

CRSQ

CREATION RESEARCH SOCIETY QUARTERLY



Volume 45

Spring 2009

Number 4

Creation Research Society Quarterly

Volume 45

Spring 2009

Number 4

Articles

- Neandertal DNA and Modern Humans 246
Daniel Criswell
- Evidence for the Lack of Snake Evolution 258
Jerry Bergman
- Mutation And Natural Selection
The Central Dogma
of Neo-Darwinian Evolution 271
Per A. Larssen
- Lysenkoism:
The Tragedy of Government-
Enforced Darwinism:
The Effect of Darwin on Soviet Communism 285
Jerry Bergman

Cover design by Michael Erkel:

Michael Erkel and Associates, 1171 Carter Street,
Crozet, Virginia 22932

Design services by Cindy Blandon, cblandon@aol.com.

The *Creation Research Society Quarterly* is published
by the Creation Research Society, 6801 N. Highway 89,
Chino Valley, AZ 86323, and it is indexed in the *Christian
Periodical Index* and the *Zoological Record*.

Send papers on all subjects to the Editor:
Kevin L. Anderson, Van Andel Creation Research Center,
6801 N. Highway 89, Chino Valley, AZ 86323.

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

Authors' opinions expressed in the *Quarterly* are not neces-
sarily those of anyone else associated with the Creation
Research Society.

Copyright © 2009 by Creation Research Society. All rights
to the articles published in the *Creation Research Society
Quarterly* are reserved to the Creation Research Society.
Permission to reprint material in any form, including the
Internet, must be obtained from the Editor.

ISSN 0092-9166

Printed in the United States of America

Departments

- Editorial: What Is New Is Old Again 241
- Book Reviews
- The Shack* by William Paul Young 245
- The Man Who Found Time* by Jock Repcheck 254
- The Genesis Debate (DVD)*
by Answers in Genesis 269
- The Harmony of Science and Scripture*
by Harry Rimmer 270
- The Privileged Planet* by Guillermo Gonzalez
and Jay W. Richards 282
- The Edge of Evolution* by Michael Behe 283
- The Devil's Delusion* by David Berlinski 291
- Understanding Intelligent Design* by William A.
Dembski and Sean McDowell 292
- Heaven Without Her* by Kitty Foth-Regner 298
- The Committee* by Clay Cornelius 299
- Hallmarks of Design* by Stuart Burgess 300
- Notes from the Panorama of Science:
- Two Mystery Mountains 293
- Normal Insect Flight with Abnormal Wings 298
- Instructions to Authors 301
- Membership/Subscription Application
and Renewal Form 303

Editorial Staff

Kevin L. Anderson, Editor
Jerry Bergman, Biology Editor
George F. Howe, Assistant Biology Editor
John K. Reed, Geology Editor
Eugene F. Chaffin, Physics Editor
Ronald G. Samec, Astronomy Editor
Don B. DeYoung, Book Review Editor
Jarl Waggoner, Managing Editor
Robert Mullin, Assistant Managing Editor

Board of Directors

Don B. DeYoung, President
Eugene F. Chaffin, Vice-President
Gary Locklair, Secretary
Mark Armitage, Financial Secretary
Danny Faulkner, Treasurer
Glen W. Wolfrom, Membership Secretary
Theodore Aufdemberge D. Russell Humphreys
David Kaufmann Lane Lester
Michael J. Oard John K. Reed
David Rodabaugh Ron G. Samec

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

Creation Research Society Conference

Creation Research Society Conference July 10-11, 2009

University of South Carolina Lancaster
Lancaster, SC

Registration:

CRS Member—\$35
Non-member—\$70

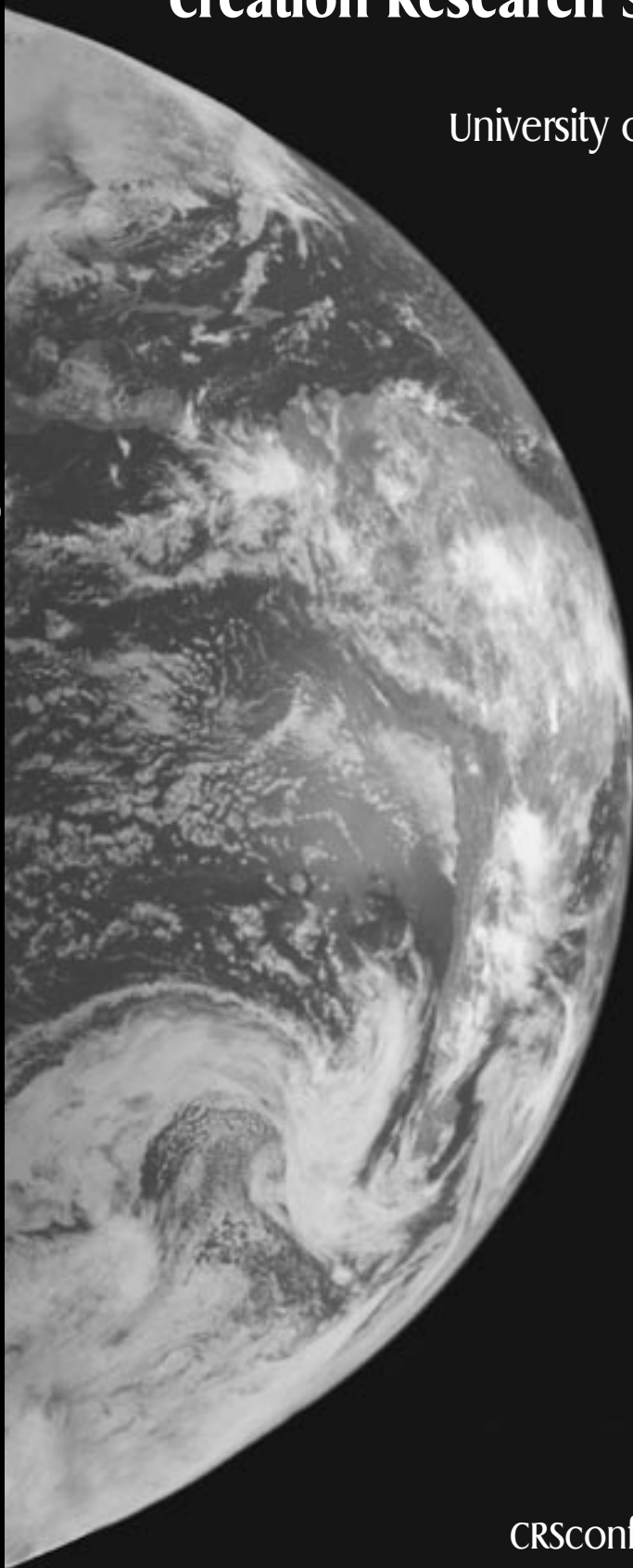
Henry M. Morris Memorial Lecture

Friday, July 10
8:00 pm
Open to public

For more information visit
www.CreationResearch.org

or contact

CRSconference@creationresearch.org
Phone (928) 636-1153





Editorial

What Is New Is Old Again

Following one of my presentations a few years ago, a professor of evolutionary genetics in the audience told me that he did not disagree with anything I had said—it was just ten years out of date. His claim was that findings from the study of evolutionary development (commonly known as Evo/Devo) answered most of my challenges. (I had not dealt with Evo/Devo in this particular talk because there is only so much that can be described in a popular-level, 50-minute presentation.) While I did not agree that my material was dated, I wondered if ten years ago he would have admitted that he could not disagree with anything I had said. I also realized that some evolutionists (especially the more knowledgeable ones) are sometimes willing to admit an earlier weakness in evolutionary teachings once they think that particular problem has been solved.

This raises another question: over the years how many people were highly influenced by so-called evidence for evolution that has subsequently been clearly shown to be wrong or misleading? And, if this has happened before, is it still happening today?

I Now Love Lucy

As an undergraduate in college, I began to read and hear about a sensational fossil

find dubbed *Lucy*. Regarded as the most fully preserved hominid fossil, *Lucy* was supposed to represent a new level of fossil evidence for human evolution. At that time it was claimed that *Lucy* provided such solid support for evolution that this was surely the last “nail in the coffin” of scientifically ignorant creationism. I remember that when creationists offered critical evaluations of the fossil and its reconstruction, they were ridiculed for ignoring the obvious nature of this fossil and the overwhelming support it provided to human evolution. In other words, creationists’ views about *Lucy* were considered too ignorant to even waste time refuting (the same kind of approach evolutionists are using with most creationists’ arguments today).

Time, however, has not been kind to *Lucy*. Other evolutionists eventually began to challenge some of the previous claims made about her (Richmond and Strait, 2000; Stern and Susman, 1983). In addition, a *Nova* episode (“The Story of Lucy,” Oct 11, 1994) aired an interview with Dr. Own Lovejoy (the primary anatomist involved in *Lucy*’s reconstruction). In this interview, Dr. Lovejoy described how the anatomy of *Lucy*’s pelvic bone (only one was found) caused her hips to conform more to a primate than human anatomy. Since he knew that she walked upright, much as modern humans, Lovejoy assumed that

the pelvic fossil remains must have been damaged. He then described how he proceeded to reshape a cast of the pelvis to give it a human anatomy. His conclusion was that this represented a more accurate reconstruction. This reshaped pelvis was subsequently incorporated into the “official” *Lucy* reconstruction.

There is really very little comment needed. Clearly, *Lucy* cannot be offered as a wonderful example of fossil evidence for human evolution when the assumption of human evolution was a key in her reconstruction. This type of circularity renders her impotent.

Yet, a major exhibit of *Lucy*’s fossils has been traveling throughout the United States in recent years, continuing to promote her as a wonderful fossil exhibit of evolution. As part of this display (as well as other permanent *Lucy* displays around the world) is a lifelike reconstruction of what *Lucy* allegedly may have looked like. Interwoven into these various reconstructions is not only the hip reshaped by Lovejoy, but other unsubstantiated features as well. (The more appropriate description would be factious features.) For example, many of these reconstructions have given her a white sclera (the white of the eye). This is almost certainly erroneous since only humans, not primates, have white sclera. *Lucy* clearly has no fossilized eyes to determine her sclera color. Thus, giv-

ing her a white sclera in these displays is purely an attempt to make her look more human, regardless of how unwarranted. Many of the reconstructions also give *Lucy* very human fingers and toes, complete with manicured nails. This is hardly appropriate, even by the most ardent evolutionist's standards.

When creationists use the scientific literature to help support their own position, frustrated evolutionists call it "quote mining." Interestingly, when I pointed out some of the factious characteristics attributed to *Lucy* reconstructions during a recent presentation I gave at a university, I was accused of "picture mining." I guess I have come to understand that "quote mining" is when creationists use the scientific literature in an inappropriate way, i.e., helping to support a creation model—a way it could not possibly have been intended to be used. Therefore, "picture mining"

**How many may have
seen these fossils as
sufficient evidence that
humans have evolved
and now
count themselves
ardent evolutionists
because of what
they were taught
about *Lucy*?**

must be when creationists have the audacity to show that pictures and other illustrations of evolutionists' claims are misleading (or just plain bogus). It does not mean that creationists have said anything incorrect; it just means they have "cheated."

So, the fossilized creature known as *Lucy* cannot rationally be offered as "Exhibit A" of evidence for human evolution. In fact, she clearly never should have been. Yet, how many people, especially 30 to 35 years ago, were strongly influenced by the claims being made of her? How many may have seen these fossils as sufficient evidence that humans have evolved and now count themselves ardent evolutionists because of what they were taught about *Lucy*?

Human Genome

At the beginning of this decade, while attending a science conference, I was speaking with a scientist who was directly involved in the Human Genome Project (a major—and costly—undertaking to map and subsequently sequence all DNA of the human chromosomes). This scientist informed me that several congressmen were very concerned about the genome results that were soon to be published. Why? Because, he claimed, many of their constituents were fundamentalist Christians, and the genome results were going to be a devastating blow to their ignorant creationist ideas. Since I was one of those "ignorant creationists," I proceeded to quiz him more on why he thought the genome sequences were such strong support for evolution. Ultimately, his arguments centered on junk DNA and chimp/human similarity.

Junk DNA is the concept that the human genome is comprised largely of nonfunctional (i.e., useless) segments of DNA. Allegedly, during the human genome's long evolutionary history, many genes (such as genes for making fins and scales) were no longer needed

as our human ancestors evolved. Instead, they were replaced with new genes (such as those for hair and skin). The unused genes were not removed from the genome; rather they remained and their sequences were steadily randomized by mutations. Thus, junk DNA is assumed to be the result of years of mutations degrading the DNA sequence of these unneeded genes, hence, rendering them useless (i.e., junk). Evolutionists conclude that junk DNA proves the human genome is a product of millions of years of genes forming and degenerating, leaving behind massive amounts of useless segments of DNA: a genetic version of vestigial organs.

They further argue that junk DNA contradicts creation. No creator would make the human genome with massive amounts of useless DNA. So, junk DNA is claimed to be evidence against creation, as well as evidence for evolution.

However, the concept of so-called junk DNA was strictly an evolutionist supposition. The fact that no function could initially be assigned to large segments of the human genome did not mean that these segments had no function. In fact, why would such an assumption even be considered, except for the fact that it appealed to evolutionists? Recent evidence has suggested that much (if not virtually all) DNA in the genome not only does have a function but also is vital to the full function and activity of the genome (Kapranov et al., 2007). This totally contradicts evolutionists' original assumptions and claims of junk DNA but supports previous predictions by creationists (Anderson, 2003). Will evolutionists now admit that initial creationist criticism of junk DNA was correct after all?

In 1975 a *Science* paper argued that there is only a 1% difference between the sequence of the human and chimpanzee genomes (King and Wilson, 1975). Since then, evolutionists have accepted this claim almost as a "given." Why? I would assume because it fits so well with

their expectation of the data. This claim was even repeated at the same time that the initial sequence of the human genome was published (Pääbo, 2001). Presumably, since chimpanzees are the closest human evolutionary relative, this mere 1% difference is clear demonstration that both we and chimpanzees evolved from a common ancestor some 5 to 6 million years ago. The argument of 1% has even been used by various activist groups to promote radical animal rights agendas, including a proposal in the Spanish parliament to grant basic human rights to chimpanzees, gorillas, and orangutans.

However, the chimpanzee genome is 11.5% larger than the human genome (CSAC, 2005). Thus, how could there be only a 1% difference between the two genomes if the chimpanzee genome contains almost 12% more DNA? The answer? There cannot. The 12% difference simply is not counted, almost as if that extra DNA of the chimpanzee genome is unimportant (I am not sure the chimpanzee would agree). What is more, the claimed 98–99% similarity of human and chimpanzee is based on a comparison of less than 80% of the respective genomes (Britten, 2002; CSAC, 2005). And of this 80%, the comparison really only involves stretches of DNA where the human and chimp genome can be directly aligned (that is directly compared without huge regions that do not match in sequence) (Britten, 2002). Of the 20% (or more) of the human genome not yet aligned with the chimpanzee, it is very possible that the differences will be far more distinct than what has been found in the 80% so far compared.

The true similarity of the entire human and chimpanzee genomes is not known. It may not be known for many years. Geneticists Svante Pääbo (an early enthusiast for the 1% claim) now admits, “I don’t think there is any way to calculate the number ... in the end, it’s a political and social and cultural thing about

how we see our differences” (quoted in Cohen, 2007, p. 1836). In other words, the claim of 1% was always more about evolutionists’ assumptions (dare I say religion?) than it ever was about genetic evidence. Yet, how many people were influenced by the 1% claim to the point of doubting creation or even doubting Biblical teachings of the uniqueness of humans?

Based on current information, I would predict the genomic difference between human and chimpanzee may be more than 20% (and certainly at least 16.5%). For years creationists have been challenging both the accuracy and the meaning of the 1% myth. Now that even evolutionists are beginning to acknowledge it was a bogus claim, will creationists be given credit for having been right after all?

mtDNA

Cells in the human body contain small organelles called mitochondria. Mitochondria possess a small piece of DNA, which is separate from the chromosomal DNA in the nucleus. This mitochondrial DNA (mtDNA) is generally passed from mother to child and like all DNA is subject to mutations with each passing generation. Based upon how many new mtDNA mutations occur per generation, a genealogy of various human lineages (i.e., family trees) can be constructed from a study of mtDNA sequences.

Over twenty years ago some evolutionists proposed a genetic lineage of human mtDNA. They claimed their proposed lineage showed that all modern humans descended from just one female (Cann et al., 1987). In other words, all mtDNA in humans today was passed down from just one mother. This female was named mitochondrial “Eve” (mtEve). Many Biblical creationists viewed this as genetic evidence of the Biblical description of Eve as “the mother of all” humans (Gen. 3:20). However, the study also claimed that mtEve lived

between 140,000 and 290,000 years ago: A direct genetic challenge to young-earth Biblical creation.

What needs to be understood, however, is that a key component of the 1987 study was the assumption that humans and chimpanzees shared a common ancestor 6 million years ago. This assumption became part of the researchers’ calculations, which gave a very slow mutation rate for human mtDNA over the last 6 million years. Thus, an old age for mtEve was an inevitable result of the study. The assumptions imposed in the calculations, in fact, made it impossible for mtEve not to be “old.”

The mtDNA mutation rate of modern humans, however, is much faster than the rate used in the 1987 study (Gibbons, 1998). Therefore, if the actual human mutation rate is applied to the 1987 study’s data, rather than a mutation rate derived from evolutionary supposition, the age for mtEve shrinks to less than 10,000 years (Gibbons, 1998). Also, a recent study has determined the original mtDNA sequence of “Eve” to within an accuracy of at least 99.99% (Carter, 2007). This is a much more accurate sequence than the “Eve” sequence used in the 1987 study. Interestingly, human lineages derived from this sequence are fully consistent with mtEve living only a few thousand years ago (Carter et al, 2008). Yet, how many people originally concluded that mtEve gave wonderful genetic support to evolution, or at least “old-earth” creation?

Index Fossils

In the early nineteenth century, British geologist William Smith was credited as the first to apply the concept of index fossils. This system, known as biostratigraphy, uses the fossil fauna in a given geologic region to assign a correlative age with other geologic regions. For example, the geologic strata of Grand Canyon, Zion National Park, and Bryce Canyon are all correlated with

each other by the fossil content of their rocks (United States Geological Survey, 1997).

Index fossils are specific fossils (1) assumed to not have existed very long in earth history (evolutionarily speaking), (2) are easy to identify, and (3) were widely distributed. For example, archaeocyathids are assumed to have lived only during the Cambrian Period. Thus, rocks containing archaeocyathids are identified as Cambrian. *Siphonodella sulcata*, a species of conodont, is assumed to have lived only at the beginning of the Carboniferous Period. It serves as an index fossil for that geologic time.

Since Smith's first application, the use of index fossils has been widely employed and practiced (Dunbar and Waage, 1969). In fact, using index fossils, geologic strata around the world was dated and correlated long before concepts of radiometric dating were even conceived. Von Englen and Caster (1952) acknowledged that at one time "historical geology [relied] chiefly on paleontology, the study of fossil organisms," which "utilizes knowledge of organic evolution" to "correlate the [rock] records of ancient time" (p. 423).

Clearly, biostratigraphy is based specifically on assumptions of evolutionary descent. Thus, a geologic stratigraphy based upon index fossils cannot be offered as geologic evidence of evolution or as evidence for contemporary geologic time scales. "By doing so, we are guilty of circular reasoning if we then say the fossil record supports [evolution]" (West, 1968, p. 216). Yet, creationists are mockingly told over and over that they are guilty of denying the overwhelming evidence of the fossil record. I have found that terms such as "overwhelming" are often used as a deceptive description for the very opposite.

Biostratigraphy is no longer emphasized as a tool for dating and correlating geologic strata (I'm not sure that means

it is no longer used, just not emphasized that it is still being used). In fact, no reliable chronometer has yet been found for dating the entire rock record. As a consequence, currently the International Commission on Stratigraphy is effectively assigning dates more by committee decision than by physical evidence (Reed, 2008). An observer of all this might begin to think that creationist criticism of evolutionary paleontology and geology has not been so erroneous after all. Yet, how many people were convinced (and still are) that fossils and rocks prove evolution and prove the earth's age to be billions of years?

Examples continue to arise where even many evolutionists now acknowledge the original claim was mistaken or bogus. Will creationists finally be given credit that they had been right in challenging the claim, that they had been right in their alternative interpretations? If this were strictly a scientific discourse, then I would say yes. But it is not likely, because that is not how this "game" is played.

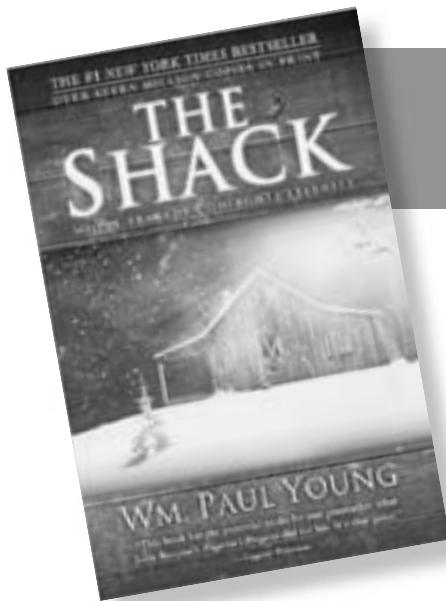
Kevin Anderson, Ph.D.

Editor

Creation Research Society Quarterly

References

- Anderson, K. 2003. Creation, evolution, and the molecular revolution. *Creation Matters* 8(5):1–2.
- Britten, R.J. 2002. Divergence between samples of chimpanzee and human DNA sequences is 5%, counting indels. *Proceedings of the National Academy of Sciences (USA)* 99:13633–13635.
- Cann, R.L., M. Stoneking, and A.C. Wilson. 1987. Mitochondrial DNA and human evolution. *Nature* 325:31–36.
- Carter, R. 2007. Mitochondrial diversity within modern human populations. *Nucleic Acids Research* 35:3039–3045.
- Carter, R.W., D. Criswell, and J. Sanford. 2008. The "Eve" mitochondrial consensus sequence. In Snelling, A.A. (editor), *Proceedings of the Sixth International Conference on Creationism*, pp. 111–116. Creation Science Fellowship, Pittsburgh, PA, and Institute for Creation Research, Dallas, TX.
- Chimpanzee Sequencing and Analysis Consortium (CASC). 2005. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature* 437:69–87.
- Cohen, J. 2007. Relative differences: the myth of the 1%. *Science* 316:1836.
- Dunbar, C.O., and K.M. Waage. 1969. *Historical Geology*, 3rd ed. John Wiley and Sons, New York, NY.
- Gibbons, A. 1998. Calibrating the mitochondrial clock. *Science* 279:28–29.
- Kapranov, P., A.T. Willingham, and T.R. Gingeras. 2007. Genome-wide transcription and the implications for genomic organization. *Nature Reviews. Genetics* 8:413–423.
- King, M.-C., and A.C. Wilson. 1975. Evolution at two levels in humans and chimpanzees. *Science* 188:107–116.
- Pääbo, S. 2001. The human genome and our view of ourselves. *Science* 291:1219–1220.
- Reed, J.K. 2008. Toppling the timescale. Part IV: Assaying the golden (FeS₂) spikes. *Creation Research Society Quarterly* 45:81–89.
- Richmond, B.G., and D.S. Strait. 2000. Evidence that humans evolved from a knuckle-walking ancestor. *Nature* 404:382–385.
- Stern, J.T., and R.L. Susman. 1983. The locomotor anatomy of *Australopithecus afarensis*. *American Journal of Physical Anthropology* 60:279–317.
- United States Geological Survey. 1997. Relative time scale. <http://pubs.usgs.gov/gip/geotime/section.html> (accessed March 3, 2009.)
- Von Englen, O.D., and K.E. Caster. 1952. *Geology*. McGraw-Hill, New York, NY.
- West, R.R. 1968. Paleontology and uniformitarianism. *Compass* 45:212–218.



Book Review

The Shack: Where Tragedy Confronts Eternity

by William Paul Young

Windblown Media, Newberry Park, CA, 2007, 248 pages, \$15.00.

Author Young initially self-published fifteen copies of this book for friends. It caught fire and a year later has passed one million copies in sales. The Christian novel has been praised by many while others accuse Young of promoting feminism, heresy, open theology, and universalism. This review will limit itself to the creation connections rather than the broader theological issues.

Young grew up in Dutch New Guinea, the son of missionary parents. His worldview was darkened by sexual abuse from outside contacts. After decades of anger, this book pictures Young's return to God through a fictional story. In the telling, a father named Mack loses his young daughter to a serial killer. The details are chilling and the reader needs reminding of the fictional setting. Mack's life is overcome by what is called *The Great Suffering*. Compounding the problem, Mack's own dad had left many "religious scars." As a result, a strong faith was not present to help with the family tragedy. One dreary day a letter arrives, inviting Mack to the remote,

forest shack where his daughter died three years earlier. There he is comforted by the God of the universe including the three persons of the Trinity. Most unusual, the heavenly Father is a jolly black woman, named PaPa, who likes to cook. This sounds bizarre but it works well in the story. The author's obvious intent is to alter common religious preconceptions.

What follows are many practical theological discussions with the Father, Jesus, and the wispy Holy Spirit. Scripture is woven into the conversations in a meaningful way. Topics which Mack brings up for clarification include the presence of evil, free will, the Trinity, and the Cross. At one point, Mack asks Christ what he thinks of the bracelet slogan, What would Jesus do? The reply: "Good intentions, bad idea...Being my follower is not trying to 'be like Jesus,' it means for your independence to be killed" (p. 149). As the story progresses, Mack's life is renewed by redemption.

Mack asks, "Was there really an actual garden [of Eden]...There are

lots of people who think it was only a myth." The answer from the Creator: "Of course [it's real]...I have a thing for gardens" (p. 134). Mack also asks why poison plants were created. The answer: "Many of these so-called bad plants...contain incredible properties for healing or are necessary for some of the most magnificent wonders when combined with something else" (p. 133). The presence of sin is said to be "for purposes that we cannot possibly understand now" (p. 222). As a reviewer, I am delighted that a million readers are exposed to such sentiments.

The book may be too uncomfortable for some readers. The description of Jesus enjoying his world by fishing and skipping stones may be a bit "over the top" (p. 147). Also, author Young comes down rather hard in his description of local churches. Still, the book leads to lively discussion, mainly by a Christian audience.

Don DeYoung
DBDeYoung@Grace.edu

Neandertal DNA and Modern Humans

Daniel Criswell*

Abstract

The variation of mitochondrial DNA (mtDNA) between modern humans and Neandertal sequences lie outside the mtDNA sequence variation within modern humans. This variation has led several researchers to conclude that Neandertals did not contribute to modern human DNA and are a separate species that went extinct in Europe. It is feasible that DNA can be retrieved from specimens that died thousands of years ago, given the ideal preservation conditions and extraction protocols. However, DNA also decays as the organism decomposes. Spontaneous hydrolysis, oxidation, and nucleotide modifications are a few of the processes that cause DNA decay and likely interfere with reliably obtaining a mtDNA sequence that accurately reflects the Neandertal mtDNA sequence.

In addition to DNA decay, contamination of samples is also apparent in published Neandertal mtDNA sequences. A comparison of conserved sequence block 2 (CSB2) in hypervariable region II (HVRII) between Neandertal mtDNA and modern man, primates, and other mammals indicate that excess thymine in CSB2 of published Neandertal mtDNA is likely the result of contamination.

Introduction

A strong case has been made for the position that Neandertals were fully human, varying slightly, but not significantly, in skeletal structure from modern humans (Lubenow, 1992). The contrasting view that Neandertals are not fully human and never contributed to the modern human gene pool has received support from extracting and amplifying ancient

DNA (aDNA) from Neandertal remains. Eleven Neandertal mitochondrial DNA (mtDNA) sequences have been published (Krings et al., 1997; Krings et al., 1999; Krings et al., 2000; Ovchinnikov et al., 2000; Schmitz et al., 2002; Lalueza-Fox et al., 2006; Caramelli et al., 2006; Orlando et al., 2006; Krause et al., 2007), and recently over one million base pairs

of Neandertal nuclear DNA (nuDNA) were sequenced (Green et al., 2006; Noonan et al., 2006). These sequences claim to be evidence that Neandertals are distinctly different from modern humans and likely did not contribute to the modern human genome (Krings et al., 1997; Serre et al., 2004; Currat and Excoffier, 2004).

The average sequence difference between some of the published Neandertal mtDNA sequences and modern humans is about three times the number of average variation between modern humans. In fact, the putative mtDNA

* Daniel Criswell, Ph.D., Institute for Creation Research, 1806 Royal Lane, Dallas, TX, Phone 214-615-8300, dcriswell@icr.edu

Accepted for publication October 22, 2008

variation between modern humans and Neandertals lies completely outside the range of variation within modern humans (Krings et al., 1997). If currently obtained Neandertal mtDNA sequences accurately represent their original sequence, it would provide strong evidence that the two groups did not exchange DNA and they could be classified as different species or subspecies (*Homo sapiens* and *Homo sapiens neanderthalensis*). The relatedness between modern humans and Neandertals using mtDNA (or nuclear DNA) is dependent, however, on retrieving uncontaminated DNA from Neandertal bones and teeth that has been sufficiently preserved to prevent significant DNA decay.

Mitochondrial DNA and Contamination

mtDNA provides the best opportunity for acquiring templates to sequence ancient DNA. It is a 16,569 base pair, circular DNA strand divided into two functional regions—the control region (1120 base pairs, 16,024–16569 and 0–576) and the coding region (the remaining 15,450 base pairs), where proteins, transfer RNA, and ribosomal RNA are transcribed (Cutticchia, 1995). The control region is where transcription is regulated and is taxonomically significant, meaning there is enough variation in this region to distinguish sequences between species, members of different ethnic groups within a species, or even one human family from another. The two hypervariable regions, hypervariable region I, or HVRI (16,024–16,383), and hypervariable region II, or HVRII (57–372), in the control region are the sources of Neandertal mtDNA. Nine Neandertal mtDNA sequences are from HVRI and two sequences were obtained from HVRII.

An important factor in obtaining useful ancient DNA from mitochondria is the number of mtDNA molecules that can be extracted from a sample. Each

sample from a living organism should have thousands of cells, 100–1000 mitochondria in each cell, and 5–10 copies of DNA in each mitochondrion, providing the >1000 mtDNA molecules required for efficient amplification (Krings et al., 1997). However, bone or tooth samples that provide mtDNA for sequencing will have far fewer intact cells, if any, and the DNA that is retrieved is likely bound to the hydroxyapatite of the bone or tooth. The loss of cells and DNA post-mortem damage emphasize the value of mtDNA with thousands of copies for sequencing targets in a living organism, and many successful aDNA sequences have started with under 100 templates (Hofreiter et al., 2001).

Each copy of mtDNA provides a target for primers (short oligonucleotides) that initiate the polymerase chain reaction (PCR) in amplifying enough mtDNA for sequencing. It is assumed that enough undamaged Neandertal mtDNA molecules are still present to provide a template for the PCR. Theoretically, several PCR amplifications with extracted template mtDNA provide sufficient sequences to derive a consensus sequence and accurately represent the original Neandertal mtDNA sequence. The more template mtDNA that is available at the start of the amplification process, the less likely the PCR product will be contaminated by extraneous sources of DNA.

Contaminating DNA can block the PCR amplification process, incorporate foreign DNA bases into targeted DNA, or result in the amplification of only non-targeted DNA (Pusch and Bachmann, 2004). Contamination is a constant obstacle for obtaining authentic ancient DNA sequences, and the evidence for contamination has been observed in ancient mtDNA samples as well as ancient nuclear DNA (Wall and Kim, 2007). Valid research requires adequate experimental protocols to prevent the incorporation of contaminated DNA (Cooper and Poinar, 2000; Gilbert et

al., 2005; Willerslev and Cooper, 2005). These requirements include a facility reserved only for ancient DNA research, the independent verification of the putative sequence in another laboratory, treatment with enzymes to remove damaged bases, and a sufficient number of clones to derive a consensus sequence (Cooper and Poinar, 2000; Gilbert et al., 2005; Bower et al., 2005; Willerslev and Cooper, 2005).

DNA Decay

Precautions can be taken to minimize contamination in aDNA samples, but the problem of DNA decay poses more difficult problems to obtain authentic ancient mtDNA sequences. As soon as an organism dies, DNA begins to degrade, and the repair mechanisms that maintain DNA sequence fidelity in living systems no longer function. Spontaneous hydrolysis and oxidation result in double-strand breaks, abasic sites, and nucleotide modifications or miscoding lesions (Lindahl, 1993). Double-strand breaks and abasic sites (most commonly depurination) can prevent PCR amplification, while nucleotide modifications can be incorporated into the amplified PCR product, mimicking the expected evolutionary changes in the putative DNA sequence.

Spontaneous hydrolysis results in approximately 2,000–10,000 depurination events in each human cell per day. This is due to the instability of the N-glycosyl bond between a purine (adenine and guanine) and the 2' carbon of the deoxyribose sugar (Lindahl, 1993). In living systems, endonucleases rapidly initiate repair processes to maintain the integrity of DNA (Lindahl, 1993). However, after the organism dies, depurination results in small fragments of DNA, which are more difficult to amplify than intact DNA from a living organism. Kinetic calculations predict that amplifiable fragments less than 400 base pairs will survive no longer than 10,000 years

at temperate conditions (Poinar et al., 1996). As the temperature decreases, the rate of DNA decay also decreases, making samples in permafrost the best candidates for aDNA sequencing (Smith et al., 2001; Willerslev and Cooper, 2005).

All of the environmental factors that affect DNA decay are not completely understood, but higher temperatures and increased moisture appear to be two of the more significant factors that accelerate DNA decay. Whether or not aDNA sequences are damaged or accurately represent the original sequence of the living organism, the retrieval of any DNA from ancient organisms is evidence for a *recent existence* of less than 1 million years for permafrost specimens (mammoth and bacteria) and less than 10,000 years for temperate specimens, including Neandertals (Poinar et al., 1996; Smith et al., 2001; Willerslev and Cooper, 2005).

The most common result of decay in DNA is the deamination of cytosine resulting in a base change to uracil (Hansen et al., 2001; Hofreiter et al., 2001). This change is easily defined by the chemical nomenclature of the two bases. Cytosine is 2-oxy-4-amino pyrimidine and uracil is 2-oxy-4-oxy pyrimidine. Post-mortem damage from cytosine deamination can accumulate fairly quickly in the context of aDNA, considering that the half-life of a cytosine residue is about 200 years under human physiological conditions (37°C and 7.4 pH) (Lindahl and Nyberg, 1974). Cytosine deamination occurs an estimated 100–500 times a day in a living cell (Lindahl, 1993), where accompanying repair mechanisms are able to correct the damage. Uracil is a base not normally incorporated into the DNA sequence of any organism; consequently many organisms, including humans, have an enzyme, uracil-N-glycosylase (UNG), to remove deaminated cytosine (uracil) when it is incorporated into DNA. When an organism dies, spontaneous cytosine deamination can

occur through a hydrolysis reaction that removes the amine group converting cytosine to uracil (Lindahl, 1993). Without UNG to repair the damaged base, any postmortem sequencing reaction will identify the deaminated cytosine as uracil and pair it with adenine on the complementary strand. In mtDNA, if the deaminated cytosine is on the heavy strand (H strand), an adenine will be incorporated on the complementary light strand (L strand) in place of the original guanine.

Deamination of adenine to hypoxanthine and guanine to xanthine also occurs, but at less than 2–3% of the rate of cytosine deamination (Lindahl, 1993), making them less likely to cause major changes in aDNA sequences. Cytosine to thymine (C→T) and guanine to adenine (G→A) transitions are classified as Type 2 transitions in the context of aDNA sequencing, representing the deamination of cytosine to uracil (Hansen et al., 2001). Type 1 transitions represent the possible deamination of adenine→hypoxanthine, which results in an A→G and T→C transition on complementary DNA strands (Table I).

Obviously, scientists who sequence aDNA are aware of the problems that deamination can cause; one of the required protocols is to treat the samples with UNG to remove deaminated cytosine residues that could produce erroneous sequences from PCR amplification. UNG is believed to remove all deaminated cytosines eliminating Type 2 transitions from DNA (Hofreiter et al.,

2001). However, treatment with UNG before amplification is not without problems. The removal of deaminated cytosine leaves an abasic site, creating strand nicks that can prevent amplification of the aDNA strand (Hofreiter et al., 2001). This is particularly worrisome when there might only be 100 templates available for amplification. Reducing the number of templates increases the risk of incorporating contaminating extraneous DNA into the targeted sequence, or completely sequencing contaminants (Pusch and Bachmann, 2004).

Evidence exists that cytosine deamination is not the only source of Type 2 transitions in aDNA. Gilbert et al. (2007) and Hoss et al. (1996) both found that UNG treatment left behind half of the C→T Type 2 transitions that were identified from damaged sequences in controlled experiments. Presumably, the C→T transition resulted from the decay of guanine to adenine on the complementary strand. Gilbert et al. (2003; 2007) noticed this, at first speculating that UNG did not remove all deaminated cytosines and was successful mainly on longer templates. Apparently, these C→T transitions might occur from an (as yet) unidentified degradation of guanine to adenine and be as frequent as cytosine deamination in nonliving samples (Gilbert et al., 2007). The C→T transition would result from sequencing the complementary strand opposite the G→A deamination event. This observation has prompted Gilbert et al. (2007) to observe that most of the knowledge

Table I. Type 1 and Type 2 Transitions. DNA decay will result in transitions on both strands when sequenced. Cytosine deamination is the most common form DNA damage in living systems.

Transition Type	H Strand	L Strand	Composite Change
Type 1	T→C	A→G	TA→CG
Type 2	C→T	G→A	CG→TA

about DNA damage comes from living systems and not from aDNA, leaving the possibility that post-mortem DNA is damaged from processes that are not yet understood (Gilbert et al., 2007).

One possible explanation for post-mortem conversion of G→A is the co-extraction of divalent metal ions that have been shown to damage DNA (Pusch and Bachmann, 2004). Concentrations of some divalent metal ions increase several times (up to 5,000 times) in aDNA when compared to contemporary samples, raising the possibility of mutagenic effects when aDNA is extracted and amplified through PCR (Velasco-Vazquez et al., 1997). This is particularly true of manganese. The G→A transition frequently occurs at site 1138 of the human *FGFR3* gene in the presence of 0.25mM MnCl₂. The same mutation occurs when human template DNA is spiked with aDNA, indicating that aDNA is the source for the mutagenic manganese (Pusch et al., 2004). It also explains why independent sequencing of putative aDNA samples would incorporate the same Type 2 transitions; the source of the mutagenesis (manganese) is in the bone or tooth material supplying the aDNA. The possibility that mutagenic effects from divalent metal ions cause sequence divergence between Neandertals and modern humans casts serious doubt on aDNA sequences being validated by independent laboratories.

Neandertal DNA

Neandertal DNA Decay

A decrease in the Neandertal to modern human Type 1: Type 2 transitions in mtDNA, compared to a modern human to modern human ratio, is an expected result of the deamination of cytosine to uracil or damage to guanine that would result in a transition to adenine. To determine the difference in Type 1: Type 2 transitions, a reliable ancestral sequence for both modern humans

and Neandertals is required as a baseline. The Eve1.0 Consensus Sequence (Carter, 2007) provides this baseline for a comparative study between Neandertal and modern human mtDNA. Not only does the Eve1.0 provide a baseline, but the evidence that all humans descended from one woman (Cann et al., 1987) and the overwhelming statistical consensus sequence from Eve1.0 (Carter, 2007) provides confidence that Eve1.0 is reasonably comparable to the first human mtDNA sequence. Even in an evolutionary scenario, Eve1.0 would predate the Neandertal specimens by more than 100,000 years, again making it a feasible source as a baseline sequence. In HVRI, the Eve1.0 consensus sequence is also identical to the revised Cambridge Reference Sequence (Anderson et al., 1981).

Therefore, the Eve1.0 consensus sequence was used as a baseline sequence to determine if the mtDNA Type 1: Type 2 transitions from Neandertals and modern humans are significantly different from the ratio within modern human sequences. Figure 1 shows a sequence alignment for the HVRI from nine Neandertals and Eve1.0. The alignment was made using ClustalX 2.0.7, employing the suggested pairwise and multiple alignment parameters for nucleic acids (Hall, 2004). Type 1 and Type 2 transitions and transversions were selected visually. Chi-square analysis (Moore, 2000) was used to evaluate the significance of differences in the Type 1: Type 2 transition of mtDNA between Neandertals and modern humans and the Type 1: Type 2 transitions within modern humans. The alignment identifies 40 transition sites between the nine Neandertal HVRI sequences and the Eve1.0 HVRI. Of these 40 sites, 16 are Type 1 transitions and 24 are Type 2 transitions. The number of transitions for HVRI in modern humans was determined from over 4300 partial and full modern human mtDNA sequences available on the National Center for Biotechnology Information (NCBI) Web site.

From these sequences (Ruiz-Pesini et al., 2007) 232 transitions were identified in the HVRI. Of these, 128 are Type 1 transitions and 104 are Type 2 transitions (data not shown). The frequency (44.8%) of Type 2 transitions is in agreement with the G+C content for Eve1.0 HVRI (46.03%) and gives the expected results for the number of Type 1 to Type 2 transitions found among modern humans. A chi-square test for the difference between Type 1: Type 2 transitions in Neandertal: modern human, and modern human: modern human gave values of $X^2 = 3.7$, with a P value = <0.10 and much closer to 0.05. A P value of 0.05 or less is arbitrarily chosen as the level for “significance” in a chi-square test (Moore, 2000). The P value given for the Neandertal: modern humans Type 1: Type 2 transitions, is barely outside of the 0.05 standard but cannot be dismissed as being insignificant. The P value of 0.05 denotes that the events tested might occur by chance less than 5% of the time. The P value for the Type 1: Type 2 transitions between Neandertal and modern humans are slightly above this 5% level of chance. This indicates that the results are most likely affected by some other factor than chance. In this case, the other factor suggested is DNA damage.

The differences in the Neandertal and modern human Type 1 to Type 2 transitions clearly points to some factor affecting this ratio other than random chance or a small sample size. A good explanation for the increase in Type 2 transitions is the activity of DNA decay through the deamination of cytosine to uracil, damage from high concentrations of divalent metal ions such as manganese or an as yet unidentified decay process of guanine to adenine and not simply sequence variation between Neandertals and modern humans.

Neandertal DNA Contamination

Without an original, living Neandertal mtDNA sequence, it would seem

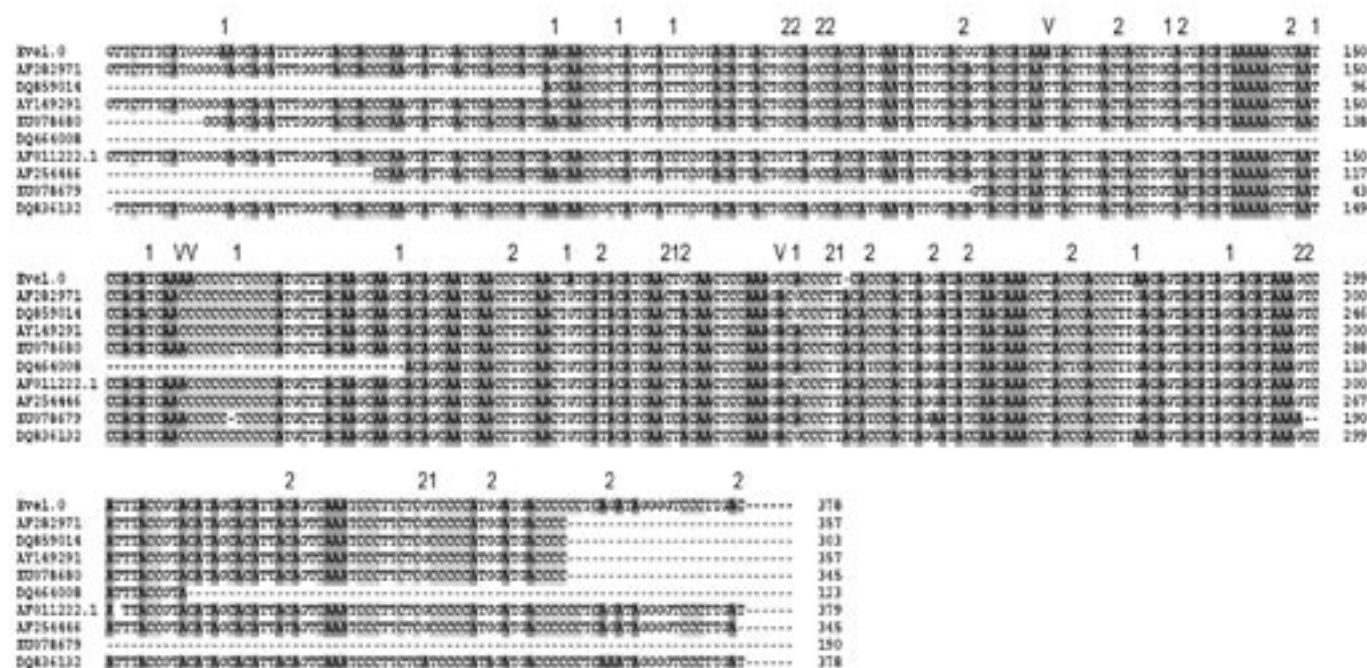


Figure 1. ClustalX alignment for nine Neandertals and Eve1.0 hypervariable region I (HVRI). Eve 1.0 position one in the alignment is position 16023 in HVRI. Type 1 transitions are labeled “1,” Type transitions are labeled “2” and transversions are labeled as “V.” Type 1 and Type 2 transitions were determined by comparing base changes from Eve 1.0 to the Neandertal sequences.

difficult to identify contamination or artifacts in any of the putative Neandertal sequences extracted from bones. Sequence differences between Neandertals and modern humans could be real differences and not the result of contamination. However, comparisons between Neandertal mtDNA and conserved sequences in other vertebrates, including man, can help identify problems within a putative ancient DNA sequence by identifying base changes or indels (insertions and deletions) that are not present in any of the other conserved sequences. (Here, conserved sequences can be defined as “similar” sequences and not necessarily because they were conserved through evolution from one kind of organism to another.)

To be identified as contaminants, sequence divergence from a conserved region would have to be so irregular from all known conserved sequences

that its presence would likely interfere with normal transcription and replication, or the sequence could be shown to be identical to a known sequence from another organism (e.g., a fungus), or another part of the organism’s genome (e.g., a pseudogene). Typically, searches for conserved sequences require comparisons of protein-coding genes. Fortunately, the arrangement of the mitochondrial genome in all vertebrates is essentially identical and there are conserved sequence elements in the mtDNA control region. Several of these conserved sequences are found in the HVRII for which there are two Neandertal mtDNA sequences. Within all vertebrate HVRII regions are three highly conserved sequences called conserved sequence blocks (CSBs). In humans the three sequences are located at sites 213–235 (CSB1), 299–315 (CSB2), and 346–363 (CSB3) (Ruiz-Pesini et al.,

2007), and all three of these are included in the two Neandertal HVRII sequences. Of these conserved sequences, CSB2 is the most informative for the identification of contamination in Neandertal sequences. CSB2 is an important part of the transcription machinery in mitochondria. It has been identified as a transcription termination element, and mutations in this region can impair or abolish transcription termination (depending on the degree of divergence from the optimal CSB2 sequence) (Pham et al., 2006).

To identify any unusual elements in the Neandertal HVRII sequences, a comparison was made with Eve1.0 and several primates. The identification of CSB2 for 21 *Simiiformes* primates was made by comparing all three human conserved sequence blocks, and their relative position to each other, with each primate mtDNA sequence available

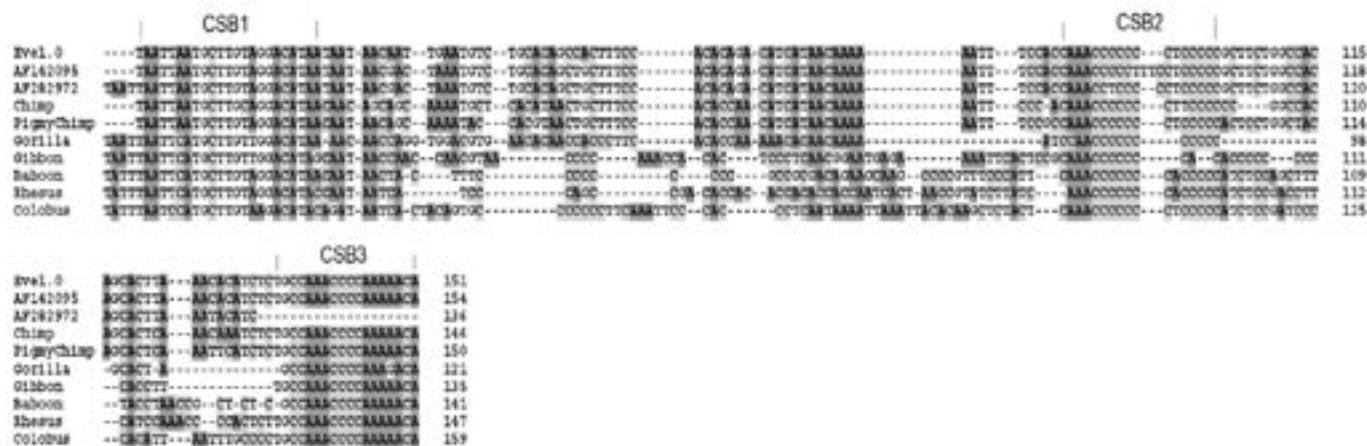


Figure 2. ClustalX alignment of HVRII with all three conserved sequence blocks (CSBs) for Eve 1.0, two Neandertals (AF142095 and AF282972), and seven representative primates from the NCBI database. AF282972 ends before CSB3. Gorilla has a long intervening sequence between CSB2 and CSB3 not found in other primates. This region (Gorilla 16194–16339) was deleted to shorten the alignment. The homology of all three CSBs is obvious as well as the thymine insertion in Neandertal AF142095.

at NCBI. A ClustalX alignment of all three conserved sequence blocks, two Neandertals, Eve1.0, and seven of the 21 primates was made for comparison (Figure 2). The ClustalX alignment was used with the same parameters as in Figure 1. The alignment was manually adjusted to bring the three conserved sequence blocks for each primate into alignment. The conserved elements of CSB2 are obvious from the alignment, as are also the two Neandertal insertions. In the alignment, Neandertal AF142095 has a thymine trimer inserted into the middle of what is called the poly-cytosine tract (polyC 309). A thymine trimer has not been identified for any of the 4300 modern human sequences (Ruiz-Pesini et al., 2007; Carter, 2007), and none of the 21 primates have this insertion. A thymine insertion is present between sites 304-305 in Neandertal AF282972. This insertion is also not present in any of the primates in the alignment and is not listed among any of the modern human polymorphisms (Ruiz-Pesini et al., 2007; Carter, 2007). This is strong evidence that the thymine trimer in AF142095 and the thymine insertion in AF282972

are artifacts and not part of the original Neandertal sequence. The addition of all 21 primate sequences does not remove the Neandertal insertions, nor does an alignment including the entire HVRII region with conserved sequence blocks 1–3 (rCRS 213–363), as no primate sequence has a thymine trimer in this region (CSB2) of mtDNA.

Removing the thymine insertions in both Neandertals produces a sequence that is identical to Eve1.0 and the rCRS. Neandertal AF142095 CSB1 and 3 are both identical to Eve1.0, strengthening the argument that the original Neandertal CSB2 sequence also should be identical to modern humans. It is possible that the single thymine insertion in AF282972 would not severely interfere with CSB2 function, but it is difficult to suggest that the thymine trimer in AF142095 would not interfere with CSB2 function regardless of its location in any primate. The absence of this type of insertion in 4300 modern human sequences and the aligned primates suggests that the thymine trimer is lethal to human mitochondria and is not a unique feature of Neandertal CSB2.

Neandertal Thymine Trimer and DNA Decay

A realignment of CSB2 provides another possible scenario to explain the existence of the thymine trimer in Neandertal AF142095 (Krings et al., 1999). The thymine trimer in AF142095 might be a sequence length polymorphism in CSB2 similar to that observed in modern humans (Figure 3). Although CSB2 is highly conserved in humans and primates, this research, and that of others (Santos et al., 2005; Carter, 2007), show that a sequence length polymorphism designated at site 309 is the most variable in the entire human mitochondrial genome (Table II). This poly-cytosine tract has four different sequence length polymorphisms identified in humans (Carter, 2007) with anywhere from 7–10 cytosines. The poly-cytosine tract ranges from sites 303 to 309 and many humans are heteroplasmic in this region, having mtDNA with two different lengths in their cells.

The addition of cytosine to this region has not been associated with any specific disease (Ruiz-Pesini et al., 2007) or disorder, and the variations here are

Eve1.0	CAAACCCCC - - - CCTCCCCCGCT
PolyC309.1	CAAACCCCC - - CCCTCCCCCGCT
PolyC309.2	CAAACCCCC - CCCCTCCCCCGCT
PolyC309.3	CAAACCCCCCCCCCTCCCCCGCT
AF142095	CAAACCCCCT T TCCTCCCCCGCT

Figure 3. A manual alignment for conserved sequence block 2 of Eve1.0, three human variants PolyC309.1, PolyC309.2, PolyC309.3, and Neandertal AF142095. Position 1 is Eve1.0 or rCRS position 299 in the mitochondrial DNA control region.

quite common, indicating the addition of cytosine has little if any effect on the functioning of CSB2. In Figure 3, an alignment between a modern human sequence with 10 cytosines in the poly-cytosine tract (polyC309.3) and AF142095 can be made with no gaps. Could the original Neandertal sequence have 10 bases in this tract with the thymine trimer substituting for the three extra cytosines that rarely appear in human poly-cytosine tracts? Probably not, since neither man nor primates have three thymine bases in the poly-cytosine tract. A unique sequence divergence that is this dramatic in a conserved region is an indication of contamination or decay and not a species-specific characteristic. If the thymine trimer is not an insertion from a contaminating source of DNA, it likely resulted from post-mortem deamination in an individual with 10 cytosines in the poly-cytosine tract.

Summary

Advances in the extraction and amplification of ancient DNA from Neandertals has provided a glimpse into the genomes of ancient humans. However, documented problems with contamination and DNA decay (Pusch et al., 2004; Wall and Kim, 2007) continue to plague efforts to show phylogenetic relationships between Neandertals and modern humans (in a Biblical sense) from aDNA sources. In this study, the high number of Type 2 transitions in

Neandertal mtDNA HVRI sequences indicates that decay processes, such as the deamination of cytosine or guanine, are incorporated onto putative Neandertal mtDNA HVRI sequences.

The novel thymine trimer present in CSB2 of Neandertal AF142095 (Krings et al., 1999) is not found in any other primate and is not one of several possible variations in any of the 4300 human HVRII sequences, indicating that it is an artifact from DNA contamination or the product of DNA decay. Removal of the CSB2 thymine trimer in Neandertal AF142095 makes this Neandertal identical to humans in all three HVRII conserved sequence blocks and is evidence that the original Neandertal mtDNA was not significantly different than modern humans. In spite of the rigorous controls instituted to eliminate damaged

and contaminated aDNA sequences, evidence continues to mount that the current methodology is inadequate to eliminate all possible sources of DNA decay and contamination. Because of these problems, conclusions made about the relationship of Neandertals to modern humans cannot be fully assessed using currently available Neandertal DNA sequences, and the problems described in this paper will need to be assessed with every new ancient DNA sequence that becomes available.

References

- Anderson, S., A.T. Bankier, B.G. Barrell, M.H. de Bruijn, A.R. Coulson, J. Drouin, I.C. Eperon, D.P. Nierlich, B.A. Roe, F. Sanger, P.H. Schreier, A.J. Smith, R. Staden, and I.G. Young. 1981. Sequence and organization of the human mitochondrial genome. *Nature* 290 (5806):457–465.
- Bower, M.A., M. Spencer, S. Matsumura, R.E. Nisbet, and C.J. Howe. 2005. How many clones need to be sequenced from a single forensic or ancient DNA sample in order to determine a reliable consensus sequence? *Nucleic Acids Research* 33 (8):2549–2556.
- Cann, R.L., M. Stoneking, and A.C. Wilson. 1987. Mitochondrial DNA and human evolution. *Nature* 325 (6099):31–36.

Table II. Frequency of sequence length polymorphisms and heteroplasmy in human conserved sequence block 2 polyC 309.

Study	No. Sequences	309C	309.1CC 309.2CCC	309.3CCCC
Present ^a	37	0.46	0.54	None
Carter 2007 ^b	827	0.52	0.48	0.001
Ruiz-Pesini 2007 ^c	4300	present	present	present
Santos 2005 ^{a,d}	48	0.46	0.54	N/A

^a Frequency of heteroplasmic families

^b Frequency for 309.1CC is 0.37, and 309.2CCC is 0.11

^c Only the presence of these polymorphisms are given

^d Individual sequence length polymorphisms are not identified

- Caramelli, D., C. Lalueza-Fox, S. Condemi, L. Longo, L. Milani, A. Manfredini, M. de Saint Pierre, F. Adoni, M. Lari, P. Giunti, S. Ricci, A. Casoli, F. Calafell, F. Mallegni, J. Bertranpetit, R. Stanyon, G. Bertorelle, and G. Barbujani. 2006. A highly divergent mtDNA sequence in a Neandertal individual from Italy. *Current Biology* 16 (16):R630–632.
- Carter, R. W. 2007. Mitochondrial diversity within modern human populations. *Nucleic Acids Research* 35 (9):3039–3045.
- Cooper, A., and H.N. Poinar. 2000. Ancient DNA: do it right or not at all. *Science* 289:1139.
- Curat, M., and L. Excoffier. 2004. Modern humans did not admix with Neanderthals during their range expansion into Europe. *PLoS Biology* 2 (12):e421.
- Cuticchia, A.J. (editor). 1995. *Human Gene Mapping 1995: A Compendium*. Johns Hopkins University Press, Baltimore, MD.
- Gilbert, M.T., E. Willerslev, A.J. Hansen, I. Barnes, L. Rudbeck, N. Lynnerup, and A. Cooper. 2003. Distribution patterns of postmortem damage in human mitochondrial DNA. *American Journal of Human Genetics* 72 (1):32–47.
- Gilbert, M.T., H.J. Bandelt, M. Hofreiter, and I. Barnes. 2005. Assessing ancient DNA studies. *Trends in Ecology and Evolution* 20 (10):541–544.
- Gilbert, M.T., J. Binladen, W. Miller, C. Wiuf, E. Willerslev, H. Poinar, J.E. Carlson, J.H. Leebens-Mack, and S.C. Schuster. 2007. Recharacterization of ancient DNA miscoding lesions: insights in the era of sequencing-by-synthesis. *Nucleic Acids Research* 35 (1):1–10.
- Green, R.E., J. Krause, S.E. Ptak, A.W. Briggs, M.T. Ronan, J.F. Simons, L. Du, M. Egholm, J.M. Rothberg, M. Paunovic, and S. Paabo. 2006. Analysis of one million base pairs of Neandertal DNA. *Nature* 444 (7117):330–336.
- Hall, B.G. 2004. *Phylogenetic Trees Made Easy*, 2nd Edition. Sinauer and Associates, Sunderland, MA.
- Hansen, A., E. Willerslev, C. Wiuf, T. Mourier, and P. Arctander. 2001. Statistical evidence for miscoding lesions in ancient DNA templates. *Molecular Biology and Evolution* 18:262–265.
- Hofreiter, M., V. Jaenicke, D. Serre, A. Haeseler Av, and S. Paabo. 2001. DNA sequences from multiple amplifications reveal artifacts induced by cytosine deamination in ancient DNA. *Nucleic Acids Research* 29:4793–4799.
- Hoss, M., P. Jaruga, T.H. Zastawny, M. Dizdaroğlu, and S. Paabo. 1996. DNA damage and DNA sequence retrieval from ancient tissues. *Nucleic Acids Research* 24:1304–1307.
- Krause, J., L. Orlando, D. Serre, B. Viola, K. Prufer, M.P. Richards, J.J. Hublin, C. Hanni, A.P. Derevianko, and S. Paabo. 2007. Neanderthals in central Asia and Siberia. *Nature* 449:902–904.
- Krings, M., A. Stone, R.W. Schmitz, H. Krainitzki, M. Stoneking, and S. Paabo. 1997. Neandertal DNA sequences and the origin of modern humans. *Cell* 90:19–30.
- Krings, M., H. Geisert, R. W. Schmitz, H. Krainitzki, and S. Paabo. 1999. DNA sequence of the mitochondrial hypervariable region II from the neandertal type specimen. *Proceedings of the National Academy of Sciences* 96:5581–5585.
- Krings, M., C. Capelli, F. Tschentscher, H. Geisert, S. Meyer, A. von Haeseler, K. Grossschmidt, G. Possnert, M. Paunovic, and S. Paabo. 2000. A view of Neandertal genetic diversity. *Nature Genetics* 26:144–146.
- Lalueza-Fox, C., J. Krause, D. Caramelli, G. Catalano, L. Milani, M.L. Sampietro, F. Calafell, C. Martinez-Maza, M. Bastir, A. Garcia-Tabernero, M. de la Rasilla, J. Fortea, S. Paabo, J. Bertranpetit, and A. Rosas. 2006. Mitochondrial DNA of an Iberian Neandertal suggests a population affinity with other European Neandertals. *Current Biology* 16 (16):R629–630.
- Lindahl, T. 1993. Instability and decay of the primary structure of DNA. *Nature* 362:709–715.
- Lindahl, T., and B. Nyberg. 1974. Heat-induced deamination of cytosine residues in deoxyribonucleic acid. *Biochemistry* 13:3405–3410.
- Lubenow, M.L. 1992. *Bones of Contention: A Creationist Assessment of Human Fossils*. Baker, Grand Rapids, MI.
- Moore, D.S. 2000. *The Basic Practice of Statistics*, 2nd Edition. W.H. Freeman, New York, NY.
- Noonan, J. P., G. Coop, S. Kudaravalli, D. Smith, J. Krause, J. Alessi, F. Chen, D. Platt, S. Paabo, J.K. Pritchard, and E.M. Rubin. 2006. Sequencing and analysis of Neandertal genomic DNA. *Science* 314:1113–1118.
- Orlando, L., P. Darlu, M. Toussaint, D. Bonjean, M. Otte, and C. Hanni. 2006. Revisiting Neandertal diversity with a 100,000 year old mtDNA sequence. *Current Biology* 16 (11):R400–402.
- Ovchinnikov, I.V., A. Gotherstrom, G.P. Romanova, V.M. Kharitonov, K. Liden, and W. Goodwin. 2000. Molecular analysis of Neandertal DNA from the northern Caucasus. *Nature* 404:490–493.
- Pham, X.H., G. Farge, Y. Shi, M. Gaspari, C.M. Gustafsson, and M. Falkenberg. 2006. Conserved sequence box II directs transcription termination and primer formation in mitochondria. *Journal of Biological Chemistry* 281:24647–24652.
- Poinar, H.N., M. Hoss, J.L. Bada, and S. Paabo. 1996. Amino acid racemization and the preservation of ancient DNA. *Science* 272:864–866.
- Pusch, C.M., and L. Bachmann. 2004. Spiking of contemporary human template DNA with ancient DNA extracts induces mutations under PCR and generates nonauthentic mitochondrial sequences. *Molecular Biology and Evolution* 21:957–964.
- Pusch, C.M., M. Broghammer, G.J. Nicholson, A.G. Nerlich, A. Zink, I. Kennerknecht, L. Bachmann, and N. Blin. 2004. PCR-induced sequence alterations hamper the typing of prehistoric bone samples for diagnostic achondroplasia mutations. *Molecular Biology and Evolution* 21:2005–2011.
- Ruiz-Pesini, E., M.T. Lott, V. Procaccio, J.C. Poole, M.C. Brandon, D. Mishmar,

- C. Yi, J. Kreuziger, P. Baldi, and D.C. Wallace. 2007. An enhanced MITO-MAP with a global mtDNA mutational phylogeny. *Nucleic Acids Research* 35 (Database issue):D823–828.
- Santos, C., R. Montiel, B. Sierra, C. Bettencourt, E. Fernandez, L. Alvarez, M. Lima, A. Abade, and M.P. Aluja. 2005. Understanding differences between phylogenetic and pedigree-derived mtDNA mutation rate: a model using families from the Azores Islands (Portugal). *Molecular Biology and Evolution* 22:1490–1505.
- Schmitz, R.W., D. Serre, G. Bonani, S. Feine, F. Hillgruber, H. Krainitzki, S. Paabo, and F.H. Smith. 2002. The Neanderthal type site revisited: interdisciplinary investigations of skeletal remains from the Neander Valley, Germany. *Proceedings of the National Academy of Sciences* 99:13342–13347.
- Serre, D., A. Langaney, M. Chech, M. Teschler-Nicola, M. Paunovic, P. Mennecier, M. Hofreiter, G. Possnert, and S. Paabo. 2004. No evidence of Neanderthal mtDNA contribution to early modern humans. *PLoS Biology* 2 (3):E57.
- Smith, C.I., A.T. Chamberlain, M.S. Riley, A. Cooper, C.B. Stringer, and M.J. Collins. 2001. Neanderthal DNA. Not just old but old and cold? *Nature* 410:771–772.
- Velasco-Vazquez, J., M. Aray-de-la-Rosa, E. Gonzalez-Reimers, and O. Hernandez-Torres. 1997. Paleodietary analysis on the prehistoric population of El Hierro (Canary Islands). *Biological Trace Element Research* 60:235–241.
- Wall, J.D., and S.K. Kim. 2007. Inconsistencies in Neanderthal genomic DNA sequences. *PLoS Genetics* 3:1862–1866.
- Willerslev, E., and A. Cooper. 2005. Ancient DNA. *Proceedings: Biological Sciences* 272:3–16.



Book Review

The Man Who Found Time: James Hutton and the Discovery of Earth's Antiquity

by Jock Repcheck

Perseus Books, Cambridge, MA, 2003, 256 pages, \$28.00.

I recently picked up a copy of this biography of James Hutton by Jack Repcheck. I expected an erudite discussion that reflected modern historical scholarship. What I found was a combination of a smug anti-Christian bias combined with what Stephen Jay Gould (1997) referred to as the “cardboard empiricist myth,” and that was before I got past the prologue. Having read several recent (and far superior) sources, I found this author completely out of touch with modern research. So, for the first time in my writing career, I find myself reviewing only the prologue of a book. Anyone in-

terested in the rest of the content should see the review by Walker (2004).

Ordinarily, I would not consider it worth the effort to bother with such a review, but I think it is helpful on occasion to remember that our opponents are, all too often, the very things of which they accuse us: biased and uninformed. Repcheck begins with the usual drivel about the victory of “science” over the repressive forces of “religion.”

Yet the reverence accorded to biblical answers caused problems, the most serious being that it prevented rigorous and systematic examination

of the very world that God had created. Scholars who investigated fields that did not touch on church doctrine were relatively unaffected, but those who explored the natural world were playing with fire—the figurative fire of controversy, the real fire of the heretic’s pyre, and the eternal fire of damnation if the church felt they had stepped too far (p. 2).

These two sentences reflect a profound ignorance of the history and nature of science, and the history and nature of the Christian church. First, he claims that the Bible precludes

knowledge of nature, when the truth is exactly the opposite. Starting with Adam naming animals and tending God's garden, believers have always been keenly interested in God's creation. Science would not be possible apart from the same medieval Christianity that Repcheck apparently detests.

Moreover, the so-called Scientific Revolution of the sixteenth century was the normal result of development begun by Scholastic scholars starting in the eleventh century. Thus my attention shifts to why the Scholastics were interested in science at all. Why did real science develop in Europe at this time? Why did it not develop anywhere else? I find answers to those questions in unique features of Christian theology (Stark, 2003, p. 123).

Not only did the axioms of science arise from Christian theology, the methods and early investigations of science came out of European universities founded and supported by the Roman Catholic (and later by the Protestant) churches. Finally, one's eternal destiny has nothing to do with any particular view of science but with the gospel clearly preached in the same Bible.

Repcheck argues for the "heroic" view of science: a few noble individuals created science while standing against the forces of evil represented by the church.

A surprising number of individuals had this unique form of intellectual courage, but it was largely the work of just four men who shattered the biblically rooted picture of Earth and separated science from theology (p. 2).

He chose Copernicus, Galileo, Hutton, and Darwin. If Mr. Repcheck wants examples of intellectual courage, he should read biographies of Wycliffe, Luther, or many early Christians. It takes a few paragraphs, but Mr. Repcheck later admits that Copernicus and Galileo were Christians. How then did

they deliver us from their own faith? It was not the heliocentric universe, as Mr. Repcheck believes; that concept had been floating around scholastic academia for some time. As Stark (2003, p. 139) noted,

Thus the "Scientific Revolution" does not begin with Copernicus. As the distinguished I. Bernard Cohen put it, "In short, the idea that a Copernican revolution in science occurred goes counter to the evidence...and is an invention of later historians."

Regarding Galileo, the anti-Biblical hero, Stark (2003, p. 163–164) notes,

But there is far more to the story than this, and these overlooked or ignored facts put things in a somewhat different light: that Galileo's troubles stemmed as much from his arrogance as from his scientific views.

There is no doubt that Hutton indirectly influenced culture away from the Christian worldview, as did Darwin, but Gould (1997, p. 66) points out that Hutton did so as Lyell's cardboard myth, not as a real man.

Charles Lyell's self-serving rewrite of geological history...demanded a certain type of hero, and Hutton best fitted the requirements. Simple chauvinism decreed a British character, and Hutton prevailed.

Repcheck, following secular propaganda, conflates the Bible's clear teaching of man's significance in God's eyes with the location of the planet Earth.

If the earth was no longer the center of things, was it still special? Why would God choose a place other than the center of the universe as the home for a creation made in His own image? (pp. 2–3).

What he misses is the clear teaching that the cosmos was special because it was created by a special God. Man is even more special because he is created in that God's image, not because his home is located at a particular point in

the universe. Given Mr. Repcheck's worship of empirical science, one wonders if he has seen the ends of the universe, thus confirming that Earth is not located at its center.

The Copernicus myth continues:

Because of the cryptic introduction and the technical nature of the work, Copernicus' book did not have a profound impact immediately. It took Galileo, the first celebrity scientist, to publicize the true meaning of what Copernicus had written (p. 3).

In the university system of the time, Copernicus's work was probably widely read. The real reason that it was widely ignored for some time was that its insistence on circular orbits prevented it from being better at predicting planetary motions than Ptolemy.

If one does not want to acknowledge that the rise of scientific astronomy was begun by Scholastics, then the beginnings of the field must be moved forward in time to the work of Johannes Kepler...whose elegant model got everything right that Copernicus had gotten wrong (Stark, 2003, pp. 139–140).

In Repcheck's mythology, there is an odd 150-year gap between the persecuted Galileo and the next liberator from religious bondage, James Hutton.

James Hutton, a Scottish natural philosopher, boldly confronted this centuries-old wisdom. Writing in 1788, he formally presented proof that the earth was significantly older than 6,000 years. In fact, its age was incalculable—it could be hundreds of millions of years old, it could be billions. Hutton reached his conclusions about the age of the planet through his revolutionary theory of the earth (p. 4).

It's hard to know where to begin with a quote like this. Hutton was not bold; he wrote for like-minded elites. His "deep time" was hardly original, as

Hutton's concept of time was in fact a commonplace among Enlighten-

ment savants. Like Buffon with his “eternal road of time,” Hutton treated time as a dimension that necessarily stretched without limit into past and future (Rudwick, 2005, p. 169).

He never presented “proof” in 1788 (actually, he presented the paper in 1785; it was first published in the Transactions of the Royal Society of Edinburgh in 1788); he merely presented a theory, and one that had no empirical proof in the sense we know it today.

Far from inferring a vast timescale from observation, Hutton deduced it from first principles and then explained away the awkward fact that its effects were unobservable (Rudwick, 2005, p. 169).

He never defined “deep time” as history, because he rejected history in his cyclical world machine.

However, he did not infer a vast scale of time by extrapolating from a very slow observable rate of erosion. On the contrary, he flatly denied the validity of anything like de Luc’s natural measures of time; he claimed that no clear evidence of the rate of erosion of the continents could be detected, even within the whole of recorded human history back to the ancient Greeks: “It is vain to attempt to measure a quantity which escapes our notice, and which [human] history cannot ascertain; and we might just as well attempt to measure the distance of the stars without a parallax, as to calculate the destruction of the solid land without a measure corresponding to the whole” (Rudwick, 2005, p. 169).

However vast—indeed infinite—its putative timescale, nothing could have been more profoundly ahistorical. Hutton showed no interest in plotting the particularities of geohistory; indeed, he explicitly rejected that kind of project (Rudwick, 2005, p. 172).

Unconstrained, Repcheck soldiers

through the factual difficulties to retell the heroic myth.

Most previous scholars who had developed hypotheses about the earth had never questioned the church’s teachings. They saw Noah’s Flood or the waters of the unformed earth as the explanation for all odd geologic formations, thus allowing the age of the earth to fit within six millennia.... Hutton completely ignored the Bible and the Deluge, and as a result he was able to clearly see what rock formations told him (p. 4).

As before, it’s hard to know where to start. Most scholars of the eighteenth century had rejected the Biblical account of the Flood and Earth’s recent origin. In fact, Rudwick (2005) notes that the savant Jean-Jacques de Luc was in an extreme minority in his attempt to defend the Flood! The rejection of the Flood had been a *fait accompli* for much of the eighteenth century among the intellectual elite; hand in glove with their more general rejection of Biblical authority. Hutton’s rejection of the Bible—and his deism—was merely mainstream at the time. Finally, it was not just the Bible Hutton ignored; it was also the rocks—he did his fieldwork *after* he had derived his theory.

When Christians present their worldview, they are “religious fanatics,” “intolerant,” “superstitious,” etc. When secularists present theirs...

Still, these men [Hutton and Darwin] were not bent on battling with their respective churches; they were simply seeking the truth unconstrained by past biases (p. 5).

I’m sure that Darwin and Hutton helped little old ladies across the street, too.

Then we get to the heart of the matter: Religion and science are like oil and water. As the heroic myth comes to its dramatic conclusion, we see that

Copernicus, Galileo, and Darwin are regarded as the key figures in the freeing of science from the

straightjacket of religious orthodoxy (p. 5).

Repcheck says that religious orthodoxy is a straightjacket; Jesus of Nazareth says that the truth will set you free. Pick one. The history of science has demonstrated beyond any doubt that the discoverers of science required the comforting confines of Biblical philosophy to justify the foundations of science. Once again, Repcheck’s personal religious bias blinds him to historical reality.

Having demonstrated his lack of knowledge of the history of science, Repcheck now demonstrates his ignorance of the history of Christianity.

In fact, biblical chronology, as the discipline of precise biblical dating was called, was one of the most rigorous “sciences” of the pre-Renaissance era. Beyond scholars, many of the holiest figures from church history, including the prophet Elijah, St. Augustine, St. Bede, St. Thomas Aquinas, and even Martin Luther had commented on the age of the earth and all had reached the same conclusion: the earth was nearly 6,000 years old (pp. 5–6).

Most people for most of church history did not concern themselves with Biblical chronology. That is because most accepted without a second thought that the earth was young, and because the esoteric modes of hermeneutics during much of that time made it irrelevant. Chronology grew in popularity after the Reformation, thanks to a new emphasis on Biblical authority, a more restrictive hermeneutic, and the growth of textual studies in the original languages. Repcheck does not cite anything in support of his mischaracterization. It would be interesting to know exactly what chronology Elijah derived, and even more interesting to know how it was preserved and passed down. The rigorous sciences prior to the Renaissance included linguistic and textual studies, engineering, mechanics, astronomy, etc. Repcheck could not be citing the curriculum guide

of any major medieval university—the incubators of science. Furthermore, what's wrong with Biblical chronology as an area of investigation? It has a better internal coherency and external consistency than modern methods of dating prehistory (Reed, 2008).

Now we come to Repcheck's explanation of the "missing link"—why was Hutton virtually ignored between 1788 and 1830?

Lyell had rediscovered Hutton's work a generation after it had been forgotten (p. 6).

Oops! Wrong again! It is odd that such a great scholar would be forgotten, especially given Repcheck's enthusiasm for the vigor of the Scottish Enlightenment. The other typical excuse is that he was too hard to read until Lyell and Playfair "translated" his great theory. But again, Repcheck has it all wrong.

It is not surprising then, that one of the two points on which Hutton was criticized most vigorously by his contemporaries was his eternalism. It was not his concept of the vastness of time that they rejected, but his scarcely concealed claim that the earth—and by implication the cosmos as a whole—had had no origin and would have no end (Rudwick, 2005, p. 170).

Hutton, I will argue, did not draw his fundamental inferences from more astute observations in the field, but by imposing upon the earth, a priori, the most pure and rigid concept of time's cycle ever presented in geology—so rigid, in fact, that it required Playfair's recasting to gain acceptability. Playfair aided Hutton's victory by soft-pedaling the uncompromising and ultimately ahistorical view of his late and dear friend (Gould, 1997, p. 63).

The hoary legend of Hutton's unreadable prose has served various ideological purposes during the past two centuries. Soon after Hutton's death, Playfair, *Illustrations* (1802), used it as a reason for bowdlerizing the work by detaching it from its teleological framework and suppressing its teleology. He has been followed by countless other scientific commentators ever since (Rudwick, 2005, p. 161).

In other words, Hutton derived a theory that no self-respecting geohistorian of his time would touch. They liked his rock cycle but not his view of history, nor his lazy empirical approach. It fell to Lyell to dig up the body and dress it in an entirely new suit. Hutton ended up as a pawn for Lyell, a hero of the new science only to the extent that he was misinterpreted.

Repcheck gets to St. Darwin, who was evidently a staunchly orthodox Christian until he learned otherwise.

The ancient age of the earth came as a revelation to Darwin (p. 6).

He must not have been paying any attention to his grandfather, Lamarck, Cuvier, Buffon, Buckland, Sedgwick, Murchison, Lyell, etc. Darwin may have become convinced of geological uniformitarianism by Lyell but almost certainly knew that most intellectuals, including many in the church, accepted an extended prehistory.

Finally, another series of misstatements about Hutton grace the pages,

Hutton devised the first rigorous and unified theory of the earth.... It was a completely original story.... Unlike all previous hypotheses of Earth's workings, there was no call for catastrophes, such as Noah's Flood (p. 8).

Strike one: it was not the first rigorous and unified geothory of earth's past. It was not even close. Strike two: it was original only in some aspects, such as the igneous formation of sediments, which was universally rejected. Hutton rejected history in favor of an eternal, cyclical earth—that was not unique, either, but was also rejected (which explains why Hutton needed Lyell to revive him). Strike three: many current hypotheses, in fact most, had shed any pretense of deriving accurate history from the Biblical account of the Flood.

In summary, Repcheck's prologue contains numerous errors of fact and bias. Keep that in mind if you are of a mind to bother with the rest of the book. If you want to learn about James Hutton's work, try Gould's *Time's Arrow, Time's Cycle* (1997) or Martin J. S. Rudwick's *Bursting the Limits of Time* (2005).

References

- Gould, S.J. 1997. *Time's Arrow, Time's Cycle: Myth and Metaphor in the Discovery of Geological Time*. Harvard University Press, Cambridge, MA.
- Stark, R. 2003. *For the Glory of God*. Princeton University Press, Princeton, NJ.
- Reed, J.K. 2008. Toppling the timescale, part III: madness in the methods. *CRSQ* 45:6–17.
- Rudwick, M.J.S. 2005. *Bursting the Limits of Time: The Reconstruction of Geohistory in the Age of Revolution*. University of Chicago Press, Chicago, IL.
- Walker, T. 2004. The man who made the wedge: James Hutton and the overthrow of Biblical authority. *TJ* 18(2):55–57.

John K. Reed
915 Hunting Horn
Evans, GA 30809
Jkenr2@comcast.net

Evidence for the Lack of Snake Evolution

Jerry Bergman*

Abstract

The fossil record of snakes, when reviewed, shows no evidence for the origin of snakes by neo-Darwinian evolution. The most common evolutionary theory is that modern snakes developed from four-legged reptiles that lost their legs. As evidence for this theory, evolutionists point to snake spurs and putative vestigial leg structures that exist on some modern snakes. These spurs and other structures are not evidence of legged ancestors, but rather are functional organs that have an important role in mating. It is also shown that evolution from tetrapod to snake would require major anatomical changes in the skeleton and the body organs as well as the production of several new organ systems, such as the sensory system.

Introduction

Feared by many—and worshiped by some—snakes are found in almost every part of the world. Snakes (suborder Serpentes or Ophidia), one of the most specialized vertebrates known, boast 18 families, each one containing hundreds of species, totaling about 3,000 species (Holman, 2000; Mattison, 2007). Only about 400 of the 3000 species are venomous, and fewer than 100 species are dangerous to humans.

Snakes can thrive in an enormously wide variety of habitats. Besides terrestrial and sea snakes, there exist burrowers, climbers, crawlers, and even air gliders, each of which, if it evolved, should have

left some evidence in the fossil record of its descent (e.g. Shine, 1991, p. 37). Evolutionists suggest that snakes evolved from either four-legged, lizard-like, land animals or aquatic (or perhaps amphibious) vertebrates that came to shore to breed and lay eggs (Simon, 1973). Their evolution should be easy to document because the “evolution of snakes involved major changes in the vertebrate body plan organization,” as reflected in the skeleton (Cohn and Tickle, 1999, p. 474). Although the typical lizard and the typical snake possess a number of traits in common, many major anatomical and physical differences exist between them (Parker and Grandison, 1977).

The Differences Between Tetrapod Reptiles and Snakes

Differences between the common tetrapod reptile and a snake include not only the fact that snakes lack limbs but also that they have a greatly increased number of vertebrae—from 120 to as many as 500 compared to 32 in humans, and approximately the same number of thoracic vertebrae typically found in lizards (Benton, 2005). Snake vertebrae are also more complex with extra processes on the neural arches that control the sideways movement and bending of its long body (Benton, 2005). Their vertebrae are connected to curved ribs that lack differentiation of the neck, thorax, abdomen, and other major body parts. A snake’s elongated body requires either a reduction of paired internal organs, such as lungs or kidneys, compared to other reptiles, or a normally paired organ positioned so that one organ is located behind the others, allowing the organism

* Jerry Bergman, Ph.D., Biology Department, Northwest State College,
jbergman@northweststate.edu

Accepted for publication June 11, 2008

to fit within the snake's long, slender, legless body.

Snakes are so well designed for several different types of movement that they have been able to effectively occupy an amazingly large variety of ecological environments (Holman, 2000). The snake's very flexible, long skeleton allows it to travel by sinuous side-to-side lateral undulations, similar to the method by which an eel swims (Parker and Grandison, 1977). Their mode of travel is so efficient that some snakes can travel as fast as seven miles per hour. On sandy or muddy surfaces snakes use a sidewinding movement; on slick surfaces they use a slide-pushing and concertina locomotion. They also can use a saltation movement, involving jumping forward by rapidly stiffening its body from head to tail (Holman, 2000). Snakes can flatten themselves, enabling them to squeeze through cracks smaller than their bodies. They can even vigorously spin their bodies to escape enemies when seized by the tail (Holman, 2000).

The snake, *Chrysopelea ornate*, can flatten itself to the degree that it can actually glide like a flying squirrel and, for this reason, is called a "flying snake." Some snakes are excellent climbers and can spend most of their lives in trees. Others are fossorial (earth burrowing) with vermiform (wormlike) bodies that are designed to burrow. Snakes can swim using lateral undulations to propel themselves through the water. Sea snakes have a caudal fin that enables them to swim much like fish. Some snakes even lock their vertebra to form a stiff polelike structure that allows them to stretch horizontally from one tree limb to another. Achieving all of these abilities requires a uniquely designed vertebral system.

Eels, caecilians, some amphibians, and certain lizard species are also limbless like snakes. All of these vertebrates, though, differ markedly from snakes. Eel and caecilian possess vertebrae that are simple biconcave spindles, and legless

lizards often have simple, flat-bottomed vertebrae (Holman, 2000).

Snake skulls are of a very light construction, and, in contrast to lizards and other reptiles, their braincase is both low and flat (Carroll, 1988). A snake can easily swallow prey two or more times the diameter of its own body. Their jaws use kinetic (movable) skull and jaw systems that form a "swallowing machine that is unique among terrestrial vertebrates" (Holman, 2000, p. 4). Their double-jointed jaw hinge moves backward and then forward so as to move their prey, which they swallow whole, down towards their elongated stomach; this technique is called unilateral feeding (McClung, 1993).

The double jaw hinge allows for large gape expansion to permit snakes to swallow prey two to three times as thick as its body diameter. The "remarkably stretchable skin is also *designed* to swallow very large prey" (Holman, 2000, p. 6, *italics added*). Digestion begins in the mouth and continues along the digestive track, where finely tuned, powerful digestive enzymes rapidly break down prey.

The enormous contrast between tetrapod reptiles and snakes makes the study of snake evolution an excellent test of the theory of common descent. As Holman noted, just observing a "disarticulated snake skeleton in a box one immediately senses the *uniqueness* of these animals" (Holman, 2000, p. 4, *italics added*). For example, snake vertebrae have more extra-articular surfaces than any other vertebrate group known (Holman, 2000). These distinct skeletal differences make it comparatively easy to identify snakes in the fossil record. In contrast, lizards have a skeleton far more like a typical mammal than a snake.

Snake Sensory Systems

The snake's sensory systems are very different from that of most other reptiles (Simon, 1973). Unlike most lizards, snakes lack external ears and hence

cannot "hear" sound, but instead sense ground vibrations. The eye design of snakes is also very different from that of lizards. Snakes do not have movable eyelids as do most lizards (a gecko is one exception), and snakes have a transparent cap called a brille that covers the eye (as do most crocodilians), offering extra eye protection. Snakes also smell and taste through their flickering forked tongue, which uses a highly innovative chemoreception system located inside their mouth (Holman, 2000). This last trait is more common among lizards.

A snake's tongue is unique in that it can extend to the outside of the head without opening the mouth (Simon, 1973). The tongue is associated with a paired vomeronasal (Jacobson's) organ to form a sophisticated chemoreceptor system used to evaluate chemical information that can tell the snake much about the air, ground, water, or even potential prey. Pit vipers have what are called "sensory pits" between the nostrils and eyes, which are "probably the most sensitive heat receptors in the zoological world," so sensitive that they are able to detect both the direction and distance of warm objects (Holman, 2000, p. 6).

Snakes' eyes are actual image-forming systems working in the lower energy portion of the infrared spectrum, just below visible light. This is why these reptiles can enter a deep burrow in total darkness to find, kill, and consume prey. In contrast, honey bees and certain other insects can "see" well into the ultraviolet portion of the electromagnetic spectrum, enabling them to see the sun and navigate even on heavily overcast days.

Evolution of Venom

If snakes evolved, these many unique snake traits must be explained by neo-Darwinian descent. However, plausible evolutionary scenarios are distinctively absent. For example, snakes have the "most efficient venom-injecting system ever evolved in terrestrial vertebrates"

(Holman, 2000, p. 4), but how “it came about that snakes manufactured poison is a mystery” (Crompton, 1987, p. 69). One theory is that their toxin was once saliva produced by mouth digestive glands, and the saliva glands evolved into poison glands. The problem with this explanation is that the use of toxin

was not forced upon them by the survival competition; they could have caught and lived on prey without using poison just as the thousands of non-poisonous snakes still do. Poison to a snake is merely a luxury; it enables it to get its food with very little effort, no more effort than one bite. And why only snakes? Cats, for instance, would be greatly helped; no running fights with large, fierce rats or tussles with grown rabbits—just a bite and no more effort needed. In fact, it would be an assistance to all the carnivorae—though it would be a two-edged weapon when they fought each other. But, of the vertebrates, unpredictable Nature selected only snakes (and one lizard). One wonders also why Nature, with some snakes, concocted poison of such extreme potency (Crompton, 1987, p. 69).

Another problem with the speculation that saliva evolved into venom is that snakes can manufacture very different poisons that function in very different ways. Some act on the nervous system (neurotoxic), which causes paralysis and blocks the nervous system. Another type, called the hemolytic poison, acts on the blood-clotting system and breaks down the capillaries, causing internal bleeding. The problem for evolution is that the toxin apparatus is a complex unit with many irreducible parts. For example, the poison glands are connected to specially designed teeth, and the brain and nervous system must coordinate the whole system (Holman, 2000).

These are just a few of the major differences between snakes and other reptiles. A major skeletal trait of snakes is

limblessness, and it is this trait on which many evolutionists focus for evidence of evolutionary descent.

Theories of Snake Origins

The two most popular theories for the origin of snakes by neo-Darwinian evolution are that they arose from small fossorial lizards or that they had a more direct aquatic origin (e.g. Holman, 2000, p. 7). Ellis added that for sea snakes it is not even “evident whether snakes evolved as aquatic animals and then some came out on land, or whether they are land animals, some of which returned to the sea” (Ellis, 2001, p. 151). Sea snakes have numerous unique traits in contrast to land snakes, indicating a “separate evolution” (Ellis, 2001, p. 15). Sea snakes possess special features allowing them to stay submerged for extended times and dive to considerable depths.

The many changes required to evolve terrestrial snakes into sea snakes would include evolution of a thin muscular tail to allow them to move through the water and both salt excreting glands and valvular nostrils to keep out seawater. They would also need a radically modified breathing apparatus and a much larger set of lungs to allow them to stay under water. The transition to a marine animal would involve much more than lung size changes; it would also require larger hemoglobin and myoglobin levels, a larger and differently designed muscle system, and a host of other adaptations existing in diving mammals.

The theory that snakes evolved from burrowing lizards has been postulated as a more feasible alternative. Although many differences exist between snakes and burrowing lizards, they both possess some remarkable similarities, including intrinsic eye muscles and lack of structures such as eyelids, tympanum, and middle ear cavities. Because there are many major differences between various kinds of snakes, different phylogeny has been postulated for several groups

of snakes. Egg-laying sea snakes, for example, are theorized to have arisen from “terrestrial elapids or perhaps from a very early Australian species” of some type, a theory also lacking fossil evidence (Ellis, 2001, p. 152).

Most theories of snake origin state that snakes evolved from tetrapod ancestors, requiring loss of their limbs (Caldwell and Lee, 1997). The many other modifications required for snakes to evolve from tetrapods include loss of legs and their appendicular muscle, loss of the appendage system, and the evolution of a whole new complex system of axial muscles to move the body. This includes complex mechanisms involving bone, nervous, and brain structures that allow snakes to travel by some type of serpentine locomotion (Holman, 2000). The common theory of snake evolution is that when fish first “invaded land they had to make several radical anatomical alterations” (Crompton, 1987, p. 11) in order to survive on land. For example, they had to evolve legs, since the better adapted they were moving in water, the less adapted they were to traveling on land. Crompton added that among the

fishy mob of pioneers were the foreparents of snakes and men, and these, together with the rest, grew legs. Not very good ones, but they improved as time went on, and time did go on: many millions of years passed and the snake still ran about on legs. Then, towards the beginning of the mammalian era, when the reign of the reptiles was drawing to a close, the snake discarded its legs. Now the fishes grew legs because they could not move about on land without them, and it seemed quite impossible that any vertebrate with well-developed ribs and backbone could do so. How did the snake get on? Well, had it held a theory about legless propulsion and set about to prove it, it could not have succeeded better. ... Legless, it can travel as fast as a human being, climb trees, travel

along the top branches, shooting from there like an arrow and resuming its rapid course along the ground, and it can rejoin the element from which it came, its new shape enabling it to swim fast and gracefully (Crompton, 1987, pp. 11–12).

This “just so” story lacks evidence, fossil and otherwise.

Potential Transitional Forms

The three most important snake fossils used to argue for snake evolution are the Squamate (snakelike) *Pachyrhachis*, *Lapparentophis* (a 1.5 meter-long reptile with 146 presacral vertebrae), and *Dinilysia*, all known back to the Cretaceous (Holman, 2000, p. 8). The theory that snakes evolved from an aquatic animal is supported by the marine creature, *Pachyrhachis problematicus*, an animal similar to varanoid lizards; a species that includes a large number of aquatic lizards. Of all known

modern lizard groups, the varanoids are most similar to snakes. These similarities include (1) the type of tooth replacement that occurs, (2) the detailed structure of the tongue and vomeronasal organ, (3) some cranial characteristics, and (4) the presence of an intermandibular joint in the lower jaw.... *Pachyrhachis* and *Ophiomorphus* from the early Upper Cretaceous were snakelike in body form, had similar vertebrae to snakes, and completely lacked forelimbs and girdles (Holman, 2000, p. 7).

Although Carroll concluded that *Pachyrhachis* and *Ophiomorphus* “may be intermediates between” snakes and varanoid lizards, much evidence exists against this position (Carroll, 1988, p. 237). From their study of *Pachyrhachis* and *Ophiomorphus*, Caldwell and Lee (1997) concluded that they were the same animal because, although *Pachyrhachis* had a “slightly” more pronounced pachyostotic rib structure (ribs thought to be adapted for a marine

existence) than *Ophiomorphus*, the two genera were “otherwise almost indistinguishable” (Caldwell and Lee, 1997, pp. 705–706). They also concluded that *Pachyrhachis* had many non-snake traits, including a well-developed pelvis, sacrum, and hind limbs that included a femur, a tibia, a fibula, and tarsals (Caldwell and Lee, 1997). This evidence strongly argues that *Pachyrhachis* was not related to snakes but rather was a long-bodied varanoid lizard.

Furthermore, evidence indicates that *Lapparentophis defrennei* was about the same “age” as *Pachyrhachis*, removing it from the fossil ancestor position. Mattison (2007) wrote that the “earliest known snake is *Lapparentophis defrennei*,” but no evidence exists of a “link with earlier snake-like reptiles and so its origin is a mystery” (p. 13). It appears that this oldest snake, *Lapparentophis defrennei*, is merely an extinct snake and not a transitional form.

Another proposed snake transitional fossil is *Dinilysia patagonica*. *Dinilysia*, a large-bodied, six-foot-long animal, is the first known snake in which the skull—which resembles that of a pipesnake but appears to have some lizardlike snake traits—is well documented (e.g. Greene, 1997, p. 271, 274). Dated from the upper Cretaceous, it is a modern snake in design, and for this reason is called the first known snake. Its vertebrae are “clearly those of snakes” (Carroll, 1988, p. 235), but it has some minor lizard traits (Holman, 2000, p. 8). The existence of this snake has been known since 1901, and a large number of exceptionally well-preserved skulls and skeletons are now known to exist. For this reason we can arrive at many conclusions about the animal with some confidence, including *Dinilysia* is an extinct snake—and not a transitional form.

Nonetheless, *Dinilysia* “has inspired and challenged efforts to understand snake origins” (Greene, 1997, p. 274). Specifically, the fossil inspired the theory that snakes evolved from an

animal that structurally resembled an Asian pipesnake, a view that Greene concluded is unlikely: “A more likely alternative is that the earliest snakes were small creatures and, like limbless anguimorphs and blindsnakes, primarily ate tiny arthropods” (Greene, 1997, p. 271).

In summary, the “question of whether snakes evolved from burrowing or aquatic lizard ancestors is still open to argument, and the knowledge of the origin of snakes gained from the fossil record remains cloudy” (Holman, 2000, p. 8). Carroll speculated that the

ancestors of snakes probably diverged from the lizards before the end of the Jurassic. Although the evidence is not conclusive, their affinities are probably close to the base of the varanoid stock, from which their primary specialization was toward great elongation of the body and limb reduction. The early members may have been relatively large terrestrial carnivores that became further specialized by an increase in jaw mobility that enabled them to swallow prey whole. Great elongation of the body and a relative reduction of its girth would have preadapted snakes for both aquatic locomotion and burrowing, which have been elaborated in divergent lines many times during their evolutionary history (1988, p. 236).

The Monitor Theory

Another theory is that snakes evolved from reptiles known as monitors. The problem is that most monitors are fairly large and move in jerks very unlike a snake. The monitor family includes the Komodo dragon, a large lizard now existing in only a few small East Indonesian islands. It bears a striking resemblance to the mythical dragon of legends. One characteristic typical of many monitors is that they, like snakes, swallow their food whole without chewing (Simon,

1973). The evidence for a monitor-snake ancestor is clearly based on an arbitrary selection of certain anatomical features that are shared by both snakes and monitors, ignoring many others in order to

link them to some common ancestor. Neither the snakes nor the monitors can break off portions of their tails voluntarily and later regrow them—an ability that is a hallmark of other lizard groups, including the legless worm lizards that superficially look enough like snakes to be frequently mistaken for them. The breakable tail is a handy defensive device permitting many a lizard to escape while its enemy is tackling the wriggling tail tip. Lacking this ability, a monitor or a snake that loses a portion of its tail must live for the rest of its life with a permanently shortened tail. Another feature attesting to the relationship between the two groups is the long, flexible, forked tongue, which is used to pick up the scent of prey with the help of a taste-sensitive organ located in the roof of the mouth. Jacobson's organ, as it is known to zoologists, is most highly developed in snakes, but in monitors it is much more developed than in [most] all other lizard groups (Simon, 1973, pp. 31–32).

The problem with postulating evolutionary trees by comparing morphological traits of living animals is illustrated by the fossorial and aquatic lizard theories. This method is largely conjecture, with a lack of fossil or other evidence to demonstrate the claim. A vertebrate paleontologist who carried out research in the last decade on snakes has concluded that since 1997,

twenty or more papers have appeared that purport to tackle the question of snake origins. The issue is still unresolved: are the snakes closely related to amphisbaenians, or are they part of the anguimorph clade, close to the mosasaurs and aigialosaurs (mosasauroids)? If the former, their origin

is from land-dwelling burrowers, if the latter, snakes were primitively marine (Benton, 2005, p. 291).

The Fossil Record

The fossil record of snakes is comparatively limited because snake skeletons are especially fragile. In the majority of cases only disarticulated vertebrae, ribs, and a few cranial bones are found (e.g. Parker and Grandison, 1977, p. 11; Holman, 2000, p. 4). A major means of differentiating snakes from lizards is the morphology of individual vertebrae, which often cannot be determined from the fossil record due to its incompleteness (Holman, 2000). Fortunately there “are wonderful exceptions to the poor fossil record of snakes,” including a number of essentially complete skeletons (Greene, 1997, p. 274). However, these “wonderful exceptions” in the fossil record have not been very helpful to evolutionists.

Although “it is now accepted that snakes arose from lizards,” Parker and Grandison (1977) admitted that “no specific designation of the ancestral group can yet be made” (p. 11) because the fossil record provides no evidence for any specific evolutionary path. More recently, Mattison (2007) concluded that no fossil evidence links snakes to lizards in spite of the fact that enough fossil evidence exists to conclude that “by the time the dinosaurs became extinct, snakes had already diversified and became widespread” (p. 11). In other words, a wide variety of snakes existed early in the fossil record, and, although many papers exist documenting adaptive and microevolutionary changes, no evidence of their evolutionary descent from lizards or other non-snakes exists.

Formal collections of snake fossils date back at least to the middle 1800s (Holman, 2000). The oldest snake fossils are dated by evolutionists as belonging to the Early Cretaceous period, about 95 million years ago, and they radiated

greatly during the Tertiary (Greene, 1997; Benton, 2005). The first snakes appear in the fossil record very early—estimates range from 100 to 150 million years ago (Mattison, 2007, p. 11). Only vertebrae have been found that are considered “unquestionably snake like” (Parker and Grandison, 1977, p. 11). The reason only vertebrae have been found may be that snakes did not evolve from tetrapods.

The claim that snakes are the “most recently evolved of all the reptilian lineages” and “appear later in the geological record than any other reptile” argues that, if they evolved from tetrapod fossils, evidence of their evolution should be abundant in the fossil record (Holman, 2000, pp. vii, 1). The first clearly recognized snake in the fossil record is *Lapparentophis defrennei*, dated from the Lower Cretaceous about 130 million years ago and found in the Sahara desert (Parker and Grandison, 1977, p. 11). Although only its vertebrae have been found, their distinctive features are unquestionably snakelike (Parker and Grandison, 1977, p. 11).

The very first snake fossils, as far as we can determine from the extant evidence, are characterized by all the same traits found in modern snakes, including an elongated body, greatly reduced limbs and eyes, a highly developed chemosensory system, and cloacal scent glands used for defense (Greene, 1997). A key trait needed to support snake evolution from tetrapods is the progressive streamlining and elongation of the snake body in the fossil record. The common theory is that once the snake body was long enough and undulant motion was perfected, the legs were no longer needed and possibly even a hindrance (Palmer, 1992).

The assumption that these snakes had legs in their evolutionary past but slowly lost them through evolutionary selection completely lacks fossil evidence. The only evidence for loss of legs is the putative leg remnant, which, as we will

show, is actually not a leg remnant but a functional organ. Also, in spite of the “discovery of limbed snakes with hind limbs, the precise group that gave rise to snakes remains uncertain and hotly contested” (Bejder and Hall, 2002, p. 452). Gradual loss of a bone-based structure, such as the loss of legs, would have been well preserved in the fossil record if this gradual loss had actually occurred. It would also seem such ancestral snakes would be at a huge selective disadvantage as their legs were becoming reduced in size but still not allowing the required streamlined body. It is difficult to postulate an advantage for these intergrades, and, if they in fact existed, it is difficult to explain their absence in the fossil record. Although many skinks (*Scincidae*) have very reduced limbs, they also have another adaptation allowing them to fold their limbs to one side during locomotion.

A major problem that results from lack of fossil evidence includes the fact that the “origin of snakes is largely speculative and little documented. Their fossil record is scanty and in the great majority of cases based only on vertebrae” (Parker and Grandison, 1977, p. 11). Stahl concluded, “The origin of the snakes is still an unsolved problem,” and Colbert added, “Unfortunately, the fossil history of the snakes is very fragmentary, so that it is necessary to infer much of their evolution from the comparative anatomy of modern forms” (Stahl, 1974, p. 318; Colbert et al., 2001, p. 154).

Some paleontologists have pointed to a fossil known as *Pachyrhachis problematicus* as the ancestor to snakes because it appears to have had very tiny legs and a pelvic girdle. This find, though, “exhibits such a blend of snakelike, lizardlike, and unique characteristics that herpetologists still argue about whether this creature was indeed a snake” or just a unique animal (Greene, 1997, p. 274).

In spite of the lack of evidence, it is now widely “accepted that snakes arose

from lizards, although no specific designation of the ancestral group can yet be made” (Parker and Grandison, 1977, p. 11). Nonetheless, debate continues as to whether or not any modern lizard families are evolutionarily related to snakes, and there even exist “conflicting views as to the environment in which snakes evolved” (Carroll, 1988, p. 235). To explain modern snakes, some herpetologists propose that they evolved in many environments, postulating a burrowing stage, followed by a land-surface stage. Others herpetologists argue that snakes never went through a burrowing stage.

Snakes resembling modern pythons have been found in the fossil record estimated by evolutionists to date back 95 million years, specifically *Haasiophis* and *Pachyrachis*, which evidently had limblike structures located on their caudal posterior. Both of these animals, though, were fishlike aquatic animals with flattened tails, indicating they are not transitional forms (Sodera, 2003).

Significantly, none of these snake fossils shows “even a trace of the pectoral girdle or forelimbs” (i.e., shoulder blades, collar bones, etc.) or breast bone (Carroll, 1988, p. 234; see also Parker and Grandison, 1977, p. 11). More recent studies confirm their lack of even a trace of a pectoral girdle and forelimbs (Cohn and Tickle, 1999; Burchfield et al., 1982). In those fossils clearly recognized as snakes, only vertebrae have been found and no clear evidence of limbs. One possible exception to lack of limbs and girdles is *Najash rionegrina*, which has a sacrum, a supporting pelvic girdle, and “robust functional legs outside of the ribcage” (Apesteguia and Zaher, 2006, p. 1037). The problem with this fossil as an example of snake evolution, however, is that it appears to be a limbed snake, not a snake losing its limbs:

Pachyrhachis problematicus, *Haasiophis terrasantus* and *Eupodophis descouensi*, three marine fossil snakes from the Tethyan coasts of

Northern Gondwana, were until now the only known snakes with well-developed hindlimbs. The presence of fully formed hindlimbs enforced the idea that these were the most primitive (basal) snakes and perfect transitional taxa linking extant snakes to an extinct group of marine lizards, the Mosasauridae. However, the presence of several other features typical of the more advanced macrostomatan snakes such as pythons, boas and colubroids supports the competing hypothesis that these fossils were advanced (macrostomatan) snakes instead, with no special bearing on the origin of snakes (Apesteguia and Zaher, 2006, p. 1037).

As Greene noted, new fossil snakes are now being “discovered even more frequently, and with luck and careful study,” these fossils will help us further understand snake origins (Greene, 1997, p. 275). So far all of the many discoveries have made the mystery of their evolution even more elusive and serve instead as examples of intelligent design.

Loss of Limbs

Lacking a convincing fossil record, herpetologists rely on comparisons of extinct and living organisms to “infer changes in their attributes through time,” as well as research on embryonic tissue interactions and shifts in developmental timing (Greene, 1997, p. 271). One major trait that is used to infer changes is the existence of spurs.

One of the earliest views of snake origins is that they lost their limbs and acquired their long, thin, legless bodies by trying to squeeze through tight places (Palmer, 1992). The two other theories as to why snakes lost their legs are:

the ancestors of snakes had legs and that those limbs were lost either in a burrowing lizard that required legs less and less, or in a marine form that lost its limbs as it came to rely more

and more on serpentine locomotion (Benton, 2005, p. 241).

As evidence for the theory that limbs were lost, herpetologists point to what they claim are rudimentary legs in snakes, organs that are actually spurs. An evaluation of whether these spurs are vestigial legs concluded that they are not, but they are functional (Bergman and Howe, 1990). To maintain the loss-of-limb theory in the face of much contradictory evidence, herpetologists have been forced to postulate that leglessness has “evolved independently in several unrelated lizard families” (Mattison, 2007, p. 11).

Although it is commonly thought that snakes underwent a progressive loss of limbs, recent “paleontological discoveries suggest a more complex scenario of limb reduction,” an event that is “still poorly documented in the fossil record” (Apesteguia and Zaher, 2006, p. 1037). One reason why a more complex scenario is postulated is that many extinct forms exist—some that had limbs, and others that did not—and they lived contemporaneously, ruling out an ancestral relationship for the limbed forms.

Snake Spurs

One of the more commonly cited evidences of snake evolution is the presence of claws or spurs on the posterior part of a few types of snakes. Darwin concluded that these snake spurs are “rudiments of the pelvis and hind limbs” that are evidence of the evolution of snakes from limbed ancestors (Darwin, 1859, p. 450). Since then Darwinists have used the argument that the support system for these clawlike, horny spur structures are vestigial “legs” left over from the snakes’ limbed past. Bobrowsky (2005) used this claim to argue against Intelligent Design by claiming that many animals

contain both nonoptimal characteristics and vestigial organs, both of which would not be expected from a truly intelligent designer.... Examples of vestigial organs include

... the vestigial leg bones in whales and snakes. These characteristics would be expected from evolutionary development but not from an intelligent designer. (p. 12)

It is still further claimed that

even at the present time, the snake has not entirely got rid of its legs. At least, tiny, vestigial remains of what were once hind legs are found inside the bodies of many snakes, while the python has two small external protuberances as leg relics, and carries in its inside the remains of a pelvis (Crompton, 1987, p. 12).

Their primary support for the view that spurs represent somewhat vestigial legs is the fact that spurs are anatomically in a location roughly similar to where the hind legs develop in other reptiles. But the “vast majority” of snakes do not have evidence of

vestiges of hind limbs or a pelvis either; only in the boas and pythons and three other small groups are there persistent remains of hind limbs, which usually appear externally as small horn-sheathed claws ..., and some vestiges of a pelvis inside the ribs. Reduction of limbs to the same extent also occurs, however, in amphisbaenians and in some lizards (e.g., Slow-worm, Glass-lizard, etc.) and these, like the snakes, progress mainly by sinuous side-to-side undulations of the body in much the same way that an eel swims (Parker and Grandison, 1977, p. 11).

Evolutionists interpret the pelvic bones and the spurs in certain snakes as “vestigial pelvic bones and anal spurs that represent the remnants of hind legs. These remnants of legs have, of course, lost all function in locomotion” (Griehl, 1982, p. 11). The common claim is that all modern snakes have lost all traces of their forelimbs but some have retained very small rudiments of their hindlimbs.

The vast majority of snakes have no vestiges of hind limbs or of a pelvis (Park-

er and Grandison, 1977, p. 10). Snakes that do have putative traces of pelvic and lower limb bones include only pipesnakes (Anilidae), boids (boas and pythons), blindsnakes (Typhlopidae), and worm snakes (Leptotyphlopidae). In most snakes that have these “legs,” including the anaconda and the python, the end parts are slightly exposed and form small horn-sheathed claws (Williams, 1970; Carr, 1963; Iverson, 1986; Murphy et al., 1978).

Congenital abnormalities, such as the ones caused by the drug thalidomide involving misshapen limbs in humans, cause the maldeveloped/shortened limbs to appear *outside* of the body surface, not embedded deep within it as is the case of the “pelvic” bones of living and fossil snakes and whales. This indicates that the so-called “pelvic” bones of living and fossil snakes and whales are not homologous to rear limbs. Comparisons of the snake’s so-called “limbs” with the extinct dolphinlike *durodontine*, which definitely had tiny rear limbs outside of its body, illustrate this.

These vestigial limbs are used as evidence that the ancestral snake was a lizardlike animal or a lizard that lost its legs as it evolved (Murphy and Henderson, 1997). One problem with this conclusion is that some lizards have both legs and spurs (Sodera, 2003). How and why snakes lost their limbs “remains enigmatic” (Bejder and Hall, 2002, p. 452). Reasons given include the claim that it gives the snake better mobility in the underbrush. Many leg-possessing creatures are very mobile in underbrush, and loss of legs would seem to put snakes at a decided disadvantage in the struggle for life.

Another theory to explain their loss of legs is that they “originally lost them adapting to aquatic life” (Hanes, 1999, p. 246). Even if the loss theory is true, such changes show evidence of loss mutations and degeneration, not the evolution of apomorphic structures as is required by Darwinism. The claim that natural

selection once selected for limbs and then later selected against limbs is also problematic. A problem is that tetrapods needed to lose not only legs but many other structures:

This mobility was not attained merely by shedding the legs. Other alterations had to take place. All inequalities were smoothed out; neck, shoulders, hindquarters went and the snake emerged as a long, symmetrical cylinder. It seemed to have become all tail, though actually it had shortened its tail, which was now merely a small appendage at the end of an amazingly long body. The body, indeed, seemed ludicrously long but the length was just another of those alterations that had to be made for the snake's new method of locomotion (Crompton, 1987, p. 12).

Other changes include snakes having more ribs that have a very different design than limbed animals—and a very different muscle design too. Crompton (1987) added that the “loss of a member in evolution is generally called a degenerate or ‘recessive’ step, yet most of the improvements of the snake came about by discarding” structures (p. 97). An example includes the fact that in its legged state it possessed eyelids that moved up and down like those of most of the higher vertebrates. It is theorized to have discarded eyelids at the same time it discarded its legs, thus acquiring the fixed, unblinking stare for which it is notorious.

Eyelids lubricate and protect the eyes, but evolutionists claim that this protection was insufficient for a snake, going on its belly through thick, often thorny vegetation or traveling down small holes in search of prey. It also obscured the vision, so a transparent disc was substituted for the eyelid. In other words, the snake put on spectacles, or rather goggles. These goggles are set neatly in the skin and are, in fact, transparent scales, which give full protection to the eyes without obscuring the vision.

The eyes behind are still lubricated and emit water that is drained into a gland, where it is used for other purposes. Gradually, however, the discs get scratched and vision becomes impaired, but the snake sheds its skin several times a year, and with each skin change it gets a new pair of goggles (Crompton, 1987).

It is on the basis of the limb-loss theory that snakes with spurs are labeled “primitive” (Parker and Grandison, 1977, p. 13). The assumption is that “more advanced” snakes, such as colubrids, elapids, and viperids, have lost all traces of their limbs, and the “less evolved” snakes have retained these traces (Murphy and Henderson, 1997, p. 101). A problem with the use of the word “advanced” here is that many “advanced” snakes, such as cobras and vipers, still lay eggs, but some of the snake kinds that are believed to be “primitive,” such as boas, which have rear spurs, use “advanced” means of reproduction, meaning they give birth to live young instead of laying eggs (Sodera, 2003, p. 225).

The Function of the Spurs

One claim is that these appendage claws, although very small—particularly in the case of large constrictors—assist in locomotion. The claws would be especially useful when climbing trees (their natural habitat) or when hanging from tree branches (Dewar, 1957, p. 169). Over 150 years ago, naturalist Edmond Gosse wrote that the “spurs” are unquestionably of use to the snake, such as to “help maintain a firm hold on a tree branch while watching for an approaching prey” (quoted in Murphy and Henderson, 1997, p. 101).

Evidence for the spurs’ usefulness includes the complex system involved in attaching them to the animal’s pelvis. Although morphologically slightly homologous to the femur, they are actually specialized structures. Judging from the bone and muscle structure, the claws do not appear to be vestigial

legs but a specially designed, functional structure (see Figures 1 and 2). The “femur” is constructed from “bone or calcified cartilage of variable shape and development ... [which] bears a cornified claw-like cap” (List, 1966, p. 44) (see Figure 3).

Their claws can be moved by muscles anchored to bone, and the bone-muscle system allows the claws to function as strong grabbers (Bergman and Howe, 1990). They also enable snakes to strike more powerful blows against enemies with its body (Storer and Usinger, 1977). The claws’ fighting role is mainly employed in male territorial combat. To effectively achieve this task, the spurs have hard, black-pigmented, horny caps attached to the bone structure (Storer and Usinger, 1977; Cardew and Goode, 2001). Conversely, they cannot be large enough to interfere with locomotion. Sodera (2003) notes that the spurs in a 15-foot-long python he dissected are “comparatively tiny” (p. 225).

A more common claim is that the spurs are used for courtship. Males use these movable spurs to scratch or stroke (and stimulate) the female during courtship and mating (Shine, et al., 2003; Vences and Glaw, 2003; Murphy and Henderson, 1997; Carr, 1963; Parker and Grandison, 1977). Specifically, the spurs are used by the “male to stimulate the female during copulation” (Griehl, 1982, p. 11). The role of the spurs in courting and copulation for the anaconda snake were described by herpetologist R. R. Mole as early as the 1920s (Mole, 1924, p. 237–238).

In one study, the male persistently raked his spurs on the sides of the female’s body (Charles et al., 1985). The spurs in females are usually smaller, an indication that scratching is primarily a male courtship behavior. Another study observed that, during the courtship behavior of the Indian python, the

male would attempt to align his body with the female as she slowly crawled forward. When the female

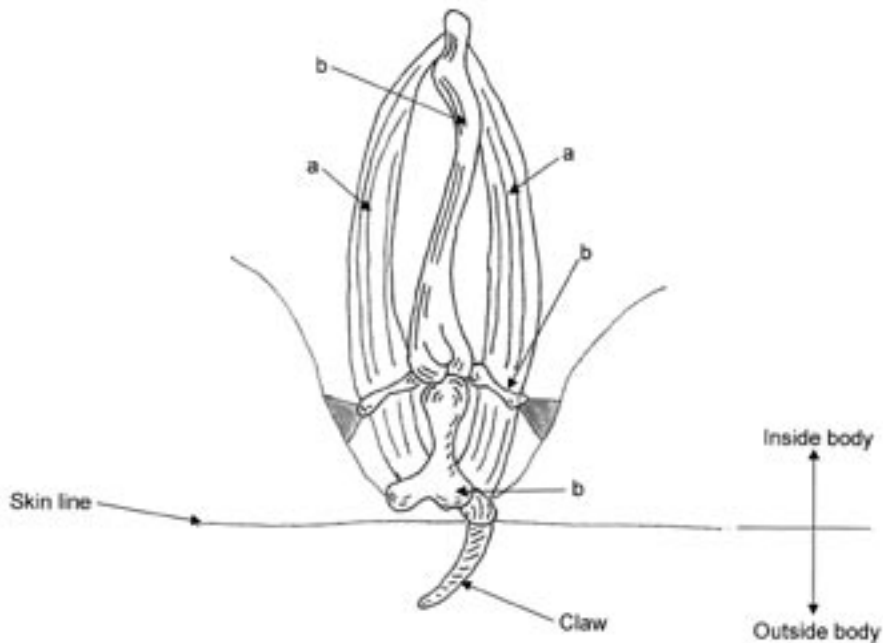


Figure 1. The hind leg skeletal structure and associated musculature from a snake, species not given. Musculature is denoted by “a” and bone by “b.” Note it is a complex structure that functions in climbing, fighting, and mating. Originally from Martin (1843, p. 226). Adapted from Murphy and Henderson (1997, p. 102) by B.L. Lindley-Anderson.

would stop forward motion, cease tongue flicking, and raise her head to a height about 75 cm above the substrate, the male would initiate vigorous courtship. The female would hold her position for 10 seconds to several minutes, while the male would loop his body over the female’s back and rapidly tongue flick the top of her head and back. The cloacas would then be aligned, and the male would begin vibrating his vestigial limbs 30–80 times per minute against the female’s body in the region above her cloaca. At this point the female would sometimes become receptive, arch her tail, gape her cloaca, and the male would insert one of his hemipenes. During the 45–365 minute coitus, the male continued to stimulate the female with his spurs (Murphy and Henderson, 1997, p. 102).

Support for the theory that claws of certain snakes function for courtship includes evidence that the spurs of these snakes protrude “only at the breeding season, functioning in courtship as does the similar spur of some male birds” (List, 1966, p. 44). From this evidence Bergman and Howe (1990) drew the conclusion that the “claws” function during courtship. Reproductive use of these spurs has been reported for reticulated pythons (Lederer, 1944). Evidence that the spurs are used for mating includes the fact that some limbed lizards also have spurs.

Other evidence for spur involvement in reproduction includes the observation that snakes with spurs lack erectile spines that are present in most other kinds of snakes (Boulenger, 2000). Snakes without spurs are forced to mate in very different ways than spurred snakes.

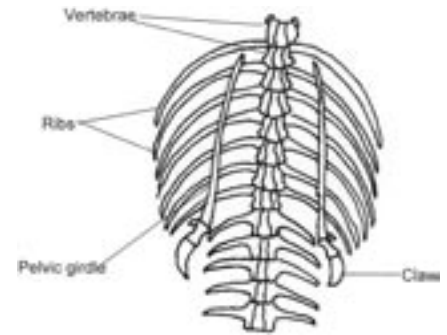


Figure 2. The snake claw structure showing it is a well-designed system. The species was not given. These supposed “vestigial” organs have been shown to function for mating and defense uses. Adapted from Murphy and Henderson (1997, p. 102) by B.L. Lindley-Anderson.

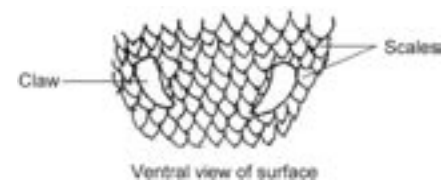


Figure 3. A picture of the snake scales and claws, species not given, showing the claw protruding slightly out from the body. This structure plays an important role in mating and defense. Adapted from Murphy and Henderson by B.L. Lindley-Anderson.

In many of the boas and pythons the next phase of the courtship consists of the male using his claw-like vestigial hind limbs to scratch or stroke his mate’s sides, but in ‘limbless’ snakes the male’s body is thrown into a rapid series of rippling waves which run forwards from tail to head. If the female is not receptive these actions evoke no response and the partnership dissolves; but if she is

physiologically ready for reproduction she responds by opening her cloaca and coitus follows (Parker and Grandison, 1977, p. 51).

The snake pelvis and rudimentary legs are also used as evidence against the belief in an intelligent designer. The argument is usually framed as follows: "Vestigial structures, such as the rudimentary pelvis of snakes and whales ... are extremely puzzling if organisms are rationally designed or are constructed according to some universal law" (Barton, et al., 2007, p. 75). As we have seen, these structures are neither vestigial nor irrationally designed but function very well for their intended purpose. Other herpetologists argue that snake limbs were lost and then reevolved again:

The discovery of limbed snake fossils has raised the possibility, depending on the phylogenetic hypothesis assumed, that limbs also may have reevolved in some snake lineages. Fossils of three marine snakes, *Haasiophis*, *Eupodophis*, and *Pachyrhachis*, present developed hind limbs and were placed in a more derived position than the terrestrial fossil snake *Najash rionegrina*, by Apesteguia and Zaher (2006). This strongly suggests a second evolutionary origin of tetrapod limb in the group. Some authors claim that this idea would be reinforced by the evidence for regulation of vestigial leg morphogenesis in living pythons by hox genes (Kohlsdorf and Wagner, 2006, p. 1908).

Conclusion

Snake evolution from non-snakes should be relatively easy to document in the fossil record because of major structural changes required to evolve from its hypothetical tetrapod ancestors. Our review has supported Parker and Grandison's (1997) conclusion that, although a large number of excellent snake fossils have

been found, no fossil evidence exists for its putative evolution and, therefore, the "origin of snakes is largely speculative and little documented" (p. 11). The fact is that the "competing phylogenetic hypotheses for snake origins are controversial and under constant debate" (Kohlsdorf and Wagner, 2006, p. 1908). Although it is widely believed that snakes evolved from some type of lizard, no viable evidence of their specific lizard relatives have ever been identified (Caldwell and Lee, 1997, p. 705).

For this reason "how the origin of snakes from lizards took place is still a matter of conjecture" (Holman, 2000, p. 7). The reason is because the earliest snakes are clearly snakes, and although an enormous amount of variety exists, no fossil evidence of snake evolution from lizards or another non-snake creatures exists (Hennigan, 2005). Furthermore, Holman (2000) added that he "will not make a judgment call as to the origin of snakes ... because in vertebrate paleontology, one learns that about the time one hypothesis is chosen over the other, a new fossil is found that changes the picture" (p. 8). For this reason the phylogeny of snakes is based almost entirely on the anatomy of living animals (Carroll, 1988, p. 236).

Acknowledgements

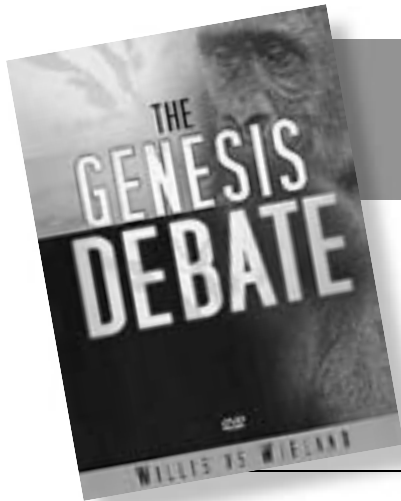
I wish to thank Jody Allen, Clifford Lillo, Norbert Smith and two anonymous herpetologists for their comments on an earlier draft of this paper, and B. L. Lindley-Anderson for producing the figures and George F. Howe for editorial assistance.

References

- Apesteguia, S., and H. Zaher. 2006. A cretaceous terrestrial snake with robust hindlimbs and a sacrum. *Nature* 440:1037–1040.
- Barton, N.H., D. Briggs, J. Eisen, D. Goldstein, and N. Patel. 2007. *Evolution*.

- Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
- Bejder, L., and B. Hall. 2002. Limbs in whales and limblessness in other vertebrates: mechanisms of evolutionary and developmental transformation and loss. *Evolution and Development* 4:445–458.
- Benton, M. 2005. *Vertebrate Palaeontology*. Blackwell, Malden, MA.
- Bergman, J., and G.F. Howe. 1990. *Vestigial Organs are Fully Functional*. Creation Research Society Books, St. Joseph, MO.
- Bobrowsky, M. 2005. Dealing with disbelieving students on issues of evolutionary processes and long time scales. *Astronomy Education Review* 4:95–118.
- Boulenger, G. 2000. *The Snakes of Europe*. Arment Biological Press, Landisville, PA.
- Burchfield, P., T. Beimler, and C. Doucette. 1982. Herpetological notes. *Copeia* 1982:193–196.
- Caldwell, M., and A. Albino. 2002. Exceptionally preserved skeletons of the cretaceous snake *Dinilysia patagonica* woodward, 1901. *Journal of Vertebrate Paleontology* 22:861–866.
- Caldwell, M., and M. Lee. 1997. A snake with legs from the marine cretaceous of the middle east. *Nature* 386:705–709.
- Cardew, G., and J. Goode (editors). 2001. *The Molecular Basis of Skeletogenesis*. John Wiley and Sons, New York, NY.
- Carr, A. 1963. *The Reptiles*. Time Inc., New York, NY.
- Carroll, R. 1988. *Vertebrate Paleontology and Evolution*. W.H. Freeman, New York, NY.
- Charles, N., R. Field, and R. Shine. 1985. Notes on the reproductive biology of Australian pythons, genera *aspidites*, *liasis* and *morelia*. *Herpetology Review* 16:45–48.
- Cohn, M., and C. Tickle. 1999. Developmental basis of limblessness and axial patterning in snakes. *Nature* 399:474–479.
- Colbert, E.H., M. Morales, and E.C. Minkoff. 2001. *Evolution of the Vertebrates: A History of the Backboned*

- Animals through Time*, 5th edition. Wiley-Liss, New York, NY.
- Crompton, J. 1987. *The Snake*. Nick Lyons Books, New York, NY.
- Darwin, C. 1859. *The Origin of Species*. John Murray, London, UK.
- Dewar, Douglas. 1957. *The Transformist Illusion*. Dehoff Publications, Murfreesboro, TN.
- Ellis, R. 2001. *Aquagenesis: The Origin and Evolution of Life in the Sea*. Penguin, New York, NY.
- Greene, H.W. 1997. *Snakes: The Evolution of Mystery in Nature*. The University of California Press, Berkeley, CA.
- Griehl, K. 1982. *Snakes, Giant Snakes and Non-venomous Snakes in the Terrarium*. Barrons Educational Series, New York, NY.
- Hanes, T. 1999. *Walking with Dinosaurs*. Dorling Kindersley, New York, NY.
- Hennigan, T. 2005. An initial investigation into the baraminology of snakes: order-Squamata, suborder Serpentes. *CRSQ* 42:153–160.
- Holman, A. 2000. *Fossil Snakes of North America: Origin, Evolution, Distribution, Paleoecology*. Indiana University Press, Bloomington, IN.
- Iverson, J. 1986. Notes on the natural history of the Caicos Islands dwarf boa, *Tropidophis greenwayi*. *Caribbean Journal of Science* 22:191–198.
- Kohlsdorf, T., and G. Wagner. 2006. Evidence for the reversibility of digit loss: a phylogenetic study of limb evolution in *Bachia* (gymnophthalmidae: squamata). *Evolution* 60:1896–1912.
- Lederer, G. 1944. Nahrungserwerb, Entwicklung, Paarung und Brutfursorge von Python reticulatus (Schneider). *Zoologische Jahrbuch (Anatomie)* 68:363–398.
- List, J. 1966. *Comparative Osteology of the Snake Families Typhlopidae and Leptotyphlopidae*. The University of Illinois Press, Champaign, IL.
- Mattison, C. 2006. *Snakes*. Harper Collins, New York, NY.
- Mattison, C. 2007. *The New Encyclopedia of Snakes*. University Press, Princeton, NJ.
- McClung, R. 1993. *Snakes: Their Place in the Sun*. Henry Holt and Company, New York, NY.
- Mole, R. 1924. The Trinidad snakes. *Proceedings of the Zoological Society of London* pp. 235–278.
- Murphy, James B., David G. Barker, and Bern W. Tryon. 1978. Miscellaneous notes on the reproductive biology of reptiles. 2. Eleven species of the family Boidae, genera *Candoia*, *Corrallus*, *Epicrates* and *Python*. *Journal of Herpetology* 12:385–390.
- Murphy, J., and R. Henderson. 1997. *Tales of Giant Snakes: A Historical Natural History of Anacondas and Pythons*. Krieger, Malabar, FL.
- Palmer, T. 1992. *Landscape with Reptile: Rattlesnakes in an Urban World*. Ticknor and Fields, New York, NY.
- Parker, H.W., and A.G.C. Grandison. 1977. *Snakes: A Natural History*, 2nd edition. Cornell University Press, Ithaca, NY.
- Shine, Richard. 1991. *Australian Snakes: A Natural History*. Cornell University Press, Ithaca, NY.
- Shine, Richard, T. Langkilde, and R. T. Mason. 2003. Cryptic forcible insemination: male snakes exploit female physiology, anatomy, and behavior to obtain coercive matings. *The American Naturalist* 162:653–666.
- Simon, H. 1973. *Snakes: The Facts and the Folklore*. The Viking Press, New York, NY.
- Slip, D., and R. Shine. 1988. The reproductive biology and mating system of diamond pythons, *morelia spilota* (Serpentes: Boidae). *Herpetology* 44:396–404.
- Sodera, V. 2003. *One Small Speck to Man*. Vij Sodera Productions, West Sussex, UK.
- Stahl, B. 1974. *Vertebrate History: Problems in Evolution*. Dover, New York, NY.
- Storer, T., and R. Usinger. 1977. *Elements of Zoology*. McGraw-Hill, New York, NY.
- Vences, M., and F. Glaw. 2003. Phylogeography, systematics and conservation status of boid snakes from Madagascar (*Sanzimia* and *Acrantophis*). *Salamandra Rheinbach* 39:181–206.
- Williams, J. 1970. *The Other Side of Evolution*. Williams Brothers Publishers, La Vemge, TN.



Book Review

The Genesis Debate (DVD)

by Answers in Genesis

AIG, Hebron, KY, 2003,
105 minutes, \$12.00.

Paul Willis, an evolutionary paleontologist and science journalist, was voted Australia's "skeptic of the year" in 2002. This title does not come lightly, although in Australia there are certainly fewer skeptics to pick from than in America. This title deserves someone capable of defending it and also someone capable of competing and overtaking it. That someone is Carl Wieland, CEO of Creation Ministries International in Australia. The two tangled at Northside Church in Australia, and what we learn from this debate is that Willis, the atheist, despite his pretensions of having bed-rock evidence, is countered successfully at every turn by Wieland.

Willis says Christians have nothing to fear from what science tells us about the history of the world and the evolution of life. He explains that many Christians differ from Wieland and other creation scientists in that they do not believe in the literal creation account of Genesis. Here Willis appears to ally himself with theistic evolutionism, a position that has numerous irreconcilable Biblical and philosophical problems.

Willis says the courts have determined that creation science is religion, not science, and he lists numerous decisions for support, although his list is difficult to read in the DVD version of this debate. Here I think Willis misstates

and misunderstands the nature of the debate. Phillip Johnson cites the opinion of Judge William Overton in a lawsuit to overturn the 1981 Arkansas legislature statute requiring balanced treatment of evolution and creation. Overton said creation science is not scientific because it does not appeal to natural law and is not falsifiable. Johnson points out that this ruling is an intellectual "snow job" because creation science makes predictions that, according to Johnson, have been proven correct (Johnson, 1993). Hence, bad philosophy underlies poor court decisions. This is not the only problem with Willis and other atheists because a sitting judge is not in a position to render decisions on matters left to philosophers of science. That oddity, however, means little if it advances the evolution cause.

Willis's remaining arguments are countered by Wieland at every turn. Willis argues that the Answers in Genesis group changed its name from the Creation Science Foundation to AIG because it backed away from science and realized it is a ministry with nothing to do with science. Wieland counters that AIG has always been a ministry and has never denied it. In fact, the group has been confused with the Christian Science and Scientology cults. Willis argues that a global flood would produce

a mixture of sediment and animals, not layers. Wieland rebuts this by noting that the Mt. St. Helens eruption in 1980 shows that thousands of laminations can form within a short time. Guy Berthault points out that horizontal grades appear when particles of different size are sent through a flume, and this suggests that such a sorting mechanism may have been present in a global flood, thus giving the illusion of numerous geologic eras (Berthault, 1988). Willis mentions the dating of a piece of wood from Sydney at 230 million years old. Carbon 14 dating revealed it to be no more than 33,720 years old. Willis notes that this was the wrong test to do, much like using a mile-long ruler to measure the size of a baby. This comment, unfortunately, misses the point of the test entirely. Willis says the error is even worse than this because the wood wasn't wood at all but an "Einsteinian concretion." Wieland counters that the laboratory that did the experiment would have detected the error if in fact this identification were the case. AIG has published numerous articles that show carbon 14 still present in animal and plant life in strata supposedly millions of years old.

While watching this video, I found it informative and certainly not indicative that creationists are in the weaker scientific position in debates. Rather,

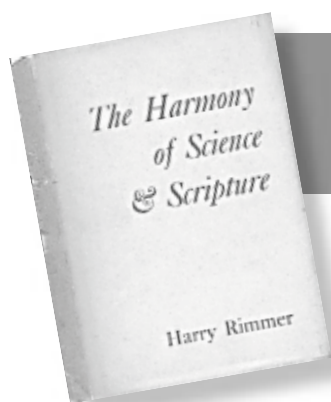
Willis was uninformed of some recent creationist papers that rebut his positions. He appears desperate to disprove creationist arguments by relying on legal

decisions that cannot adequately deal with this issue. Rather than laying atheist bedrock, Willis's position is shown to be nothing but sinking sand.

References

- Johnson, Phillip. 1993. Darwin on Trial. InterVarsity, Downer's Grove, IL.
 Berthault, Guy. 1988. <<http://www.answersingenesis.org/tj/v3/i1/lamination.asp>>

Jeffrey Stueber
 jstuber@charter.net



Book Review

The Harmony of Science and Scripture

by Harry Rimmer

Wm. B. Eerdmans Publishing Co., Grand Rapids, 1944 (10th edition), 283 pages, Out of print.

This classic book was first published in 1936. This review, seven decades later, is a reminder of the rich and colorful history of creation studies. Author Harry Rimmer (1890–1952) was a boxer, fossil hunter, debater, evangelist, preacher, and much more. What he lacked in education, Rimmer made up for with self-study and boldness. He claims to have spoken on Bible-science topics in 4,000 high school assemblies over a 25-year period (Wikipedia, 2008). If true, this is an amazing schedule of speaking every other day, month after month, over the quarter-century period. One detects a bit of sarcasm toward those with university training: he calls them the captains of science and kings of education (p. 74). Rimmer was granted honorary doctorates by Wheaton College and John Brown University (Morris, 1984, p. 89).

Rimmer's style of writing is a delight. As an example, spiral galaxies are described as "silver snails in the garden of God" (p. 21). Rimmer also comments on the "thin reasoning" and "poverty of ideas" used by the atheists of his day (pp. 15, 161), an apt description of modern skeptics. Theistic evolution was popular a century ago and was strongly opposed by Rimmer. He pictured this compromise as similar to a circus performer attempting to stand on two horses galloping in opposite directions (p. 72). Rimmer favored the gap theory and a local Genesis Flood but was not dogmatic in these positions. He suggested that dinosaurs may have been used for early transportation, somewhat like elephants (p. 141).

The book spends many pages defending the building of Noah's Ark, the long day of Joshua, and Jonah and the

whale. Rimmer goes astray on occasion, as when he declares that Joshua's time extension has been absolutely verified by eclipse records.

This volume and other early creationist books are valuable reading. There are many "lost treasures" of ideas in old books. In the creationist realm, it is found that many contemporary issues were hotly debated a century ago.

References

- Wikipedia. 2008. Harry Rimmer. http://en.wikipedia.org/wiki/Harry_Rimmer (as of June 1, 2008)
 Morris, Henry M. 1984. *History of Modern Creationism*. Master Books, Green Forest, AR.

Don DeYoung
 DBDeYoung@Grace.edu

Mutation And Natural Selection: The Central Dogma of Neo-Darwinian Evolution

Per A. Larssen*

Abstract

The central dogma of neo-Darwinism is: Mutations provide variety that is selected by natural selection. Mutations and natural selection are ultimately the only driving force of evolution, but they are effective only if one or more mutations prove beneficial to an organism in a given environment. In evolution, natural selection can do nothing without mutations. Since macromutations are virtually all near-neutral or harmful, micromutations are the only means by which new species could possibly evolve. The probability that micromutations will lead to new species is so low as to be close to zero. One reason is the net deterioration of the genome that occurs as a result of mutations, especially near-neutral mutations, which selection and medical advances cannot counteract. Furthermore, nonrandom “mutations” are controlled by in-built cellular processes and, therefore, cannot be a cause of evolution. A large number of studies clearly show that the central dogma has failed, and this devastates the credibility of neo-Darwinism. Furthermore, the increasing knowledge of the immense complexity of life at the molecular level has buttressed both the Creation and Intelligent Design movements.

Introduction

What drives the alleged evolutionary process? Does science know the underlying mechanism that can convert one genera into a new genera, one basic type into a new basic type, or explain the origins of the differences between

the higher level taxa? Darwin thought of evolution primarily in terms of the natural selection of normal biological variations existing in all life, resulting in survival of the fittest in the struggle for existence. The literature today refers to natural selection as a process, a force,

or a mechanism, and even as an active, almost intelligent, agent that “picks” what will survive. Darwin thought that normal biological variation could be extended to the point that entirely new species are formed over long periods of time. His major proposed mechanism of pangenesis (reviewed in Bergman, 2003) has been scientifically discredited.

Genetic information is contained in the aperiodic arrangement of nucleotides in DNA and is unique not only for any species in organisms but also for variations and individual mem-

* Per A. Larssen, Ph.D., 18332 Oak Ridge Drive, Santa Ana, CA 92705,
plarssen@earthlink.net

Accepted for publication September 21, 2008

bers within a species. New genetic information would be the *additional* information contained in species B if it were unique from and required for it to evolve from species A or if new species B had been created independently from species A. Unless it is experimentally proven that as a result of random mutations the aperiodic arrangement of nucleotides in species B positionally fits exactly (or almost exactly) the aperiodic arrangement of nucleotides in species A that is already known, there is no basis for concluding that species A evolved into species B. Such proof does not exist.

Other attempts to explain the source of new genetic information are summarized by Bergman (2003). They include Lamarckianism, orthogenesis, Bergson's creative evolution theory, theistic evolution, DeVries's macromutations, Goldschmidt's "hopeful monster" theory, panspermia, punctuated equilibrium, symbiogenesis, and chaos theory. None of these theories has survived scientific scrutiny, and none has been able to successfully challenge the present-day neo-Darwinian theory of mutation as the source of new genetic information, a mechanism that is also increasingly recognized as inadequate. As will be shown, mutations have not been able to explain the source of new genetic information.

Neo-Darwinism

According to the modern or synthetic theory of evolution, now called neo-Darwinism, evolution's driving force is random mutations that cause phenotypic variations, which are then acted on by natural selection. The discovery of the DNA double helix molecular structure, the function of genes, and the laws of inheritance all have provided neo-Darwinism with a mechanism to allow organisms to evolve by altering the genetic program encoded in the genes. Darwin knew nothing of DNA,

the material of inheritance that transmits an organism's characteristics to its descendants, or of mutations, the laws of inheritance, or the extreme specified complexity of living cells.

Naturalistic evolution theorizes that nonliving simple molecules evolved into the first living cell (through self-organization), and from there all life, including humans, developed through the selection of beneficial mutations by natural selection. The process occurred without guidance, direction, or purpose, except for the purpose of survival itself. It began about three billion years ago with the appearance of the first unicells, followed by the Cambrian explosion of complex, multicelled organisms 530 million years ago, and since then the evolution of all complex life on earth has occurred. This theory gradually overthrew the once dominant view called creationism, and conquered academia, education, and the media.

The mechanism of evolution at the molecular level consists of the rearrangement of DNA base pairs of a particular species by copy errors in such a way that they produce new genetically encoded traits that are selected, eventually producing a new species. Since mutations can only produce a few base pair changes at a time (because a large number of changes tend to be lethal), a new species is slowly evolved. If it could be demonstrated that evolution through random mutation of DNA bases is highly unlikely, or even impossible, then no known mechanism to generate new information for evolution of new species would exist. As will be shown, natural selection, and thus macroevolution, cannot work without mutations.

The nonexistence of information-adding mutations has equally serious ramifications for both naturalistic and theistic evolution, because, while some theistic evolutionists have difficulty accepting randomness, they assume the same history and mechanisms for evolution as do naturalistic evolutionists.

Random Mutations

Can Macro- and Micromutations Produce New Species?

The major driving force of the naturalistic theory of neo-Darwinism is random mutations. No macroevolutionary process can exist without a constant supply of mutations (Bergman, 2005a). The concept of macromutations appears to have different meanings, or at least different formulations: (1) Apparently it was first used of saltational changes in Goldschmidt's "hopeful monster" theory. (2) The concept depicts macromutations as affecting regulatory genes that activate other genes, which cause the synthesis of proteins. (3) The concept depicts macromutations as the cause of major alterations in the phenotype, the visible properties of an organism, which virtually always, if not always, are destructive to the organism. This is the way macromutation is used in this paper.

Mutations can have both external causes (radiation from the sun, space, or earth) and internal causes (toxins, radiation from food, and free radical damage) that damage the genes. Several thousand mutated genes that lead to serious illnesses and death have now been identified. Since these destructive mutations cannot be the driving force of evolution, I will ignore harmful and fatal mutations in this analysis of evolutionary mechanisms.

Most known macromutations are harmful and, therefore, cannot be a significant source of genetic variation for evolutionary development. For this reason, micromutations (small changes in the structure or arrangement of the genes, usually in a single nucleotide change) will be considered. These micromutations are assumed by both evolutionists and some creationists to be the ultimate source of genetic variation that produces phenotypic variation within the species, but in general only evolutionists ascribe micromutations to

be the cause of the step-by-step continual formation of new species over millions of years. So far no documented examples of mutations exist that meet the necessary conditions for the cumulative selection required to evolve new life forms.

Most micromutations cause small changes, resulting in no clear destructive genetic effects, and for this reason the cell often can tolerate them. The smallest mutation type, a point mutation, changes one base into another and is usually the result of a copying error that occurs when chromosomes duplicate themselves during cell division. Most copying errors are random, a requirement of naturalistic evolution. Although a small number of errors remain, the cell's ability to "proofread the text" and repair mistakes reduces the errors a hundredfold or more.

The large number of highly effective genetic repair systems in the cell fall into three major categories: error avoidance, error correction during DNA replication, and advanced repair of errors missed by the first two systems (Bergman, 2005b). These small errors demand millions of years of evolution to be able to produce a substantial change in a gene. If certain errors cannot be repaired, tumor suppressor genes send the cell into a complex programmed destruction cycle called apoptosis (Bergman, 2008a). Creationists believe that the many repair systems are part of the Creator's design to maintain the information in the basic created genome.

Proteins are constructed according to instructions emanating from the information in DNA. The proteins consist of long amino acid chains that are "folded into specific, intricate, three-dimensional shapes that contain all the twists, turns, folds, pockets, and loops essential for performing the numerous functions required by the cell" (Bergman, 2006). Proper folding requires "chaperones" and other molecular machinery called "folding factors." The folding is double-checked several times

by numerous other quality control systems. Mutational changes sufficient to produce new proteins would also likely require a new set of custom chaperones and enzymes to fold the new protein properly. These new chaperones and enzymes would also require new genetic information. After folding, a protein must successfully pass through multiple layers of monitoring before it can be sent to the needed location in the cell. Both the astounding genetic repair systems involved in the transcription step and the elaborate quality control factory for proteins are major problems for neo-Darwinian evolution and support the concept that the origin of life was by direct, miraculous creation.

Another serious problem for evolutionary theory is that, due to these error correction/quality control systems, copying errors are relatively rare. Neo-Darwinism assumes only slight genotypic and phenotypic changes that occur over long periods of time; otherwise the organism usually will not survive. The frequency of copying errors escaping the repair mechanisms for most organisms is about one per ten billion transcriptions per nucleotide (Spetner, 1997). Spetner calculated the possibility that a new species can be formed by random micromutations by determining the following parameters:

- (1) the chance of a mutation occurring, i.e., the mutation rate
- (2) the fraction of the mutations that have a selective advantage
- (3) how many replications occur in each step of the chain of cumulative selection
- (4) how many steps are required to achieve a new species.

Values for these parameters are all either known or can be estimated. For organisms other than bacteria, the first of these parameters, the mutation rate, is about 10^{-10} per nucleotide per live birth (Spetner, 1997, notes p. 123). However, not just any copying error can serve as a step that aids cumulative selection; it

must add information to the genome that produces a phenotype having a positive selective value. Fisher, who did much of the original work in population genetics, found that even "beneficial" mutations are likely to disappear from the population for various reasons and that a single mutation, even if favorable, will have only a very small chance of establishing itself in the species population (Fisher, 1958). Although Fisher, an English statistician, evolutionary biologist, and geneticist, published this 50 years ago, his conclusions are still valid today (Spetner, 1997).

If evolution is to function, large numbers of adaptive mutations must appear. Only then could mutants survive the vagaries of selection. But adaptive mutations are very rare. Simpson, generally acknowledged as the dean of modern evolution, determined a "frequent selective" value at about 0.1% (Simpson, 1953). Although published 45 years ago, Spetner and others use Simpson's 0.1% as a typical selective value (Spetner, 1997).

From the inferred changes in the fossil record of the so-called horse evolution during the past 65 million years, Spetner concluded that one typical small step of evolution would require about 50 million births (Spetner, 1997). The probability of at least one such mutation during this time is 50 million times 10^{-10} , or one in two hundred per nucleotide (for how Spetner arrived at 50 million births and a mutation rate of 10^{-10} per nucleotide, see Spetner 1997, pp. 121–124). Assuming that there is an equal chance that the base will change to any one of the other three bases in the nucleotide triplets (codons) that specify a single amino acid, the chance of obtaining a specific change in a specific nucleotide is a third of that, or 1 in 600. (Spetner, 1997, p. 100, slightly altered). This probability is the second of the above parameters.

Fisher's calculations (see reference above) show that for only one mutation

with a 0.1% selective value, the chance is 1/500 that it will survive, and this is the third parameter used. The chance that a specific copying error will appear is 1/600, and for it to both appear and survive to take over the population is $1/600 \times 1/500 = 1/300,000$ —less than the chance of flipping 18 coins and coming up with only heads.

G. Ledyard Stebbins (1966), considered the founder of evolutionary botany, 40 years ago estimated that to evolve a species requires about 500 steps, an estimate still accepted as the lower level today. Spetner uses this as the fourth of the above parameters (Spetner, 1997). Other researchers estimate a much larger number of steps or transitions are required to evolve a new species, which would considerably lessen the probability for this to occur. The adaptive mutation must survive each of these steps. The chance for this is estimated at $(1/300,000)^{500}$ or about 2.7×10^{-2739} , or more than 2500 orders of magnitude below 10^{-50} , which statisticians consider the level of probability approaching impossibility!

Therefore, there appears to be an impenetrable wall separating the basic organism types. On this basis Spetner rejected neo-Darwinian theory. His calculation spans several pages, some of which is included in Larssen (2001), with a more detailed presentation in a book by Larssen (2004). Using different paths, others, such as Ho and Saunders (1979), have come to the same conclusion as Spetner. Using a different mathematical proof in a book of surprisingly few pages, Hoyle and Wickramasinghe (1982) arrived at close to the same result.

Gnawing doubts about beneficial results of random mutations have led some to propose the idea of quantum mutations. One proponent of this idea is Kenneth R. Miller, a theistic evolutionist, professor of biology, and outspoken anti-creationist (Miller, 2000). Quanta at the subatomic level allegedly can evolve the first living cell by chance fluctua-

tions of vibrational energy changing a molecule's configuration and producing a spontaneous mutation. That quantum effects can be actualized and magnified in this way is not accepted by most evolutionists. Furthermore this constant vibrational energy would cause havoc in the genome.

Mutational Deterioration of the Genome

The deterioration of the genome as a result of mutations is well known and widely acknowledged by geneticists. Examples include a book focusing on the aging part of genomic deterioration (Vijg, 2007), the article "Darwinism and the Deterioration of the Genome" (Bergman, 2005a), and the work of John Sanford (Sanford, 2005), which will be discussed in the next section. Bergman concludes that the production of new information by mutations is at the core of the validity of neo-Darwinism. He attributes the degradation of the genome to many causes, such as (1) the tendency for mutations to produce a highly disproportionate number of certain nucleotide bases, and (2) many mutations occur in only a relatively few places within the genes called hot spots. Bergman finds that there is little or no evidence for beneficial mutations that can produce macroevolution and that the genome is deteriorating. He shows that nearly neutral mutations create major problems for evolutionary theory because they cannot be removed by selection, eventually causing mutational meltdown (Bergman, 2008b).

Origin and Maintenance of the Complex Genome

The genome is not only extremely large but also exceedingly complex and full of bends and branches, with genes that control other genes that control still other genes. The same row of genetic letters can code for completely different instructions. Tens of thousands of different types of sophisticated nanomachines

carry out incredible chemical feats in the living cell. The information used to produce and regulate these components is encoded by the genome. When asked how all this could have come into existence, the standard answer is what Sanford calls "The Primary Axiom": "Mutations combined with selection have created all biological information" (Sanford, 2005).

Sanford concludes that the overwhelming deleterious effect of mutations can clearly be seen in the demonstrated lack of information-creating mutations. He is not convinced that a single, clear example exists of a mutation that unequivocally has created new information, even in the case of antibiotic resistance in bacteria. Anderson (2005) provided a detailed analysis of antibiotic resistance, and showed that they are the result of deleterious genetic events, the opposite of new information. Bergman made a literature search, finding that of over 450,000 "mutation" hits, only 186 even mentioned the word "beneficial." or similar terms. Those labeled beneficial were beneficial only in a very narrow sense and consistently involved loss of information (Bergman, 2005a).

Population geneticists know by experience that virtually all mutations are largely neutral or deleterious. Mutations that have positive effects on fitness are so rare that they are excluded from distribution diagrams that show mutational effects on fitness as a function of mutation frequency. Kimura (1979) argues that most mutations are nearly neutral and are, therefore, not subject to selection. He shows this in distribution curves that include a relatively narrow box on each side of the zero point, representing a "no-selection zone." No beneficial mutations are shown to the right of the zero point (see Figure 1). Sanford (2005) shows a corrected distribution (see Figure 2), compared to the one used by Kimura. An interesting feature incorporated in Sanford's diagram (Figure 2) that is not found in Kimura's diagram is the tiny

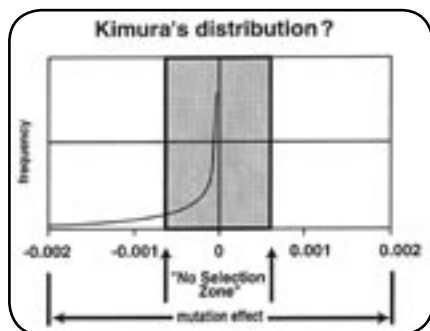


Figure 1. Distribution diagram of mutation effect adapted from Kimura (1979). Most mutations are nearly neutral approaching the zero point. Deleterious mutations are farther to the left. The “no-selection zone” is shown by the box.

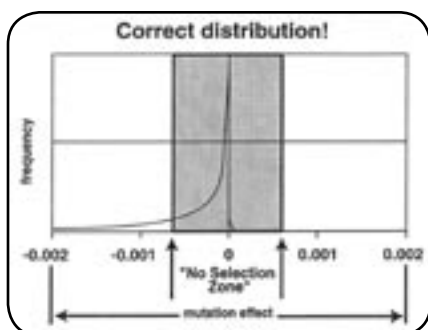


Figure 2. A corrected Kimura diagram (from Sanford, 2005) showing where beneficial mutations would occur. Their distribution is reduced in range and scale by a factor of ten thousand to one million. This part of the mutation distribution could not be drawn small enough, and a relatively large triangle is shown just to the right of the zero point. Even with beneficial mutations greatly exaggerated, essentially all beneficial mutations will still fall within Kimura’s “no-selection zone.”

triangle slightly to the right of the zero point, entering the beneficial mutation area. Because of the diagram’s scale, Sanford could not draw this section of the distribution diagram in proportional

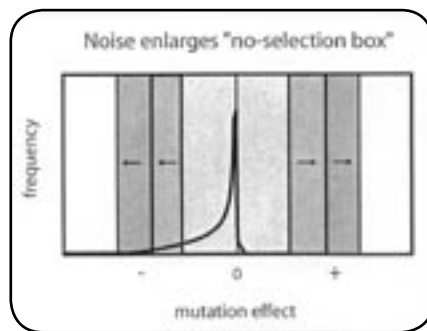


Figure 3. Sanford’s much larger no-selection zone due to several noise factors (reproduced from Sanford, 2005, Figure 9, p. 104).

scale to the deleterious section. The chance of a beneficial mutation is so rare that it would otherwise not show up in the distribution diagram.

Sanford (2005) believes that there *are* beneficial mutations in some sense, but they are still usually part of an overall erosion of information and are much too rare for genome building and thus are well inside the “no-selection zone.” The box size should further be enlarged by all nongenetic factors that affect reproductive probability, and “anything that decreases the signal-to-noise ratio will make proportionately more of a genome’s nucleotides utterly un-selectable” (Sanford, 2005, p. 22). Sanford shows a distribution with this and other noise factors (see Figure 3) that has a much wider no-selection zone than the one used by Kimura (see Figure 1). This implies that the chance of the appearance and survival of a beneficial mutation through 500 steps of supposed evolution is infinitesimal and, in fact, impossible (Spetner, 1997). Further, there exists no selection scheme that can reverse the damage caused by continuous mutations (Sanford, 2005). This agreement between the conclusions of a molecular biologist and a geneticist is notable and compelling.

Newer discoveries show that the mutation rate for reproductive cells

in humans is at least 100 nucleotide substitutions per person per generation (Sanford, 2005, pp. 34, 70, 120, 125). Even if a good portion of DNA is actually “junk,” every person is a mutant carrier. Most “junk” DNA also deteriorates. Although these data are valid only for point mutations, there are many other common mutations, such as frame-shifts, redistributions, duplications, inversions, etc. These nonrandom “mutations,” which are discussed further below, also do not support neo-Darwinism.

Sanford asserts that neither natural nor artificial selection (such as human countermeasures from advances in medicine) can eliminate this deterioration. For this reason, reducing the continued accumulation of damaging mutations by denying large segments of the population worldwide the right to bear children is both impracticable and socially unacceptable.

Mutations and natural selection, Spetner’s calculations on species formation, and Sanford’s mutational deterioration of the genome are discussed in Larssen (2007).

Nonrandom “Mutations”

Genetic Changes

Neither macro- nor micromutations can be the driving force of evolution, and natural selection is impotent without them. What, then, is the cause of variation within the species? Part of the answer is nonrandom genetic changes. These changes are still considered by some to be “mutations,” although evolutionary theory is based on randomness. Nonrandom “genetic rearrangements appear to be just as normal in the cell as cell division, although they do not occur often. They are affected by specific enzymes, which the cell synthesizes precisely for that purpose” (Spetner, 1997).

Genetic recombinations show evidence of having been initiated by the en-

vironment (climate, temperature, food) to achieve adaptation by mechanisms such as epigenetics. The possibility of adaptation to the environment already exists in the genome. An example of these variations is the long and short beaks of the Galapagos Islands finches, which Spetner discusses in some detail (Spetner, 1997, pp. 202–205). Spetner argues that the diversity of finches (1) could have come from nonrandom variation, (2) could have come from the direct influence of the environment, and (3) alternatively, could have happened through a built-in genetic switch triggered by the environment.

Another example is the ratio of light to dark peppered moths on the dark tree trunks caused by pollution during the industrial revolution in England, which was reversed when the tree trunks later became lighter due to pollution control. Light and dark moths are always present at some level, indicating that the difference exists in the moths' wild type gene pool. Evolutionary literature often erroneously describes peppered moths as normally sitting on tree trunks, when in fact they typically rest high up in the canopies protected by the foliage (Wells, 2002, p. 149). Both finches and peppered moths possess variations within their species or basic type, and they both demonstrate that genetic changes are controlled by processes in the cell.

While random macromutations alter genes, recombinations (including duplications, inversions, deletions, and translocations) only move existing genes around. Recombination is not a simple process, and we do not fully understand how it proceeds as precisely as it usually does. Specific genes exist that affect recombination effectiveness. These genetic rearrangements occur in response to the surroundings and can result in phenotype changes, but not in new species. These nonrandom genetic rearrangements that appear as a response to the surroundings may explain the enormous variation existing within most

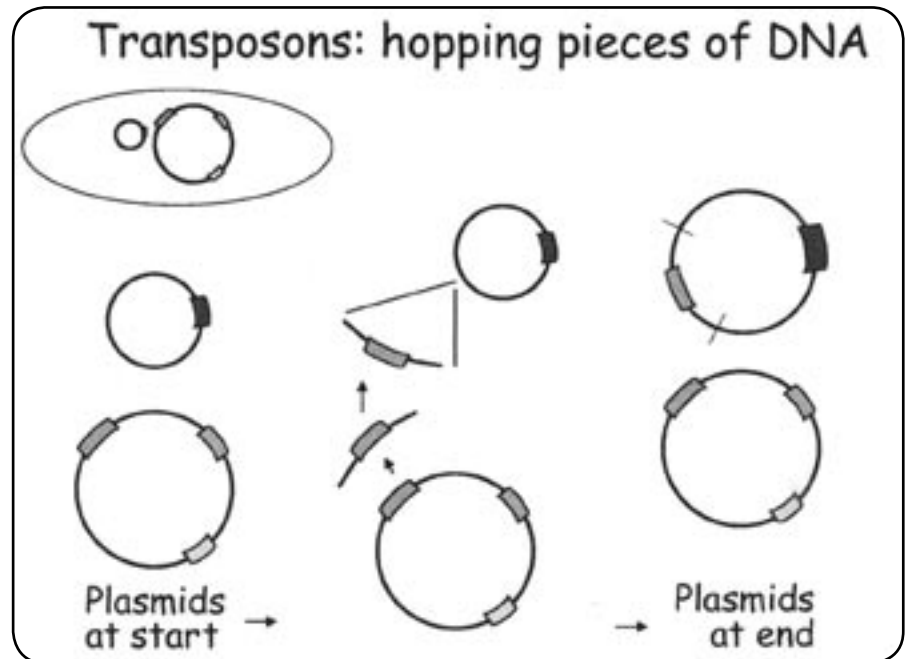


Figure 4. Transposons, containing DNA segments (larger units not shown), can jump from one location to another in a chromosome. Plasmids are small ring forms of DNA containing genes. The genes are “curved parallelograms.” Plasmid to the left ends up identical in another place on the chromosome to the right. The center illustrates how the jumping occurs (from a lecture to students by Luca Comai in 2001, University of California-Davis).

every species, such as finch beak size differences and in the appearance of dogs. These recombinations cannot contribute to Darwinian evolution because as far as we know they do not increase information and do not occur as a result of randomness.

The inbuilt ability to respond to the environment also may be due to epigenetics, which refers to heritable traits that do not involve changes in the underlying DNA sequence but rather methylation that turns certain genes on or off. Further, some variations may be caused by micromutations, which, as shown above, are too rare or too minor to have any significant evolutionary effect. These also are not neo-Darwinian changes. When the very first of any basic species type was created, it already had the mechanisms and a genetic pool

broad enough to produce the variations necessary to adapt to many environmental changes.

Transposons

One means of nonrandom genetic variation is found in the transposition system. DNA segments termed transposons, which consist of as many as several thousand nucleotides, can move to different positions of the genome of a single cell (see Figure 4). Transposons have DNA components that code for the two required enzymes that facilitate their movement. Integration of a transposon into a gene results in its disruption. These “mutations” are under strict cellular control and therefore are not the result of a random process. The more notorious transposons in bacteria have genes that confer resistance to several

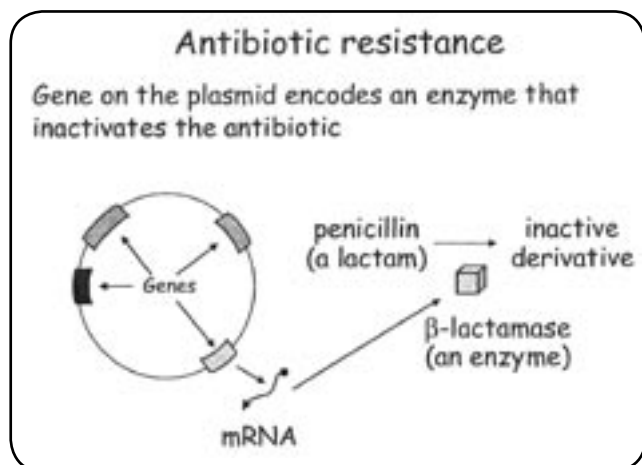


Figure 5. Antibiotic resistance. One gene in a plasmid, through messenger RNA, is coding for an enzyme, beta-lactamase, shown as a small cube. The enzyme produces penicillin immunity by making it inactive in the bacterium (from a lecture to students in 2001 by Luca Comai, University of California-Davis).

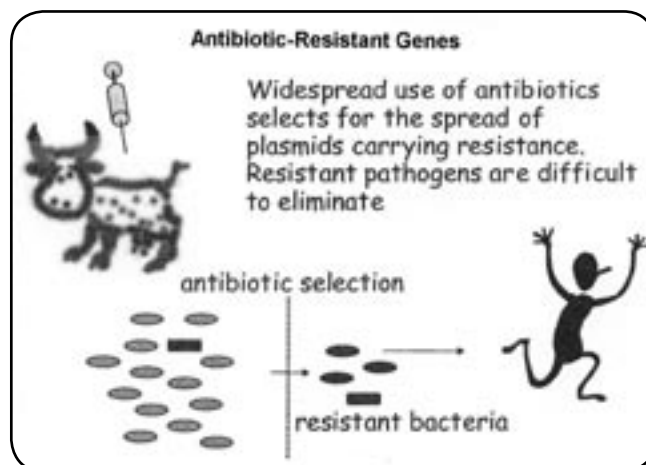


Figure 6. Antibiotic-resistant genes. Transposons contain such genes as seen in the plasmids in Figures 4 and 5 above. After injection of the antibiotic in the animal, the resistance-carrying plasmids, which are naturally found in bacteria and are inherited, are spreading among bacteria. The bacteria to the left become the resistant bacteria shown on the right. The bacteria causing illness are difficult to eliminate, illustrated by the reluctant black figure (from a lecture to students in 2001 by Luca Comai, University of California-Davis).

types of antibiotics. These transposons can be quite large—the transposon that carries resistance against ampicillin, streptomycin, and sulfanilamide contains around 20,000 nucleotides.

Plasmids, small ring-shaped extrachromosomal DNA naturally existing in all bacteria (see Figure 5), copy themselves without external control. They can carry transposons and are inherited by the host cell's progeny. Plasmids are passed between bacterial cells during conjugation and transposon-carried genes can move from a plasmid of one bacterium into the genomic DNA of another bacterium (Spetner, 1997, p. 187). Aside from spreading antibiotic resistance, the normal functions of transposons are not fully understood, but we do know that the resistance they provide does not occur as a result of evolution (see Figure 6). On the experiments with bacteria, Spetner writes that if

adaptive mutations are stimulated by the environment, they contradict

the basic dogma of neo-Darwinism. ...that mutations are random, and the kind of mutations that occur are independent of the environment. If mutations are...non-random (and/or) the environment can stimulate adaptive mutations, the paradigm of Darwinian evolution, which has dominated the biological sciences for close to 150 years, must be replaced (Spetner 1997, p. 190).

A comprehensive review of genetic transposition has been published by Bergman (2001). He describes the discovery of transposons, their complicated mechanisms and functions, their types, movements, molecular biology, and significance for creation. In agreement with Spetner, Bergman refers to experiments showing that the movement and placement of transposons are regulated by enzymes and elaborate control systems in the cell, negating the randomness demanded by neo-Darwinism. He concludes that the “extremely complex

transposition mechanism could not exist without simultaneous presence of all its main parts, supporting the concept of irreducible complexity” (Bergman, 2001, p. 145).

Selection

Natural Selection Is Not a Selective Force

Organisms with mutations regarded as beneficial are presumed to be “chosen” by the process of natural selection. Natural selection is a descriptive term meaning that some members of an organism's offspring are more likely to survive in the struggle for existence. Unaware of mutations and the laws of genetics, natural selection was the only “mechanism” Darwin could use to explain how evolution occurred. His overemphasis on selection has been maintained by most in the evolutionary community ever since.

French zoologist Pierre-Paul Grassé, a former president of the French Academy of Sciences, rejects both of the assumed mechanisms of evolution, random mutations and natural selection. He asserts that the role of natural selection in evolution is not based on a single fact: "Guided by the overwhelming selection, randomness becomes some type of providence which, under cover of atheism, is not mentioned but is worshiped in secrecy" (Grassé 1973, translated 1977, p. 107). In a review of the original French edition, the Russian geneticist Dobzhansky says of Grassé's book:

[It] is a frontal attack on all kinds of "Darwinism." Its purpose is "to destroy the myth of evolution, as a simple, understood, and explained phenomenon," and to show that evolution is a mystery about which little is, and perhaps can be, known. Now one can disagree with Grassé but not ignore him. He is the most distinguished of French zoologists, the editor of the 28 volumes of *Traité de Zoologie*, author of numerous original investigations, and ex-president of the Académie des Sciences. His knowledge of the living world is encyclopedic (Dobzhansky, 1975).

For the purpose of this analysis, let us assume that no new mutations exist in the zygote and only the genetic laws of inheritance operate. If the descendants share only the parents' characteristics and nothing new exists on which selection can work, evolution is effectively dead. Natural selection depends on the existence of mutations: no mutations, no natural selection, and no evolution.

Macromutations are destructive, and beneficial micromutations (such as copying errors) are too rare to be able to furnish anything on which selection can work. The assumption in the above statement is therefore immaterial and unnecessary. Accordingly, there is no evolution!

Some leading evolutionists openly

admit that, in practice, the theory of natural selection is a tautology, a way to say the same thing twice. The theory predicts that the most viable organisms will produce the most offspring, and the most viable organisms are defined as those that will produce the most offspring. Harvard University geneticist Richard Lewontin opines:

Evolution cannot be described as an adaptive process, because all organisms are already adapted. Natural selection is functioning essentially to make it possible for organisms to maintain their status of adaptation instead of improving it. Natural selection does not seem to improve the chance of the species to survive in the long run, but simply makes it possible for them to trace, or keep up with the surroundings, that constantly change (Lewontin, 1978, pp. 213).

The famous founder of the strictly methodical research on heredity, Danish professor and physiologist W. L. Johannsen, concludes from his crucial early experiments on hens:

What happens in natural or artificial selection is merely that a fixed life form steps forward from its hiding place in the mixture. Selection is therefore not able to produce anything new. It can only select something that already exists. ... It is quite evident that genetics has removed the foundation from the Darwinian selection theory (Johannsen, 1915, p. 169 as quoted in a book by professor and theologian I.P. Seierstad, 1946, pp. 64–65).

Johannsen uses "mixture" instead of "gene pool" because he was not familiar then with later developments about what "mixture" really meant. Nonetheless, his conclusion is still valid today.

Can Selection Stop Genomic Deterioration?

Sanford determined that the human genome deteriorates due to mutations.

Mutations are either near neutral or deleterious, leading to the loss of genetic information that in time will result in reduced adaptation. This decline in adaptation is assumed to occur at the rate of 1–2 percent per generation. A steadily increasing adaptation loss will lead to dramatic degeneration of the human race within around 300 generations. Although medical and technical advances are still increasing our life span, "human geneticists would probably all agree that eventually selection must be increased if we are to stop genetic degeneration" (Sanford, 2005 p. 45). Conversely, Sanford concludes that no form of selection can ultimately stop genetic degeneration, only slow it down (Sanford, 2005, p. 117).

The question is, how much selection is required to stop the degeneration, and can it be stopped altogether? A small, closely-knit and highly specialized group of population geneticists tied to the primary axiom ideology have analyzed what selection can and cannot do. These population geneticists have effectively demonstrated the limitations of natural selection, with some even talking about a "mutation meltdown" (Sanford, 2005, p. 115; Lynch et al., 1995a).

Lynch defines mutational meltdown as when "the population size declines, random genetic drift becomes a more significant evolutionary force and the rate of accumulation of deleterious mutations increases, causing further decline in population size. We refer to this extinction phenomenon, which can be quite rapid, as a mutational meltdown" (Lynch, 1996, p. 488; see also Lynch et al., 1995a, p. 1069).

The Lynch et al. (1995a) article deals primarily with asexual populations but one illustration (Figure 6a, p. 1075) deals with a sexual population. When the mean time to extinction is plotted against the reproductive rate, the mean extinction time is short only for very low populations, from 8 to over 32,000 generations for populations of only 4

to 16 individuals. Conversely, Sanford (2005) deals with higher organisms and with the largest human population that can be considered, over 6 billion people (see below).

Lynch et al. (1995a) present results based on computer simulations supported by analytical approximations. For higher organisms they use a genomic mutation rate of one per gamete per generation (Lynch et al., 1995a, p. 1067) and one per individual per generation (p. 1068). They arrive by this process at very long mean extinction times as a function of reproductive rate for sexual populations at various population sizes (p. 1975, Figure 6a), even for populations of 16 individuals and smaller. However, they state that credible arguments have been made that the mutation rate may actually be greater than one, in which case the mean extinction time that they have reported to be very long “may be vastly overestimated,” and “it appears that sexual populations as large as 1000 individuals.... are potential victims of the mutational meltdown” (Lynch et al., 1995a, p. 1078).

Neel et al. (1986) show that the deleterious mutation rate must be much higher than one per person per generation, in which case mean extinction time is substantially decreased. Sanford (2005) quotes Lynch as saying, “Our results provide no evidence for the existence of a threshold population size beyond which a population is completely invulnerable to a mutational meltdown” (Sanford, 2005, p. 173, quoting Lynch et al. 1995b, p. 510).

Mutation rates have been investigated by a number of other geneticists. Drake et al. (1998) report mutation rates in higher eukaryotes are roughly 0.1–100 per genome per sexual generation, and for humans 1.6 per effective genome per sexual generation. Nachman and Crowell (2000) report that the genomic deleterious mutation rate for humans is at least 3 per genome per generation, concluding that synergistic

epistasis among harmful mutations may be common. They also indicate that male mutation rate is 4 times the female mutation rate. Kumar and Subramanian (2002) conducted computational analysis of several thousand genes from major groups of placental mammals to determine mutation rate differences among genes in a genome and among various mammalian lineages. They find that the average mammalian genome mutation rate of 2.2×10^{-9} per base pair per year is constant and largely similar among genes and also similar among lineages with vastly different generation lengths and physiological attributes (Kumar and Subramanian, 2002., p. 803). This is at variance with current thought that mutation rates widely vary among genes within a genome and among lineages in mammals.

Can this genomic degeneration problem be solved? Several possibilities exist, but they all fail. For example, if we could select against all “mutations,” no life-form could reproduce, causing rapid extinction. Every life-form inherits a large number of deleterious mutations and so collectively carries billions of near-neutral or harmful mutations. From the estimated total of 600 million new mutations that enter the entire human gene pool in our own generation, it is estimated that in a 6-billion world population as many as one third, or 2 billion people, would be precluded from having children (Sanford, 2005, p. 71). This would still leave 400 billion new mutations to burden the next generation. Even if we assume that two thirds of the remaining mutations are completely neutral, about 133 billion harmful mutations would be added to the population in the next generation. If we doubled the intensity of selection, we still would have 67 billion damaging mutations for the next generation. The cost of selection sets distinct limits to how many mutations can be eliminated per generation and for this reason “*mutations will continue to accumulate, and*

the species must degenerate!” (Sanford, 2005, p. 72).

Crow agrees that because mutations are accumulating, population fitness is declining, and due to chance some individuals would experience more mutations than others (Crow, 1997). If more mutations in the population could be eliminated at less “cost” (by focusing selection on the individuals with the most mutations), the number of mutations per person might be stabilized, and the fitness decline of the population would taper off. However, of primary importance is not who has the most mutations, but who has the most damaging mutations. Crow’s model answers only the former and ignores the latter. The fitness impact of different nucleotides can vary by many orders of magnitude, and one minor mutation can overshadow the effects of a million near-neutral mutations. Crow’s model has limited significance in the real world because it is based on several unreasonable assumptions (Sanford, 2005, pp. 106–108 and Figure 10a, p. 112). Crow’s model is unrealistic because

[it] is designed to make the problem of mutation accumulation “go away”. It assumes all mutations have equal value, are all individually very subtle, yet none are so subtle as to be “nearly neutral”, that all selection is based upon “mutation count.”... None of these assumptions are even remotely reasonable. Even though all these assumptions are artificial and unreasonable, the numerical simulation still shows severe mutation accumulation (Sanford, 2005, p. 112).

Walter ReMine (2005) has developed software for doing numerical simulations of Crow’s model (represented by Sanford’s [2005] Figure 10a, p. 112). This shows a fitness curve *versus* generations (Sanford, 2005, Figure 10b, p. 113), where fitness clearly declines to zero after roughly 300 generations. If the

Lynch et al. (1995a) reservation about “vast overestimates” is not considered, this finding deviates sharply from the long extinction times result (Lynch et al., 1995a). If it is considered, there is less disagreement between Lynch et al. (1995a) and Sanford (2005).

Without intervention, the extinction of the human genome appears as certain as the extinction of stars and the death of organisms. We as individuals will not only die as a result of the deterioration of our own genome, but without outside intervention the human race also will eventually die for the same reason. This agrees with current speculation by some evolutionists that over 99 percent of all species that have existed in the past have gone extinct.

In the previous section it was concluded that there is no evolutionary process. In this section Sanford's (2005) findings lead to the conclusion that living organisms exhibit a process of devolution that he calls genetic entropy.

Plotting the human life spans of the descendants of Noah against the number of centuries after Noah when a given individual was born shows a dramatic reduction in life spans, which has a strong likeness with a biologic decay curve (see Figure 7). The data reveal an exponential curve that fits well with a correlation coefficient of 0.90. The Biblical data are in very good agreement with modern theories of genomic degeneration caused by mutation accumulation (Sanford, 2005, pp. 148–149, Figure 14, p. 152). The curve is very similar to theoretical curves shown by Sanford that reflects genomic degeneration (Sanford, 2005, Figure 4, p. 65 and Figure 10b, p. 113).

Summary

Random mutations combined with natural selection is the central dogma of how the neo-Darwinian theory works. This review shows why macromutations cannot be the driving force of evolution,

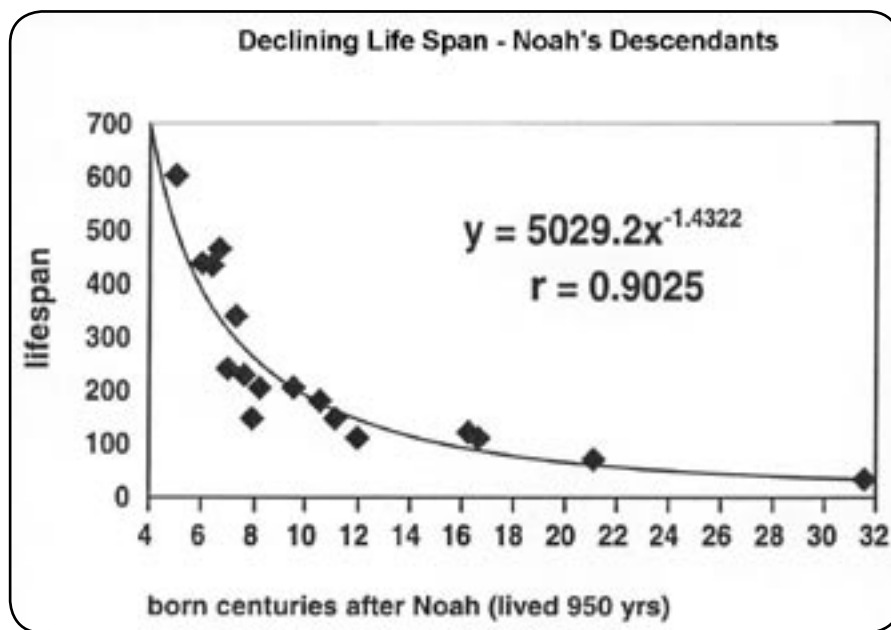


Figure 7. Human life spans in early history (from Sanford, 2005). When Biblical life spans are plotted against time for generations after Noah, a dramatic decline in life expectancy is shown. The curve shows a strong evidence of biological decay. It reveals an exponential curve following the formula $y = 5029.2x^{-1.43}$. The curve is consistent with the concept of genomic degeneration caused by mutation accumulation.

and calculations show that micromutation copying errors are far too rare and cannot be the basis for evolving new species. Natural selection's role in evolution depends on the existence of mutations, and natural selection is inadequate to halt genomic degeneration.

How the complexity and the incredible chemical feats of the living cell came into existence through random mutations and natural selection, referred to as the primary axiom or the central dogma, defies explanation and is considered, as shown, an impossibility. The nearly neutral mutations within the “no-selection zone” of the mutation distribution curve creates major problems for evolutionary theory due to their increasing accumulation. The adaptation loss at 1–2% per generation will lead to dramatic degeneration of the human race within around 300 generations,

and this genomic deterioration cannot be rescued by selection.

The combined impact of the inability of mutations to produce new species and selection's inability to halt genomic deterioration demonstrates the failure of evolution's central dogma to explain the complexity that we see in the realms of molecular, cellular, and systems biology, and strikes a devastating blow to neo-Darwinian evolution theory.

These facts are a sufficient blow to motivate a paradigm shift. The well-known Swedish evolutionary biologist, the late Søren Løvtrup of Umeå University, in his book *Darwinism: The Refutation of a Myth*, evidently perceived such an outcome when he wrote, “I believe that one day the Darwinian myth will be ranked the greatest deceit in the history of science” (Løvtrup, 1987, p. 422).

Acknowledgments

I want to thank Jerry Bergman for steadfast support and for pointing to a number of related works, including several of his own, that have strengthened the thesis of this paper that the central dogma of evolution, mutations and natural selection, does not work. Thanks also to an anonymous reviewer for keeping the subject matter focused and improving the readability and clarity of the text.

References

- CRSQ: *Creation Research Society Quarterly*.
- Anderson, K. 2005. Is Bacterial Resistance to Antibiotics an Appropriate Example of Evolutionary Change? *CRSQ* 41(4): 318–326.
- Bergman, J. 2001. The molecular biology of genetic transposition. *CRSQ* 38:139–150.
- Bergman, J. 2003. The century-and-a-half failure in the quest for the source of new genetic information. *Technical Journal* 17:19–25.
- Bergman, J. 2005a. Darwinism and the deterioration of the genome. *CRSQ* 42:104–114.
- Bergman, J. 2005b. The mutation repair system: a major problem for macroevolution. *CRSQ* 41:265–273.
- Bergman, J. 2006. The elimination of mutations by the cell's elaborate protein quality control factory: a major problem for neo-Darwinism. *CRSQ* 43:68–74.
- Bergman, J. 2008a. Origins of apoptosis: selfish genes or intelligent design? *CRSQ* 44:204–212.
- Bergman, J. 2008b. Progressive evolution or degeneration? In Snelling, A. (editor), *Proceedings of the Sixth International Conference on Creationism*, pp. 99–110, Creation Science Fellowship, Pittsburgh, PA.
- Crow, J.F. 1997. The high spontaneous mutation rate: is it a health risk? *Proceedings of the National Academy of Sciences* 94:8380–8386.
- Fisher, R.A. 1958. *The Genetical Theory of Natural Selection*. 2nd Revised Edition. Dover, New York, NY.
- Dobzhansky, T. 1975. Darwinian or “oriented” evolution? *Evolution* 29:376–378.
- Drake, J.W., B. Charlesworth, D. Charlesworth, and J.F. Crow. 1998. Rates of spontaneous mutation. *Genetics* 148, 1667–1686.
- Grassé, P. 1973. *L'Evolution du Vivant*. Translated 1977 as *Evolution of Living Organisms*. Academic Press, New York, NY.
- Ho, W.M., and P.T. Saunders. 1980. Beyond complexity. *Journal of Theoretical Biology* 104:399–446.
- Hoyle, F., and C. Wickramasinghe. 1982. *Why Neo-Darwinism Does Not Work*. Cardiff Press, Cardiff, UK.
- Johannsen, W.L. 1915. Experimentelle Grundlagen der Deszendenzlehre (Experimental Foundations of the Descendant Theory). *Kultur der Gegenwart*, III, 4, 1: *Allgemeine Biologie*. As quoted in I.P. Seierstad's 1946 book *Skapelsesberetningen og naturvitenskapen* (*The Creation Account and Natural Science*), Lutherstiftelsen Publishing, Oslo, Norway.
- Kimura, M. 1979. Model of effective neutral mutations in which selective constraint is incorporated. *Proceedings of the National Academy of Sciences* 76:3440–3444.
- Kumar, S., and S. Subramanian. 2002. Mutation rates in mammalian genomes. *Proceedings of the National Academy of Sciences* 99:803–808.
- Larssen, P.A. 2001. Utviklingslæren i krise (The Theory of Evolution in Crisis). *Origo* 75:14–21.
- Larssen, P.A. 2004. *Darwins lære faller* (*Darwin's Theory is Falling*). Prokla-Media Publishing, Ottestad, Norway.
- Larssen, P.A. 2007. Darwinismens sentrale dogme. *Origo* 106:7–12.
- Lewontin, R.C. 1978. Adaptation. *Scientific American*, 239 (Sept.):213–230.
- Lynch, M. 1996. A quantitative-genetic perspective on conservation issues. In Avise, J.C., and J.C. Hamrick (editors), *Conservation Genetics: Case Histories*, pp. 471–501. Kluwer Academic, Norwell, MA.
- Lynch, M., J. Conery, and R. Burger. 1995a. Mutational meltdown in sexual populations. *Evolution* 49:1067–1080.
- Lynch, M., J. Conery, and R. Burger. 1995b. Mutation accumulation and the extinction of small populations. *The American Naturalist* 146(4):489–518.
- Løvtrup, S. 1987. *Darwinism: The Refutation of a Myth*. Croom Helm, New York, NY.
- Miller, K.R. 2000. *Finding Darwin's God*. HarperCollins, New York, NY.
- Nachman, M.W., and S.L. Crowell. 2000. Estimate of the mutation rate per nucleotide in humans. *Genetics* 156:297–304.
- Neel, J.V., C. Satoh, K. Goriki, M. Fujita, N. Takahashi, J. Asakawa, and R. Hazama. 1986. The rate with which spontaneous mutation alters the electrophoretic mobility of polypeptides. *Proceedings of the National Academy of Sciences* 83:389–393.
- ReMine, W. 2005. Cost of selection theory. *Technical Journal* 19:113–125.
- Sanford, J.C. 2005. *Genetic Entropy & the Mystery of the Genome*. Elim Publishing, Lima, NY.
- Simpson, G.G. 1953. *The Major Features of Evolution*. Columbia University Press, New York, NY.
- Spetner, Lee. 1997. *Not by Chance! Shattering the Modern Theory of Evolution*. The Judaica Press, Brooklyn, NY.
- Stebbins, G.L. 1966. *Processes of Organic Evolution*. Prentice Hall, Englewood Cliffs, NJ.
- Vijg, J. 2007. *Aging of the Genome. The Dual Role of DNA in Life and Death*. Oxford University Press, Oxford, UK.
- Wells, J. 2002. *Icons of Evolution*. Regnery Publishing, Washington, DC.

Book Review



The Privileged Planet: How Our Place in the Cosmos Is Designed for Discovery

by Guillermo Gonzalez
and Jay W. Richards

Regnery Publishing, Inc.,
Washington, D.C., 2004,
444 pages, \$30.00.

This interesting book is by two researchers in the intelligent design (ID) movement, Guillermo Gonzalez and Jay Richards. The book's thesis is twofold. The authors openly maintain that the requirements for "habitability," the ability of a habitat to sustain life, and the requirements for scientific measurement of the universe, are almost the same. More subtly, they demonstrate that the requirements for life evolving are so stringent and the conditions needed so rare that it is highly improbable that complex life has evolved anywhere, including on earth.

The book's subtitle encapsulates the main thesis of the authors quite well: "How Our Place in the Cosmos Is Designed (intelligence) for Discovery" (human discovery of the natural world, its laws, etc.). Gonzalez and Richards argue that our earth, solar system, galaxy, universe, and even the physical laws that characterize the known world are fine-tuned for life. They maintain that the characteristics that make our world habitable also allow the greatest possible degree of scientific exploration and discovery. One example given is perfect

solar eclipses. Eclipses are very valuable tools for the study of the sun, as they allow us to see the sun's chromosphere and measure certain characteristics of the sun ordinarily hidden by the sun's brightness. Many of the factors that produce such eclipses also aid our survival: a terrestrial planet at the right distance from the right kind of star, a relatively large, stabilizing moon, and a transparent atmosphere.

The book discusses the history of the Copernican principle, the idea that our earth, solar system, and galaxy are typical and average in the universe. The authors demonstrate how many actual observations have shown that in fact, our earth, moon, solar system, and galaxy are exceptional in the universe. For example, our moon is relatively large compared to the earth and has a stable orbit when contrasted with other planetary moons in our solar system. Also, our location outward from the center of the galaxy helps to protect us from harmful levels of radiation.

The authors embrace the standard idea of an old earth, and some of their

examples of the correlation between habitability and measurability are based on this belief. For example, they feel that our location in the galaxy is the best for habitability, and this also allows us to observe the cosmic background radiation and determine that the universe began with a big bang. However, many of their other arguments are compatible with and could support young-earth creation, and many of their observations of design in the universe are valid.

Gonzalez and Richards have done a fine job of presenting the question of design in the universe to those who have ignored the arguments of creationists. It is a must-read for those who want to keep up with the trends in the intelligent design movement, as well as anyone who wants to keep up with the latest evidence of design in astronomy. The book includes two appendices on panspermia and the Drake equation. It is thoroughly referenced, indexed, and extensively footnoted.

Jeremy Maurer
maurerjl@grace.edu

Book Review



The Edge of Evolution

by Michael Behe

Free Press, New York, 2007,
321 pages, \$28.00.

The title page of the book is a bar graph summarizing the book's purpose and conclusions. The top is labeled "The Surprising Depth of Fine Tuning of Nature for Life on Earth." It summarizes the primarily astronomical evidences for design of the universe and everything in it. The lower portion introduces us to the issues of life and the principal concern of the book: At what point do the evolutionary mutation and natural selection processes become inoperable and design take over? At the current state of scientific knowledge, Behe cannot offer a sharp line but instead shows a band. The upper edge lies between classes and orders with Linnaean design responsible above that line. Below, in Behe's view, Darwinian processes are sufficient.

The book is a devastating quantitative empirical evaluation of the Darwinian mechanism for macroevolution. It essentially reduces the mechanism of macroevolution to something close to an absurdity. The book is highly recommended and is very well written. Opening it we read Behe's starting assumptions: Darwinian evolution can be viewed as a three-stage process: ran-

dom mutation, natural selection, and common descent. The uniformitarian multibillion-year time scale is assumed to be true. The author believes strongly in common descent. He cites the deleterious mutations common to both man and chimpanzees as evidence. However, evolution does not require vast amounts of time for its action to be seen available for study. It requires rather a large population of available creatures. Each creature in essence becomes an evolutionary experiment. The long lives and relatively small family sizes of mammals means that long times are involved in order to get the large numbers evolution requires. This effectively eliminates direct testing of the putative mechanism of evolution with mammals. The twentieth century has seen this problem overcome by the development of microscopic techniques that permit the study at the cellular level, in a relatively short time, of large numbers of creatures having large numbers of offspring and short reproductive cycles.

The central core of the book is a detailed study of the principle malaria parasite strain (*Plasmodium falciparum*),

the human response to malaria, and the parasitic response to the human actions against it. Emphasis is placed on the development of resistance to chloroquine.

The odds in favor of a particular parasite developing chloroquine resistance by random mutations are observationally determined as one in 10^{20} . The number of malaria parasites on earth on average in any year is about 10^{20} . Multiplying these numbers together we get a likelihood of one that in any year, a chloroquine resistant malaria parasite will surface. This agrees with the fact that over the 40 years of observation, chloroquine resistance broke out independently in several different parts of the planet. The resistance seems to be the result of mutations damaging at least two amino acid locations, namely 76 and 220, in a particular protein. These mutations convert a one-way portal into a two-way portal allowing chloroquine, otherwise concentrated in the parasite, to escape.

Conclusions include the following.
1. The mutations lead to a benefit for the parasite under the stress of chloroquine

poisoning, just as Darwin predicted. 2. The benefit is at the cost of damage to a useful feature of the parasite. 3. No new information increase or novel features appears as a result of these mutations, or any other mutations occurring over the 40-year observation period. Nothing appears that would support evolution, which of course requires an increase in complexity, information, and novelty.

Similar work has been done on a virus (HIV under anti-HIV medicinal stress) and a prokaryote (*E. coli* under 30,000 generations of laboratory study). The results are identical to those noted above for the malaria parasite. Similar conclusions follow from detailed studies of the various natural forms of resistance to malaria that humanity has developed such as sickle cell, thalassemia, and Duffy antigen.

In 200 million years of evolution, Behe estimates that about 10^{18} mammals have existed along the evolutionary track from mammal-like reptiles to man. This is to be compared with the 100 times as many malaria parasites that live and die in a single year where they are fully available to study. The issue is not time but the number of creatures available for evolution to work on. Furthermore not just one beneficial mutation complex is required along the mammal-to-man evolutionary trail, but many.

Behe labels the odds of developing a mutational complex of 1 in 10^{20} as a chloroquine complexity complex (CCC). The odds then of a beneficial mutational complex twice complicated as a CCC are a CCC squared or one in 10^{40} . This then is used as a reference

standard subsequently. Bacteria are the most numerous living organisms on earth. The total number of these that have occurred in the last billion years is on the order of 10^{39} . Multiplying this with the CCC squared measure gives a likelihood of less than one of a positive mutation. The implication then is that any beneficial mutational complex twice as complex as a CCC is most unlikely to occur even in a billion years by any unintelligent process such as Darwinism. A double CCC then sets the upper edge of evolution.

A study of protein-protein binding sites follows. It is known that in a cell few proteins are lone rangers. Rather six or more proteins combine at protein-protein binding sites to produce a product needed by the cell. A new binding site might then be the source of some novel product that would provide true evolutionary advance.

Binding sites are extremely complex structures typically involving up to 20 complementary amino acids on each side of the binding area. Michael Behe, using available data, the double CCC complexity standard, and a reasonable argument shows that even two weak binding sites produced are beyond evolutionary capabilities. This would only bind three proteins together, not the six generally required. Furthermore the typical cell has about ten thousand binding sites, not just two.

Behe now introduces the question as to whether unaided unintelligent processes might move single eukaryote cells into multicellular creatures like humans. His first answer is to point out the

awesome complexity of control networks for multicellular creatures, far exceeding that of producing individual proteins or of the 1 in 10^{20} complexity standard. However, that introduces the possibility of mutations in control systems moving evolution forward in large jumps. Behe answers that with the lengthy history of mutating control systems in fruit flies (*Drosophila melanogaster*). Startling results are certainly achieved. Fruit flies have been produced with legs coming out of their antenna sockets and useless extra wings where they don't belong. At the end of it all, a fruit fly is still a fruit fly. There is no evidence of novelties that would advance the fruit fly along the evolutionary trail.

There is, however, an interesting result from this work. Mutations in control systems have been found to produce the minor differences observed at the species level. For example, flies have obtained wing spots and dogs slight variations in bone structure. Noting this and his earlier considerations, the author sets the upper edge of what Darwinism can do at just beyond the species level but below genera.

How far down from the Kingdom into the Linnaean organizational system does design go? The author ties together the mutation and binding site work along with recent work on control systems. He then proceeds level by level down to vertebrate classes. Behe concludes that purposeful design extends into biology at least to the major classes of vertebrates.

Ker C. Thomson
kt37321@bellsouth.net

Lysenkoism

The Tragedy of Government-Enforced Darwinism

The Effect of Darwin on Soviet Communism

Jerry Bergman*

Abstract

The story of the Russian scientist Lysenko is a tragic example of what can happen when the science establishment and the government uncritically support Darwinism and oppose competing theories of origins. The enforcement of Darwin's ideology by government and organized science had disastrous effects on Russian agriculture, which led to major repercussions to the Russian economy, contributing to the Soviet famines that killed multimillions of people. Only when the tragedy became all too evident did the public and academia rise up to resist the Lysenko-Darwin orthodoxy and work to correct the harm that it caused in the Soviet Union. This incident is an important lesson for current governments that support neo-Darwinism and persecute Darwin dissenters.

Introduction

Karl Marx had a keen interest in Darwinism, as illustrated by the fact that his reading in natural science centered chiefly on material "dealing with change or development, such as biological evolution" (Joravsky, 1961, pp. 7–8). His interest was shared by many of his compatriots because of what they saw as a "parallel between Darwin's theory and political economy" and because Darwin's work was the foundation

for the view of human history that was the primary basis of communist theory (Joravsky, 1961, p. 12). Both Marx and Engels enthusiastically embraced Darwinism because it dealt a "mortal blow" not only to theology, but also to all similar teleology in natural science (Joravsky, 1970, p. 230). Many socialists, though, accepted evolution but opposed natural selection, especially when applied to humans (Weikart, 1999).

The first known Russian intellectual to attempt to blend Marxism and Darwinism was Peter Tkachev (Rogers, 1963). Soon after, Tkachev and other Russian intellectuals also attempted to achieve a seamless synthesis of the two major ideologies, Marxism and Darwinism, that were the foundational concepts in the Soviet Union (Rogers, 1963). In addition, both Lenin and Stalin were so heavily influenced by Darwinism that they also were forced to blend it with Marxism. The Soviet government accepted Darwinism early in its history to the degree that the

theory of biological evolution, with its relevance for the historical origin of man and its reputation for opposition to religious myths, became

* Jerry Bergman, Ph.D., Biology Department, Northwest State College,
jbergman@northweststate.edu

Accepted for publication April 5, 2008

a central part of the official Soviet worldview. In 1931 the first chair (kafedra) of “dialectics of nature and evolutionary theory” was established at the University of Leningrad with Isaak I. Prezent as head (Roll-Hansen, 2005, pp. 86–87).

Prezent also became an active and influential member of the Communist party. He worked diligently for much of his life to implement the Communist party’s political program, which emphasized creating a new science supporting the “class struggle” ideology and stressing the influence of environment on the development of life. For this reason, the “inheritance of acquired characteristics” theory was a critical tenet for Marxism. Prezent was a committed Darwinist and even organized a museum at Leningrad University to honor his hero Charles Darwin (Medvedev, 1969, p. 259). Prezent’s ideology was Darwinistic to the core, including Darwin’s acceptance of pangenesis and Lamarckian biology. Specifically, “Darwin held that environmental changes, acting either on the reproductive organs or on the body, were necessary to generate variation,” and Darwin “increasingly emphasized somatically-mediated variations at the expense of germinally-mediated variations” as he developed his evolution theory (Winther, 2000, pp. 425, 440). Mendelism, which concluded that genetic traits were “inherited rather than acquired, was contrary to the party’s political program” (Roll-Hansen, 2005, p. 87).

Prezent opposed scientists who argued that many mental abilities were inherited and stressed that Soviet science should always be practical and supportive of the proletariat, a statement that was interpreted to mean the environment was critically important, as Lamarckian biology stressed. Implied in Lamarckism was the belief that people could become more perfect if they put forth the effort, an idea that fit into the chief article of faith in the Soviet social-

ists’ paradise ideal of the innate perfectibility of humans (Marshall, 2001).

Darwinism was enthusiastically accepted in Russia to even a greater degree than in Western Europe (Rogers, 1973, p. 484). One reason Darwinism was so rapidly accepted in Russian culture was because, in contrast to Western Europe, where

Darwin’s theory encountered firmly established religious traditions among many of the educated elite [in Russia the appearance of Darwinism] ... coincided with the rise of a secular intelligentsia that venerated the natural sciences. The young radical thinkers of the 1860’s looked to the natural sciences for the ultimate solution of all problems. They enthusiastically received Darwin’s theory of evolution as the corollary in biology of Newton’s laws in physics. Biology had been the last refuge in the natural sciences of teleological and religious interpretations, and the young radicals saw in Darwin’s theory a splendid materialistic interpretation which explained the evolution of all organic life (Rogers, 1963, p. 457).

Darwinism profoundly influenced not only science but also all areas of thought in Russia, especially after the Russian Revolution (Vucinich, 1988).

Trofim D. Lysenko

Trofim D. Lysenko (1898–1976) was a Ukrainian orthodox Darwinist agronomist who achieved a high position in both the Soviet scientific establishment and the Soviet government. Lysenko “for nearly thirty years exercised a virtual monopoly over Soviet agricultural and biological sciences” (Krementsov, 2006, p. 386). Furthermore, he is recognized as

undoubtedly one of the most notorious scientists of the twentieth century. Already during his lifetime, his name—like those of Charles

Darwin, Karl Marx, and Gregor Mendel—was transformed into a catchall label. “Lysenkoism” came to denote ... the political suppression of Lysenko’s scientific opponents and the direct endorsement of his doctrine by political authorities (Krementsov, 2006, p. 386).

The fact that “Darwin’s theory of evolution was enthusiastically accepted in the 1860s by nearly all the Russian intelligentsia” set the stage for the acceptance of Lysenko’s pure Darwinism, uncontaminated by the findings of Gregor Mendel (1822–1884) (Rogers, 1963, p. 459). Lysenko concluded that Mendelism or “Western genetics” was “unscientific” because it was “metaphysical,” partly because Gregor Mendel was an Austrian Catholic Monk (Gajewski, 1990, p. 425). Lysenkoism was “the only truly scientific and materialistic theory of heredity constructed on the basis of dialectical materialism” (Gajewski, 1990, p. 425).

Lysenko was also “very close” to the leading Soviet Darwinist, A.I. Oparin—Lysenko’s *docha* (country home) on the outskirts of Moscow adjoined that of Oparin (Yockey, 2005, p. 153). Lysenko rose to prominence in the 1930s and had a major influence on Soviet agriculture in both the 1930s and 1940s and for decades thereafter (Hossfeld and Olsson, 2002). Lysenko was even supported by certain prominent Western biologists, such as “England’s most admired geneticist, J. B. S. Haldane” (Gardner, 1992, p. 244). Lysenko’s formal fall from grace did not occur until Khrushchev’s ousting in 1964 (Krementsov, 2006).

As documented by historians, the result of Lysenkoism was a disaster for both Soviet food production and the Soviet people (Soyfer, 1994; Gajewski, 1990). The disaster resulted from Lysenko’s acceptance of Darwinism, as taught by Darwin toward the end of his life—including natural selection, Lamarckism, the rejection of Mendelian genetics, and the rejection of the mutation theory of

Thomas Hunt Morgan (now called the “modern synthesis” or neo-Darwinism). Although Darwin accepted Lamarckism as one possible explanation for variation in the first edition of *The Origin*, he increasingly accepted Lamarckism, as is evident in later editions of *The Origin*. One reason he accepted Lamarckism is because Darwin believed that “Thomson’s views of the recent age of the world have been for some time one of my sorest troubles” and he needed a mechanism that allowed for rapid evolution (Browne, 2002, p. 315). As Browne noted,

The 100 million years that Thomson allowed was not nearly long enough for the exceedingly slow rates of change Darwin envisaged in nature. The fifth edition of the *Origin* bore witness to his discomfort. Rattled, he tried various ways to speed up evolution. He was aware that he was becoming more environmentalist, more Lamarckian ... the age of the earth was the single most intractable point leveled against his theory during his lifetime (Browne, 2002, p. 315).

Lysenkoism became the “official ideological doctrine in the Soviet Union,” approved by Stalin. It further became a “canonical text” that rejected “neo-Darwinism” as well as Mendelism. It also rejected the mutation research done by Thomas Hunt Morgan (Morganism) and August Weismann’s work on mice, which disproved Lamarckism. This “official ideological doctrine” stressed that Darwinism, as taught by Darwin himself, contradicted Western philosophy. Lysenkoists taught that neo-Darwinian biologists for this reason did everything within their power to overthrow the old Darwinism.

In the post-Darwinian period “the overwhelming majority of biologists”—far from further developing Darwin’s teaching—did all they could to debase Darwinism, to smother its scientific foundation.

The most glaring manifestation of such debasement of Darwinism is to be found in the teachings of Weismann, Mendel, and Morgan, the founders of modern ... “reactionary” genetics (report quoted in Rossianov, 1993, p. 737).

Another reason for the Soviet government’s embrace of Lysenko was that he accepted the macromutation views of DeVries, which taught that “heritable changes could occur by big, sudden leaps” (Rice, 2007, p. 252). The Soviets believed this view mirrored the goal of the Russian Revolution, which they believed propelled them in a single year from the Middle Ages into the modern world.

Prezent, who became Lysenko’s chief theorist in 1934, wrote that “creatively developed Darwinism,” or what was often called the “new biology,” must play a critical role in both “the struggle against metaphysics in questions of life” and in “reconstruction of biological science” (quoted in Medvedev, 1969, p. 46). Because Lysenkoism was in many ways an anti-creation movement, or at least an anti-theism movement—as was Marxism—the two ideologies fit together well. A major claim of Lysenko was that “one species of plant can undergo transformation into another” simply by altering the environment (Gajewski, 1990, p. 427).

Once Lysenko achieved power, his supporters, including many leading scientists and the Soviet government, ruthlessly suppressed his critics. Many lost their jobs, some suffered imprisonment, and a few, such as geneticists Israil Agol and Solomon Levit, microbiologist Georgy Nadson, and Russia’s leading Mendelian geneticist Nikolai A. Vavilov, died in prison or were even executed, often on false charges (e.g. Soyfer, 1994, p. 156; Medvedev, 1969, p. 258). Vavilov was sentenced to death for, among other things, belonging to a political rightist organization (Gould, 1983). Among other things, Vavilov was “guilty” of

interpreting his data “in a manner uncongenial with strictly Darwinian or Larmarkian views” (Gould, 1983, p. 137). Little tolerance existed for deviating from strict Darwinian interpretations. In fact, Vavilov’s views were not really anti-Darwinian, but non-Darwinian, in that he accepted evolution, but not by means of the mechanism that Darwin proposed.

So important was the Lysenko affair that it has “commanded the attention of biologists, historians, sociologists, philosophers, and Sovietologists” for decades after the movement fell (Krementsov, 2006, p. 386). The effect was so widespread that the term “Lysenkoism” has come to mean scientific oppression of minority science by the dominant science with the aid of the government.

Although Darwinism was essential to the Soviet worldview from the very beginning (Karl Marx, V.I. Lenin, Joseph Stalin, and many leading Soviet leaders were all committed Darwinists), Lamarckism-style Darwinism was never dominant in the Soviet Union until Lysenko achieved formal government support for orthodox Darwinism. Although repeating Lysenko’s experiments under more stringent conditions shed major doubts on his results, Lysenko and his followers believed so strongly in his ideology that they stubbornly refused to admit that they could be wrong (Gould, 1983). Some studies were even falsified or were based on faulty methodology (e.g. Gajewski, 1990, p. 427; Putrament, 1990, p. 443). Julian Huxley (1949, p. 10) concluded that Lysenko genuinely believed that he had scientifically proven the inheritance-of-acquired-traits theory and most of the Soviet scientific community unthinkingly went along with the program.

Darwin’s Support for Lamarckism

Many theories of evolution existed at the turn of the last century in Russia,

as well as in Europe and the Americas. Darwin openly advocated Lamarckism until he died. Lamarck supported, as did Darwin, the theory of the inheritance of acquired characteristics. This theory essentially taught that characteristics acquired during an organism's lifetime, such as strength, could be passed on to its progeny. The classic example is that giraffes must stretch their necks in order to reach the higher levels of trees, and this stretching modifies the animal's gametes as a result of the action of particles that Darwin called *gemmules*.

The modified *gemmules* were given off by various body structures and traveled to the eggs or the sperm, allowing changes that occurred in the animal's body to be passed on to its offspring (Bergman, 2006). Thus, those giraffe ancestors that stretched their necks to reach leaves would have offspring that had longer necks. This process eventually caused giraffes to acquire the long necks and legs as seen today.

Although Lysenko did publish a set of lectures about the effects of temperature on plant development, he had little formal training in biology. Lysenko was not a Marxist, and he never joined the Communist party; but he was introduced to evolutionary theory early in life, evidently by the society of Marxist biologists, and eagerly embraced Darwinism along with the Lamarckian ideas that Darwin espoused (Wells, 2006, p. 185). Lysenko attracted the attention of agricultural scientists partially because he was an eloquent and articulate spokesman for classical Darwinism. No doubt many of the Marxist biologists who had accepted Lamarckian ideas were a major source of support to Lysenko.

Widespread famine was occurring in the Soviet Union during that time, and Stalin's government was forced to respond to the problem. One response was to encourage Soviet scientists to find with a solution. Lysenko, probably more of an opportunist than an ideologue, jumped at the opportunity to apply his

Larmarkian ideas to the agriculture sector. After Lysenko had the full support of the government, persecution of dissidents soon followed.

Among the many supporters of Lysenko was the Soviet minister of agriculture, Jakov Jakovlev, whom argued that Mendelian genetics is incompatible with true Darwinism. Jakov demonized Mendelians as the "powers of darkness" and praised Lysenko for marching "under the banner of reconstruction of biological science on the basis of Darwinism raised to the level of Marxism" (Roll-Hansen, 2005, pp. 218–220). The level of Lysenko's support is illustrated by a 1948 address he gave to the Lenin Academy of Agricultural Science. In his talk, he reported that the central committee approved his program, and the response was described as "stormy applause" (Gould, 1983, p. 135).

When Mendelian biologists criticized Lysenko, his defense was not always rational or supported by scientific arguments. Lysenko often evaded their arguments or tried to claim that Mendelian genetics was wrong because it "was incompatible with true Darwinism" (Roll-Hansen, 2005, p. 219). In addition, in the Soviet Union "loyalty to 'Darwinism' had become a touchstone for scientific truth in genetics" (Roll-Hansen, 2005, p. 219). As Wells noted,

science in the Soviet Union was government-supported on a scale unprecedented in history. Driven by a desire to surpass the West, the Soviet Union devoted a larger share of its budget to science than did any other industrialized nation. Unfortunately, unprecedented government support also meant unprecedented government entanglement (Wells, 2006, p. 184).

Herein lies the problem: no geneticist "dared openly to reject Darwinism" in the Soviet Union (Roll-Hansen, 2005, p. 219). The penalty could be, and sometimes was, death or long terms of imprisonment in Siberia. At the least, bi-

ologists who refused to conform to the requirement that they teach Lysenkoism as fact had their teaching duties taken away (Gajewaki, 1990). The textbooks were "full of Lysenkoism," which professors were required to teach, and Mendelian genetics was disparaged. A problem is that many well-known geneticists, some even outside of communist countries, were sympathetic to Marxism, including J. B. S. Haldane and Herman J. Muller. Unfortunately, the Marxist sympathies of some biologists may have implied support for aspects of Lysenkoism that they did not support (Berg, 1990).

As the scientific evidence against Lamarckism accumulated, many scientists eventually realized that the theory was false and had to be rejected. When Mendel's work on garden peas was rediscovered, more and more scientists welded Mendelian genetics to Darwinism. Mendel's work, first published in 1866, was almost totally ignored until after 1900, and even at late as the 1930s some Western biologists remained skeptical of Mendel's views. Reasons for their skepticism include the fact that genes were unobserved abstractions until the middle 1900s and the fact that well-known exceptions to Mendel's laws existed.

Lysenkoism adversely affected not only the USSR but other nations as well, especially the Communist Bloc countries such as Poland and Czechoslovakia (Gajewaki, 1990; Orel, 1992). The introduction of Lysenkoism into these nations had disastrous effects. Utilization of techniques that interfered with efficient crop production not only negatively affected the Polish economy and agriculture production, but also the "national economy" in several Eastern Bloc countries (Gershenson, 1990, p. 447).

Lysenko's Contributions to Science

Lysenko did not rise to prominence without some valid scientific support

for his work. Liu (2004) argued that he did do some good scientific research and actually made some contributions to several fields of biology. Lysenko had to have some credibility in order to convert so many prominent scientists to his position. Examples Liu provides include research on the so-called cold treatment of plants that induces or accelerates flowering, a process called vernalization. Usually the “cold treatment” involved chilling moistened seeds for a few weeks. Roll-Hansen noted that the “continued use of this term is an indication of the international scientific impact that Lysenko’s work had” (2005, p. 113).

It was this technique that brought the ordinary farmer Lysenko to the attention of the Soviet authorities. Lysenko had collected much data on the effect of time and temperature variables on the vernalization process (Roll-Hansen, 2005, p. 116). Rice (2007) noted that if “Lysenko had stopped here, he might today be revered as the man who helped save Soviet agriculture, but he went further,” wrongly claiming that the chilling process actually changed the seeds in ways that were heritable (p. 252).

Contemporary Analogy

The Soviet Union has provided history with “the major example of how a science can be crippled by political dogma,” namely by the “abandonment of modern genetics for the crackpot Lamarckian views of plant-breeder Trofim D. Lysenko” (Gardner, 1992, p. 244). The Lysenko tragedy was primarily a result of government interference in science, imposing the dogmatism of certain Darwinist ideologues, especially on scientists. Otherwise, Mendelists likely would have prevailed—as it did in most of the rest of the world—because the proponents of Mendelism had the scientific evidence supporting their basic theory. The history of the Lysenko affair provides an important contemporary lesson when Darwinian fundamentalism

is dogmatically supported by many governments, including the United States. The fact is, throughout his entire career, Lysenko was a “Darwinist because most of his ideas are consistent with Darwin’s ideas” (Liu, 2004 p. 490). Gershenson (1990) wrote that after the basic theory of Lysenko was shown to be completely erroneous, it was necessary to learn the lesson of

how important it is, always and everywhere, to stand for scientific truth, and to what fatal results the violation of ethical standards in science may lead. Such violations were typical of Lysenko’s supporters, who used every means in their power to eliminate their scientific opponents in order to establish their own careers and to reach their personal goals. It is necessary to understand clearly how dangerous ignorance can be when it is in power. Beyond taking notice of all this, it is necessary to speak out about it, because even now Lysenkoism continues to exist, and no one should pretend that now all is well. (p. 447)

The same conclusion is true of the crusade against Darwin skeptics today. What happened in the Soviet Union with Lysenkoism is now happening in other countries as a result of state enforcement of neo-Darwinism. Under Lysenkoism “expressing one’s personal views was regarded as a declaration of hostility toward ... science” (Gajewski, 1990, p. 427). Today, under the control of Darwin fundamentalists, the same charges leveled against Lysenko’s critics are now leveled against creationists. As Gajewski (1990) observed, after he returned from Sweden in 1948 he

still continued for some time to lecture on genetics in Warsaw University.... Soon, however, the Lysenkoist version of genetics became official, and the Council of the Faculty of Biology asked me to abandon teaching the old, erroneous genetics and to introduce in its place the correct,

new one. My answer was that there is only one genetics—that which is based on well-established evidence. Then a compromise was offered: I should teach both the “new” and the “old” genetics. I retorted that this could not be done, inasmuch as they were contradictory. I was then temporarily forbidden to teach genetics at all. Professor Petruszewicz wanted to convert me, so took me for an excursion to the Soviet Union. As a special privilege, he organized for me an official visit to Lysenko in his office at the Institute of Agronomy in Moscow, so that I could learn at the very source of enlightenment and ... change my views. (p. 426)

Summary

Lysenko’s rapid rise to power and his plan to save Russia from famine by relying on the refuted theory of Lamarckianism is an important event in history. The suppression of dissidents and Lysenko’s ultimate failure and fall from grace (upon the eventual realization that many of his ideas were wrong) is the heart of the problem that results when Darwin ideologues attempt to muzzle those who disagree. The cost is harm to both science and society. The lesson of the Lysenko tragedy, that government-enforced orthodoxy in science can lead to blocking of scientific inquiry and progress, strongly parallels current events of government enforcement of orthodox neo-Darwinism resulting in suppression of dissidents (Joravsky, 1961, 1970). Looking back, scientists today have judged him as ignorant, yet he had the backing of many, if not most, scientists, as well as the governments of several nations (Putrament, 1990, p. 435).

Although dissidents today are not sent to gulags, the lesson of Lysenko applies to the contemporary suppression of those scientists and others who have concluded that neo-Darwinism does not fully explain the natural world. They are

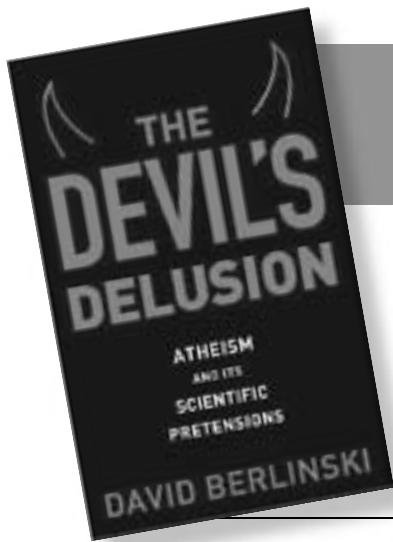
labeled ignorant, but their conclusions about abiogenesis, vestigial organs, junk DNA, ontogeny recapitulates phylogeny, and other areas have largely all been proven correct. Furthermore, Lamarckism is still inferred in science, such as when an evolutionist implies that a life-form developed a structure because it needed it in order to exploit its environment.

Acknowledgements

I wish to thank Jody Allen RN, Clifford Lillo, MA, James Owen, MA, George Howe, PhD, and John UpChurch for their comments on earlier drafts of this article.

References

- Bergman, J. 2006. Pangenesis as a source of new genetic information: the history of a now disproven theory. *Rivista di Biologia/Biology Forum* 99:425–444.
- Berg, R.L. 1990. In defense of Timofeff-Resovsky. *The Quarterly Review of Biology* 65:457–479.
- Browne, J. 2002. *Charles Darwin: The Power of Place*. Knopf, New York, NY.
- Gajewski, W. 1990. Lysenkoism in Poland. *The Quarterly Review of Biology* 65:423–434.
- Gardner, M. 1992. Notes of a fringe-watcher: the sad story of professor Haldane. *Skeptical Inquirer* 16:244–248.
- Gershenson, S.M. 1990. Difficult years in Soviet genetics. *The Quarterly Review of Biology* 65:447–456.
- Gould, S.J. 1983. *Hen's Teeth and Horse's Toes*. Norton, New York, NY.
- Hossfeld, U., and L. Olsson. 2002. From the modern synthesis to Lysenkoism, and back? *Science* 297:55–56.
- Huxley, J. 1949. *Soviet Genetics and World Science*. Chatto and Windus, London, UK.
- Joravsky, D. 1961. *Soviet Marxism and Natural Science*. Routledge and Kegan Paul, London, UK.
- Joravsky, D. 1970. *The Lysenko Affair*. Harvard University Press, Cambridge, MA.
- Krementsov, N. 2006. Review of the Lysenko effect. *Isis* 97:386–387.
- Liu, Yongsheng. 2004. Lysenko's contributions to biology and his tragedies. *Biology Forum* 97:483–498.
- Marshall, R. 2001. *Living Anatomy: Structure as the Mirror of Function*. Melbourne University Press, Melbourne, Australia.
- Medvedev, Z. 1969. *The Rise and Fall of T. D. Lysenko*. Columbia University Press, New York, NY.
- Orel, V. 1992. Jaroslav Krizenecky (1896–1964), tragic victim of Lysenkoism in Czechoslovakia. *The Quarterly Review of Biology* 67:487–494.
- Putrament, A. 1990. How I became a Lysenkoist. *The Quarterly Review of Biology* 65:435–445.
- Rice, S. 2007. *Encyclopedia of Evolution*. Facts on File, New York, NY.
- Rogers, J.A. 1963. The Russian populists' response to Darwin. *Slavic Review* 22:456–468.
- Rogers, J.A. 1973. The reception of Darwin's *Origin of Species* by Russian scientists. *Isis* 64:484–503.
- Roll-Hansen, N. 2005. *The Lysenko Effect: The Politics of Science*. Humanity Books, Amherst, NY.
- Rossianov, K.O. 1993. Joseph Stalin and the 'new' Soviet biology. *Isis* 84:728–745.
- Soyfer, V.N. 1994. *Lysenko and the Tragedy of Soviet Science*. Rutgers University Press, New Brunswick, NJ.
- Vucinich, A. 1988. *Darwin in Russian Thought*. University of California Press, Berkeley, CA.
- Wells, J. 2006. *The Politically Incorrect Guide to Darwinism and Intelligent Design*. Regnery Publishing, Washington, DC.
- Weikart, R. 1998. *Socialist Darwinism: Evolution in German Sociologists Thought from Marx to Bernstein*. International Scholars Publications, Lanham, MD.
- Winther, R. G. 2000. Darwin on variation and heredity. *Journal of the History of Biology* 33:425–455.
- Yockey, H. 2005. *Information Theory, Evolution, and the Origin of Life*. Cambridge University Press, New York, NY.



Book Review

The Devil's Delusion: Atheism and Its Scientific Pretensions

by David Berlinski

Random House Inc., New York, 256 pages, \$24.00.

I first ran across author Berlinski in 1996 as a casual reader of his article "The Deniable Darwin" in the journal *Commentary*. This article hit evolution at its foundations: Darwinism is not only lacking in evidence but devoid of explanatory power or method of operation. A theory that lacks these features is therefore without use. Richard Dawkins leaped to Darwinism's defense by using the only intellectual card in his deck: Berlinski is just another dumb creationist. Berlinski has steadfastly maintained he has no creationist beliefs and this frustrates evolutionists, because they cannot understand how well-educated non-creationists can disbelieve in evolution.

Forward twelve years later Berlinski is still frustrating Darwinists, this time taking a swing directly at modern atheists who agree with Dawkins that Darwin made it possible to be an intellectually fulfilled atheist. They are not satisfied to find room in life for both religion and science. Rather, as skeptics on an anti-religious campaign, they openly proclaim that one view is wrong and that religious view must be eliminated.

Theists frequently assert that one cannot have full moral knowledge or be fully moral without knowing and obeying a divine ethical source, but modern evolutionists believe otherwise. Sam Harris, one of Berlinski's subjects, proudly reveals the violence in religion's

past to argue that we do not need religious moral underpinnings since their result is poor moral outcomes. Berlinski's retort to this is artful and here he is most brutal. Nazis and other totalitarians, Hitler included, may have believed in a higher power or occasionally mouthed pieties, but what they did not believe is that God, certainly not the God of Christianity, was watching them or demanding they act different than their violent predispositions.

Who at this point cannot agree with Berlinski? Do not the ACLU and other strongly anti-religious organizations operate under this exact principle, that no God shall control our behavior? Dawkins, in *The God Delusion* (1996), argues that we would not fall into ruin if we lost our acceptance of divine moral commands. Again, Berlinski's reply is artful and worth quoting.

"Why *should* people remain good when unobserved and unpoliced by God? Do people remain good when unpoliced by the police? If Dawkins believes that they do, he must explain the existence of the criminal law, and if he believes that they do not, then he must explain why *moral* enforcement is not needed at the place where law enforcement ends" (p. 34).

In essence, people do not behave unless coerced to do so either by criminal law or by moral law that compels people

to behave when criminal law is absent. Dawkins' retort to this is that people who find they do ill when criminal law or moral laws are absent will find their behavior reflects poorly on them. However, this retort is shallow and unpersuasive. Exactly why should people not misbehave if no criminal or moral law supervenes on their behavior even if it reflects badly on them? What do they gain by obeying a moral law that does not exist when criminal law is absent? Under what moral pretenses would we consider them immoral if they acted so?

Berlinski is a brilliant wordsmith but his verbiage most always gets in the way of the point he tries to make. For instance, after opening this book and slowly warming up to the challenge of absorbing his brilliance, we are exposed to the fact that "Until just yesterday, it was fashionable for scientists carefully to cast their bread upon various ecclesiastical waters" (p. 1). Come again? One has to digest that nugget of information before going on to the main course and even at that it leaves a lump in one's throat.

Later, Berlinski deflects Dawkins' assertion that one cannot explain the existence of something that is improbable postulating another entity that is more improbable. Berlinski deals with this by nicely asking why an improbable universe demands an even more improbable God, a question Dawkins does not answer, and then suggesting that because

something is improbable does not mean it cannot exist. It is unlikely a rich man can get to heaven, the Bible informs us, but most likely there are rich men in heaven. Likewise, an improbable god might still exist to create an improbable universe. Improbable events happen all the time and who is Dawkins to tell us different? My summary of Berlinski's brilliant master stroke is the meat of this retort, but one must wade through murky waters to retrieve it in this book.

Religious euphemisms come and go frequently in this book and one can be forgiven for asking what religious beliefs he has, but I find little to suggest that Berlinski has taken the leap from a Darwinian doubter to theism or even

Christianity. His chapter on miracles criticizes Christopher Hitchens' attempt to relegate miracles to the intellectual dust bin, only to explain that evolutionary theory has little facts and much ideology. Berlinski abuses Eugene Koonin who expresses what we already know: There is a "big bang" of biological life in the fossils and what natural mechanism would explain these nobody knows (except God, maybe). Reaction to Koonin's article urged him to keep his thoughts to himself for fear that creationists may latch on to his words as evidence of their beliefs. It would seem a miracle is exactly what we witness in the fossils and Berlinski doesn't openly advocate a Christian theistic interpretation of them.

The Devil's Delusion is a brilliant piece of writing which attacks many of the core modern tenets of atheism which, of course, attack many of the core beliefs of theism. What Berlinski does is show us that these beliefs have no power to strike a mortal blow against theism and, after this intellectual battle, theist beliefs are left standing.

References

- Berlinski, David. 1996. The deniable Darwin. *Commentary* 101(6):19-29.
Dawkins, Richard. 2006. *The God Delusion*. Bantam Books, New York.

Jeffrey Stueber
jstueber@charter.net



Book Review

Understanding Intelligent Design

by William A. Dembski
and Sean McDowell

Harvest House Publishers,
Eugene, OR, 2008, 233 pages,
\$14.00.

The authors of *Understanding Intelligent Design* are spearheading another scientific revolution. They say that "Darwinism has run its course" (p. 172), and the ideology of "Darwinism is dead in the water" (p. 63).

"Design is now revolutionizing the way we see the world, much as Darwinism did more than a century ago" (p. 172). However, "Scientific revolutions are nasty affairs. They impact everything from fundamental scientific research to science education. If you do not like the sight of blood, better to stay away" (p. 176). We are called "not to please

the world" but rather "to proclaim the truth to the world," namely, that "ID (Intelligent Design) is the cutting edge in science" (p. 178). The authors very briefly mention their belief that the universe was brought into existence 13.8 billion years ago at the time of the "big bang" and that this event points to a designer.

Coverage in this book includes: Dedication to Ben Stein, Forward by Josh McDowell (the father of author Sean McDowell), ID to the rescue, story from the rocks, origin of life, challenge to join the revolution, websites, books,

DVDs, "Ten questions to ask your science teacher about design," "Dealing with difficult critics of ID," "Evolutionary logic: A parody of Darwinian educational philosophy," nine pages of notes with chapter references, and an 11-page index.

Regardless of one's understanding of the age issue, this book can be useful for gaining a current basic conception of ID with its antievolutionary impetus.

Wayne Frair, Ph.D.
1131 Fellowship Road
Basking Ridge NJ 07920

Notes from the Panorama of Science

Two Mystery Mountains

Introduction

The study of the earth, its structure and history, is facilitated by those areas where mountain building or erosion has exposed the rocky framework of the earth. The Rocky Mountains of North America display a wide range of geology. In Colorado, the granite core is often exposed. Farther north, especially in the Yellowstone Region, volcanics have shaped the landscape. Breccia and conglomerate composed of basalt, andesite or other volcanic products can be seen. Still farther north (Glacier National Park, for instance), Precambrian sediments predominate.

Two mountains in southwestern Montana contain mysteries concerning provenance and time. Lone Mountain, elevation 11,186 ft., the backdrop for Big Sky Resort in the Madison Range, contains fossil clams of the genus *Inoceramus* in volcanic ash near the top. Since the clams appear to have been transported, the question concerning their provenance arises. Sphinx Mountain, elevation 10,869 ft., also located in the Madison Range but south of Lone Mountain, is composed of conglomerate that is in reverse stratigraphic order. The lack of a near source for the conglomerate, the size of the rock, and the presence of large cross-beds, suggest rapid movements of large quantities of water. Both of these mountains have features of water volume and speed that comport with the global flood described in Scripture.

Lone Mountain

Throughout the greater Yellowstone area, volcanic ash is often seen and



Figure 1. Lone Mountain in Southwestern Montana. Big Sky Resort is located at the base of the mountain. The mountain is composed of volcanic ash.

occasional beds of basalt show up. It was with a study of volcanic ash that a real surprise occurred. Three of us (Dennis Bokovoy, John Hergenrather, and I) were doing geological research and reconnaissance in the Yellowstone area. We had heard of a mountain (Lone Mountain) southwest of Bozeman, Montana that was composed mostly of volcanic ash (see maps, Bolm, 1969). It rises to a height of 11,186 feet just south

of the Spanish Peaks. A number of years ago, the area around Lone Mountain was developed into a major resort (Big Sky). Lone Mountain is now a major ski area. An impressive hotel is located at the base of the mountain, and many cabins and dwellings are scattered around the valley (Figure 1).

One unusual question about Lone Mountain (among others, as we discovered later) is the source of the volcanic

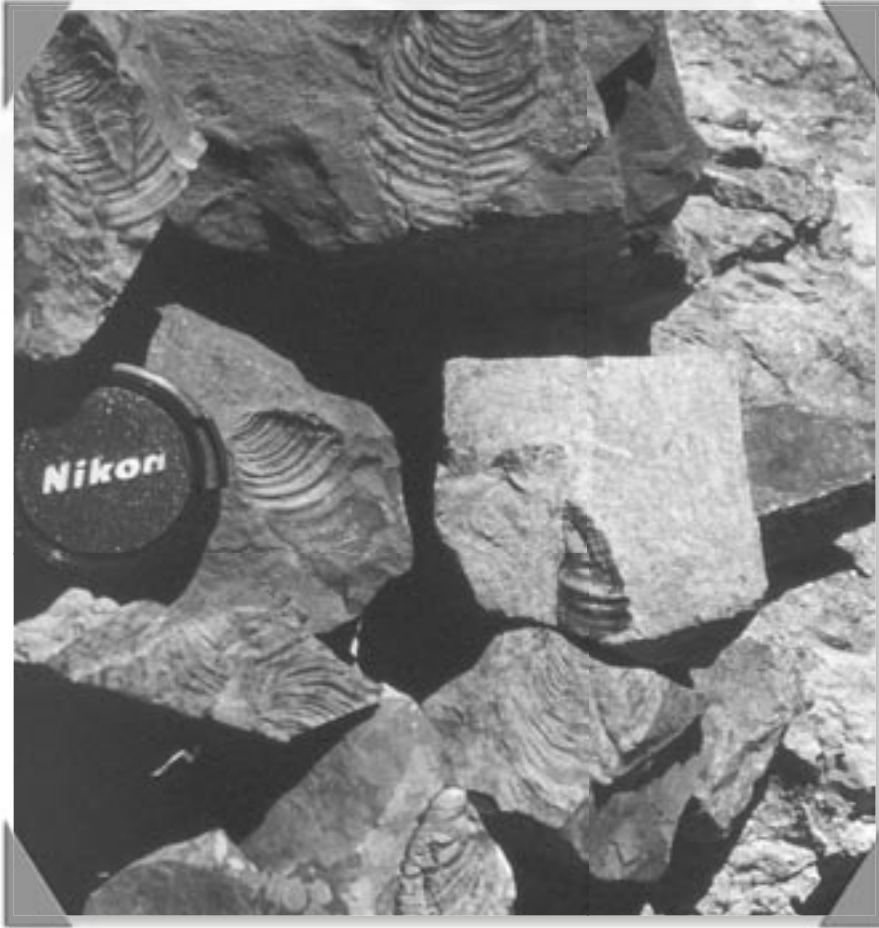


Figure 2. Marine clams, Genus *Inoceramus*, were found high on the shoulders of Lone Mountain.

ash. Elsewhere in the Yellowstone area, ash appears either as thin layers associated with the levels of petrified trees or beds of several feet thickness located between beds of breccia or basalt. Here several thousand feet of ash was piled up bed upon bed, most of it horizontal or nearly so. Furthermore, it is considered to be from air-fall. Where did this ash come from? No obvious volcanic centers exist in the area. The ash seems to be limited mostly to Lone Mountain. Was Lone Mountain itself the source of the ash? That has to be considered even though the horizontal nature of the ash layers seems to speak against that interpretation. Geologists suggest that Lone Mountain is a volcano that did not erupt;

the magma did not reach the surface. It is thought that if the mountain were sliced in half, a Christmas tree laccolith would be visible.

On this occasion the four of us hiked up the mountain part way to examine the outcrops. We also took the ski lift to a higher elevation and proceeded to hike toward the top of the mountain. At the time we were there, major construction was occurring to extend the ski lift to the top of the mountain. Near the top we paused to examine an area of freshly bulldozed rock of indurated ash. A few minutes later I said to Dennis, "This looks like some organic matter." He looked at the rock I was holding that contained some markings that faintly

looked like plant fossils. "That's not clear enough to impress anyone," was his reply after a quick look. I threw the rock away. In general the rocks looked very sterile; likely no fossils.

Only a few minutes later, I was startled to find myself gazing at what was clearly a fossil. It was the corrugated impression of a clam shell. I took it over to Dennis and made some vague remark about these poor fossil evidences! He was speechless for a moment. "Wow! There isn't any question about that one." With that discovery there began a frantic search for more. Quickly more were discovered (Figure 2). These were all located in broken blocks of rock resulting from the bulldozing. Before long we were able to locate the source and photograph fossil clams located directly in the undisturbed rock (genus *Inoceramus*). Some of the clams, which are bivalves, still had both valves connected together. This would seem to indicate that they had not been transported great distances.

These fossils were isolated, not in layers or beds. There was very little other organic matter present. Other than the clam fossils, only a few fragments of plants were found; the rock was clean, dark, hard volcanic ash. What was the explanation for these sea animal remains located high up in the ash layers on this mountain? This was truly unexpected and puzzling. Elsewhere, farther south in the area of the petrified forests of Yellowstone, only plant fossils have been found. No animals are associated with the petrified trees, leaves, and plant debris. Here the situation was somewhat opposite. Here were marine animals, whereas elsewhere there was no evidence of marine environments. Both situations suggest sorting by water. For days the four of us pondered the riddle concerning these fossils. Where was the source and what conditions brought them to this location?

Just across the valley entirely different conditions existed. Instead of volcanism,



Figure 3. Sphinx Mountain, composed entirely of conglomerate, is located in the Madison Range in southwestern Montana.

normal stratigraphy was seen. Mesozoic and Paleozoic beds lapped up against the Precambrian core of the Spanish Peaks (Lee Metcalf Wilderness Area) (Spencer and Kozak, 1973). Obviously the Mesozoic and Paleozoic have been removed from the top of these mountains when the mountains rose. Could it be possible that these marine animals were removed from some marine habitat that originally existed where the Spanish Peaks now stand? If that were the case, why were not other animals or plants also moved and why were there no sediments other than volcanic ash? The transportation and sorting by water would seem to be required.

To the west, east, and south, suitable sources of either the ash or fossils seem to be absent except for the volcanic

peaks in the western part of Yellowstone Park. However, it is difficult to envision ash or marine animals coming from that distance and accumulating in one isolated mountain. Were the clams not transported but buried where they were living? That seems unlikely also because there is little evidence in the volcanic ash of the environment that clams need.

Another factor to consider is that these fossils were at a high elevation. Normally, the source from which these animals were transported would need to be at even a higher elevation. The only heights higher for many miles around would have been the Spanish Peaks.

These are several unanswered questions connected with this unusual situation. More detailed study for the whole

area as well as the actual fossil site will be needed before the questions can be answered with any degree of confidence. However, one scenario that other scientists are unlikely to consider is that of a major flood of water. One could visualize the entire area being covered with water. It would not take much water movement to lift these concave/convex clam shells, transport them in the water, and deposit them onto the layers of ash. This would result in isolated clams deposited in the ash largely free from any debris associated with them in their original environment.

Study of the Yellowstone petrified trees suggests drift in water. The Bible tells of a major inundation by water. This Flood could be the explanation for the puzzling presence of clams high on a mountain of volcanic ash.

Sphinx Mountain

Northwest of Yellowstone National Park is the Madison Range. In 1959 a major earthquake shook these mountains. Part of a mountain plunged into the Madison River Canyon. Twenty-eight campers were buried by this giant slide and by falling rocks and trees in adjacent areas.

These mountains are unlike the volcanic mountains and terrain just to the east. They show the normal stratigraphy of the Rocky Mountains in this part of Montana—Mesozoic and Paleozoic flanking Precambrian cores of the mountain peaks. A few miles north of the Madison River Canyon and the earthquake area, an entirely different mountain dominates the skyline (Figure 3). However, it is visible only along a short stretch of U.S. Highway 287 in the Madison River Valley.

Sphinx Mountain is unusual because the whole mountain is composed of conglomerate (Figure 4). Lone Mountain is volcanic ash, but Sphinx Mountain is not volcanic and has no or little ash. Directly adjacent to it is The Helmet, a lower pinnacle that also consists of



Figure 4. Sphinx Mountain conglomerate. Some of it (as seen in this photo) is angular and could be called breccia.

conglomerate (Figure 5). These two represent the limit of the conglomerate in this area. All the rest of the adjacent mountains are stratigraphically typical of the Madison Range.

Sphinx Mountain rises to a height of 10,860 Feet. With conglomerate all the way to the top, the source of the conglomerate obviously must be higher. None of the surrounding mountains are higher. The conglomerate obviously came from elsewhere. Where could it have come from? The Gravelly Mountain Range to the west has had some of the Phanerozoic removed. It is the opinion of some students of Sphinx Mountain that the conglomerate came from these mountains on the west. Since these mountains now are lower

than Sphinx Mountain, we need to consider that they were either higher in the past when erosion deposited the conglomerate that produced Sphinx Mountain or that Sphinx Mountain was lower. A puzzle is why the conglomerate is limited to this one mountain and adjacent pinnacle. If the conglomerate came from the west, why would it not be scattered broadly over the mountains to the east?

The conglomerate of Sphinx Mountain is in reverse stratigraphic order (Decelles et al., 1987)! The conglomerate that consists of Paleozoic blocks and cobbles appears at the top, whereas the conglomerate lower on the mountain is composed of Mesozoic rocks. This is reverse to the order for the Paleozoic and

Mesozoic beds found throughout the West. Evidently, if the Gravelly Mountains are the source of the conglomerate, the erosion that brought the rock over to Sphinx Mountain must have occurred after most of the stratigraphy of the Gravelly Mountains was in place. Thus the currents first removed the top Mesozoic sediments off the Gravelly Mountains. These were dropped as Sphinx Mountain was building. Then as erosion cut down, water reached the Paleozoic beds and moved and dropped rock on top of the Mesozoic.

This may be too simple a scenario. Isolated deposits of conglomerate (some thousands of feet thick) are found widely scattered east of the Rocky Mountains. Most of these deposits are quartzite, but some are mostly limestone pebbles, cobbles, and boulders similar to those of Sphinx Mountain. Some of the boulders are a meter or more long. Because local sources are usually absent, the suggestion appears reasonable that originally a broad blanket of this conglomerate extended over portions of the Rocky Mountains. Mountain uplift and erosion has removed most of it (Oard et al., 2005).

Currents able to move conglomerate several miles across the Madison River Valley or even farther from the west obviously must have been very strong. There is evidence of this violent water movement. Some of the conglomerate on Sphinx Mountain is cross-bedded.

Although some of the questions such as why the extent of the conglomerate is limited and how it could have been deposited at so high an elevation may not be fully answered, certain conclusions are obvious.

1. The erosion off the top of the Gravelly Mountains was produced by a large amount of fast-moving water. The conglomerate is composed of rocks of fist size or larger. The movement of such coarse-grained sediment requires fast-moving water that is



Figure 5. The Helmet adjacent to Sphinx Mountain is also composed of conglomerate. It is connected to Sphinx Mountain by a high saddle and originally probably was continuous with Sphinx Mountain.

not limited to mountain streams. The distance of movement was 20 or more miles if the conglomerate came from the Gravelly Mountains.

2. The erosion cut down through Mesozoic into Paleozoic beds rapidly. If the erosion had been punctuated by hiatuses of any considerable length of time, there would be periodic changes in sediment size or weathering surfaces as the sediments accumulated. These we did not see.

We did see that the conglomerate consisted mostly of harder rock; most of the softer rocks did not survive the transport across the miles or were deposited elsewhere.

Two mystery mountains, Lone Mountain and Sphinx Mountain, are evidences among many others that water beyond that seen on the continent today sculptured the landscape. For Lone Mountain, water was responsible for moving clams several miles and laying them down on volcanic

ash. Sphinx Mountain also displays evidences of large amounts of water moving rapidly.

Many of the major mountain ranges of the West have their top sediments removed, laying bare the lower Paleozoic beds and Precambrian granite cores. Often coarse conglomerates are piled up along the flanks of these ranges. Such evidences, along with those of Lone Mountain and Sphinx Mountain imply major erosion by water in the past. Most of this activity appears to have occurred at the same time (Upper Mesozoic) over much of the country. It is difficult to deny that a major catastrophe by water was involved. The Biblical worldwide Flood qualifies as such an event.

References

- Bolm, J.G. 1969. Geology of Lone Mountain area, Southwestern Montana. M.S. Thesis, University of Idaho, Moscow, ID. p. 2.
- DeCelles, P.G., R.B. Tolson, S.A. Graham, G.A. Smith, R.V. Ingersoll, J. White, C.J. Schmidt, R. Rice, I. Moxon, L. Lemke, J.W. Handschy, M.F. Follo, D.P. Edwards, W. Cavazza, M. Caldwell, and E. Bargar. 1987. Laramide thrust generated alluvial-fan sedimentation, Sphinx Conglomerate, Southwestern Montana. *American Association of Petroleum Geologists Bulletin* 71(2):135–155.
- Oard, M.J., J. Hergenrather, and P. Klevberg. 2005. Flood transported quartzite — east of the Rocky Mountains. *Journal of Creation* 19(3):76–90.
- Spencer, R.W., and S.J. Kozak. 1973. *Geology of the Spanish Peaks area of the Madison Mountains, Montana*. Montana Bureau of Mines and Geology Open File Report 55.

Harold G. Coffin
427 Switch Connector Rd. SW
Calhoun, GA 30701
hgcof@bellsouth.net

Normal Insect Flight with Abnormal Wings

Erebomia exalloptera, a fly with one wing significantly larger than the other, has been discovered in the Amazon River region. Its amazing feat is that it flies very well, but just how it is able to fly no one yet knows (Anonymous, 2003, p. 14).

This peculiar species of fly shows that the Creator is extremely versatile, being able to make flies that can move correctly even though their wings are abnormal. More information will be

needed to discover what advantage such disproportionate wing size may confer on this species. It would be interesting to study the wing conditions of other fly species that are taxonomically close to *E. exalloptera* to see if its wings derived from the genetic potential latent in that group (Brown, 1996).

Acknowledgments

I thank George Howe for editorial assistance and computer typing.

References

- Anonymous. 2004. The fly that shouldn't be able to. *New Scientist* 180:14.
- Brown, C. 1996. Devonian fish and amphibians and the gene-theme model. *Creation Research Society Quarterly* 33:13–15.

Colin Brown
61 Derby Road
Golborne, Warrington
WA3-3LE, England, U.K.



Book Review

Heaven Without Her

by Kitty Foth-Regner

Thomas Nelson, Nashville,
2008, 272 pages, \$15.00.

This book chronicles the author's personal journey from agnosticism to Biblical Christianity. During early professional years, Kitty was a successful contract writer and novelist. Her free-spirited, feminist lifestyle was the envy of many as she resisted occasional nudges from those who offered a testimony of faith. However, her mother's fatal illness upended Kitty's world. Mom was a strong believer and expressed regret in entering heaven without her daughter. Kitty made a promise to her mom: "I'll see you there" (p. 2). Thus began a search for assurance about the next life. Kitty researched holy books, cults, and philosophies. Over time, the Holy Spirit

led her to realize the beauty and truth of Scripture. She was further influenced by apologists such as Lee Strobel, R. C. Sproul, and the classic works of C. S. Lewis. Also, as is true for many in our CRS family, creation studies helped Kitty absorb the gospel message.

In Darwin's day, it was the loss of ten-year-old daughter Annie that quenched Darwin's immature faith. He could not reconcile a loving God with the death of a favored child. Such pain remains a stumbling block for many today. For author Kitty, sorrow for her mom came to be understood in terms of the Fall of mankind, which has placed a dark shadow over the earth. Only those with an acquaintance of the Curse in Genesis 3 can correctly process the pain of

this present world. And only those with such understanding have real hope for a redeemed future that is free from the Curse.

In her new life as a believer, Kitty has gone on with a shining testimony, including the rich testimony of this book. She feels greatly indebted to many creationist writers who helped her understand life, and their books are listed with positive comments. This book has some outstanding chapters with titles such as "The Heavens Declare: How Could I Have Missed All This?" Thanks, Kitty, for a book that encourages the ministry of the Creation Research Society.

Don B. DeYoung
DBDeYoung@Grace.edu

Book Review



The Committee

by Clay Cornelius

Tate Publishing & Enterprises,
Mustang, OK, \$13.00.

The Committee left me with a sense of amazement. I don't remember ever seeing an approach to writing this unique. It is a story of Clay's fight with alcohol, drugs and lust, first by recounting the reality of what was happening in his life, and then by playing a recap of what was going on in his life represented by members of a committee in his mind, negotiating for control.

The initial members of his committee are allegorized as Life, Happiness, Pleasure, Logic, and Conscience. Pleasure is chairman of the board and dictates all affairs. By the time he is 22 years old, Competition, Finance, Society and Health are added to the committee. Pleasure, with support of Society and Logic, rules the committee and supports anything that will cause him to feel good.

Clay talks about his entry into the world of alcohol and drug use under the influence of Pleasure. To the outside world, Clay's life looks stable, but inside a battle rages to maintain the very structure of his being. Committee meetings are infrequent, and Conscience is the first to report that something is wrong. The other members of the committee do not think much of Conscience's comments at first, but after a number of events get Clay's attention, the committee begins to question the direction

his life is taking. "Something is wrong, and I couldn't deny it. Pieces of my life that were really important to me were beginning to slowly disintegrate."

Society convinces the committee over the objection of Finance that it is necessary to trade in his Plymouth Colt Vista (not so cool) for a really hip Ford Expedition. But while under the influence, he wrecks the vehicle when he attempts to avoid hitting a deer. Life, who has quietly remained in the background of the committee, begins to agree with Conscience that something must be done, and suggests that God might be the answer.

Pleasure, Logic, and Society are not too keen on the idea, and Finance protests, but takes on the challenge Life suggests to contribute to the church. This does not make sense to Logic, but he grudgingly goes along with it.

The partying, drug and alcohol use, and a live-in girlfriend are all suggested by Pleasure and lead to a number of near catastrophes. An overdose and the loss of his girlfriend cause Happiness to be at a new low, and a new urgency comes over the committee.

During one of these meetings, Logic introduces a new member, named Greater Good. Under his influence, the committee begins to consider the consequences of this lifestyle over the

long term. But while living a double lifestyle, going to church but partying on the weekends, he is struggling for self-control.

During that time, Life enters a critical debate with Logic.

"Logic, do you think that all of this is chance? This life, this earth, and this universe?"

"Yes I do," replied Logic, "and I have really seen no evidence to the contrary."

"And 'chaos' makes sense to you as a human origin?" asked Life.

"More sense than 'magic'," answered Logic.

"Do you remember our first car?" asked Life, apparently changing the subject.

"Uh, yeah," replied Logic, a little thrown off.

"What a beautiful sight that faded old Reliant was to seventeen-year-old eyes," reminisced Life. "Where is that car today?"

"What on earth...?" asked Logic.

"Humor me," said Life. "Where is that car now?"

"At Dad's house, I guess," answered Logic, still hesitant. "Sitting in the field, rusting. Why do you ask?"

"It is certainly rusting; decaying away," Life agreed. "In fact, the same is true of everything on this earth; it will

all eventually decay. Eventually there will be nothing left in that field, as the car disintegrates completely. Its natural tendency is to fall apart.”

“So what?” said Logic.

“So why do you believe that out of chaos, in a universe with constant laws and a tendency toward disorder, the complete opposite would happen?” asked Life.

“What do you mean?” asked Logic.

“How could this universe just appear out of thin air, in contradiction to everything we know about nature’s laws?” inquires Life. “This earth is a beautiful symmetry of life, and you are telling me that chaos put it together? That’s like telling me that the car in

the field could ‘build itself’ under the right circumstances of chance. But every human being knows the only way the car gets built is with the addition of intelligent life into the equation. And the only thing that could keep the car from rusting is continued maintenance, again from intelligent life. How could you believe otherwise?”

Life makes further arguments concerning the existence of a creator, and though Logic doesn’t buy into it at first, circumstances surrounding the disasters caused by the party scene cause the committee to consider the advantages of attending church.

Eventually, Alcohol, Pot, and Lust come out from behind the shadows and

attempt a hostile takeover of the committee, dethroning Pleasure. Life is beaten to a pulp, Happiness is slapped up, Society is told to forget his new church friends, Finance is told to stop giving to the church, Competition is limited to video games, and Conscience and Greater Good are told to shut up. Logic is told: No more God research.

The Committee illustrates the internal battle that many people go through in their minds struggling with the question of their existence, and the treatment of the basic questions surrounding the origin of life and its meaning reveals the importance of finding answers.

Douglas B. Sharp
Sharpdb@rae.org



Book Review

Hallmarks of Design

by Stuart Burgess

Day One Publications,
Leominster, Herefordshire,
England, 232 pages, \$13.00.

Author Burgess is a design engineer at Bristol University, England. This is an attractive, clearly written book with many figures. Chapters describe the design of the human knee, bird flight, bird song, and the peacock’s tail. This latter discussion is valuable. The “barbules segments on adjacent barbs coordinate perfectly with each other to produce the eye pattern” (p. 83). Burgess goes on to show the complex mathematical curves within the peacock feather including cardioids and ellipsoids.

Thorough discussion shows the many differences between mankind and animals. Dozens of unique human distinctions are listed. There is interesting speculation, including the horse as being directly created and designed for the purpose of human transport. We are rightly reminded that evolutionary progress, if actual, should have left multiple layers of fossils which are poorly designed, imperfect, misfits. Instead, however, the fossil record shows an exquisite history

of incredible design right from the start. Check the website DiscoveryofDesign.com for more discussion on this topic. The book includes an index and a list of British creation organizations. The Creation Research Society is not mentioned anywhere, although there are many Society members throughout the British Isles.

Don DeYoung
DBDeYoung@Grace.edu

Instructions to Authors

Submission

Submit an original plus two copies of each manuscript to the editor of the *Creation Research Society Quarterly* (see the inside front cover for address). Concurrent submission of an electronic version (Word, WordPerfect, or Rich Text Format) of the manuscript text and graphics is also encouraged. The manuscript and graphics will not be returned to authors unless a stamped, self-addressed envelope accompanies submission. Manuscripts containing more than 30 pages are discouraged. An author who determines that the topic cannot be adequately covered within this number of pages is encouraged to submit separate papers that can be serialized.

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

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

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

Appearance

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

Submitted manuscripts should have the following organizational format:

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

2. Abstract page. This is page 1 of the manuscript, and should contain the article title at the top, followed by the abstract for the article. Abstracts should be between 75 and 200 words in length and present an overview of the material discussed in the article, including all major conclusions. Use of abbreviations and references in the abstract should be avoided. This page should also contain at least five key words appropriate for identifying this article via a computer search.

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

4. Body of the text. Two types of headings are typically used by the CRSQ. A major heading consists of a large font bold print that is centered in column, and is used for each major change of focus or topic. A minor heading consists of a regular font bold print that is flush to the left margin, and is used following a major heading and helps to organize points within each major topic. Do not split words with hyphens, or use all capital letters for any words. Also, do not use bold type, except for headings (italics can be occasionally used to draw distinction to specific words). Italics should not be used for foreign words in common usage, e.g., "et al.", "ibid.", "ca." and "ad infinitum." Previously published literature should be cited using the author's last name(s) and the year of publication (ex. Smith, 2003; Smith and Jones, 2003). If the citation has more than two authors, only the first author's name should appear (ex. Smith et al., 2003). Contributing authors should examine

this issue of the *CRSQ* or consult the Society's web site for specific examples as well as a more detailed explanation of manuscript preparation. Frequently-used terms can be abbreviated by placing abbreviations in parentheses following the first usage of the term in the text, for example, polyacrylamide gel electrophoresis (PAGE) or catastrophic plate tectonics (CPT). Only the abbreviation need be used afterward. If numerous abbreviations are used, authors should consider providing a list of abbreviations. Also, because of the variable usage of the terms "microevolution" and "macroevolution," authors should clearly define how they are specifically using these terms. Use of the term "creationism" should be avoided. All figures and tables should be cited in the body of the text, and be numbered in the sequential order that they appear in the text (figures and tables are numbered separately with Arabic and Roman numerals, respectively).

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

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

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

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

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

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

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

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

Special Sections

Letters to the Editor:

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

Editor's Forum:

Occasionally, the editor will invite individuals to submit differing opinions on specific topics relevant to the *Quarterly*. Each author will have opportunity to present a position paper (1500 words), and one response (750 words) to the differing position paper. In all matters, the editor will have final and complete editorial control. Topics for these forums will be solely at the editor's discretion, but suggestions of topics are welcome.

Book Reviews:

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

Creation Research Society

Membership/Subscription Application and Renewal Form

The membership/subscription categories are defined below:

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

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

Please complete the lower portion of this form and mail it with payment to CRS Membership Secretary, P.O. Box 8263, St. Joseph, MO 64508-8263, or fax for credit card payment to (816) 279-2312. Applications may also be completed online at creationresearch.org.



This is a ☐ new ☐ renewal application for the subscription year beginning Summer ☐ 2008 ☐ _____. (Please type or print legibly.)

Name _____ Address _____

City _____ State _____ Postal/Zip code _____ Country _____

Phone (optional) _____ Email _____

Degree _____ Field _____

Year granted _____ Institution _____

Presently associated with _____

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

For foreign orders, including Canadian, payment must be made in U.S. dollars by a check drawn on a U.S. bank, international money order, or credit card. *Please do not send cash.*

Indicate applicable category 	Indicate payment 			
	Paper**			Paperless†
☐ Voting ☐ Sustaining	USA	Canada Mexico	Other countries	
☐ Regular [per year]	☐ \$35	☐ \$53	☐ \$70	☐ \$31
☐ Senior [per year]	☐ \$30	☐ \$48	☐ \$65	☐ \$26
☐ Life member	☐ \$500	☐ \$500	☐ \$500	☐ \$500
☐ Student* [one year; multi-year not permitted]	☐ \$30	☐ \$48	☐ \$65	☐ \$26
☐ Subscriber [per year]	☐ \$38	☐ \$56	☐ \$73	☐ \$34
* Student members are required to complete the bottom portion of this form. ** Rates for the paper option include postage for First Class Mail International (FCMI), which is equivalent to airmail. Surface mail delivery is no longer available.				

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

Member/Subscriber	\$_____ per year
(multi-year not permitted for students)	x _____ years
SUBTOTAL	\$_____
Optional contribution	+ \$_____
Life membership	+ \$_____
TOTAL	\$_____
☐ Visa ☐ MasterCard ☐ Discover ☐ American Express ☐ Check/money order	
Card number	_____
Expiration date (mo/yr)	_____
Phone number (_____) _____	
Signature	_____

Student Members are required to complete the following:

School or institution now attending _____

Your current student status: ☐ high school; ☐ undergraduate;
graduate program ☐ MS ☐ PhD; ☐ other _____

Year you expect to graduate or complete your degree _____

Major, if college or graduate student _____

Signature _____

Order Blank for Past Issues

Cost of complete volumes (per volume): members (all categories) – \$18.00 + S/H

nonmembers and subscribers (libraries, schools, churches, etc.) – \$25.00 + S/H

Cost of single issues (per issue): members (all categories) – \$5.00 + S/H

nonmembers and subscribers (libraries, schools, churches, etc.) – \$7.00 + S/H

Volume	Number				Volume	Number			
	1	2	3	4		1	2	3	4
21	☐	☐	☐	☐	34	☐	☐	☐	☐
22	☐	☐	☐	☐	35	☐	☐	☐	☐
23	☐	☐	☐	☐	36	☐	☐	☐	☐
24	☐	☐	☐	☐	37	☐	☐	☐	☐
25	☐	☐	☐	☐	38	☐	☐	☐	☐
26	☐	☐	☐	☐	39	☐	☐	☐	☐
27	☐	☐	☐	☐	40	☐	☐	☐	☐
28	☐	☐	☐	☐	41	☐	☐	☐	☐
29	☐	☐	☐	☐	42	☐	☐	☐	☐
30	☐	☐	☐	☐	43	☐	☐	☐	☐
31	☐	☐	☐	☐	44	☐	☐	☐	☐
32	☐	☐	☐	☐	45	☐	☐	☐	☐
33	☐	☐	☐	☐					

CRSQ on CD, version 2.0

Members, \$75; nonmembers and subscribers, \$100.
Upgrade: Members, \$40; nonmembers and subscribers, \$55. (Prices on this item include postage and handling.)

Two-set CD contains volumes 1–41 (through March, 2005) of the *Creation Research Society Quarterly* and volumes 1–9 (through December, 2004) of *Creation Matters* in Adobe Acrobat format.

Volumes 1–20 are available on CD. See “CRSQ on CD” advertisement on right for details.

Add 20% for postage (for U.S. orders: min. \$5, max. \$25; for Canadian orders: min. \$10, no max.; for other foreign orders: min. \$15, no max.)

Total enclosed: \$ _____

Make check or money order payable to Creation Research Society. Please do not send cash. For foreign orders, including Canadian, please use a check in U.S. funds drawn on a U.S. bank, an international money order, or a credit card.

(Please type or print legibly)

Name _____ Address _____

City _____ State _____ Zip _____ Country _____

☐ Visa ☐ MasterCard ☐ Discover ☐ American Express Card number _____

Expiration date (mo/yr) _____ Signature _____

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

Creation Research Society

History—The Creation Research Society was organized in 1963, with Dr. Walter E. Lammerts as first president and editor of a quarterly publication. Initially started as an informal committee of 10 scientists, it has grown rapidly, evidently filling a need for an association devoted to research and publication in the field of scientific creation, with a current membership of over 600 voting members (graduate degrees in science) and about 1000 non-voting members. The *Creation Research Society Quarterly* 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 a research and publication society, and also engages in various meetings and promotional activities. There is no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund and research center are maintained to assist in such projects. Contributions to the research

fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates The Van Andel Creation Research Center in Chino Valley, Arizona.

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

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

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

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

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

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