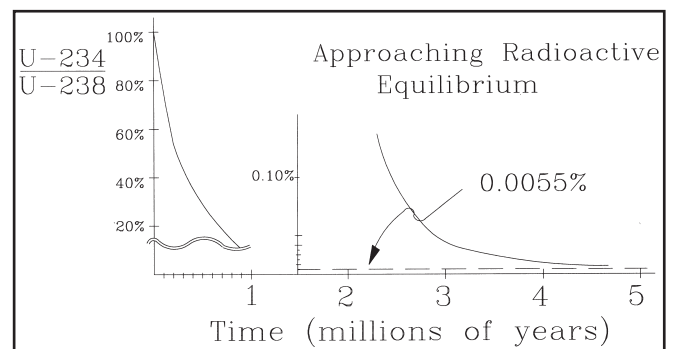


Figure 2. Graph of the U-234 abundance versus time, assuming the U-234 starts with a 100% abundance, or was equal in abundance to that of U-238. The time scale shown assumes that no accelerated decay occurred.

ated decay, this assumption thus implies an earth age of at least 1.2 million years.

To justify the young-earth viewpoint, one would be logically correct in claiming that the rocks may have been created already in a state of radioactive equilibrium, with no time needed to reach that state. However, a more natural explanation seems to be provided by accelerated radioactive decay. We do not know the original ratio of U-234 to U-238 in the created materials of the early earth, but if we make some reasonable guesses, then a period of accelerated decay would adjust this ratio to the 0.0055 % ratio presently found in the bulk of earth materials. This may be evidence that such accelerated decay did, in fact, occur. Furthermore, by the time of the Garden of Eden, radioactive equilibrium would have been in existence, and decay rates of uranium much smaller, possibly even zero.

The U-235 abundance, compared to U-238, also seems to support this point of view. If the initial abundances of these two isotopes were of the same order of magnitude, then several half lives of U-235 are needed to establish the present 0.72% and 99.27% isotopic abundances, implying sample ages of a few billion of years (Chaffin, 1985). As in the U-234 cases, we do find slight variations in U-235 percent abundances between different minerals collected at different sites (see for example Malyshev et al., 1977). However, the variations are small. To advocate a young earth without accelerated decay or very rapid initial decay after the creation of the elements, one seems forced to assume that the uranium isotopes were created in isotopic per cent abundances approximating those found today (Chaffin, 1985).

When considering evidence for the presence of plutonium-244 in solar-system rocks (Chaffin, 2000b), evolutionary astronomers have concluded that a supernova must have occurred close in time and space to the existence of the hypothetical pre-solar nebula. Although young-earth assumptions would not favor the solar nebula idea, the rock data on Pu-244 nevertheless should be considered. If these rocks did in fact contain Pu-244 (half life 8.0×10^7 years), this would be additional evidence for accelerated decay.

Dating with Stars

In recent years, astronomers have attempted to date the universe independently of the assumed models of inflationary expansion and other assumptions (Meyer and Truran, 2000; Arnould and Takahashi, 1999). One of the ideas is to measure the abundance of U-238. Another idea uses Th-232. Now Th-232 is the starting element of the *thorium series*, while U-238 is the starting member of the so-called *uranium series*, so they are in different decay chains and do not decay into each other. The method em-

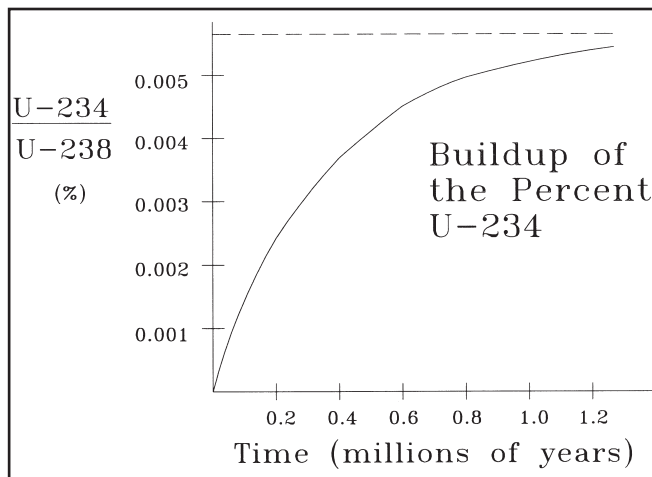


Figure 3. Graph of a possible alternative assumption — that there was no U-234 at all at the start. Assuming no accelerated decay, this leads to an earth age of at least 1.2 million years.

ploy *measured* abundance ratios in a large number of ultra-metal-poor (UMP) stars, and compares the present-day, *measured* abundances to theoretical values to calculate the age of the star. For UMP stars, studies have shown that s-process model abundances are under-represented as compared to r-process stars. The s[low]-process is a build up of heavy elements by capture of neutrons in nuclei, with enough time in between captures for beta decays to take their course. The r[apid]-process is a rapid capture of neutrons with no time in between captures. Many evolutionary astronomers now think that large-mass, Type II supernovas are a likely location for the r-process type of nucleosynthesis.

Actually, the idea of using U-238 or Th-232 abundances to date stars is not a recent one (Butcher, 1987). However, measurements have only recently begun to provide the type of data in UMP stars that is needed (Westin, Sneden, Gustafsson, and Cowan, 2000) According to a news story (“Dating a star like a rock,” 2000) and a press release on the web site of the European Southern Observatory (www.eso.org), a paper is in preparation by Gustafsson, Mitzuno-Weidner, Hill, Primas, Bonifacio, Molaro, and Nissen which will report a new observation of uranium in a spectral line of the UMP star CS22892-52. What is done is to compare the measured abundance of uranium or thorium to that of europium to extract an age, based on the r-process model for initial abundances. The press release stated that the lower limit for the age, based on the U-238 measurement, is determined for the CS22892-52 star as 12 billion years. For the star HD115444, a lower limit of 11 billion years is already in print (Westin, Sneden, Gustafsson, and Cowan, 2000).

The r-process model can only be applied to stars which are thought to be very old stars, such as these galactic halo stars, CS22892-52 and HD115444. Stars of that “age” are

thought to have been produced before much s-process material was mixed into the interstellar medium. Any admixture would ruin the whole method. It is possible that, after around 20–30 stars have been measured, the results may not be uniform and these assumptions will therefore be proven wrong. Meanwhile, this remains an active area of research. Interestingly, the high-temperature environments of stars are known to alter half lives, particularly those of elements such as Re-187 (Meyer and Truran, 2000). However, attempts are made to factor these effects into the equations.

The r-process models produce initial abundance ratios for U-235/U-238 of 1.35 ± 0.14 and for Th-232/U-238 of 1.58 ± 0.15 , where the errors are the standard deviations based on the eight different models reported by Pfeiffer, Kratz, and Thielemann (1997). Thus, according to these models, slightly more U-235 is initially produced than U-238, and after 12 billion years, radioactive decay will have reduced the abundance ratio of U-235/U-238 considerably. Since the half-life of U-235 is 7.04×10^8 years, and of U-238 is 4.47×10^9 years, calculations show that the present-day U-235/U-238 ratio in these UMP stars should be about $6.4 \times 10^{-3}\%$. Hence, it will be interesting to see if some future measurements will be able to determine U-235 abundances in these stars. On earth the ratio is 0.72%. Since the evolutionary model has more recent r-process material contributing to the solar material, this does not necessarily disprove the stellar evolution scenario. But it does not prove it either.

Accelerated nuclear decay, if it occurred uniformly throughout the galaxy, would of course destroy the validity of these methods of calculation. It would also change rates of nuclear processes in the cores of stars. Hence, although we may reject the evolutionary assumptions for stars, it is a field of future research to determine exactly which assumptions we reject or accept in a young-earth model.

With these data in mind, we now turn again to the subject of how accelerated decay could occur. In Chaffin (2000a), a sketch of a mechanism was presented. We now attempt to provide some possible further details for the sketch.

Topology and Strings

Multidimensional string theories quickly lead to the branch of mathematics known as *topology*. This, of necessity, is what happens when one takes these extra coordinates, or dimensions, seriously. An *n-dimensional manifold* is a space which is defined to be smooth, or that every point can be surrounded by a collection of other points which is equivalent to the interior of an n-dimensional ball (Alexandrov, 1961; Pontryagin, 1999). For example, the surface of a sphere is a two-dimensional manifold, which mathe-

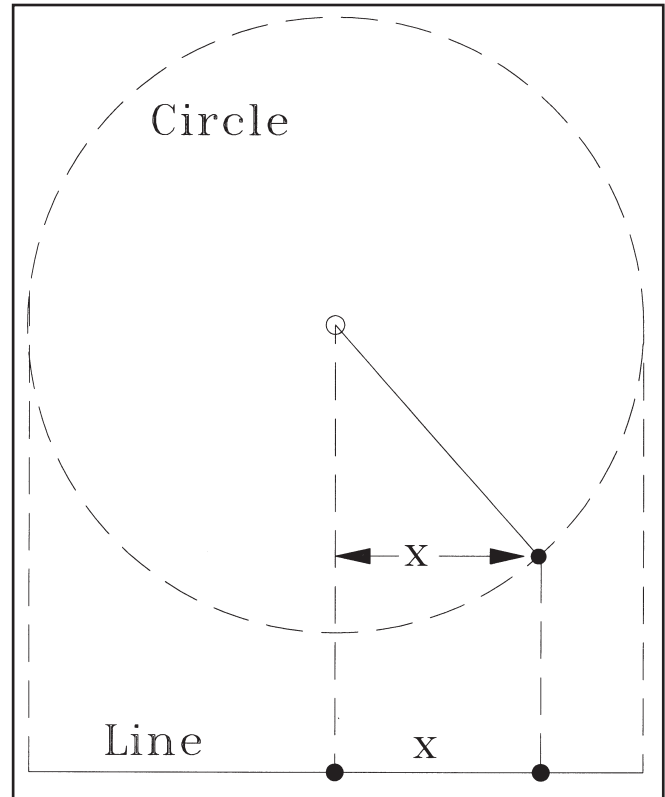


Figure 4. The position of a pendulum bob, confined to move in a single vertical plane, can be completely specified by a single linear coordinate x , provided the pendulum does not swing over the support's level. If the pendulum is free to swing higher than the support, then the circular topology is needed to specify the position. (Figure drawn after Rourke and Stewart, 1986).

maticians write as S^2 (pronounced *S-two*, not *S-squared*). One needs two numbers to specify a point on this manifold, hence the number 2 means it is two-dimensional. Another two-dimensional manifold is the surface of a torus, T^2 . For precise, mathematical purposes, the sphere S^2 and the torus T^2 are distinct entities, and should not be confused.

For example, suppose we are trying to describe the motion of a pendulum (Figure 4). Initially, let us suppose that the pendulum is swinging back and forth, staying perfectly within the confines of a vertical plane. Then we could draw a line, or projection, down to the point on a flat, horizontal surface directly below the pendulum ball. A single coordinate x would then suffice to specify the position of the pendulum ball, this coordinate specifying the position on a *straight line*. However, for large oscillations of the pendulum, and if the pendulum was fixed by a universal joint at the top, the pendulum could swing over the top. Our single coordinate would then not suffice to distinguish positions above the support from positions below the support. Hence, a more correct mathematical model for the pendulum would be the *circle*. If, in addition, the pen-

dulum were now able to swing in all directions, and not confined to one vertical plane, then the circular topology becomes inadequate, and a more correct model is the sphere, S^2 .

Suppose now that the problem is that of two pendulums, each confined to move in a vertical plane but allowed to swing over the top. The two pendulums move *independently* of each other, assuming positions on two different circles. The combined coordinates now have a different topology, the topology of the torus, T^2 .

One of the early pioneers of topology was Henri Poincaré, whose active work on the subject occurred during the 1890's up to his death in 1912. Poincaré analyzed different surfaces by thinking in terms of deformations of loops, which links to what are now called *homology* and *homotopy*. In mathematical topology, homology theory concerns itself with the question of the number of holes in the space. Shown in Figure 5 are three curves, a, b, and c on the surface of a torus. The curves a, b, and c have something in common, they cannot be shrunk to a point by continuous sequence of deformations. For curves a and b it is because the hole is there. For curve c it is because the curve is wound around a closed circumference and cannot be shrunk unless one cuts the curve, moves it, and then pastes the ends together. In topology, this is described by stating that a and b belong to the same homology class, whereas c belongs to a different class. Similarly, the concept of homotopy concerns itself with deforming loops. Two loops are homotopic if they can be continuously deformed into each other. These concepts, and others, become important tools in analyzing topology and ultimately multidimensional string theory.

Within the last five to ten years research has uncovered numerous *dualities* relating different limits and formulations of string and membrane theories. Greene (2000, pp. 231-262) and Duff (1998) have discussed the duality between ordinary vibrational modes and winding modes of a string (see Figure 6). A value of the radius for compactified dimensions leads to the same results or equivalent results for a different radius, in which the winding modes and ordinary vibrational modes change roles in the equations of the theory (Dai, Leigh, and Polchinsky, 1989). Another type of duality relates the *strong coupling* limit of one theory to the *weak coupling* limit of another. A *coupling constant* is a number which gives the strength with which an elementary particle is coupled to the field that it experiences. For example the coupling constant for interaction with the electromagnetic field is the electric charge. In some work by Witten (1996) and Lykken (1996), it was speculated that, contrary to previous thought (Kaplunovsky, 1988; 1992), strong coupling limits of certain string theories were more relevant to accelerator physics. This led to some more realistic applications of string theory than had been previously been possible (Nath and Yamaguchi, 1999).

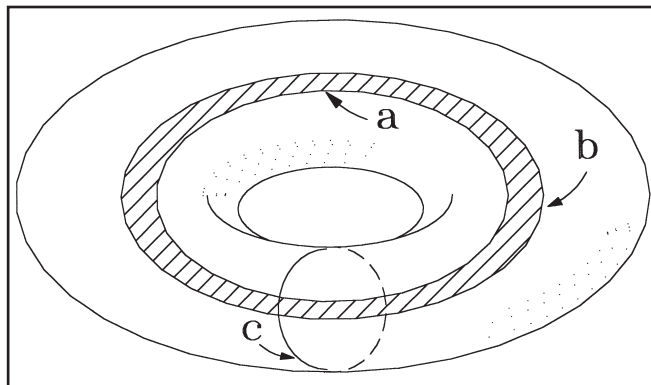


Figure 5. Three closed curves on the surface of a doughnut (torus) illustrate inequivalent and equivalent closed paths. Curves a and b, which bound the hatched area, can be smoothly distorted into each other, whereas curve c winds around a different direction and cannot be distorted into a or b, without cutting and pasting the ends (Figure drawn after Eguchi, Gilkey and Hanson, 1980).

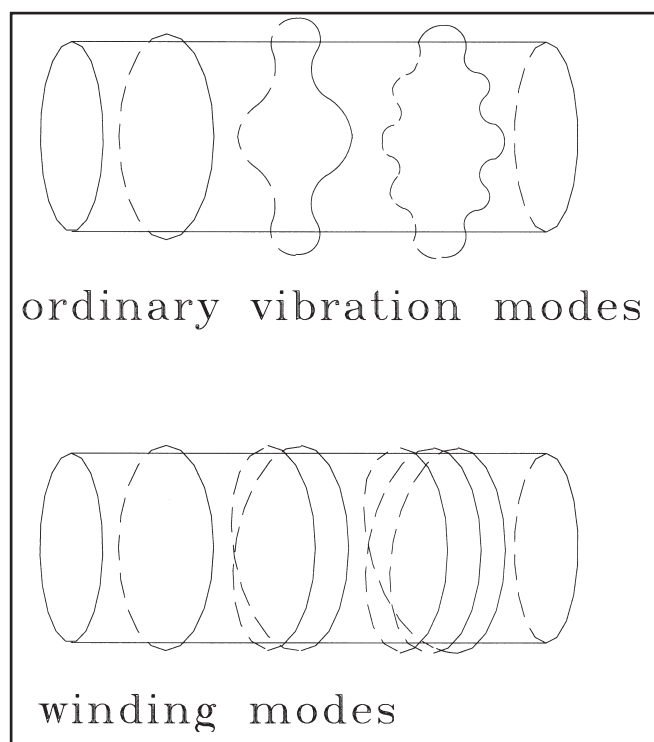


Figure 6. The ordinary vibration modes of closed strings (above) and the winding modes (below). In the equations of string theory, these two modes carry energy, and exchange roles when the radius of the compactified dimension moves from small to large.

Compact Circumferences and Coupling Constants

Weinberg (1983) used generalized Kaluza-Klein models having $4+N$ dimensions to find a relation between coupling constants and the root-mean-square (rms) circumfer-

ences of the compactified dimensions. As discussed in Chaffin (2000a), the original Kaluza-Klein model had only one extra dimension besides the usual four of ordinary spacetime. Witten (1981) discussed the generalization to the case where there are more compact dimensions. Weinberg applied this idea to reduce some assumed higher-dimensional equations of gravitation theory to the four-dimensional case, and worked out the results of his equations for some simple examples. These examples assign an assumed topology to the compactified dimensions, and then calculate the rms circumferences. For one example, he assumed that the topology corresponded to the symmetry group $SO(N+1)$, the group of rotations, contiguous to the “leave-it-alone” or identity rotation, in $N+1$ dimensional space.¹ This gave the result for the $SO(N+1)$ coupling constant:

$$g = \left(\frac{\kappa}{R} \right) \left[\frac{1}{2} (N+1) \right]^{1/2} \quad (1)$$

Here, $\kappa^2 = 16\pi G$, where G is Newton’s gravitation constant, R is the radius of this $(N+1)$ - dimensional shape with topology analogous to that of a sphere. Thus, for a highly symmetrical topology such as this, all the coupling constants would be the same.

Weinberg also considered an example having the symmetry $SU(3)$, the group of all unitary 3×3 matrices with determinant plus one. In this example there are two different possible values for coupling constants g and g' ,

$$\begin{aligned} g &= \frac{\sqrt{2}\kappa}{R} \\ \text{and} \\ g' &= \sqrt{\frac{2}{3}} \frac{\kappa}{R} \end{aligned} \quad (2)$$

Thus, the ratio of the two coupling constants is the square root of three, and does not depend on the radius R of the extra dimensional shape.

Candelas and Weinberg (1984) generalized these results to include the effects of quantum fluctuations of matter fields on the vacuum, and found slightly modified versions of the earlier relations between the radii R of the compactified dimensions and the coupling constants. They also generalized some considerations of Rubin and Roth (1983) which attempted to relate the radii of the compactified dimensions to the average temperature of the matter fields contained in the universe.

The change of the compactified radii with temperature can be understood physically through the Casimir effect (Chaffin, 2000a; Hawking, 1996). The Casimir effect is a

force between two parallel conducting plates caused by differences in zero-point energy of the electromagnetic field. In a similar manner, at zero temperature, the gravitational zero-point energy of the Kaluza-Klein ground state leads to the collapse of the fifth dimension, but in that case we deal with the topology of the compactified dimensions, not with parallel plates. In the parallel-plate case, if a gas of photons at fixed temperature is introduced between the plates, the net pressure on the plates will be the sum of two contributions: the positive pressure from thermal photons, of constant magnitude, and the negative Casimir pressure, varying in inverse proportion to the fourth power of the plate separation. The negative Casimir pressure arises because the short distance between the plates prevents standing waves of certain wavelengths from existing between the plates. If the plates start out close together, the negative Casimir pressure is stronger than that of the thermal photons and the plates collapse. If they start out at a distance such that the Casimir pressure is weaker, then the plates will fly apart with nothing to stop the separation. The thermal photon pressure changes as the plate separation changes, but only as (separation)^{-4/3}; i.e. much more slowly than the Casimir pressure.

Candelas and Weinberg (1984), and before them Rubin and Roth (1983), attempted to extrapolate from the parallel-plate case to a realistic Kaluza-Klein model. Such a model would remove the artificial constraints of an assumed external geometry and an assumed time-independent internal geometry. Realistic models would also involve more than just one compact dimension with compactification brought about by vacuum expectation values (VEVs) for non-gravitational fields, and would include fermionic (half-integral spin) fields. The presence of curvature in both the compact and non-compact dimensions, the response of the VEVs to changes in temperature, and fermion degeneracy pressure might well all contribute to behavior very different from that observed in the parallel-plate case.

This idea provides a possible mechanism for changing the radii of the compact dimensions as the universe expands and its background temperature changes. Early in creation week, it may be that the mechanism could also work in a young-earth model.

Kaluza-Klein Excitations

In superstring theory, we need to link a 10-dimensional “manifold,” which is simply a framework which can be smoothly described by 10 independent coordinates, with our observed four-dimensional spacetime. If the extra six dimensions are curled up into a compact space, this simply means that every point of four-dimensional spacetime has

¹A *group* is a set of elements plus a rule of combination of pairs of elements, satisfying certain requirements, including that every element has an inverse.

one of these compact six-dimensional spaces associated with it (In more recent theory, 11 dimensional membranes are wrapped up to make ten-dimensional superstrings, but that is just an unneeded complication as far as we are concerned.). If the size of the compactified six-dimensional space is small compared to the scale of everyday life, we would not directly detect the effect of these extra dimensions (Chaffin, 2000a).

At high enough energies, higher even than those of the abortive superconducting supercollider, the SSC—which began but did not complete construction in Texas, a particle accelerator would be likely to detect the presence of the so-called Kaluza-Klein excitations or Kaluza-Klein modes. In quantum mechanics, waves are associated with all particles. When we consider string theory, we find that if a spatial dimension is curled up, then the momentum p associated with the waves wrapping around this dimension will be quantized, with values $p = nh/(2\pi R)$, $n = 0, 1, 2, 3, \dots$, and h is Planck's constant, while R is the radius of the compactified dimension. In this picture the masses of the quantized excitations, the masses m_n of the particles, are given by $m_n^2 = m_0^2 + n^2 h^2/(4\pi^2 R^2 c^2)$, where m_0 is the mass of the mode with zero momentum and c is the speed of light.

Particles can be divided into fermions (half-integral spin) and bosons (integral spin). It is possible that the fermions or some of the fermions may not have Kaluza-Klein excitations (Dienes, Dudas, and Gherghetta, 1999). This is dependent on exactly how the extra dimensions are compactified. If the fermion corresponds to excitations located at the fixed points of an *orbifold*, then no Kaluza-Klein excitations exist. In mathematically precise formulations of topology, an *orbifold* is a way of smoothing over or “blowing up” certain fixed points at which different coordinates must be joined (Dixon, Harvey, Vafa and Witten, 1985).

In the actual multidimensional string theories, we need to make contact with the “real” world of four spacetime dimensions. The 10-dimensional superstring theory must compactify six of the dimensions on a six-dimensional compact manifold. Particle physicists have, in the last 15 years, spent a great deal of time studying just how to do this. Fortunately, mathematicians have been studying topology since the time of Poincaré in the late 1800's. While they have not fully developed all the machinery needed by the string theorists, two mathematicians, Eugenio Calabi and Shing-Tung Yau had studied a type of six-dimensional space, known as a Calabi-Yau space (pronounced *cal-lah'-bee-yah'-oo*) which particle theories needed (Greene, 2000). The topology of this space, with the requisite number of “holes,” seems to be right to allow the known quarks and leptons to be described in terms of string theory. The quarks and leptons are grouped into three “families,” which are allowed by these Calabi-Yau shapes. They allow description in terms of rep-

resentations of the $SU(3) \times SU(2) \times U(1)$ group of the so-called *standard model*.

Unified Theories

In 1974 the $SU(5)$ theory of combined strong, weak, and electromagnetic interactions was proposed (Georgi and Glashow, 1974; Georgi, Quinn, and Weinberg, 1974). The $SU(5)$ theory receives its name because it is modeled after five by five special unitary matrices (hence the nickname SU standing for special unitary), *special* meaning they have a determinant plus one. This theory allowed all the families of quarks and leptons to be combined into representations of the $SU(5)$ group, which means that we only needed particles called gluons, W^+ , W^- , Z^0 bosons, and the photon to describe the forces between the quarks and leptons (Georgi, 1989, has given a popular-level description of how this theory was formulated.). Basically, the $SU(5)$ theory had only one “coupling constant.” In accord with previous discussion, “coupling constant” may be thought of as a number which describes how much force originates from placing particles of known type a certain distance apart. Each type of force has its own coupling constant, but the $SU(5)$ theory implied that the coupling constants for strong, weak and electromagnetic forces all originated from a single constant, diverging into their various values as the energy of the interactions is lowered from high energies down to low energies. The reason for the divergence of these values has to do with what is called *renormalization*, and with the *effective field theory* which results from performing the renormalization appropriate to a given energy scale. In quantum field theory, a particle is surrounded by a cloud of virtual particles, which cloud will be penetrated to varying degrees by a second particle interacting with it (Georgi, 1989). A more energetic particle penetrates further. For example, a real particle with positive electric charge will be surrounded by pairs of virtual electrons and positrons. On the average, the virtual positrons are pushed farther away from the real particle, while the virtual electrons are nearer to it. So on the average, the real particle has more negative charge near to it than far from it. A second real particle, depending on its energy, will penetrate this cloud to a lesser or greater degree. For this reason, the effective interaction depends on the particle energy, and the coupling constant of electromagnetic interactions is less for smaller energies. In the case of the strong force, the gluons cause the force to get weaker at larger energies (Georgi, 1989, p. 432).

Renormalization theory says that not only the coupling constants, but also the masses of particles appear to vary on different energy scales (Nelson, 1985). While quantum theory connects this effect to varying energy scales, the basic ideas are actually much older. J.J. Thomson discovered

the so-called electromagnetic mass in 1881 (Thomson, 1881). Thomson correctly noted that a charge moving through a dielectric experiences a resistance, which is non-dissipative, and hence is best described by an additional contribution to the mass. The resistance is comparable to that of a sphere moving through a perfect fluid. Motion of the sphere is impeded by the presence of the fluid. Using James Clerk Maxwell's theory of electricity and magnetism, Thomson showed that the charged sphere, moving through the dielectric, would experience an additional mass. Thomson's equation for the new mass m is:

$$m = m_0 + \frac{4}{15} \frac{\mu_0 e^2}{a} \quad (3)$$

where e is the charge, a is the radius of the sphere, and μ_0 is the magnetic permeability. While quantum theory does not assign a radius to the electron, the "vacuum polarization" effect is nevertheless a real effect (Georgi, 1989, p. 434; Bjorken and Drell, 1964, section 8.2). In many lab experiments, the particles have low energy and are nowhere near the large energies that bring out these effects. However, for experiments involving modern particle accelerators, these effects become evident: the effective coupling constants and effective masses vary with energy.

The SU(5) theory of Georgi and colleagues had an unfortunate failure. It predicted the decay of the proton, with a half-life greater than 10^{29} years. As a result of this prediction, experiments were set up to detect this proton decay, and no conclusive evidence for such decays was found. The half-life of the proton, if not infinite, was shown to be higher than the range which the SU(5) theory seems to allow. Other unified theories based on other groups or on string theory are possible, and this is still an active field of research. For example, Shiu and Tye (1998) discussed the possible suppression of proton decay by an additional symmetry, while Dienes, Dudas, and Gherghetta (1998) discussed a *higher-dimensional* mechanism involving selection rules for the Kaluza-Klein excitations which allow all proton-decay processes to have vanishing probability. In the SU(5) theory and in similar theories allowing proton decay, there are particles, either X-bosons or Higgs particles, which are responsible for the proton's decay. In the Dienes, Dudas and Gherghetta theory, however, the proton does not have Kaluza-Klein excitations which leads to a zero probability for its decay (Technically, the proton is said to be restricted to the fixed points of an orbifold, at which point the probability for interacting with the X-bosons or Higgs particles is zero.). Of course, these theories are untested at present, so the correct explanation for the lack of proton decay is still undecided.

Unfortunately, this also leaves open the question of whether or not the SU(5) theory was correct in predicting that there is only one coupling constant at high energies. If the radii of compactified dimensions varied over the early

history of creation, then a related question also seems to be unanswered for us. Could the rates of alpha and beta decay vary relative to each other over the history of the universe? This is an interesting question, and needs to be answered in order to correctly interpret radioisotope data. A start in this direction will be provided in the next section.

Kaluza-Klein Excitations and the Fermi Coupling Constant

Humphreys (2000) provided a model for accelerated beta decay. However, his approach involved different assumptions than will be addressed here. Nath and Yamaguchi (1999), considered the question of whether Kaluza-Klein excitations contribute to the so-called Fermi constant, which determines the fundamental rates of beta decays. Enrico Fermi, the Italian-American of the Manhattan project, was responsible for the first realistic theories of beta decay, so this coupling constant G_F , as applied in beta decay theory, is named after him. For the case of one extra dimension, Nath and Yamaguchi showed that to leading order in the ratio of the W boson mass M_W to the mass proportional to $1/R$ (the compactification scale mass M_R), the effective Fermi constant G_F^{eff} is given by

$$G_F^{\text{eff}} \cong G_F^{\text{SM}} \left(1 + \frac{\pi^2}{3} \frac{M_W^2}{M_R^2} \right) \quad (4)$$

Here, G_F^{SM} is the value of the Fermi constant which may be calculated from the standard model of quantum field theory (Nath and Yamaguchi, 1999, comment that the standard model agrees very well with experiment), which does not involve any assumptions about extra dimensions. For the case of more than one extra dimension, Nath and Yamaguchi derived a simple formula similar to the above but depending on the extra dimensions. From the results of standard model calculations, plus experimental measurements (Abachi, et al., 1996; van Ritbergen and Stuart, 1999), Nath and Yamaguchi showed that the energy M_{RC}^2 was at least 1.6 TeV. This encourages particle physicists to hope that, with the completion of the Large Hadron Collider (LHC), expected in 2005 or so, evidence for these extra dimensions may be found (see Kane, 2000, for a semi-fictitious account of expectations).

Now, because we are interested in the possibility of accelerated decay in the early universe, we need to take the discussion a step further than Nath and Yamaguchi did. In their paper, they only considered present-day measurements. Because of our interest in explaining radioisotope data in terms of a young earth, we may think as follows. If, over the early history of the universe, the radius of compact dimensions should change, then so would the mass scale

M_R , and hence the value of the Fermi constant. Under the simplifying assumption that other factors in the equation do not change as radically as M_R does, decreases in the sizes of extra dimensions would increase M_R , and hence decrease the values of G_F . This in turn would mean that half-lives for beta decays of nuclei would become larger as the extra dimensions became smaller. Thus, one would expect accelerated decay to have occurred early in the history of the creation.

Conclusion

We have seen that a straightforward biblical interpretation does not rule out a period of accelerated decay early in creation week. Since life does not appear until some time on day three, the cessation of the accelerated decay at that point prevents life from receiving abnormally large radiation doses. The models presented depend on the compactification of extra dimensions, with the compactification being completed early in creation week. Other models may lead to accelerated decay at other points, for instance during the Fall of Genesis 3 or during the Flood of Noah, but it would seem that these other episodes would probably have to be explained using alternative models, and could not allow as much accelerated decay as could be accommodated early in creation week.

Since God is the origin of physical principles, it would be wrong to state that He must act in a certain way. However, Scripture is a reliable record of His actual creation. The models considered here merely point out some unnecessary assumptions involved in interpreting radioactive decay: half lives may not have been constant.

I have also discussed the explanation of uranium and plutonium-244 abundances using accelerated decay, and given explicit equations for the determination of the variation of the Fermi constant. These results enable one to conjecture about how much the variation must have been in order to explain present-day isotopic abundances. Since there is no precise number to match with theory, and since various approaches to the final, present-day abundances are possible, these results remain explanatory in nature. Perhaps future studies will be able to connect more precisely with the data.

Acknowledgments

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Book Review

Origins: Linking Science and Scripture by Ariel A. Roth

Review and Herald Publishing Association, Hagerstown, MD. 1998, 384 pages, \$29.99

This is an impressive book for its depth of scholarship, its clarity of expression, and its perceptive analysis of the current principal theories of origins: young-earth creation and old-earth evolution. The writer is respectful of the claims of evolution, but he shows through careful analysis and many literature references how far short these claims fall in agreement with the evidence. In contrast, the same evidence from biology and geology is shown to be eminently compatible with the concept of an earth filled with life by God some thousands of years ago.

Dr. Roth opens the discussion with a section entitled “The Questions” giving some historical background on the origins controversy. A chapter called “Fashions in Thinking” describes various paradigms which have been dominant in the past, only to go out of fashion when prevailing opinion changed. Paradigms come and go, and may be true of false.

As we search for truth, we can avoid letting ourselves be trapped by erroneous paradigms by practicing both independent thought and thorough investigation. We must always base our conclusions only on the firmest data (p.44).

Succeeding sections of the book include “Living Organisms” which is a detailed description of the biosphere and theories of its origin; “The Fossils,” a study which essentially falsifies the theory of evolution; and “The Rocks,” in which evidence indicates that sedimentary rocks were deposited rapidly by flood waters rather than slowly over eons of time.

One section is entitled “An Evaluation of Science and Scripture” in which the author points out that science deals with only part of reality. Naturalistic science can tell us nothing of morality, freedom of choice, consciousness, or purpose. “There exists a vast realm beyond the simple cause-and-effect explanations of science” (p. 286). Likewise the investigation of historical events is largely outside the purview of science since these are non-repeatable, in contrast to experiments in physics or chemistry.

A chapter entitled “Scripture: Something Unusual” deals with authentication of the Bible. Evidences includes independent historical records, archaeological discoveries, the prevalence of flood stories among all peoples, and the remarkable fulfillment of prophecies centuries after they were first written. A further chapter discusses some questions on scripture interpretation, and a final chapter is entitled “Is Science in Trouble?” Here Dr. Roth quotes the philosopher Malcolm Muggeridge, who stated: “It is time to try to reestablish an equilibrium between science and spirituality, allowing mankind to find again a place in the universe” (Note 32). Dr. Roth goes on to say,

The problem is not just evolution. In a sense, evolution is only an important symptom of a more deep-seated issue. The real difficulty is more whether naturalistic science is going to persist in trying to provide answers to all questions within its own closed system of explanations. How did science get into this intellectual straitjacket? Science made its greatest error when it rejected God and everything else except mechanistic explanations... Science would not now be facing apparently insurmountable challenges to evolution if it had not adopted such a strong exclusive, naturalistic stance. Concepts of the creation life would still offer a possible explanation as they did for the pioneers of modern science (p. 334).

As a comprehensive and extremely well-researched book, this volume should be attractive to anyone interested in the subject of origins. It would be especially suitable as a textbook for high schools and colleges where the evidence for creation and criticism of evolution are allowed to be taught. The book includes numerous illustrations, a glossary of technical terms, and an index.

Carol Armstrong
(deceased)

The Molecular Biology of Genetic Transposition

Jerry Bergman*

Abstract

This paper reviews the functions, mechanisms, and types of movable genes called transposons. It is concluded that they play an important role in all living organisms, including antibiotic resistance and increased genetic diversity. This field has exploded in recent years, and indications exist that movable genetic elements are a significant part of the genome both in terms of size and importance. Research has also indicated that all transposons are controlled by

a complex genetic mechanism that functions to reduce the likelihood of inappropriate transposon placement. The evidence now indicates transposons are part of a complex designed system that serves the function of producing morphological variety. Furthermore, the transposition mechanism cannot be explained by a step-by-step evolutionary process but must exist as a complete unit in order to function.

Introduction

Transposition is a complex genetic process involving organized movement of genetic elements such as *transposable elements*, or *transposons*, to new locations on the DNA. Often called jumping genes, transposition literally means “a change in position.” Gene movement can be either to a position somewhere else on the same chromosome, or to another chromosome altogether. Transposons have been called the “smallest living creatures” because they consist of replicating units that seem to behave autonomously (Plasterk, 1993). It is now known that movable genetic elements play an important role in many living organisms, including as part of the antibiotic resistance mechanism and to increase genetic diversity. Evidence now also exists that they play a role in cancer development.

The Discovery of Transposons

The first transposable elements to be recognized include *controlling elements* (now called transposons), *activators* (now called regulators), and *disassociation elements* (now called autonomous elements). They were first identified as responsible for color alterations in *Zea Mays* corn by Barbara McClintock in the 1940s. McClintock presented her first paper on her findings at a 1951 genetics symposium at Cold Spring Harbor Laboratory on Long Island, N.Y. (McClintock, 1951). Her conclusion that genes actually move from one place to another on the genome in an organized manner was at first greeted incredulously (Dean,

1984). Her work on transposons had been an outgrowth of her earlier research confirming that genetic crossing-over during meiosis does in fact exchange genes (Landman, 1994).

A major observation which led her to postulate the transposon concept was the discovery that in plant offspring one sister cell (cells that are descended from a cell after differentiation, thus are the same kind of cell) *gained* what the other *lost* in a regular way. For example, McClintock noted that whenever one sector of a variegated chlorophyll pattern plant leaf showed a greatly increased number of green streaks on the white background, its twin showed a *reduced* number of green streaks (Dean, 1984). These plants led McClintock to conclude that one cell had gained some component that the sister cell had lost during a mitotic cycle (McClintock, 1987).

The specific factor McClintock found to be responsible for governing color was a *suppressor* gene which she called a *disassociater* or Ds element. When the disassociater lies near the gene for purple, for example, this color is repressed, but when it moves to another spot *away* from the purple gene, the color purple is expressed. The suppressor genes are in turn controlled by regulator genes that are located nearby the suppressor genes on the same chromosome.

Even after McClintock had published numerous well documented research reports in leading genetic journals, the scientific community resisted her conclusions. The response to her findings was in her words:

... in some instances, hostility. A third attempt to support the thesis of the origin of mutable loci in maize appeared in 1953 in the widely read journal

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Genetics. It was titled "The Induction of Instability at Selected Loci in Maize." This article appeared before copying machines practically eliminated requests for reprints... In this instance I received a total of only three requests for this reprint! By then I had already concluded that no amount of published evidence would be effective... There were many vocal skeptics. Therefore, the method I had chosen to record data and conclusions from them was continued into the early 1960s.... In retrospect, it appears that the difficulties in presenting the evidence and arguments for transposable elements in eukaryotic organisms were attributable to conflicts with accepted genetic concepts. That genetic elements could move to new locations in the genome had no precedent and no place in these concepts (McClintock, 1987, p. x).

A major reason for the skepticism common at this time was because McClintock's findings were so radical and the phenomena she described "could not be explained in terms of the then-current framework of genetics. This mind-set began to change with the discovery of movable DNA systems in bacteria" (Landman, 1994, p. 70). McClintock spent decades collecting reams of data and eventually her conclusions could no longer be disputed (Keller, 1983). The transposon process was eventually so well empirically confirmed that she was awarded the Nobel Prize in 1983.

The transposition field has exploded in recent years, and indications now exist that movable genetic elements are a significant part of the genome, both in terms of size and importance (Holzman, 1991; Nitasaka, Yamazaki, and Green, 1995). Their contemporary importance is indicated by the fact that a *Medline* journal search of peer reviewed research revealed 2,376 published articles on transposons from 1995 to 1999 alone. Research has also indicated that transposons are controlled by a complex genetic mechanism that is used to reduce the likelihood of inappropriate placement. Some evidence now indicates transposons are part of a complex system that serves several functions including producing morphological variety (Craig, 1997; Russell, 1996).

Two types of transposons exist, a so-called simple system and a complex system. The term *insertion sequence* (IS) refers to the simplest transposition system, and is usually used to describe transposable segments that are less than 2 kilobases long (about 2,000 bases, therefore the three base code sequence codes 667 amino acids). Conversely, the term *transposons* (Tn) describes the more complex movable genetic elements that are usually *longer* than two kilobases. The smallest insertion sequence consists of only one gene flanked by short repeated DNA sequences (Plaster, 1993; Green, Ellington and Szostak, 1990). A large

variety of mechanisms are used to achieve the complex process of organized gene movement. Mechanisms that control movement are divided into two types, *non-composite*, meaning they are not flanked with the control elements called *insertion sequences*, and *composite* which describes those that are flanked with control sequences (Xiao et al., 1995; Pearlman and Butow, 1989).

Transposable elements have now been found in both prokaryotic (cells lacking a nucleus and organelles) and eukaryotic (nucleated cells) organisms. They are presumably universal to all living things including humans (Dombroski, Scott, and Hazazian, 1993). Prokaryotic transposable elements have so far been studied most extensively in *Escherichia coli*, but much research has been completed on vertebrate transposons. This research has found that transposable elements are similar in both prokaryotes and eukaryotes as well as viruses (Russell, 1996).

The discovery of transposable elements has revolutionized genetics, proving that the gene is "fluid and mobile, changing constantly in quality and quantity, and replete with hierarchical systems of regulation and control" (Gould, 1985, p. 712). The number of transposable elements in most eukaryotic organisms is evidently large. In *Drosophila melanogaster* over 30 different families of transposons are now known, accounting for close to 10% of the total DNA (Pimpinelli et al., 1995). On the average transposons account for about 0.3 percent of the bacterial genome. In humans, evidence exists that as much as 35 percent of our genome may be transposons if the Alu family of transposons is included (Bestor, 1998; Schwartz, 1995).

Basic Mechanism of Transposition

The gene transposition process is initiated by one or more enzymes which excise the movable genetic element from one location on a chromosome then integrate it into another chromosome location. Next, the transposition enzymes repair the DNA insertion junction to enable the transplanted genes to function properly in their new location. The DNA normally is cleaved at a specific location, and the specific break site is called a *dissociation point*. *Transposase*, the primary enzyme that catalyzes the transposition process, consists of at least one polypeptide, but most other transposases are oligomers consisting of two to four polypeptides. The active unit of the Mu bacteriophage which integrates DNA in the bacteria genome is a tetramer, and all four subunits are evidently required for strand transfer to occur (Schwartz, 1995). In transcellular transposition, after a transposon is inserted the precise repair of adjacent DNA is completed by the host's DNA replication and repair system.

Replicative and Non Replicative Transposition

Two major transposition mechanisms are now known to exist, those involving *non-replicative* and those involving *replicative* transposons (Figure 1). Most organisms use either one or the other (although some systems can transpose using both methods). A few organisms, such as the bacteriophage Mu, use both types, though its replicative transposition does not use an RNA intermediate (Craig, 1995). *Insertion sequences* (IS) are named according to when they were discovered and the "1" refers to the first one discovered. This family of insertion sequence transposons alone now includes over 300 types.

Replicative transposition involves a two-step process: 1) making an mRNA copy of the transposon, and 2) moving *only* the copy to another location, leaving the original gene intact. The mRNA is then transcribed back into DNA by reverse transcriptase. This transposition method is typified by the *Tn3* bacteria transposon (*Tn* means transposon, 3 the third one discovered). The first step of integration involves a transposon forerunner unit which integrates at the DNA target site, then the transposon is replicated. The second step utilizes the co-integration process, a procedure called *resolving* that is catalyzed by *resolvase*, an enzyme coded by the transposon. The result of this process is that a single copy of *Tn3* is integrated at the target site (Moran et al., 1994). This process is common because evidently the genomes of most animals contain multiple members of the *Tc1* family of transposable elements (Avancini, Walden and Robertson, 1996).

Replicative transposition requires an mRNA intermediate called a *retrotransposon* because the process of replication it uses is similar to how retroviruses function. Examples include some yeast transposons which almost always integrate in areas *outside* of open reading frames. Their most salient trait is the fact that they encode polypeptides which have reverse transcriptase activity.

Two known types of transposons that use the retrovirus system are: 1) retrotransposons that use *long terminal repeats* (LTRs) and 2) those retrovirus systems that lack these terminal repeats called *retroposons*. Both long terminal repeats and retroposon transposon types contain sequences similar to the *gag* and *pol* retrovirus genes, and not unexpectedly both utilize mechanisms similar to those used by retroviruses.

The advantage of the reverse transcription replicative process is the fact that it does not require excision of the

gene element from the donor site. The long terminal repeat transposon type resembles retrovirus proviral DNA which also transposes by means of reverse transcription of mRNA but through a mechanism that differs in many ways from the retrovirus mechanism. One difference is the retroposons use an Adenine-rich sequence at their 3' ends in place of terminal repeats (Pimpinelli et al., 1995).

The second major transposon mechanism is called *non-replicative transposition* because it does *not* involve replication of the transposon. This method is by far the most common, and an example is the 9,300 base pair transposon *Tn10* that contains a tetracycline resistance gene. This transposition type involves excision of the strand from its original site which requires coding for the transposases that cut both DNA strands at both ends of the transposing element. Subsequently, both DNA strands are excised, leaving behind four single-stranded staggered cuts at the target site. The transposon is then inserted into the new site, bonded, and the DNA sugar phosphate backbone molecules are properly ligated together.

Transposition also has two subtypes: 1) those with both short inverted repeats at their termini that encode a transposase which is required for their transposition and 2) those which use heterogeneous central portions flanked by long inverted termini called *foldback elements*. The first class is also called *composite* or *compound* transposons because they contain insertion sequence elements at each end (usually the insertion sequence element is inverted). This type requires specific transposases which are coded by the terminal insertion sequence elements. The second class of transposons utilize terminal inverted repeats that are about 30 base pairs long which do *not* contain insertion sequences (Kendrew and Lawrence, 1994, p. 1098).

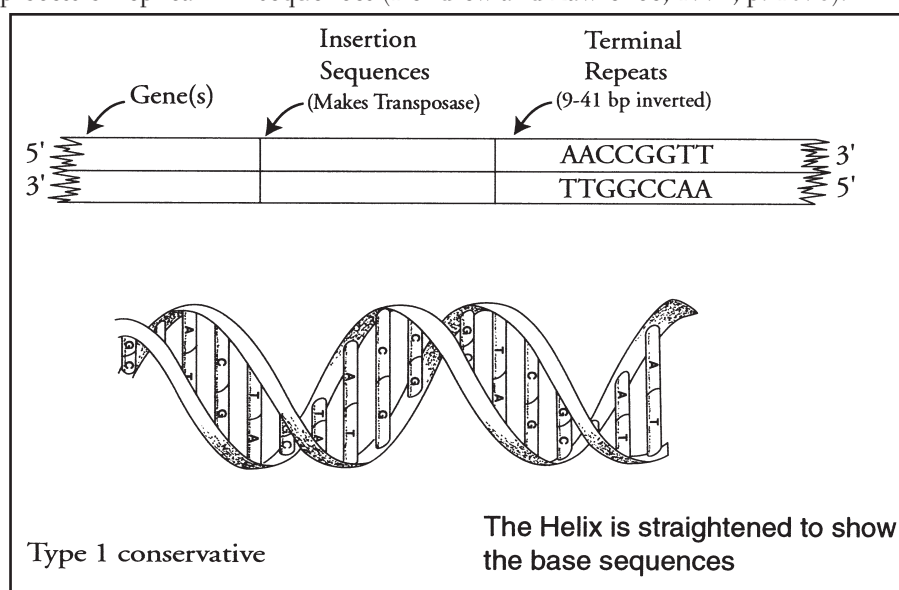


Figure 1. Non-replicative or conservative transposition which shows the process this transposon type uses to insert genes in a DNA strand. Drawings by Richard Geer.

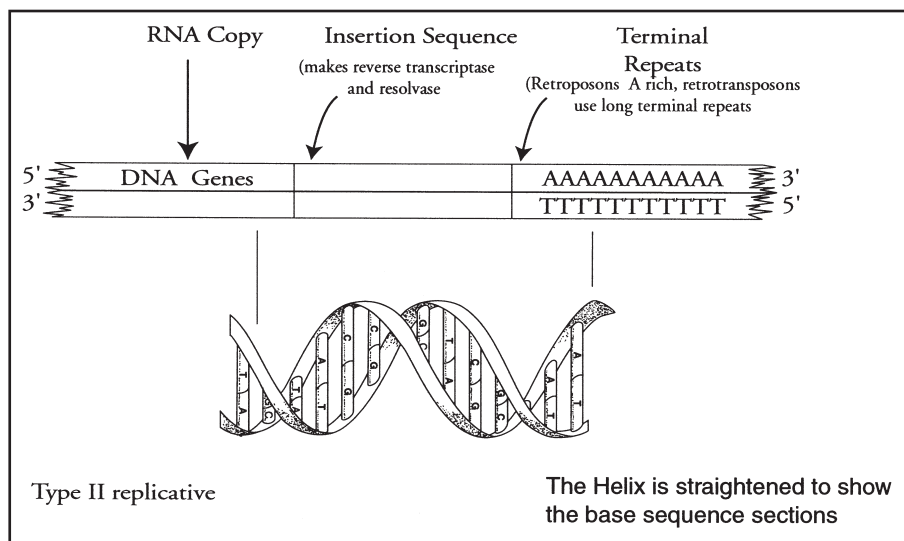


Figure 2. Replicative transposition which uses reverse transcriptase and resolvase in order to produce a gene copy.

Transposons are also now known to use mechanisms similar to those used in other biological gene exchange systems including: 1) the acquisition of bacterial genes for antibiotic resistance, 2) the replication of certain bacteriophages, 3) the integration of retroviruses, and 4) the intracellular movement of retroviral like elements.

New evidence points to unexpected parallels among these many transposition events: They all occur by similar DNA breakage and joining reactions. Moreover, the structures of transposition proteins from very different biological sources have remarkable overall structural similarity, even though they lack extensive primary sequence homology (Craig, 1995, p. 253).

Transposons can be *autonomous* (largely able to direct their own transposition), and *nonautonomous* (those that lack transposition genes and therefore must be activated by an autonomous element elsewhere in the genome) (Russell, 1996). The latter are referred to as *stable* because they cannot transpose by themselves; the former are called *unstable* because they can excise themselves to a new location. Most autonomous transposons can become stable nonautonomous elements by internal deletions or complex sequence rearrangements. This control system introduces some stability and order to the genome.

Target Choice

The criteria used to select the target choice is not yet fully understood, but some criteria likely exist because many sites attracted by transposons are largely predictable. Russell concludes that “transposons integrate at a target site by a precise mechanism so that the trans-integrated elements are flanked at the insertion site by a short duplication of target site DNA” (1996, p.629). Craig (1997, p. 437) adds that

some transposition elements “display considerable target site selectivity and others display little obvious selectivity, although none appears to be truly random.”

Generalizations in understanding target site are problematic because a variety of mechanisms are used. The hot spots are not easy to identify because identifying the obvious criteria, including primary sequences or morphological traits such as bends and kinks in the DNA, requires a greater understanding of the factors that influence DNA topography. A mechanism must normally exist, though, because in many cases strong hot spots are only a “few base pairs from sites that are not hit at all” (Plasterk, 1993, p. 782). Accessory proteins that communicate with the target DNA recombinase and direct interactions between target DNA and recombinase are all used to determine target sites (Craig, 1997).

A common target regulation method is the histone coiling-wrapping system which helps to determine where the mobile genetic element can be inserted (Wolfe, 1995). Yet another control method involves placing of transposable elements into *heterochromatin*, a specialized chromatin material which often remains tightly coiled in the non-dividing nucleus and can be seen easily in the microscope because it stains darkly during interphase. The rest of the chromatin, called *euchromatin*, stains with low intensity and uncoils during interphase, usually condensing only during mitosis. Evidently the heterochromatin condition also prevents, or at least impedes, transposable-element movement. Conversely, the euchromatin position facilitates such movement. For this reason mobile genetic elements cannot normally move to another area of the genome.

Pimpinelli et al. (1995) determined the distribution of eleven different transposable elements on *Drosophila melanogaster* mitotic chromosomes. They found that nine of the eleven transposable elements were preferentially clustered onto one or more discrete heterochromatic regions in the chromosomes of the stock they tested (the offspring of samples collected near Baria, Italy). An analysis of the location of heterochromatic transposable element clusters found that they were also very similar in geographically distant strains. Researchers also concluded that these transposable elements assumed the role of major structural components in *Drosophila* heterochromatin.

Although the integration sites for “most mammalian and drosophila retroelements” at this early stage in the research may appear “to be distributed *more* or less ran-

domly," this could be true mostly because we do not yet understand the site selection criteria. As research in this area has progressed, increased knowledge has revealed a tendency to transpose to a specific area (Labrador and Corces, 1997, p. 392). Transposase is evidently a requirement for transposition, and Labrador and Corces (1997 p. 383) concluded that transposase is normally tightly regulated at several levels including transcription, differential splicing, translation and protein-protein interactions. One regulation system involves a repressor that inhibits transposition by binding to certain sites in the genome.

A totally or largely random integration site would eventually wreck havoc to the genome even if only a small proportion of random integrations occurred in the larger mammal and vertebrate genome. This would be true even in animals that have large amounts of extra DNA compared to lower life forms such as yeast. Yeast genome contains wall to wall genes and "most or all yeast retroelements [in yeast] show target site" selectivity and random integration would commonly damage genes (Labrador and Corces, 1997, p. 393).

Furthermore, all mobile elements share fundamental biochemical and structural similarities, and for this reason all mobile elements would be expected to behave in ways similar to those in yeast and manifest tight control over the target site (Craig, 1995, p. 254). Nevertheless, the mechanism occasionally does not work properly, and a gene is damaged by a transposition insertion, causing that gene to malfunction. If the gene is a tumor suppressor gene, oncogene, or another gene implicated in cancer, tumor progression will result. Also, much of the damage caused by transposition may be blocked by methylation.

All transposable genetic elements utilize at least one transposase, and several use more than one. Transposases in bacteria are usually encoded by the insertion sequence elements located on each side of all transposons. The two known roles for transposase are, first, the cleavage of the correct DNA sequence that is to be moved, and, second, the accurate recognition of the two transposon ends. This mechanism evidently usually insures that only the proper set of DNA bases is excised and the movable genetic elements are spliced into the new correct location of the gene. The synthesis of transposases is in turn under the direct control of a *repressor* which rigidly controls transposition frequency. This tight control is necessary because transposases could otherwise damage the genome, causing cancer (McKee and McKee, 1996).

The Molecular Biology of the Process of Transposition

The enzyme catalyzing transposition is an "impressively" long rod-like structure two micrometers in length (Plas-

terk, 1993, p.783). The two transposon ends must be integrated into the target DNA strand by a rotationally symmetric reaction. The transposase then binds to the end recognition sequences. A second enzyme family called *integrases* functions as a transposase for both retrotransposons and retroviruses which are located in eukaryotes (Craig, 1997). Cointegrate resolution of Tn3 phage DNA also requires the integrase named *resolvase*. It has now been confirmed that these enzymes are all structurally similar, even though surprisingly little sequence homology exists between them:

That a retroviral integrase and a bacterial transposase are indeed fundamentally related has now been spectacularly demonstrated by the structures of the catalytic domains of these proteins at the atomic level. The overall topology of the HIV integrase and MuA transposase structures is similar, although there is little extended primary sequence homology between them. That these proteins might be structurally related was not entirely unanticipated; these and other recombinases contain a signature array of conserved acidic amino acids, the D, D(35)E motif, so-called because of the usual 35-amino acid spacing between the last two residues. These conserved amino acids are critical for the 3' end processing reactions, suggesting that these amino acids are part of (or at least closely related to) the active sites of the enzymes. Moreover, in both the integrase and MuA transposase structures, these amino acids are close together, forming a plausible binding site for a metal ion cofactor essential to recombination (Craig, 1995, p. 254).

All insertion sequences and transposons that have been sequenced so far are flanked with perfect or close to perfect *terminal repeats* that are between 9 and 41 base pairs long. The repeats are also found *inverted* with respect to each other: the same or a very similar set of sequences is found at each end but in the opposite orientation (Russell, 1996). The number of inverted repeat sequences at the transposon termini area ranges from a few to several hundred bases. The terminal repeats are essential for the transposition process because only specific sequences are recognized by transposase, and these are essential to successfully catalyze the DNA cuts and initiate transposition.

Short DNA sequences are duplicated during transposition in order to repair the insertion ends at the *target site*. The target site cut is often staggered, resulting in an overhang of from 4 to 13 bases. The last required step for both insertion sequences and transposons is for DNA polymerase and DNA ligase to repair the ladder frame by filling the 4 to 13 base gap—a process called *target site duplications*. Repair of the break in the DNA is often template dependent, usually relying on the homologous chromatids, the sister chromatid, and even *ectopic* templates (nonhomologous gene segments).

Virtually all transposable elements utilize this system to repair their insertion site DNA regardless of the transposition mechanism they use. The number of bases duplicated is either constant or may vary with each strand position or event. Why this difference exists and the exact role of these inverted repeat sequences are not understood, but it is known that they are necessary in order for transposition to occur.

Transposon sequences of one species are often more similar to those in closely related species than they are to less closely related species. Exceptions to this tendency suggest the possibility that transposable elements may occasionally be transmitted horizontally, that is from one species to another morphologically similar species. Some transposons integrate primarily in one position, others in several, and they do not normally integrate randomly. One possible reason for a variety of integration sites may be the result of mutations or structural defects in chromosomes which cause a transposon to integrate at the wrong site in the DNA.

One method of transposon control which illustrates what can go wrong is located in transposable factors called *P elements*. The 3,000 bp (base pairs) long *P elements* are prevented from jumping around on the somatic chromosomes by some unknown mechanism. They are normally able to jump only in gametes due to three introns that break up the transposase gene. These introns serve as a control element that must be removed from the mRNA before the transposase protein can be produced (Green, Ellington, and Szostak, 1990).

Normal splicing removes only two of these introns from the nuclear DNA of the somatic cells, and for this reason it cannot make transposase. Conversely, *all three introns* are evidently removed from the germ cell line (Wills, 1989, p. 266). When the third intron was removed from the cloned element and the modified *P element* was reintroduced in *Drosophila melanogaster*, it transposed “everywhere,” not just in the germ line. As a result, small patches of mutant tissue appeared in many locations on the fly. Control must normally exist because most transposons show only occasional shifts, and rarely do they transpose everywhere as indicated in the research cited by Wills above. Other possible causes of transposon movement includes environmental circumstances, or an optimal number of transposable elements may exist which will result in their blockage if this number is exceeded.

Horizontal Spread of Transposons

The *P elements* of *Drosophila* have been studied most extensively to understand the mechanism’s spread of transposons within an animal type. Research on captive populations of these flies indicates that the transposon

was transmitted from *Drosophila willistoni* into a *Drosophila melanogaster* fly about 70 years ago. Today all living *Drosophila melanogaster* flies evidently contain the *P element* except those isolated in laboratories (Plasterk, 1993). The *P elements* can be accurately detected because the repressor gene which normally regulates the *P elements’* activities does not exist in *Drosophila melanogaster*.

Both *Tcl* and the mariner superfamily of transposons exist in the genome of most insects, platyhelminthes and even mites (Plasterk, 1993). The *Tcl* transposon has been found in nematodes, fungi, ciliated protozoa, and several kinds of vertebrates. This is explained by evolutionists as a result of horizontal spread distribution, but the fact that they are “absent in whole parts of evolutionary trees and then show up with 95% nucleotide conservation in species thought to have diverged 200 million years ago” indicates either they were created as part of the genome in diverse forms of life or for the purpose of horizontal spread (Plasterk, 1993, p.781). Avancini et al. (1996, p. 131) found that this family of transposons is “extremely common in animal genomes with multiple representatives in most genomes.” Their commonality indicates transposons are important and implies that they have a central function in many living things. If their commonality is due to horizontal spread, this indicates that a mechanism exists that permits horizontal spread and they serve a purpose in the genome.

Looped Transposons

Another type of transposon control involves the disassociation of an entire transposon, which then forms a DNA ring similar to a plasmid. For this reason the DNA is usually unable to rejoin the chromosome. Consequently, all of the genetic information the ring contains is evidently lost to the genome. Many transposons are evidently repressors, and when removed by translocation all of the genes it normally represses can then be expressed. As these control sequences travel around the genome, the genes are turned on and off (Moran et al., 1994). Allowing repressors and other control sequences to randomly move around the genome surely would eventually wreck havoc to the genome, arguing for some type of control system.

Another means of transposon spread is by bacteriophages that replicate the transposon each time they reproduce. Some plasmids called *episomes* are capable of splicing their way into bacteria DNA. An example is *E. coli* fertility factor F which consists of 94,500 bp of DNA and codes for a variety of proteins (Russell, 1996). Non-mobile transposable element clusters may regulate both the activity and the copy number of mobile transposable elements.

Functions of Transposons

Many evolutionary theorists view most transposons as parasitic DNA which often randomly move around the genome. The result is a major source of random genetic variations that natural selection can select from, increasing the likelihood of producing genetic changes that convey a survival advantage for the animal from its mixed bag of largely destructive, useless, or otherwise non-functional DNA.

Although once felt to be only “rogue DNA’s that seemed to land anywhere in the genome” many transpositions are now recognized as having “profound effects on the expression of genes” (Pennisi, 1998, p. 1134). While most of the genome is not yet understood, many current findings, some of which are reviewed in this section, indicate that what is known about transposition does not seem to support this hypothesis. Rather, it suggests that the transposition system is a complex organized system of gene movement and “each system has its own highly specific requirements for how these reactions must be temporally and spatially coordinated ... [by] an intricate nucleoprotein architecture” that orchestrates transposition (Craigie, 1996).

The list of known functions for transposons is growing yearly, and transposons are now believed to play an important role in the genome of most organisms (Craig, 1997). A primary role is to produce color and trait variety, but transposase enzymes also are critical for antibiotic resistance (Pennisi, 1998). Travis (1992) concluded that transposons are a “constructive driving force” which generates much genetic variety. Most of the antibiotic resistance transposons that have been studied in detail use an adjunct transfer vector to distribute their antibiotic resistance genes. An example is the R plasmids which are located in the pathogenic bacteria *Shigella*. Some transposable elements even function as introns which are removed from the mRNA by RNA splicing (Craig, 1997).

Except for bacteria, the transposition mechanism evidently usually does not involve genes that code for trait variations that influence the survival of the animal or plant. Aside from the variety they produce related to defense against antimicrobial compounds in bacteria, transposition usually seems to be limited to influence traits such as color variety. As noted, without an organized and designed control system the transposition machinery would also soon cause deleterious mutations and changes in the genome:

Insertions and inversions can disable the gene into which they enter by disrupting the reading frame. In this way, they act as switches to turn a gene OFF. The insertion can also be precisely removed, and the inversion precisely reversed, to permit the gene once more to function. The insertion sequences (IS) have special

indicators on their ends that identify them for removal and transposition. If it were not for the precision with which they act, they would be turning genes OFF at random, wreaking havoc in the genome. Moreover, if not for the special indicators on the ends of the IS, once a gene is turned OFF in this manner there would be little chance the IS could be precisely removed to turn the gene ON again. The chance that a random deletion will precisely take out a previous insertion is very small.

The chance is also small for a random inversion to reverse a previous inversion. The chance that a transposition will occur in the genome of a bacterium is about one in a million generations... If they are random, then they would be equally likely to occur anywhere in the genome... (Spetner, 1997, p 89–90).

Spetner notes that the genome of a bacterium has about a million nucleotides. Therefore the chance that an inversion or a deletion will occur and one of its endpoints will land on a particular nucleotide would be about one per trillion replications. Such events can occur in bacteria, but cannot be important in higher animals because their reproduction and mutation levels are far less frequent. An example he gives is during the entire putative 65 million year long horse evolution, only about a trillion replications have occurred.

Research on the mechanisms of transposition reveals that this system contains a far greater level of organization and complexity than previously understood. The extremely complex transposition mechanism could not exist without the simultaneous presence of all its many parts, supporting the concept of irreducible complexity. Even the existing complex transposition system is imperfect and occasionally results in a gene being placed in an area of the genome or in another gene that causes genetic damage. Spetner concludes that

there are good reasons to believe that these genetic rearrangements are not random. Insertions and inversions are complex rearrangements of the gene. Inversions occur when two sequences recombine in just the right way. Inversions seem to have important roles to play in both cells and organisms, but we don’t yet know what those roles are. We do know, however, that they are not just genetic mistakes. They are controlled by a set of special enzymes... Some of the enzymes they need are encoded in the transposon itself, and some are encoded in other parts of the cell’s genome. The rearrangements seem to be deliberate acts performed on behalf of the cell (or the organism). They do not seem to be the random stuff that the NDT (NeoDarwinism) says propels evolution (1997, p. 89)

If further research supports the thesis of this review, transposition will be one of more than a score of systems

which eloquently support the conclusion that the amount of information necessary to control the body's genetic systems is phenomenal. This view is supported by the growing information about the complexity of the human genome and the enormous amount of information it contains.

Although the role of many transposable elements is still unknown, it would be rash to assume they have no function. Past experience of human anatomists in labeling 180 structures as vestigial organs, all which are now known to serve a function, provides an excellent illustration of the fallacy of labeling a structure useless. Transposons in eukaryotes have been studied so far mostly in yeast. Other studies have thus far been largely confined to *Drosophila*, corn, and humans. Many of these transposons aside from those that code for the transposition mechanism, also carry genes, and many of these genes have as of yet unknown functions (Russell, 1996). Nonetheless, the still widely held selfish DNA theory (Osawa, 1995; Black, 1999; Dawkins, 1976), which holds that the only role of most transposons is to reproduce themselves and spread throughout the genome is becoming less tenable as more is learned about transposable elements (Travis, 1992).

Labrador and Corces (1997, p. 389) concluded that although the functional versus selfish DNA debate has not been settled yet, recent findings support the functional view. They note that the finding that retrotransposons can serve as repair systems such as "healing *Drosophila* telomeres opens a new scenario" on this question (1997, p. 399). Furthermore, the new evidence that indicates that transposable elements can "contribute to the maintenance of heterochromatin, and consequently to chromosome structure ... opens new and exciting avenues for experimentation ..." (1997, p. 399).

In humans, the SINEs family is a 300 base long sequence that is repeated up to 500,000 times and amounts to 3 percent of the total genome. SINEs are a member of the large Alu family of genes which are all hypothesized to be transposable elements. Likewise the LINEs family member called L1 is also believed to have transposed via a retrotransposon method. The fact that as many as 100,000 copies—fully 5 percent of the human genome—consists of L1 elements, also indicates that transposons may involve a significant fraction of the human genome (Hadler, Devadas and Mahalingham, 1998; Russell, 1996).

Evidence that one function of transposons is to produce phenotypic variety is indicated by research on the P elements. Loss of a P element may cause the organism to lose "some potential for generating genetic variability" (Wills, 1989, p.268). Certain domestic animals may have lost some of their transposons as indicated by the fact that isolated laboratory flies do not have P elements. Wills (1989, p. 268) speculates that this may also have happened to humans, noting that it would be intriguing to determine if groups such as the Australian Aboriginals who have not yet

acculturated in the cities "have more mobile elements in their genomes than the effete Western man."

Transposition Can Produce an Increase in Gene Number

Replicative transposition noted above can function to increase the gene number as a result of each transposition. Transposons can also increase gene number if their removal results in a chromosomal break that can be repaired by using the sister chromatid (the homologous chromosome) as a template for DNA synthesis to effectively make a new copy of the now-departed transposon. If the donor site is restored with its transposable control gene, which is likely the case if the sister chromatid was used as the template to make the repair, the transposon command would again be initiated. This process may occur repeatedly, producing many copies of a gene (Fedoroff, 1991).

Mechanisms involved in producing these repeats are not fully understood. However, certain excessive repeats cause instability of the organism, and consequently reversion back to the wild type is common. This usually occurs as a result of a complete or partial excision of certain transposon elements. The reason they revert back to the wild type is evidently due to another repair process which determines that uncontrolled replication of the transposon has occurred and corrects the problem. Some results of this multiple transpositions process in plants include producing a striking physical appearance in the plants leaves, petals, seeds, and other tissues (Plasterk, 1993).

When the System Fails:

Transposition as Intragenomic Parasites

Although some evolutionists argue that most transposons are intragenomic parasites, the so called parasitic DNA theory (Yoder, Walsh, and Bestor, 1997), much research contradicts this view, including evidence that transposons are evidently usually tightly regulated by the host and usually insert into a specific site which does not adversely affect the host (Craig, 1997). It is known that the host can determine the transposition rate of the Tc1 transposon, and this may also be true for many other transposons (Labrador and Corces, 1997).

Furthermore, the fact that most transposable elements normally avoid certain sites and/or regions of the genome indicates that a negative feedback system exists to control transposition rates and sites (Craig, 1997, p. 438). Creationists argue that transposition is a complex system designed for a constructive purpose including to produce genetic variety, and the most important and best documented function is to transpose antibiotic resistance genes.

Some movable genetic elements *seem* to act like parasites, existing in DNA and reproducing as the cell reproduces but serving no useful purpose. To explain the existence of these transposons, some researchers assume that many of the parasitic DNA elements were mutated and could have been selected for because they benefited the host (McDonald, 1990). Intragenomic parasite transposons are evidently usually blocked by 5-methylcytosine. Evidence exists that most of the 5-methylcytosine in mammalian DNA resides in the specialized intragenomic parasite transposons (Yoder et al., 1997).

Yoder et al. (1997) also claim recent evidence indicates that reversible promoter methylation is not commonly involved in developmental gene control as once thought. Rather the primary function of cytosine methylation is evidently the suppression of parasitic or unneeded sequence elements, and the secondary role of cytosine methylation is control of allele-specific gene expression including both X inactivation and genomic imprinting.

Aside from the subset of genes subject to inactivation in females to achieve dosage compensation and genomic imprinting, no other cellular gene in non-expressing tissue has been proven to be methylated in a pattern that prevents transcription. The transposon promoters are inactivated when methylated, and the C→T transition mutations which occur at methylated sites usually destroy the parasitic transposons. Consequently, these mutated movable genetic elements are removed from the genome. Therefore, parasitic theory cannot explain most of the permanent transposons. They also conclude that

It has become increasingly difficult to hold that reversible promoter methylation is commonly involved in developmental gene control; instead, suppression of parasitic sequence elements appears to be the primary function of cytosine methylation, with crucial secondary roles in allele-specific gene expression as seen in X inactivation and genomic imprinting (Yoder et al., 1997, p. 335).

Use of Transposons for Molecular Biology Research

Implications of transposons for molecular biology is enormous. Due to various difficulties in using viruses for vectors, researchers have experimented with using transposons as gene carriers. Since many transposons insert themselves at specific sites in the gene, the researcher can clone the desired genes into the transposon by recombinant DNA techniques. Transposons have potential as a vector to transfer genes not only from one organism into another, but because transposons are evidently "not restricted in their host range," they may have the flexibility necessary to function as effective yet versatile vectors (Plas-

terk, 1993, p.785). The transposon elements of *Drosophila melanogaster* have already been used as vectors.

Transposable elements are now also important experimental tools that can be used not only as vectors but also as probes. A process called *transposon tagging* uses a transposon probe to identify recombinant DNAs in order to determine if they have successfully inserted themselves into the genome and also to determine if they have carried the gene of concern into the correct area. Many genes responsible for murine cancer have been identified by retroviral tagging.

Transposon Mutations

Occasionally the transposon mechanism does not function properly and produces a spontaneous mutation. If a transposon is inserted inside a gene, it can inactivate either necessary or optional genes which may explain the origin of some pseudogenes. Incorrect insertion can also cause gross chromosomal rearrangements, both due directly to the results of their transposase cutting an incorrect site or as a result of a transposon being spliced into an area of the genome where it interferes with normal gene function. Insertion inside a reading frame can destroy the gene, causing a *null mutation*, and insertion into a genetic control area such as a CpG island or enhancers can cause changes in genetic expression (Akopyants et al., 1998).

If the transposable element is imprecisely excised, the polypeptide that the gene produces may be altered. If the bases added or deleted are a multiple of three, the polypeptide may be functional but usually only if the changes occur at the genes' ends which are less critical in producing functional proteins. If a number of bases other than three is lost or gained, a string of nonsense genes will likely result, and totally nonfunctional protein will be produced.

Since mutations caused by transposons are relatively uncommon in humans and many other animals compared to those caused by mutagens, clastogens and transcription errors, mechanisms likely exist to reduce the likelihood of their placement between a gene or other inappropriate locations in the genome. Although it is assumed that a large proportion of spontaneous mutations in *Drosophila melanogaster* that are of laboratory origin are associated with mobile DNA elements, Nitasaka, Yamazaki and Green found that none of the mutants they examined are associated with an transposition insertion. They concluded that:

Clearly much more information, both of terms of numbers of genes studied and numbers of alleles per gene analyzed, is needed before it is possible to answer with any confidence the question of whether the spectrum of spontaneous laboratory mutations is predictive for what takes place in the wild (1995, p. 168).

Transposons and Cancer

Transposons also play a major role in the development of tumors and cancer (Cao, Brown and Sognier, 1997; Miki et al., 1996; Ramel et al., 1996). The best example is retroviruses which can function as transposons to transport oncogenes into a genome such as the papillomas virus. Understanding transposons will help researchers better understand the gene carrier initiated changes which cause cancer. Many, likely most, heterochromatin genes "have organizations that resist inactivation by insertional mutagenesis," consequently protecting them (Pimpinelli et al., 1995, p. 3808). For this reason euchromatin may be the major mutational concern.

Transposons for Cancer Therapy

The implications of transposons for curing disease is enormous. Since they insert themselves at specific places in the gene, the researcher simply clones the desired genes into the transposon by recombinant DNA techniques. Once this is achieved, one goal is to cause transposons to carry genes into cells which can cause cancer cells to react a certain way so the tumor can be effectively and accurately detected or to cause the cancer cells to revert to normal or self-destruct.

Significance of Transposons for Creationism

Evolutionists have postulated that the genome has been evolving for billions of years and is a hodge podge of not only useful genes, some which are still evolving and many others that are all but useless, but also currently non-functional DNA and genes such as pseudogenes (Travis, 1992; McDonald, 1990). Some genes were once useful but are now no longer needed due to evolutionary changes, and yet others have mixed or no clear function (Smit, 1996). Transposons have even been postulated to contribute to the "explosion of new organisms, many...bizarre in appearance [that] appeared suddenly in the Cambrian fossil record" (Travis, 1992, p. 884). The discovery of transposition at first seemed to support this evolutionary view.

Transposons were assumed to randomly move around the genome, often causing damage, and often they were selected against but would occasionally cause beneficial mutations. Some evolutionists believe they are a major source of genetic variation because they can cause random variations that selection can select from, increasing the likelihood of mutations that convey a survival advantage for the animal from its mixed bag of largely destructive, useless or otherwise non-functional DNA.

While the function of most of the genome is not yet understood, many current findings, some of which are reviewed in this paper, indicate that transposition does not support this hypothesis. Rather, it suggests an intelligent design origin because the transposition system is a complex highly organized system of gene movement and "each system has its own highly specific requirements for how these reactions must be temporally and spatially coordinated ... [by] an intricate nucleoprotein architecture" that orchestrates transposition (Craigie, 1996).

Evolutionary naturalism postulates that the genome accumulated as a result of the selection of random mutations which has occurred throughout evolutionary history. Research on the genome such as the mechanisms of transposition indicates that a far greater level of complexity exists than previously imagined. The extremely complex transposition mechanism can not function without the simultaneous presence of *all* its many parts and thus can not be explained by natural selection. The mechanism would not be selected for *unless* and *until* it confers a survival advantage to the organism. Furthermore, in the case of transposition, many of its parts such as the enzymes and DNA would damage the genome unless the control that results from the whole system existed.

Variation is critical for evolution, but a mechanism which produces variation would not be selected until it functioned properly, and until then many of its parts would be deleterious. Except for bacteria, the transposition mechanism is not known to involve trait variations that favorably influence survival. Except for the variety they produce related to defense in bacteria, the function of transposition seems to be limited to influencing traits such as color variety which usually doesn't have survival significance. Without an organized and designed control system the transposition machinery would also soon cause the genome to become chaotic.

Even the current highly perfected system occasionally results in a transposition being placed in the wrong area of the genome, causing a mutation or other damage. Furthermore, the entire system must be in place as a unit for it to function properly. If most or possibly all of its parts are not present, the system will not function or will malfunction, causing major genetic damage. In a literature search, the author did not locate a single article which even tried to hypothesize how this system could have evolved by natural selection selecting mutations. It is a prime example of Behe's concept of irreducible complexity (Behe, 1996).

Transposons are especially important for creationism because the biological mechanism it requires reveals a complexity at the molecular biology level which is far beyond the complexity that is known to exist at the gross anatomy level. The estimated 150,000 proteins that exist in humans and many times this in all life involve hundreds of enormously complex systems. Other discoveries

of the last decade include the signal transduction system, the cell cycle control mechanism, and the large cytokine and kinase families. The DNA transcription and translation control and regulatory systems alone reveal a level of complexity unsuspected only a few years ago (Quinn, 1975, 1976).

If further research supports the thesis of this paper, transposition will be one of more than a score of systems which eloquently supports the intelligence design model and worldview. The amount of information existing in the genome necessary to control these systems is phenomenal. Intelligent design is also supported by growing understanding about the complexity of the human genome and the enormous amount of information it contains which defies naturalistic explanations.

Summary

Rather than a printed book, the genome may be more accurately likened to a manuscript stored on a word processing program. The information in the manuscript is not set in stone, but is changeable in ways that biologists are just beginning to understand (Henningfeld and Hecht, 1995; Holzman, 1991; Fedoroff, 1991; Borst and Graves, 1987). The current state of research on transposons is best summarized by McClintock:

Only now, more than forty years after the discovery of transposable elements, are we beginning to understand enough about the ways that they can affect genes to decipher some intriguing new aspects of gene control from their study (1987, p. xi).

We are also finding that a designed order exists in the many systems which were once assumed to be random or disordered:

The biological and conceptual connections between many different mobile elements have long been recognized. It is now clear that biologically diverse [transposon like] systems also share fundamental biochemical and structural similarities (Craig, 1995, p. 254).

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Erratum

CRSQ 35(4), June 2001, page 46. The following is the correct equation 2.

$$\Delta S = S_f - S_i = \int_{T_i}^{T_f} C_p \frac{dT}{T} - R \ln \left(\frac{P_f}{P_i} \right) \quad (2)$$

Evolution Is Lethal Antiscience

Joseph Mastropaolo

Abstract

The foundation of evolution is abiogenesis, life spontaneously generated from nonlife. The superstructure placed upon that foundation is monogenesis, myriad spontaneously generated structures to produce every kind of simple life form then by countless spontaneous generations every kind of complex life form. The other “definitions” of evolution are change over time, common descent and natural selection. Laboratory abiogenesis has failed consistently and dredging the bottoms of the oceans yielded the inert sulfate of lime, not the fraudulent “monera.” The simulated abiogenesis of the proteins to mock-up the simplest original cell is more than a zillion ($10^{4,000,000}$, 1 followed by more than 4,000,000 zeros) times more impossible than the mathematical definition of impossible. The probability of monogenesis was not attempted because myriad multiplications of impossible yield impossible to unimaginable extremes. The common textbook instructions, “life arose in the ancient seas” from “that original organic soup,” are teaching the innumerable miracles of the evolution religion and that violates the U.S. Constitution’s prohibition of a state supported church. To meet the requirements of science and the Constitution, these lessons must be changed to “life was *created*,” as in “Henry Ford *created* the Ford automobile.”

“Change over time,” “definition one” of evolution, actually describes devolution to extinction, the exact opposite of evolution. “Common descent,” “definition two” of evolution, actually describes true-to-type devolution to extinction, again the exact opposite of evolution. A sample engineering analogue, as well as actual epidemiological data from human genetic disorders and fatal birth defects, identify “natural selection,” the alleged “primary mechanism” for evolution, as actually a mechanism for devolution to extinction, the exact opposite of evolution. Both “definitions” of evolution and evolution’s “primary mechanism” yield universal devolution to extinction. Additionally, evolution is the antithesis of science because it cloaks current permanent accelerating human and biosphere extinction in the garb of biologically advantageous progress. Evolution wantonly militates against countermeasures while myriad individuals and populations, including humans, are accelerated to the greatest mass extinction in history. Therefore, evolution is identified here as the wantonly lethal antiscience ruling the summit of criminality. As a first step for self defense against imminent permanent human and biosphere mass extinction, the evolution movement must be expunged worldwide.

Introduction

Evolution has ruled biology for more than a century. That is a remarkable achievement and the purpose of this paper is to illumine why evolution is so controversial and why it is considered here to be at the summit of criminality. The approach is to pursue the various definitions of evolution and to examine the evidence. As needed, principles from the sciences shall be brought to bear.

The foundation of evolution is abiogenesis, a living cell allegedly springing to life from nonliving matter. This apparently is based on the “monera” fraud of Ernst Haeckel (Assmuth and Hull, 1915, pp. 74–76). The nonexistent monera were misrepresented as primitive missing-link sin-

gle cells found in the slime at the bottom of oceans but in fact were inert precipitates of sulfate of lime (Rupke, 1971, pp. 169–183; Becker, 1999, pp. 14–18). To synthesize a monera, the Miller-Urey experiments failed remarkably and consistently (Yockey, 1992, pp. 231, 232, 234, 238–241; Miller and Levine, 2000, p. 344). Furthermore, the

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simulated evolution of a small protein for a small cell yielded an improbability comparable to a successful perpetual motion machine (Yockey, 1992, p. 257). In spite of no evidence from nature or the laboratory or simulation, abiogenesis persists in current high school and university biology textbooks as “life arose in the ancient seas” from “that original organic soup” (Johnson, 1998, p. 195; Miller and Levine, 2000, pp. 344, 346). To the apparent impossibility of abiogenesis, evolution concatenates the apparent impossibilities of monogenesis, the parent cell spontaneously diversifying to form all other kinds of single-cell organisms, then these in turn spontaneously complicating to all multicellular life forms.

Another approach to evolution is by way of its meanings. Apparently, there are three. “Definition one” is change over time. It is stated that evolution of this type is a fact. “Definition two” is common descent. This is treated as though it were a fact. “Definition three” is natural selection, the primary mechanism for definitions one and two (American Scientific Affiliation, 1996, p. 3).

This study will be limited to an examination of abiogenesis, monogenesis, change over time, common descent and natural selection.

Data On Abiogenesis and Monogenesis

Let us begin by examining the foundation of evolution, abiogenesis. The necessary elements in nature are believed to have spontaneously joined together and spontaneously generated life in a cell. We incompletely know, but the cell would not know at all, that its metabolic functions of digestion, circulation, respiration, excretion, movement, repair, and reproduction would depend upon the spontaneously generated polysaccharides, lipids, amino acids, alpha helixes, polypeptide chains, assembled quaternary protein subunits, and nucleotides. At least all of these extremely complex subunits must spontaneously self-combine then further spontaneously combine into the still more complex functioning cellular structures, like the mazes of conduits containing automatically moving raw materials and finished products to and from peripheral assembly organelles, energy systems, long-chain proteins, and nucleic acids. In preparation for an electrical storm, for example, exactly the right mix of the spontaneously generated DNA, mRNA, ribosomes, cell membrane material with its millions of gate-controlled apertures, enzymes, and scores of other protein structures, each a complex machine in its own right, must be spontaneously and precisely positioned (Behe, 1996, pp. 262–268; Denton, 1986, p. 263). Then with every atom in the right place at the right time the first cell might be thunderbolted together and spring to life. Even these incomplete details are not mentioned in the biology textbooks and none of the above ref-

erences are cited. No calculation of the probability of any of those events is given to the student to estimate whether or not what is being taught has the same or greater improbability of miracles, which would rule it out of science. Without evidence, the student is expected to believe on faith the dogma that a cell somehow sprang to life in the distant past “in the ancient seas” “that original organic soup” (Johnson, 1998, p.195; Miller and Levine, 2000, p. 346).

The objective determination of abiogenesis as science, or as miracles, may be approached by observing that many functions in a living cell are determined by the structures of its proteins. The trail of the first cell therefore leads us to the peculiar organic chemistry of biologically useful amino acids in viable proteins. When amino acids are synthesized in the laboratory, about half are left-handed and about half are right-handed. Yet, only the left-handed ones are biologically useful. Of the left-handed, there are 20 eligible amino acids for each of perhaps hundreds of positions in a viable protein, but almost always only one correct choice can meet the functional requirements. Almost always a peptide bond is required and any other will cause the protein to fail biologically. Sometimes with a correct primary structure, the correct secondary or tertiary or quaternary structures may not materialize because the solution conditions for the synthesis were not exact. Taking the complex biochemistry into account which yields the complex submicroscopic geometries biologically required, a search may be made for the probability of creating a protein by chance as specified by evolution. Accordingly, the probability of evolving one molecule of iso-l-cytochrome c, a small protein common in plants and animals, is an astounding one chance in 2.3 times a trillion vigintillion. A trillion vigintillion has 75 zeros. In evolution's terms, if a random mutation is provided every second from the alleged birth of the universe, then to date that protein molecule would be only 43% of the way to completion. That is devastating for evolution because there would be no time to complete that single molecule, no time to evolve the scores of thousands of proteins required for one cell, no time to evolve all the other simple cells and no time to evolve all the complex organisms for a functioning biosphere. The author of this landmark monograph concluded, “The origin of life by chance in a primeval soup is impossible in probability in the same way that a perpetual motion machine is impossible in probability” (Yockey, 1992, pp. 255, 257). That should settle the question but let us employ an extra measure of patient endurance and continue the search.

The evolutionist, Richard Dawkins, stated:

Suppose we want to suggest, for instance, that life began when both DNA and its protein-based replication machinery spontaneously chanced to come into existence. We can allow ourselves the luxury of

such an extravagant theory, provided that the odds against this coincidence occurring on a planet do not exceed 100 billion billion to one" (Dawkins, 1996, pp. 144, 146).

The 100 billion billion is 10^{20} . So Dawkins' own evolutionist criterion for the impossibility of evolution, one chance in more than 10^{20} , has been exceeded by more than 50 orders of magnitude not for a whole cell but for only one molecule of one small protein in that cell. Had Dawkins been influenced by the literature (Yockey, 1992, pp. 255, 257), he would not have said, "It is absolutely safe to say that, if you meet somebody who claims not to believe in evolution, that person is ignorant, stupid or insane (or wicked, but I'd rather not consider that)" (Johnson, 1993, p.9). Dawkins by his own probability estimate, with more than 50 orders of magnitude to spare, has identified himself as a nonbeliever in evolution and needs to ask whether he considers himself "ignorant, stupid, insane or wicked." That surfeit of evidence, more than 50 orders of magnitude, should surely settle the case but let us continue the search.

According to Dembski and Borel, specified events of small probability do not occur. Dembski estimated 10^{80} elementary particles in the universe and asked how many times per second an event could occur. He used the Planck value of 10^{45} . He then calculated the number of seconds from the beginning of the universe to the present and for good measure multiplied by ten million for 10^{25} seconds in all. He thereby obtained $10^{80} \times 10^{45} \times 10^{25} = 10^{150}$, or more exactly 0.5×10^{150} , for his Law of Small Probability to eliminate chance (Dembski, 1998, pp. 5, 62, 209, 210).

Currently, there does not seem to be a scientific criterion more generous to evolution than Dembski's one chance in 0.5×10^{150} . Anything as rare as that probability had absolutely no possibility of happening by chance at any time by any conceivable specifying agent by any conceivable process throughout all of cosmic history. To test against that criterion, we take one chance in 2.3×10^{75} for one protein (Yockey, 1992, pp. 255, 257) and multiply by the 60,000 proteins required for the abiogenesis of a minimal cell (Denton, 1986, p. 263; Morowitz, 1966, pp. 446–459) and obtain one chance in more than $10^{4,478,296}$ (Mastropaolo, 1999, p. iii). That exceeds Dembski's most generous criterion for impossible by more than $10^{4,478,146}$. Or if 0.5×10^{150} to 1 is the most generous probability science can provide to demarcate possibility from miracle, then with more than four million orders of magnitude to spare abiogenesis must be considered miraculous. To put abiogenesis in biology textbooks as evolutionists have done throughout the United States is to teach evolution religion as science and that violates the requirement of the U.S. Constitution prohibiting the establishment of a state religion (Constitution of the United States of America, 1787, Amendment I, see note).

With abiogenesis so unimaginably impossible, it is a waste of time to examine monogenesis which rests upon the abiogenesis foundation. With the innumerable spontaneous generations of abiogenesis so impossible, the additional countless spontaneous generations of monogenesis built upon that foundation are impossible to an even greater extreme. In order to document this problem of comprehending such extreme impossibilities, dimensioning the improbability of abiogenesis may be useful. Numbers like $10^{4,478,296}$ are incomprehensively large. It is the number 1 followed by 4,478,296 zeros. There is no English word for it. There ought to be some way to give a sense of such a magnitude. For example, if a perpetual motion machine is probabilistically impossible and has a probability of 10^{75} to 1 against it (Yockey, 1992, pp. 255, 257), then how many impossible perpetual motion machines would abiogenesis' $10^{4,478,296}$ to 1 against it represent? The answer is the impossibility of $10^{4,478,221}$ perpetual motion machines, also a number too large to imagine. Let us persevere and consider the Blue Fairy that animated Pinocchio (Collodi, 1883, see note) as one chance in 10^{150} , that is, she is impossible according to Dembski's criterion for impossible. The abiogenesis of only one type of simple unassembled protein raw material to mock-up a minimal original cell is more impossible than $10^{4,478,146}$ Blue Fairies. Again, this is too large a number to imagine. In passing, we may note that evolution is likely the greatest fairy tale ever told because every elementary particle, like an electron, in the entire cosmos could be occupied by a Blue Fairy playing Musical Chairs at the incredible tempo of 10^{45} changes per second for more than 20 billion years with more than $10^{4,478,146}$ Blue Fairies patiently waiting a turn to play. Instead of biology, American students are being taught evolution's peerless blend of championship science fiction with children's fairy tales. But let us not give up. Let us consider a universe 100 billion light years in diameter, probably double the size of ours, and ask how many trips across that universe we could make if each probability unit was equal to the diameter of a hydrogen atom. With the hydrogen atoms side by side, the answer would be $10^{4,478,259}$ trips, again too large for the imagination. Abiogenesis is so immensely improbable that it defies finding a reference to common experience or even a language equivalent to express it abstractly.

To give a language reference, let us define "zillion" as greater than $10^{4,000,000}$ (1 followed by more than 4,000,000 zeros) and let us define "create" as Webster renders its first meaning, "to cause to come into existence; bring into being; make; originate; esp., to make or design (something requiring art, skill, invention, etc.)." We may quite properly say, "Henry Ford created the Ford automobile," without attributing to Henry Ford any divine status. Now let us employ these definitions and properly conclude that the probability of evolution's foundation, abiogenesis, and its

superstructure, monogenesis, is more than a zillion to one against them and the probability of creation, without religious connotation, is more than a zillion to one in favor of it. Such probabilities remove every vestige of the vaguest doubt from any objective scientist. Let us close with the reminder that those probabilities are for only one type of simple unassembled protein to mock-up the simplest original cell and they represent gross underestimates. The improbabilities for a complete cell or for a complex life form of trillions of cells or for an ecosystem of millions of different interdependent complex life forms would require multiplications by myriad additional orders of magnitude. The evolutionist mind of Anaximander (611–549 B.C.) must be complimented for imagining abiogenesis and monogenesis (Durant, 1939, p. 138), concepts so improbable that human minds are incapable of comprehending the extent of their impossibility. Authors like Johnson (1998) and Miller and Levine (2000) would be well advised to discontinue violations of the Constitution by removing from their public school textbooks all mention of the countless incredible miracles, abiogenesis and monogenesis. They would bring their public school textbooks into compliance with the requirements of science and the Constitution of the United States of America and the Constitution of the State of California if they substituted, “life was created.”

Data On the Three “Definitions” of Evolution

Let us now consider “definition one” of evolution, “change over time.” “Because such changes have been repeatedly observed, evolution of this type is a fact” (American Scientific Affiliation, 1996, p. 3). According to common observation, however, all individuals in the biosphere age and die. Once dead, the plants rot and the animals putrefy to simpler nonviable elements. Individually, life forms devolve. Types of life forms as populations also regress from viable to permanent extinction. That too is devolution, not evolution. The nonviable universe also devolves (Humphreys 1978). The first definition of evolution is antonymous to the trillions of consistent observations of billions of people over thousands of years. The exclusive fact is devolution.

“Definition two” for evolution is common descent. This “view that all (or most all) life forms, extant and extinct, are related by common ancestry: a theory about the history of life . . . the common sense observation that all offspring have parents, have led [sic] many scientists to treat the inference of common ancestry as though it were a fact” (American Scientific Affiliation, 1996, p. 3). According to common observation, however, individuals age and die as the same type of individual at birth. Individuals also reproduce true to type. Types of life forms as populations dem-

onstrate variability in characteristics like size, weight, color, and speed of motion but always breed true to their type. For example, Shetland horses may weigh 300 pounds and Belgian horses may weigh a ton more than that. Horses may be described by a mean and a standard deviation for body weight or any other characteristic of horses. It is common knowledge that all variability in parents and offspring is within their type. No mare has ever given birth to a calf and no cow has ever born a foal. Life forms do not transmute to other types of life forms. Life forms as individuals and populations have been observed devolving to extinction but never evolving. The second definition of evolution is antonymous to the trillions of consistent observations of billions of people over thousands of years. Again, devolution is the exclusive fact.

“Definition three” of evolution is natural selection, “The theory (acting upon genetic variations, such as mutation) has been the *primary mechanism* for the biological changes described in definitions one and two” (American Scientific Affiliation, 1996, p. 3, emphasis in the original). As documented above, definitions one and two are definitions of devolution, not evolution. Also as documented above, the alternative definition of evolution, abiogenesis, is so impossible it strains the imagination and must be classified as countless miracles. The superstructure of innumerable spontaneous generations, monogenesis, is countless multiples more impossible than abiogenesis and also must be classified as countless additional miracles.

For the sake of discussion, let us consider whether or not genetic variations, such as mutation, may in any way mitigate those extreme impossibilities. Evolutionists would have us believe that mutations will yield new and better life forms that will result in many different kinds of plants and animals, i.e. diversification, and a progression to higher, more complex life forms. To clarify that logic, let us select one example from an almost infinite number of thought experiments. Let us take the circuit board out of an AM radio, put on a blindfold, then put a finger on the board. To simulate a mutation, if the finger lands on a connection, break that connection or if the finger lands where there is no connection, then make one. Reassemble the radio and test its range of stations for reception. Repeat the process. If the radio increases its range of stations or improves its reception, then we conclude that mutations cause improved structure and function. Or if it becomes an FM radio, then the modifications mimicking random mutations succeeded in producing diversification. If the radio becomes a TV, then the mutations succeeded in producing the equivalent of an advanced life form. Contrarily, if the radio progressively degrades to the point of no longer working, then the mutations produced extinction. Obviously, there is no chance of obtaining a TV because the AM radio has no monitor and none of the other special parts and circuits that a TV requires. And like living things,

the AM radio could not spontaneously generate all those special TV parts because that would violate the laws of physics. Obviously, there is no chance of obtaining an FM radio because the design, frequency modulation, is significantly different from an AM, amplitude modulation, radio and cannot be constructed by introducing mutations into an AM design. Obviously, the radio will degrade to the point of not working at all and that is consistent with all human experience. In all human experience, there is no analogous model to suggest that natural selection and genetic variations, like mutations, will cause diversity or increased complexity. There is no such experience with life forms, either. All human experience suggests that all things, especially the complex, nonviable and viable alike, degrade toward permanent extinction. With its genetic variations and mutations, natural selection accelerates extinction, not evolution. Let us next consider human mutations.

Mendelian inheritance in man is

an encyclopedia of human genes and the disorders and other traits with which they are associated. It has been in creation and updating for over 35 years and has been computerized for most of that time. In addition to the print edition (Figure 1), it has been distributed online (OMIM) since 1987 and by compact disc (MIM-CDTM) since late 1993. (McKusick, 1998, Vol. 1, xiii–xviii)

Apparently, this database in the National Center for Biotechnology Information at Johns Hopkins University is the best in the world for the current catalog of human genes and genetic disorders.

Medically reported human genetic disorders have been cataloged in the above reference since 1966. If evolution were true, then we should observe a decrease in genetic disorders over time according to the first definition of evolution, change over time, and the third definition, natural selection. That means that the graph would look like the hypothetical Figure 1. The data in Figure 1 are actually reversed. Like those data, evolution is false. The true data are plotted in Figure 2. As can be seen, the trend is an exponential increase in medically reported genetic disorders. Beyond any doubt, the trend is devolution. The data thereby demonstrate that the ravages of time produce mutations that result in devolution, the exact opposite of evolution (McKusick, 1998, Vol. 1, xiii–xviii).

By 2031, it is estimated ($R^2 = 0.995$) there will be 100,000 human genetic disorders and by 2096 1,000,000 (see Figure 3). "At least one clinical disorder has been related to 1,318 of the mapped loci (roughly 30%)" (McKusick, 1998, Vol. 1, xiii–xviii). That suggests genetic disorder saturation of each locus by 2031 and supersaturation by 2096. These data confirm human devolution and suggest imminent permanent genetic extinction in this century. That evolution cloaks imminent human ex-

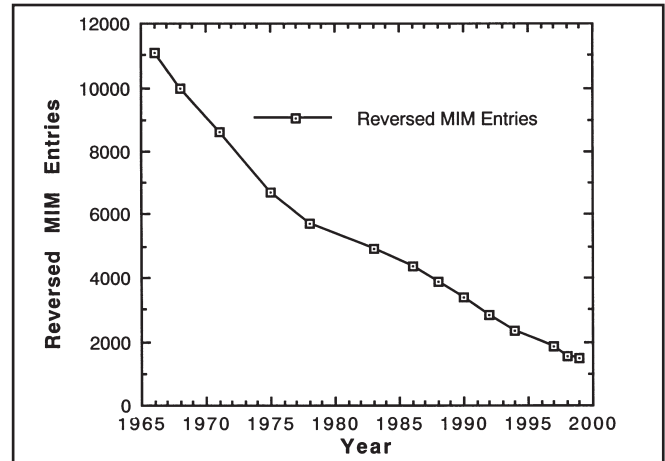


Figure 1. If evolution were true, these would be the medically reported genetic disorders from 1966 to 1999. These data are actually reversed. Like these data, evolution is false.

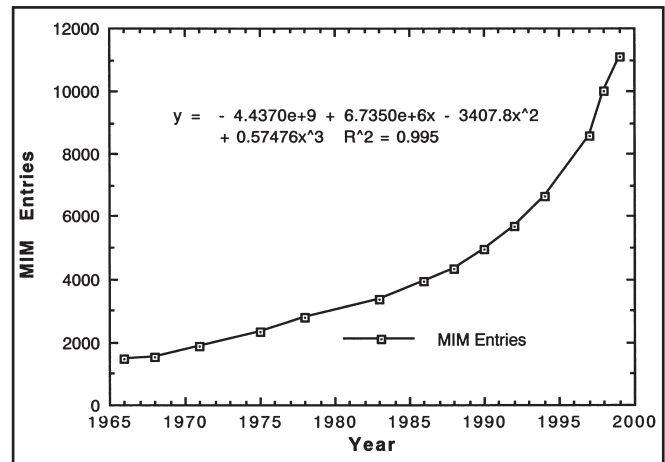


Figure 2. McKusick: *Mendelian Inheritance in Man*, Reported Genetic Disorders 1966 to 1999. The number of medically reported genetic disorders in 1966 was 1,487. The number reported by 1999 was 11,099. A curve of best fit has an R^2 of 0.995. These data are evidence of devolution.

inction as biological progress, thereby militating against countermeasures until permanently too late, identifies evolution as the summit of criminality.

Evolutionists are aware of genetic disorders like the sickle cell allele, a red blood cell mutation. For example in recent biology textbooks we find, "The sickle cell allele confers an unexpected advantage in Africa," (Johnson, 1998, pp. 128, 183) and "Why is sickle cell anemia so common in some regions . . . The answer to that question is a surprising lesson in evolution . . . That mutation conferred an advantage wherever malaria was common, and thus it was favored by natural selection" (Miller and Levine, 2000, p. 233). Evolutionists call it "a classic case of heterozygote superiority" because survival of heterozygous individuals in malarial regions of West Africa is 1.0 compared

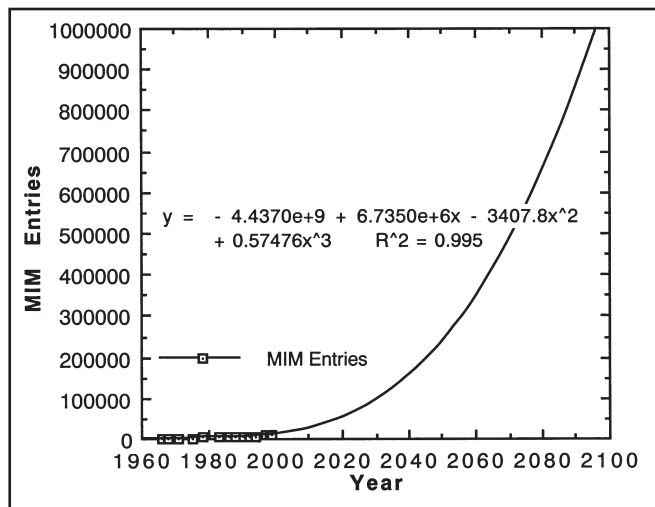


Figure 3. McKusick: *Mendelian Inheritance in Man*, Reported Genetic Disorders 1966 to 1999 with Extrapolation to the Year 2096. The number of medically reported genetic disorders in 1966 was 1,487, in 1999 11,099. A prediction equation 99.5% accurate suggests 100,000 human genetic disorders by 2031 and 1,000,000 by 2096. These data are evidence of devolution and suggest imminent human extinction.

to 0.9 for individuals with normal homozygous hemoglobin. They gloss over the fact that survival for homozygous sickle-cell individuals is 0.2. Also glossed over is that the survival average for normal hemoglobin, homozygous plus heterozygous with the sickle-cell mutation, is 0.95 compared to the sickle-cell average of 0.6. Even in malarial environments, normal hemoglobin permits a survival advantage of at least 35% and of as much as 70% (Hartl and Clark, 1997, p. 251). In a non-malarial environment, there were 75,000 hospitalizations per year of 6.1 days with significant mortality. "Thus, sickle cell disease is one of the most prevalent genetic disorders in the US" (Ashley-Koch, Yang and Olney, 2000). The evolutionists' classic case of biological superiority thus is filling hospitals and graveyards with the afflicted. The sickle-cell allele is genetic disorder-disease MIM-OMIM number 141,900 and such disorders have been increasing exponentially (McKusick, 1998, Vol. 1, xiii–xviii). This demonstrates that evolutionists choose to put at risk vulnerable students and their families rather than admit that mutations are genetic disorders documenting devolution, not evolution. Genetic disorders are reason for alarm and countermeasures, not wanton misrepresentation. Cloaking significant morbidity and mortality as biological progress called, evolution, identifies evolution as lethal antiscience.

In 1997 from genetic testing, the estimate was that everyone on average carried six genetic disorders (Gargus, 1997). The extrapolation suggests that by 2033 the average for every man, woman and child may be 60 or more genetic disorders. The data indicate that the greatest mass

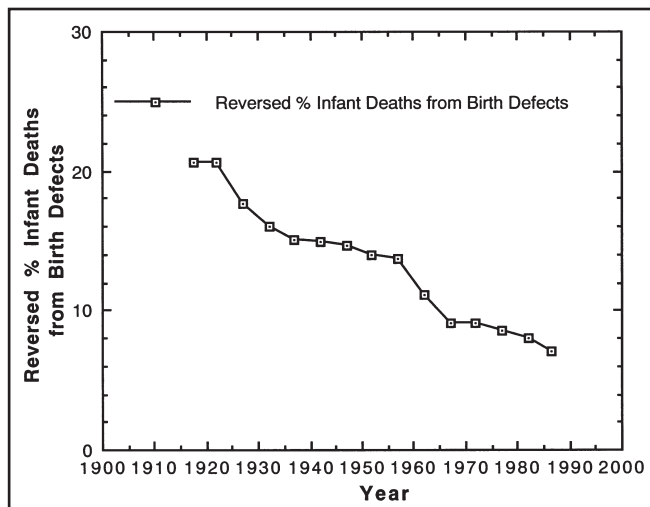


Figure 4. If evolution were true, these would be the percentage of infant deaths attributed to birth defects in the United States from 1916 to 1988. These data are actually reversed. Like these data, evolution is false.

extinction in the history of the planet is in progress in non-human life forms at a rate of 30,000 extinctions per year and accelerating (Leakey and Lewin, 1996, Chapter 13; Mass Extinction References, 1998). The clear message is that mutations accelerate the permanent extinction of all life forms, including humans. There can be no greater imperative than educating students and parents to those facts. The lethal masquerade of portraying mutations as advantageous biological evolution must be extinguished before it brings the entire biosphere, including all of humanity, to permanent extinction. Cloaking the greatest mass extinction in the history of our planet as the biological progress called, evolution, identifies evolution as the most lethal antiscience in the history of our planet.

Data on fatal human birth defects may be found in the medical epidemiological teratology literature. If evolution were true, then we should observe a decrease in fatal birth defects over time according to the first definition of evolution, change over time, and the third definition, natural selection. That means that a graph of the medically reported fatal birth defects should look like the hypothetical Figure 4. The data in Figure 4 are actually reversed. Like those data, evolution is false. The true data are plotted in Figure 5. As can be seen, the trend in spite of medical advances is an exponential increase in fatal birth defects (Sever, Lynberg and Edmons, 1993). Beyond any doubt, the trend is devolution. By 2085, it is estimated ($R^2 = 0.967$) there will be 100% human infant deaths attributed to birth defects (see Figure 6). That suggests that the genetic disorder saturation of each chromosome locus by 2031, and the supersaturation by 2096, will manifest 100% infant deaths from birth defects by 2085. These data agree with the genetic disorder data in confirming human devolution and in suggesting imminent permanent genetic extinction in

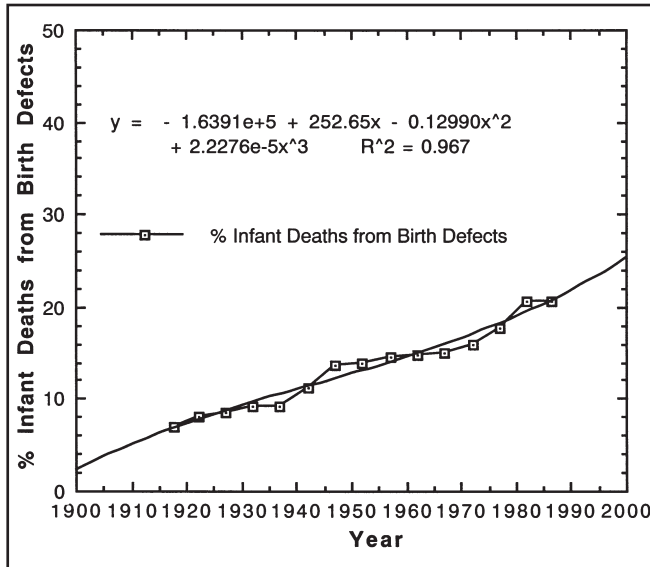


Figure 5. Percentage of Infant Deaths Attributed to Birth Defects in United States from 1916 to 1988. The percentage of infant deaths attributed to birth defects was 7% in 1916 to 1919 and rose to 20.6% for 1982 to 1988. These data are evidence of devolution.

this century. That evolution cloaks accelerating human birth defect mortality toward imminent human extinction as biological progress, thereby militating against countermeasures until permanently too late, adds additional evidence to the identification of evolution as antisience at the summit of criminality.

The World War II crimes of the Nürnberg Trials can hardly compare to the slaughter of all humanity and the entire biosphere. Crimes against peace, war crimes and crimes against humanity are minor lapses compared to the extinction of all life forms. Not just scores of strains of millions of individuals—surfeit enough in horror beyond imagining—are at stake, but rather many millions of species and many billions of individuals. And if this historically greatest of all mass bioslaughters currently under way depletes the critical biomass for sustainable ecobalance, then the universe's only known biosphere will erode irreparably to a barrenness as ghostly as the moon. No megacrime in the history of this planet, or of this universe, comes close to that summit of criminality.

Summary and Conclusions

According to the most generous mathematical criteria for evolution, abiogenesis and monogenesis are impossible to unimaginable extremes. The three definitions of evolution are disguised definitions of devolution to extinction. For the entire biosphere including all humanity, our planet currently is in the throes of the greatest mass extinction in its history. The tens of thousands of different life forms per-

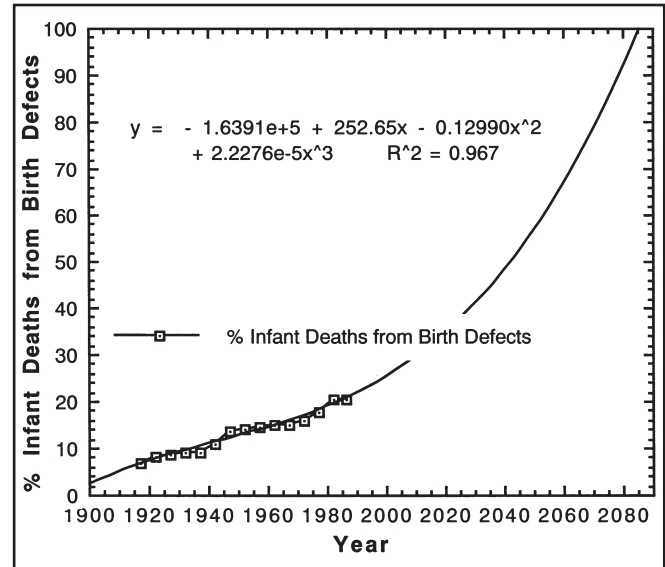


Figure 6. Percentage of Infant Deaths Attributed to Birth Defects in the United States from 1916 to 1988 with Extrapolation to 2085. The percentage of infant deaths attributed to birth defects was 7% in 1916 to 1919, rose to 20.6 % for 1982 to 1988 and is expected to be ($R^2 = 0.967$) 100% by 2085. These data are evidence of devolution and confirm imminent human extinction.

manently extinguished each year are accelerating the depletion of the biosphere to the level where it permanently will no longer support human life because no new life forms can be created and none can be evolved. That evolution cloaks these mass extinctions and the imminent permanent extinction of all humanity as biologically advantageous is identified here as wanton, lethal antisience at the summit of criminality. There can be no greater imperative for the educational and governmental institutions of the world than countering the greatest mass extinction in history as induced over the last 140 years by the evolution movement. As a first step for self defense against imminent permanent human and biosphere extinction, the lethal antisience, evolution, must be expunged worldwide.

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Book Review

Big God vs. Big Science by Bill Sardi

Here and Now Books, San Dimas, CA. 2001. 108 pages, \$7.00

Author Bill Sardi is a journalist and publisher. His book is a rebuttal to the old earth view of Hugh Ross and Don Stoner, concentrating on the science issues more than theology. In a clear informal style, progressive creation is challenged without attacking the personalities involved.

Parts of the book will confuse uninformed readers. Sardi equates new species with macro evolution (pp. 10, 67). However speciation is a micro concept. He also closely equates old earth creation, theistic evolution, the gap theory, and the day age theory (p. 10, 28). However, these are very different approaches to Genesis. Time dila-

tion is confused between the separate effects of gravity and relativistic speed.

Sardi is dismayed by Ross's big bang ideas. This book is the result, with many good ideas and helpful figures. The book has an attractive cover and a helpful index. The author may be reached at 457 West Allen #117, San Dimas, Ca. 91773.

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Notes from the Panorama of Science

The Growth Rate of *Muhlenbergia torreyi* (Ring Muhly Grass) Colonies in Central Arizona

Van Andel Creation Research Field Study Note

George F. Howe and John R. Meyer*

Muhlenbergia torreyi (ring muhly) covers a large area of the Van Andel Creation Research Society property in Chino Valley, AZ. Several features of this fascinating grass have been discussed in a previous publication (Howe, Williams, and Meyer, 1999) such as ring muhly's possible role in reducing soil erosion, its morphology, its circular growth habit, its ecology, and the position that grass family members in general may have within the creation origins model.

Growth Rate of Rings

That same paper contained the description of a growth rate experiment which was begun on June 23, 1998 in order to measure how rapidly a growing arc of *M. torreyi* moves across the soil. Rebar pegs were placed so that each peg was touching the front or outer growing edge of eight ring muhly colonies and one colony of the blue grama grass (*Bouteloua gracilis*). Measurements of colony growth progression were made on September 22, 2000, roughly two years after the stakes were positioned. The distance from the trailing edge of each stake to the new front edge of each colony was measured in the direction of growth. These experimental colonies were separated from each other by an average distance of 1.54 meters (m), with 1.0 m being the shortest distance between any two and 3.0 m the longest. All experimental arcs were located on flat terrain that was gently sloping southward with the following coordinates (latitude and longitude): 34°50.82N and 112°27.85W

Table I. Growth distances for eight *M. torreyi* colonies measured after 2 growing seasons (June 23, 1998 to September 22, 2000).

Colony Number	Compass Direction of Growth	Growth Distance (cm)
1	W	2
2	SW	5
3	SW	5
4	W	7
5	N	5
6	S	7
7	SEE	5
8	SSW	7

Average growth per colony over 2 years = 5.4 cm

Average growth per colony per year = 2.7 cm



Figure 1. Colony number 8 of *Muhlenbergia torreyi* after two growing seasons. Note how the arc has grown 7 cm in what is a SSW direction (to the left and down), leaving the rebar peg behind. Small white dot to the left of the peg is an artifact.

The direction and amount of growth for each colony was noted: see Table I. The total period of growth for each arc was 2.25 years. Although the experiment thus actually ran a little longer than two years, the average growth of each colony per year (Table I) was calculated by dividing the total average growth by two (instead of 2.25), as will be explained later. Figure 1 is a photograph of one of the eight ring muhly colonies (colony number 8) on September 22, 2000. Figure 3 shows the one *Bouteloua* colony and its two stakes after two growing seasons. In June, 1998, two stakes were placed on opposite edges of the blue grama grass clump shown in Figure 3. Figures 4 and 5 are photographs of *M. torreyi* and *B. gracilis* respectively, showing their inflorescences.

In the future growth of these colonies will be monitored more frequently throughout the year to determine if they

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Figure 2. One of the ring muhly colonies photographed in January, 2001. Note how the grass itself is brown, dry, and dormant during winter.



Figure 4. Colony of *M. torreyi* at the end of its growing season (September, 2000). Inflorescences are seen arising from the plants below.

undergo one or two growth spurts annually. We believe that there is only one and that it occurs in the spring and summer season. Support for this assumption lies in the fact that *M. torreyi* and *B. gracilis* colonies examined in the winter



Figure 3. Colony of *Bouteloua gracilis* (blue grama grass). Originally the two pegs were positioned each on opposite sides of the colony. In two growing seasons, the plant has engulfed and grown over them both, thus moving about one inch per year. Dot to left of upper peg is an artifact.

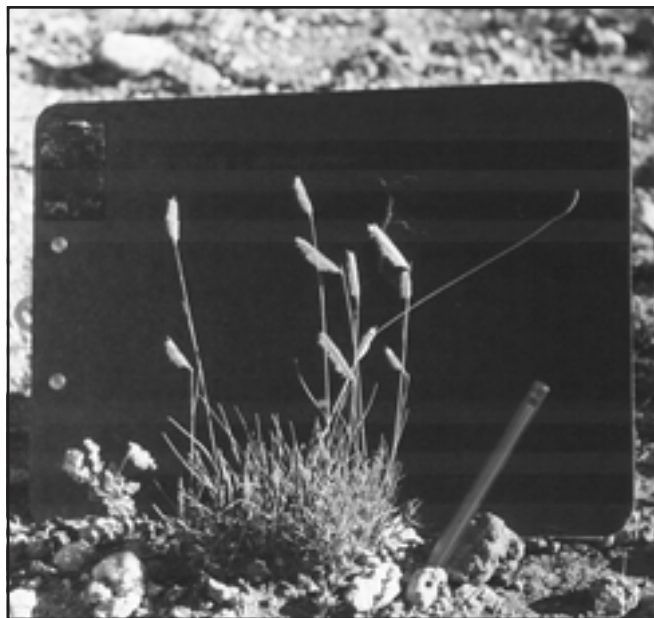


Figure 5. Colony of *B. gracilis* at the end of its growing season (September, 2000) showing leaves below and inflorescences above.

(January 2001; Figure 2) were in a completely dormant (non-green) condition. Repeat measurements made on January 11, 2001, showed no change from the data previously



Figure 6. *Muhlenbergia torreyi* rings after a light snowfall, January, 2001.

gathered on September 22, 2000. These ring muhly colonies had not expanded between September and January¹.

In the years during which this experiment has run the average annual temperatures at the nearby Prescott, AZ. airport were close to the mean for the last 33 years (U.S. Weather Bureau, 2001). The average annual rainfall in 1998 for Chino Valley was 5.18 inches ("") and in 1999 was 10.19" where the 33-year mean is 11.79". It appears that "moisture stress" on these grass colonies was somewhat greater than average. The average lateral spread of 2.7 cm per year (a little more than one inch) may therefore be somewhat low for *M. torreyi* rings and the same is true for the one colony of *B. gracilis* studied here; 2.5 cm per year. Undoubtedly the expansion rate for such grass colonies varies from year to year and from site to site, but the growth of one inch per year seen here may be useful in making rough estimates of the age of large muhly rings when it is possible to see entire rings or enough of an arc to calculate the center from which the colony started.

M. torreyi rings serve as points where snow accumulates and melts, as seen in Figure 6. There is a superficial visual resemblance between the young, mound-like muhly colonies and *Mammillaria* cacti, which grow near them (Figure 7). In the previous paper (Howe *et al.*, 1999) it was suggested that aspects of God's *creation* can be understood by observing *Muhlenbergia torreyi* and other grasses. The scene of snow melting into the ground as a moisture supply for ring muhly and other wild plants (Figure 6) can also bring the Creator's *providence* into focus. In Chapter 38, verses 25–27 God asked Job this probing question:

Who hath divided a watercourse for the overflowing of waters, or a way for the lightning of thunder; to cause it to rain on the earth where no man is; on the wilderness wherein there is no man; to satisfy the des-



Figure 7. Small, newly-formed clumps of ring muhly (right of pen) bear resemblance to *Mammillaria* cacti (left of pen) which grow nearby. While we attach no significance to this curious phenomenon, it is one of the visual features that greet those who study vegetation at VACRC.

olate and waste ground; and to cause the bud of the tender herb to spring forth?

We will continue to observe the growth rate of this interesting grass and to assess its pattern of expansion at VACRC throughout the course of the year.

Acknowledgements

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¹Late June 1998 until late September 2000, although actually 2.25 years, would thus have included only two annual growth periods corresponding to spring–summer 1999 and spring–summer 2000.

Joseph B. Prestwich: Uniformitarianism and Catastrophism

William Weston*

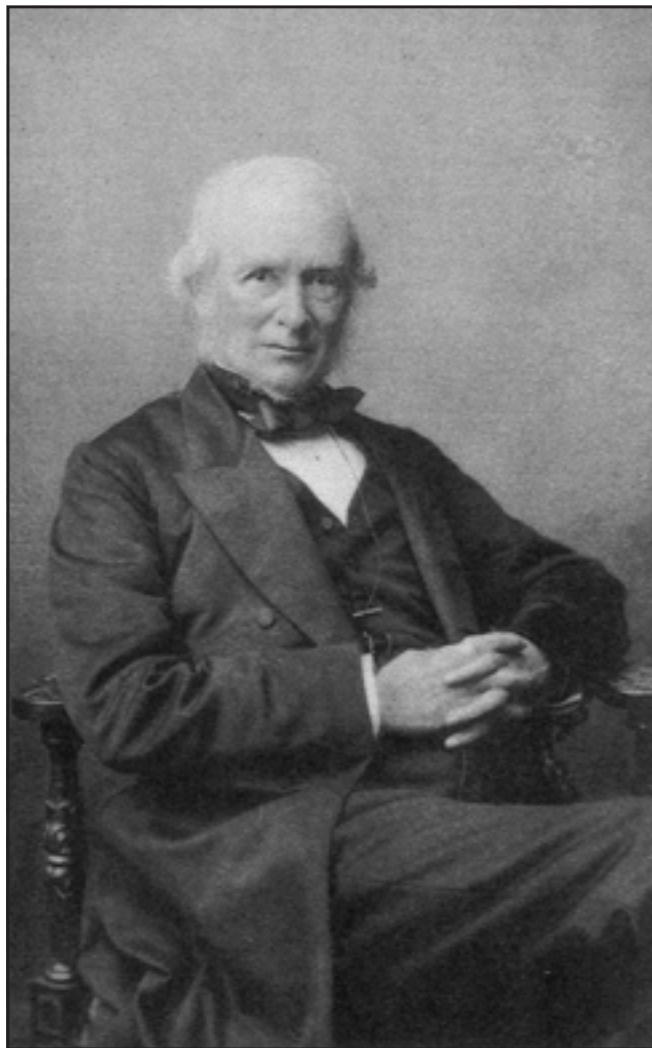
During his lifetime, Joseph B. Prestwich (1812–1896) was one of the foremost authorities on the Quaternary period. Judging by his correspondence, the great scientists of his age such as Charles Lyle and Charles Darwin were impressed with his work. He first achieved renown in 1851 after publishing a work on the Thames River called *A Geological Inquiry Respecting the Water-Bearing Strata of the Country around London*. In 1874 he was appointed to the chair of geology at Oxford. His great work *Geology: Chemical, Physical and Stratigraphical* was written in two volumes in 1886 and in 1888.

Early in his career, Prestwich's views on geology and paleontology were uniformitarian. He also believed that science should be kept separate from religion. In an 1877 letter to a friend he wrote, "...the association of the Bible and geology is one I never make, holding the two to be perfectly distinct and to be studied independently. I accept the truths concerning our moral and spiritual nature from the Bible, but in all that concerns physical nature I look to Nature herself for an explanation" (1899, p. 268).

Years later, Prestwich's view regarding the separation of science and Scripture would undergo a major change. While studying geologic formations in England, he found caves and rock fissures filled with animal bones, including tiger, hyena, wolf, horse, deer, and rabbit (1895, pp. 25–26). The bones were broken into fragments, and no skeleton was complete. What was odd about the herbivore bones was the absence of carnivore teeth marks. These fossil-filled caves and fissures pointed toward two conclusions: (1) the herbivores were congregating with the carnivores and (2) the herbivores and carnivores had died at the same time.

Prestwich also noted that the fossils occurred in association with "rubble drift." The rocks of a rubble drift were of a local origin and had sharp angles, which indicated violent rupturing of the source rocks. The only agent that seemed capable of producing such rubble drifts was a "superincumbent body of water" sweeping over the land and wrecking havoc with the terrain. This observation led him back to the question of why the herbivores and carnivores were congregating together. Were these naturally incompatible animals seeking refuge from a rising flood?

To find evidence that would answer that question, Prestwich made a trip to the Channel Islands in 1880. In a letter written shortly after this trip, he wrote "I think I am now in a position to show that the south of England,



Joseph B. Prestwich

France, and possibly the greater part of Europe, have been submerged during the early human period, and that paleolithic man was thereby destroyed (in great part). It revives in a curious way the tradition of the Noachian deluge. I have long had cause to suspect this, but hesitated even to mention so unexpected a result until I was sure of the facts I obtained in the Channel Islands" (1899, p. 311).

At the same time he made the trip to the Channel Islands, Prestwich was also studying the works of French geologists. From a report written by Albert Gaudry, Prestwich learned about a small, isolated mountain near the center of France, called Montagne de Santenay. Rising steeply to about 1030 feet from the surrounding plain, it had a nearly level platform on top. Close to the summit were limestone fissures packed with broken animal bones. One notable thing about this mixture of broken bones was the prevalence of carnivores, especially wolves. Since there were no teeth marks on the herbivore bones, Gaudry had concluded that the carnivores and herbivores had gathered together on the high platform of Santenay. He believed that

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what drove them there was a steady rise in water. The rise was slow enough for the animals to get there, yet the height of the mountain was not sufficient for them to escape. When they perished, their bloated bodies formed a mat of carcasses on the surface of the water. Since there was no current of water to carry them away, some of the decayed and detached parts fell on Mount Santenay. When the water began to subside, the upper elevations of the mountain were exposed to divergent currents. Unlike the advancing waters which had little erosive power, the effect of the retreating waters was devastating. The presence of broken angular rocks embedded in yellow or brownish earth indicated that waves had washed over and partially eroded the mountain. Wave action smashed the bones into rocky formations re-emerging above the water and drove some of the bones into the limestone fissures (1894, pp. 936–938).

According to calculations of observable geological processes, Prestwich estimated that this great flood occurred about 10,000 years ago. The submergence of the continent of Europe was short in duration, for there was an absence of marine sedimentation. Prestwich could not say what caused the flood, yet he was prepared to defend his views that it had in fact occurred. On December 15, 1892 he submitted an important paper on the subject to the Royal Society of London. It was a bold challenge to uniformitarian doctrine. In a letter written to a friend two weeks prior to submitting the paper, he said, "I am aware that I must expect opposition, as it touches upon questions which geologists and physicists must differ... The votaries of uniformitarianism are, I fear, apt to consider their doctrines as infallible, and to act accordingly. For my part, I believe that in another half century geologists will wonder that a doctrine so unphilosophical was ever held" (1899, p.

367). Prestwich underestimated the durability of uniformitarianism, yet he was right in attacking its "unphilosophical" approach to science.

In 1895, Prestwich wrote his last book called *On Certain Phenomena Belonging to the Close of the Last Geological Period and on Their Bearing Upon the Tradition of the Flood*. In this work he goes beyond his December 1892 paper and for the first time publicly proclaimed his belief that the submergence of Europe was connected to the story of Noah and the Genesis Flood. Although Prestwich was not prepared to say that Noah and his family were the only survivors of the Flood, he did say that the Biblical story was based on a genuine event of gigantic proportions and was not simply a local river flood. In publishing this final work, Prestwich had reached a turning point in his career. The man who had been so meticulous in maintaining a separation between the Bible and science was, in the last year of his life, groping for a reconciliation of the two.

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On the Origin of Feathers

It is clear that the appearance of novel structures requires simultaneous and levels (Ashley and Hall, 1991). Defining the particular changes and recognizing the emergent consequences is not always possible. The morphological revolution that produced feathers is inextricably associated with a Set of closely coordinated structural genes and a unique production machine. The mechanism appears to retain linearity, but several epigenetic processes are involved. The degree of iteration is remarkable at several levels. Consequently, simple timing changes in development can produce structures of diverse morphology. Essentially, feathers are a two-dimensional surface of variable dimensions constructed from a single family of proteins.

The hierarchical organization emphasizes that morphological changes and changes at the molecular level

may evolve in different ways. At the morphological level feathers are traditionally considered homologous with reptilian scales. However, in development, morphogenesis, gene structure, protein shape and sequence and filament formation and structure, feathers are different. Clearly, feathers provide a unique and outstanding example of an evolutionary novelty. As a key innovation they may explain the rather sudden diversification birds. The combination of simple construction, relatively inexpensive production and a plethora of functions may have afforded the subsequent avian radiation

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Letters to the Editor

How to Define the Expanse in Genesis 1

Regarding “A Critique of the Literary Framework View of the Days of Creation,” (CRSQ 37:237–243), Kulikovsky did a commendable job of exegeting the Scriptures, he shows clearly that Scripture does not allow the *raqiya*, the expanse in Gen. 1, to be defined as the atmosphere (p. 240), he follows Humphreys in identifying the expanse as “interstellar space.” But, although he criticizes Kline for not mentioning the waters *above* the expanse “presumably because they do not fit into his pattern,” Kulikovsky does not mention the waters *above* the expanse either.

Presumably he would follow Humphreys in saying that “out beyond the most distant galaxy, is a wall of ordinary water, of unknown thickness.” [Humphreys, Russell D. 1994. A biblical basis for creationist cosmology. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism* (Technical Symposium Sessions), p. 260. Creation Science Fellowship, Pittsburgh, PA.] This commendably places the water *above* the expanse exactly as the Hebrew phrase (me’al plus lainedh) used in Gen. 1:7 demands. (The very same phrase is used with reference to an expanse in Ezek 1:25, 26 to describe a voice coming from a man on a throne, and that throne is certainly above the top of the expanse.)

But, this creates two problems. If the water above is *beyond* “interstellar space.” above the top of space as the Hebrew phrase demands, there is no space available for it; and matter requires space. Secondly, Gen. 7:11 must refer to the releasing of the water above the expanse mentioned in

Gen. 1:7 since a major source of water for the Flood is inferred, but the amount of water that could be supplied by even the heaviest of ordinary rains would be insignificant. [Morris, John C., and Morris, Henry M. 1961. *The Genesis Flood* pp. 9, 121. Baker, Grand Rapids, MI.] But how can water fall to earth as rain from “beyond the most distant galaxy?”

So, if one transforms the expanse into atmosphere, Gen. 1:14–17 is violated. If it is transformed into interstellar space, physics and Gen. 7:11 are violated. I suggest the reason why neither of these interpretations of the expanse agree with Scripture is because they both assume “that a particular author living in a vastly different culture and at a time far removed from the present would write according to 20th century expectations” (Kulikovsky, p. 237). Rather than forcing upon the expanse in Gen. 1 a meaning in line with 20th century expectations, I suggest the better option is to interpret it within *its* historical and grammatical context. [Seely, Paul H. 1991. The firmament and the waters above, Part I: The meaning of *raqiya’* in Gen. 1:6–8. *Westminster Theological Journal* 53:227–240; Seely, Paul H. 1992. The firmament and the waters above, Part II: The meaning of “the water above the firmament” in Gen. 1:6–8. *Westminster Theological Journal* 54:31–46.]

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Literary Framework Critique—A Response to Paul Seely

I wish to thank Seely for his letter regarding my paper “A Critique of the Literary Framework View of the Days of Creation” and especially for his kind acknowledgment that I “did a commendable job of exegeting the Scriptures.” Seely raises a few objections to my identification of the expanse created on day 2 with interstellar space, but these objections are easily rebutted.

Firstly, Seely complains about my failure to mention anything about the waters above the expanse. There are two reasons for this: (1) The work of day 2 involves the creation of the *expanse*—not the waters above or below. In other words, the focus of day 2 is on the expanse itself, not its boundaries. (2) I do not discuss the waters above because there is not much else that can be said. The Biblical account tells us nothing more about the actual nature and final form of these waters.

Seely argues that if the expanse is interstellar space, then the waters above the expanse are *beyond* interstellar

space. Seely goes on to argue that since these waters are matter, and matter requires space, then there is no space available in which it can exist, because the waters are *beyond* interstellar space. However, it seems that Seely has mistakenly equated spatiality (ie. “space” as understood in relation to the space-time continuum) with interstellar space (ie. the empty void between stellar objects). Spatial objects can and do exist outside of interstellar space. For example, a person, an animal, a car, a house, a mountain etc. are all spatial objects, yet they all exist outside of interstellar space (ie. on the surface of this planet). Thus, there is no reason why the waters above the expanse cannot bound interstellar space while still existing in the space-time continuum.

Seely also claims that “the floodgates of the heavens” in Genesis 7:11 is a reference to the releasing of the waters above the expanse, which would imply that all this water fell through interstellar space and dumped on earth. Thus,

identifying the expanse with interstellar space violates both Genesis 7:11 and physics.

However, Seely offers no exegetical or contextual support for his assertion that the opening of “the floodgates of the heavens” is a reference to the releasing of the waters above the expanse. The only argument he presents in support of his interpretation is a scientific objection (or at least what Seely thinks is a scientific objection). Given that the water mentioned in Genesis 7:11 was a major contributor to the Flood (albeit secondary to the bursting open of the “fountains of the great deep”), Seely claims that “even the heaviest of ordinary rains would be insignificant.” This leads Seely to the conclusion that the water must have come from elsewhere, such as the waters above the expanse. Seely’s reasoning, however, is flawed on several counts. Firstly, Genesis 7:12 states that it rained for 40 days and 40 nights. I fail to see how so much water dumping on the earth for so long can be regarded as being insignificant, especially since local floods in modern times have covered extensive regions with far less rainfall. Secondly, Seely is assuming that only “ordinary” rains are in view here. Given the context (i.e., God’s judgment of the entire earth

by means of the Flood), this assumption is completely without justification. God told Noah that He would bring Floodwaters upon the earth to destroy it (Genesis 6:17) so this was no ordinary flood—it was a supernatural act of God. This is further shown by God’s promise never to send another Flood “to destroy the earth” (Genesis 9:11). Thirdly, the fact that it rained for 40 days and 40 nights— an extraordinary amount of time—also indicates that this event was a supernatural act of God. Thus, to view the rains as merely ordinary rains totally violates the context.

In light of the above, it should be clear that Seely’s objections are unfounded. Furthermore, his own published interpretation of the expanse and the waters above suffers from its own critical problems and is fatally flawed, not to mention a clear departure from Biblical inerrancy [See Holding, J. P. “Is the *raqiya* ‘(firmament)’ a solid dome?” *Creation Ex Nihilo Technical Journal* 13(2):44–51, 1999].

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Defense of CCC Model

In the December 2000 CRSQ there were five letters purporting to be critiques of Mr. Gentet’s CCC Model. It is in response to those letters and in defense of Mr. Gentet’s article that I am writing.

One letter raised the issue of adhering to Bishop Ussher’s chronology, “Let us focus on the latter. I assume that Mr. Gentet adheres to an Ussher-type Chronology. (If not, then there is no basis for claiming to be a Biblical literalist.)”

First of all, Mr. Gentet left open the date of creation. Secondly, we should keep in mind that while Bishop Ussher was sincere, he drew an erroneous conclusion that the creation of Adam was approximately 6,000 years ago. However, when one considers the genealogy of Josephus, the Jewish historian, or the genealogy in the Septuagint (the Greek translation of the old testament, circa 300 BC) one can arrive at the age of approximately 7,500 years ago. The Septuagint translation is quoted freely in the book of Acts, therefore, it carries some authority.

By combining astronomy, history, and tree ring dating, which is not absolute but still quite accurate, it has been possible to push the age of man back to at least 10,000 years ago. This does not conflict with the Bible. One needs to realize that the genealogies in the Scriptures were not put there to determine when man was created. The purpose of the genealogies is to trace the ancestry from Adam to Jesus Christ. From the first Adam to the second Adam.

If we insist on being Biblical literalists, then we should adhere to Saint Paul’s admonition to Timothy in I Timo-

thy 1:4 “Neither give heed to fables and endless genealogies, which minister questions, rather than godly edifying which is in faith: *so do*.”

Evidence of Pre-Flood Curse

Mr. Gentet proposes in his CCC Model that not all of the fossil record is the result of the Genesis Flood, but a portion of it supports the account of creation week and that other portions of the fossil record are the result of the curse on mankind. Let the evidence speak for itself. Let us first take a look at history from the Biblical perspective. Genesis tells us that God did place a curse on the land and on mankind in general as a result of Adam’s sin. We do have historical data to support the great magnitude of this curse. I refer to Mr. Gentet’s paper where he quoted Eusebius, one of the early church fathers as follows, “Eusebius... describes God’s interaction with the degenerate pre-Flood mankind, ‘While they were leading this life, God, the guardian of all, pursued them with floods and conflagration... He cut them off with perpetual famines and plagues, by wars and by thunderbolts from the high...’”

Eusebius and other church fathers had access to writings that have long since disappeared. However, occasionally, an old book will pop up. One of those is the book of Jasher. This book is referred to in at least two places in the Old Testament, Joshua 10:13, and 2 Samuel 1:17–18. Obviously the Old Testament writers place some confidence

in the historical value of the book of Jasher. (The book of Jasher referred to in Joshua and 2 Samuel was faithfully translated from the original Hebrew into English and reprinted in 1966 by Health Research, Mokelumne Hill, California 95245.) I have a portion of this book from which I will quote. Notice how it corroborates Eusebius and how in some instances it parallels the book of Genesis:

It was in the days of Enosh that the sons of men continued to rebel and transgress against the Lord to increase the anger of the Lord against the sons of men. The sons of men went and they served other gods and they forgot the Lord, who had created them in the earth and in those days the sons of men made images of brass and iron, wood and stone, and they bowed down and served them. And every man made his god and they bowed down to them and the sons of men forsook the Lord all the days of Enosh and his children and the anger of the Lord was kindled on account of their works of abominations which they did in the earth. And the Lord caused the waters of the river Gihon to overwhelm them and He destroyed a third part of the earth... And notwithstanding this the sons of men did not turn from their evil ways. Their hands were yet extended to do evil in the sight of the Lord. And in those days there was neither sowing nor reaping in the earth for there was no food for the sons of men and famine was very great in those days. And the seed which they sowed in those days in the ground became thorns, thistles and briars. For from the days of Adam was this declared concerning the earth of the curse of God which he cursed the earth on account of the sin which Adam sinned before the Lord. And it was when men continued to rebel and transgress against God to corrupt their ways that the earth also became corrupt... And on that day the Lord caused the whole earth to shake and the sun darkened and the foundations of the world raged and the whole earth was moved violently and the lightning flashed and the thunder roared and all the fountains in the earth were broken up such as was not known to the inhabitants before. And God did this mighty act in order to terrify the sons of men so that there may be no more evil upon the earth. And still the sons of men would not turn from their evil ways and they increased the anger of the Lord at that time. And did not even direct their hearts to Him. At the end of seven days in the sixth hundredth year of the life of Noah, the waters of the flood were upon the earth and all the fountains of the deep were broken up and the windows of heaven were opened. And the rain was upon the earth 40 days and 40 nights... (Compare this with Genesis 7:11–12) And Noah with his household and all the living creatures that were with him came into the ark on account of

the waters of the flood... When the sons of men assembled together, about seven hundred thousand men and women, they came to Noah unto the ark. And they called to Noah, saying, "Open to us that we may come to thee in the ark. And wherefore shall we die." (footnote says: It must be remembered that according to this book, a third part of the earth had already been destroyed by the overflowing of the river Gihon.)

Does this imply that only 700,000 human beings are left on the earth at the time of the Flood? Thus we have three witnesses as to what life was like before the flood; Genesis, Eusebius and Jasher.

Dinosaur tracks and other evidence of the passage of time.

Now take a brief look at the fossil record. There are only two ways to view it. One is from the evolutionary viewpoint, that is, the various periods and epochs are successive. The other is to view the fossil record from the Genesis viewpoint, that is, that after Creation week the various ecosystems developed parallel to each other and were contemporaneous. As Mr. Gentet pointed out in his papers, even Huxley, an evolutionist, recognized the fallacy of the evolutionist's approach:

For anything that geology or paleontology are able to show to the contrary, a Devonian fauna and flora in the British Isles may have been contemporaneous with Silurian life in North America and with the Carboniferous flora and fauna in Africa. Geographical provinces and zones may have been as distinctly marked in the Paleozoic epoch as at the present and the seemingly sudden appearances of new genera and species to which we ascribe to new creation may be simple results of migration.

God tells us in Genesis 1:9–13 that the first life on the planet was plant life:

"And God said, Let the waters under the heaven be gathered together unto one place, and let the dry land appear: and it was so. And God called the dry land Earth; and the gathering together of the waters called he Seas: God saw that it was good. And God said, Let the earth bring forth grass, the herb yielding seed and the fruit tree yielding fruit after his kind, whose seed is in itself, upon the earth: and it was so. And the earth brought forth grass, and herb yielding seed after his kind and the tree yielding fruit, whose seed was it itself, after his kind: and God saw that it was good. And the evening and the morning were the third day.

It was not until the fifth day that God created birds and marine life (Genesis 1:20–23):

And God said, Let the waters bring forth abundantly the moving creature that hath life, and the

fowl that may fly above the earth in the open firmament of heaven. And God created great whales and every living creature that moveth, which the waters brought abundantly, after their kind, and every winged fowl after his kind: and God saw that it was good. And God blessed them, saying, be fruitful, and multiply, and fill the waters in the seas, and let fowl multiply in the earth. And the evening and the morning were the fifth day.

Then the sixth day He created insects, land vertebrates and man. As stated above, these ecosystems then developed contemporaneously and spread throughout the earth and the oceans. For instance in the lower Precambrian we find stromatolites are very scarce. In the middle Precambrian, stromatolites are more abundant. By the end of the Precambrian, stromatolites are abundant and wide spread. Then comes the so-called Cambrian explosion, when marine life proliferated. This could not have been caused by the Flood, rather this is what we would expect based upon the account of what occurred on the fifth day of creation, "... And God blessed them, saying, be fruitful, and multiply, and fill the waters in the seas...."

At the same time this was going on plant life was also growing and spreading, birds were multiplying and land vertebrates and insects, as well as man, were also increasing in number. A situation eventually was reached similar to what we have today. Look at the various ecosystems we have around the world. They are different but they are contemporaneous.

Now let us consider a few examples that further corroborate Mr. Gentet's belief that not all of the fossil record was a result of the flood;

No marine fossils have been found anywhere in the Newark Group, land plants and freshwater fishes are locally abundant in the darker gray beds, and dinosaur tracks in the redbeds are more plentiful than anywhere else in the world. Ripple marks are common, and mudcracks cover many of the bedding planes. The imprints of Triassic raindrops are in places associated with the footprints and mudcracks... Thus the mud that spread over the floodplains during the wet seasons lay exposed to the sun during the dry months. Dinosaurs crossed and recrossed, leaving their tracks in the mud. The last spatter of passing showers also left imprints of raindrops where the mud was exposed and still soft. During the dry season the mud shrank and cracked and then was baked and hardened so that it could hold these surface features until they were buried by a new layer sediment." (*Historical Geology* by Dunbar and Waage, third edition 1969 pp. 330–331)

I grew up on the Atlantic seaboard. I have watched the tide go out and mudcracks form. I have watched the tide

come in and those same mudcracks disappeared. It would be inconceivable to argue that raindrop impressions could survive when mudcracks do not. Such features would never have withstood the beginning of the Flood with its torrential rains and the outpouring of vast amounts of water from subterranean sources as indicated by the Scriptures:

In the six hundredth year of Noah's life, in the second month, the seventeenth day of the month, the same day were all the fountains of the great deep broken up, (in Hebrew, great deep, subterranean water supplies burst forth and covered the Earth. The metaphor used is that of a vine spreading outward) and the windows of heaven were opened. And the rain was upon the earth forty days and forty nights... And the flood was forty days upon the earth; and waters increased, and bare up the ark, and it was lifted up above the earth. And the waters prevailed, and were increased greatly upon the earth; and the ark went upon the face of the waters. And the waters prevailed exceedingly upon the earth; and all the high hills, that were under the whole heaven, were covered. Fifteen cubits upward did the waters prevail; and the mountains were covered.

Clearly the evidence in the Newark formation indicates that normal life processes were going on. Raindrops, mudcracks and dinosaur tracks could never have withstood the violent, destructive forces of nature brought about by the hand of God.

I will give two more examples of time indicators, though there are many, many others:

A remarkable occurrence was discovered near the base of the Chinle formation at St. Johns, which is southeast of Petrified Forest in eastern Arizona. Here, from a single layer, some 1600 bones were collected representing at least 39 individuals of a single species of therapsid, *Placerias giga*, along with fragments of five other kinds of reptiles. The carcasses had been dismembered by carnivorous reptiles before burial, but they had not been concentrated by currents. The reason for such mass mortality at a single spot remains an enigma. (*Historical Geology* by Dunbar and Waage, pp. 336–337)

Clearly no Flood was involved in this deposit.

Phytosaurs were common in the streams, and several other orders of reptiles, now extinct, were adapted to various modes of life on the land. The phytosaurs resembled the modern gavials in appearance and habits but were not closely related to crocodiles. Their bones are found in association with river clams, amphibians and lungfishes. One species from western Texas had a length of 25 feet. All the phytosaurs were confined to the Triassic Period. (*Historical Geology* by Dunbar and Waage, p. 335)

The above is an example of a "Jurassic" ecosystem. There is no way that you can attribute the above to Noah's Flood, otherwise you would expect to find phytosaurs mixed indiscriminately with other animals who were not a part of the phytosaurs' eco-community. It is significant that the phytosaur is confined to "Jurassic" beds. A Flood would have scattered them throughout many different layers. These are only three of many examples that vindicate and support Mr. Gentet's CCC model.

We may not be able at the present to point to a specific example and say this is proof of the pre-Flood curse. However, I suggest that some of the following may have been the result of that curse.

There was wide spread glaciations in the Precambrian and elsewhere. For example the Gowganda tillite,

This is a poorly sorted, unstratified conglomerate greywacke that includes faceted and stratified boulders as much as 10 feet in diameter. Long heralded as evidence of Precambrian glaciations, the origin of the Gowganda as a fossil tillite had been questioned by many. That it is indeed a tillite in some areas has been unquestionably demonstrated by the discovery that at the south end of Lake Timigami in Ontario it lies on a polished and striated pavement; here the evidence indicated that the ice sheet advanced three times from the northeast during deposition of the Gowganda. The Gowganda is a widespread formation, suggesting a large ice sheet rather than a montane glaciation... (*Historical Geology* by Dunbar and Waage, pp. 140–141).

See also (*Vanished Worlds, an Introduction to Historical Geology* by Roy R. Lemon, published by William C. Brown, 1993), "Precambrian ice ages," p.199, "Ice age indicators," p. 199, "Evidence for Precambrian glaciations," p. 200, "Late Proterozoic glaciations," p. 201, and "An Ordovician ice age," p. 242.

In North America the evidence for aridity is impressive. The enormous deposits of salt in Kansas (of Leonardian Age) and of the Permian basins in Texas and New Mexico have been estimated to amount 30,000,000,000,000 tons and would have required the evaporation of 22,000 cubic miles of seawater of normal salinity. The great volume of widespread dune sand adds to the picture. Both these features suggest warmth...Europe was also the scene of intense aridity.... (*Historical Geology* by Dunbar and Waage, pp. 301–302)

These few examples demonstrate that natural processes were going on from the very beginning of creation, though in some instances the magnitude of these events were

greater than anything we have so far experienced to date. This is even acknowledged by modern day uniformitarianists. Such evidence could not be the result of the Genesis Flood and that is by no means all! If we insist upon Biblical literalism and "Biblical geology," consider the rather dogmatic statements that are made in Genesis 7:21–23:

And all flesh died that moved upon the earth, both of fowl, and of cattle and of beast and of every creeping thing that creepeth upon the earth and every man: All in whose nostrils was the breath of life, of all that was in the dry land, died. And every living substance was destroyed which was upon the face of the ground, both man, and cattle, and the creeping things, and the fowl of the heaven; and they were destroyed from the earth...

You will notice that the emphasis was on land dwelling life that would be wiped out. Nothing is said about the destruction of marine life. Yet when you study the fossil record you find wide spread destruction of marine life of all types. One might argue that bottom dwelling organisms could be inundated by sediments but not swimmers such as ichthyosaurs, sharks, plesiosaurs, etc. For example, at the end of the Cretaceous, not only did dinosaurs apparently become extinct but also so did ammonites and marine reptiles. The Flood could not account for such selective destruction of marine life. There has to be another explanation.

Summary and Conclusion

The geologic record does not prove the theory of evolution. On the contrary it corroborates and vindicates the Genesis account of creation and the events of the pre-Flood and post-Flood world. It is a record of natural processes and in some instances of catastrophic disasters. It is also a record of the migration of plants and animals, but not all of the geologic record is the result of a world-wide deluge! The Flood is an historical event recognized even by skeptics, though they do not accept its worldwide extent. I would like to suggest that in searching for the Flood break we need to take into account the archeological record. Since mankind began over again after the Flood we should find evidence of the spread of the human race and the domestication of plants and animals beginning in the area where the ark landed. This subject is much too lengthy to discuss in this letter.

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Instructions for Authors

Submission

An original plus two copies shall be submitted to the editor of the *Quarterly*. Due to the expense involved, manuscripts and illustrations will not be returned to authors.

All submitted articles will be reviewed by at least two technical referees. The editor may or may not follow the advice of these reviewers. Also, the prospective author may defend his position against referee opinion.

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After the peer review is finished and all changes have been made to the article, a final copy will be requested. This should be accompanied by a computer disk containing a copy of the article in Rich Text Format (.rtf). Authors who provide either an email address or fax number will receive a proof copy of their article just prior to publication.

Authors are requested to supply a list of key words for subjects covered in their articles.

The *Quarterly* is a journal of original writings. Only under unusual circumstances will we reprint previously published manuscripts. Never submit an article to two or three journals, including ours, hoping all of them will publish your work. When submitting an article, please state if the material has been published previously or has been submitted to other journals.

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Although it is nicer to be positive, there seem to be a lot of important negatives:

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References and Book Reviews

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CRSQ: *Creation Research Society Quarterly*. [for multiple *Quarterly* references]

Cockman, Joneen. 1988. Collecting plants for the Creation Research Society Herbarium. *CRSQ* 24:187–193.

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

———. 1971b. *Origin of eukaryotic cells*. Yale University Press, New Haven, CT.

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

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

Book review headings, like references, have a particular style which should be followed. This issue of the *Quarterly* will provide examples.

Length

Manuscripts containing more than 25 pages are discouraged. If a topic cannot be covered to the author's satisfaction in this number of pages, the author should divide his material into separate papers that can be serialized in the *Quarterly*. Book reviews should be limited to 1000 words.



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

Activities—The society is solely a research and publication society. It does not hold meetings or engage in other promotional activities, and has no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund is maintained to assist in such projects. Contributions to the research fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates The Van Andel Creation Research Center in Chino Valley, Arizona.

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

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

2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.

3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.

4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.