

# EDITORIAL

## SCIENCE, A GOOD PLACE TO BEGIN . . .

I well recall the amazement and satisfaction I found in a physics laboratory experiment in which ordinary white light was separated by a prism into many distinct colors. Intuitively I had classified white as simply another color as is seen on a typical chart of paint colors. Now, I had learned that white was a combination of many colors that could be separated with a simple spectroscope. The reverse process was likewise fascinating as I noticed that the combining of many colors from decorative Christmas lights yielded a nearly white light. Science had worked. It was a rewarding pursuit.

We are all, or should be, impressed with the accomplishments of science. We have come to expect new discoveries and explanations almost daily, and wait impatiently for the next breakthrough. Technology based on science has provided a marvelous technocracy that almost threatens to engulf us. These advances give us unequivocal evidence that the scientific method works. For discovering explanations for the natural world about us, there seems to be no better methodology than science. In addition, science deals with the more concrete aspects of reality which give us a gratifying degree of security in this successful area.

We might feel very satisfied with science, except that all does not seem well. An exclusively scientific system of thought often leaves out too many areas that, we suspect, are part of reality. One only has to mention such concepts as consciousness, meaning of reality, morality, good and evil, freedom of choice, concern, conscience, loyalty, or love to realize that there seems to be a realm beyond the simple naturalistic cause-and-effect explanations of science.

A number of thought leaders have testified in one way or another about the reality beyond science. Vannevar Bush, who had an illustrious career as a scientist and administrator and who has been called the “father of the modern computer,” has stated that “Science proves nothing absolutely. On the most vital questions, it does not even produce evidence.”<sup>1</sup> The noted astronomer Sir Arthur Stanley Eddington, in referring to the areas of meaning beyond science, observed:

*Natural law is not applicable to the unseen world behind the symbols, because it is unadapted to anything except symbols, and its perfection is a perfection to symbolic linkage. You cannot apply such a scheme to the parts of our personality which are not measurable by symbols any more than you can extract the square root of a sonnet.<sup>2</sup>*

The famous mathematician-philosopher Arthur North Whitehead emphasizes the limitations of scientific explanation by pointing out that “Scientists animated by the purpose of proving that they are purposeless constitute an interesting subject for study.”<sup>3</sup> Physician-author Oliver Wendell Holmes described the relation more graphically when he quipped, “Science is a first-class piece of furniture for a man’s upper chamber, if he has common sense on the ground-floor.”<sup>4</sup> Last century, as the theory of evolution was being developed, Alfred Russel Wallace, whose ideas of biological evolution closely paralleled those of Charles Darwin, pointed out that man’s mental nature, i.e., his moral and intellectual capacities, could not have been developed by the laws of natural selection.<sup>5</sup> The philosopher Huston Smith states the problem more directly: “In envisioning the way things are, there is no better place to begin than with modern science. Equally, there is no worse place to end....”<sup>6</sup> These words eloquently emphasize some of the limitations and the patent incompleteness of science.

The expression “scientific world view” can suggest a contradiction in terms, because science gives only a partial view of reality, and its value as an explanatory system is limited. Any wholistic world view must account for those areas of experience beyond naturalistic explanations. Tempting as it may be, we should not reduce truth to our own simplistic level of understanding. Truth must look beyond science for many explanations. That is where God comes in.

Ariel A. Roth

## ENDNOTES

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# ARTICLES

## ORIGIN OF LIFE: A LOOK AT LATE 20TH-CENTURY THINKING

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### WHAT THIS ARTICLE IS ABOUT

*The origin of life on Earth has been an enigma for mankind since written records have been kept. In the closing years of the twentieth century, there are two mutually exclusive theories in currency. Life either evolved spontaneously on Earth during a primordial period, or living organisms were brought into existence by a Creator.*

*The naturalistic explanations for life's origins outline sweeping scenarios which result in the abiotic appearance of proteins and nucleic acids. Assuming that such a case has been explained, a leap is made from macromolecules to the living cell.*

*The presence of macromolecules is not equivalent to the existence of life. This may be seen by collecting macromolecules from once-living matter and waiting to see whether life will begin.*

*Living cells must have informational macromolecules present in a steady-state, non-equilibrium system. Moreover, the information content of proteins and nucleic acids is truly meaningful only in the context of the living cell.*

*Evolutionary explanations of how proteins and nucleic acids may arise in a pre-biotic environment have insurmountable difficulties. A growing recognition of these difficulties is reflected in the resurgence of "panspermia" as an explanation for life on Earth.*

*No naturalistic scenarios are available or even possible to account for the information content of biomolecules and for the non-equilibrium steady state of key chemical reactions found within all living cells. These considerations force one to conclude that the very existence of life suggests the existence of a Creator.*

Among numerous ideas in currency 4000-5000 years ago about the origin of life was one that is still held dearly by millions. It is summarized in the fourth commandment: "For in six days the Lord made heaven and earth, the sea, and all that in them is, and rested on the seventh day ...."<sup>1</sup>

Much more recent is a radically different concept of origins which derives the present universe from a hypothetical "big bang" and its evolutionary aftermath. Accordingly, life originated on Earth by random interaction between matter and energy.

Never before has the phenomenon of life been better understood. This is due to intense research effort by tens of thousands of scientists and their often spectacular discoveries over the past 50 to 80 years. The functions of about one-third of all proteins manufactured by the simple cell *Escherichia coli* are now known, and the total elucidation of the structure of this cell is foreseeable.<sup>2</sup>

We are also learning more about structures and workings of other more complex living systems. The recent development of automated DNA sequencing has prompted suggestions that a multi-billion dollar effort be organized to determine the complete nucleotide sequence of the human genome.

Cells are the smallest living independent entities, and nothing less than a cell deserves the adjective “alive.” Cells range in complexity from the simple bacterium, such as the common colon organism *Escherichia coli*, to highly differentiated cells of our nervous system. Numerous features common to all cells are understood by creationists to signify a common designer, but are explained by evolutionists in terms of a common ancestry.

### **COMMON CONSTITUENTS OF LIVING MATTER**

All cells have similar components. By weight they are 60-70% water, 25-35% biopolymers, and about 5% small organic compounds and minerals. These cellular ingredients (with the exception of water and minerals) are unique in several ways and cannot be found in nature except as parts of living or once-living matter.

Comparatively simple molecules containing a limited number of atoms comprise our inanimate environment. These molecules are rich in oxygen atoms, resistant to heat, and generally stable under a variety of conditions. In contrast to these simple molecules, biological polymers (which constitute most of living matter after water is removed) — proteins, nucleic acids, polysaccharides and lipids — are molecules made from thousands of atoms. They are rich in carbon and hydrogen atoms and are definitely unstable in the presence of heat and oxygen. Researchers working with proteins, for example, must always be careful not to stir a protein solution too vigorously, and to keep it on ice as long as possible, so as to prevent unraveling their intricate structures.

Protein molecules and nucleic acids are *informational macromolecules*, i.e., their structures harbor biological information. The gigantic molecules of proteins and nucleic acids are made by linking hundreds (or thousands) of a small number of “building block” molecules: amino acids for proteins and nucleotides for nucleic acids. Biological information resides in the particular sequence in which building blocks are linked.

When letters of the alphabet are linked in particular sequences, meaningful words are created. Likewise, the information content of proteins and nucleic acids depends initially on the order in which their building block components are connected.

The true meaning of biological information contained within the structures of biopolymers is evident only in the context of the entire living cell, because the phenomenon of life depends on harmonious interactions of thousands of kinds of protein and nucleic-acid molecules. If biopolymers are like words, then the living cell is like an extensive monograph.

### **BIOPOLYMERS MIXED IN TEST-TUBES DO NOT YIELD LIVING MATTER**

When all biopolymers are removed from a cell and put in a test-tube with all the other ingredients normally found in cells (small organic molecules and minerals) in just the right proportions, *nothing* happens.

The living cell is more than a collection of biologically active molecules. However, the extra quality is not, as many think, a mysterious life-force which departs upon death. This may be demonstrated rather dramatically by freeze-dried bacteria.

If a liquid culture of single-celled organisms is frozen rapidly and placed under vacuum, cellular water in the form of ice gently leaves the cells through sublimation, leaving behind cells as waterless powder. The organisms are in a state of suspended animation, neither alive nor dead. They can remain in this state indefinitely, so long as they are kept dry. If the cells are placed in water along with suitable nutrients, they once again continue living. Therefore, in this instance “life” was manipulated simply by adding or removing water.

### **WHY LIVING MATTER IS MORE THAN THE SUM OF ITS INGREDIENTS**

In a living cell the thousands of chemical transformations that are necessary for life to occur must be confined to a comparatively small space. This makes the products of one reaction available as starting materials for the next reaction along the necessary biochemical metabolic pathways. Moreover, the ingredients of cells are frequently assigned spatially, some in the nuclear region, others near the cell envelope. Without cellular morphology, these components have no meaningful tasks.

The process of life is dynamic, involving the biosynthesis of new substances, degradation of old ones, pumping in fresh food supplies and secreting waste products, as hundreds of chemical changes take place

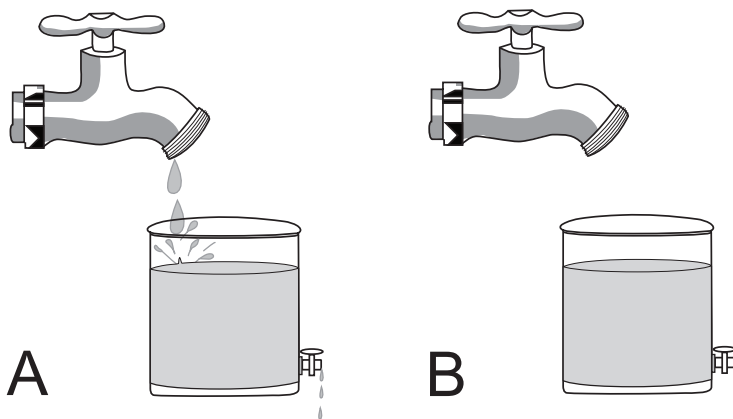
simultaneously every second. A most important property of a living cell which makes it more than just the sum of its ingredients is that the totality of its chemical transformations is not in equilibrium.

A chemical change is the rearrangement of atoms making up various molecules. Such a change may be represented as:  $A + B \rightleftharpoons C + D$ , where substances **A** and **B** interact and form products **C** and **D**. After this chemical change runs its course, a certain amount of all four substances will be present. The ratio at equilibrium of (**C**\***D**) to (**A**\***B**) is an unchanging (constant) number. At that point the reaction is incapable of any further chemical transformation. If all these chemical changes reach equilibrium, the cell dies.

Essentially all chemical reactions in a cell are facilitated by biological catalysts called enzymes. These agents tend to push reactions rapidly toward equilibrium, even though total equilibrium would be fatal to the cell. However, since chemical reactions in the cell are interconnected, the end products of one chemical transformation become the starting material for the next, and thus equilibrium is never reached. As the products are further utilized, more starting materials are manufactured, resulting in constant intracellular concentration of metabolic intermediates. This is called a steady state, non-equilibrium system, because the amounts of metabolic intermediates are relatively unchanging within the cell, and the total system is *not* at equilibrium. Such is only possible in live, intact cells. If a cell is physically disrupted or if it dies, the steady state changes into equilibrium. Figure 1 illustrates in a simple way the contrast between steady state and equilibrium conditions.

This situation can actually be approximated in the laboratory by poking holes in the membranes of live cells (so they will lose their ability to concentrate nutrients from their environment) and allowing the internal reactions to go to equilibrium. Such cells are now dead, and even if the holes of their membranes were repaired, they will not come back to life. For life to recur, non-equilibrium conditions would have to be established by the selective removal of key metabolite molecules from the cell. When the strategic reactions are once again restored to non-equilibrium, the system as a whole will be driven toward a steady state.

Manipulations involving the removal of a few small molecules from a cell containing many other molecules is beyond our present and most likely future capabilities. Such a capacity is tantamount to being able to reverse death to life on the cellular level.



**FIGURE 1.** A simple illustration of the difference between steady-state and equilibrium conditions. In both cases the volume of liquid in the container is constant. However, in A, liquid is constantly flowing through the system, while in B, the liquid is static.

### ATTEMPTS TO DISCOVER THE ORIGIN OF LIFE

The earliest historical records indicate that man has recognized the qualitative difference between living and non-living matter, and since then there never has been a shortage of theories to explain the presence of life on Earth. Yet the origin of life remains one of the greatest challenges to naturalistic interpretations. According to Nobel laureate Max Delbruck, "... there has been an immense conceptual gap between all present-day life and no life," and the "how" of the transition of earth from no life to life is "perhaps *the* fundamental question of biology."<sup>3</sup>

Nevertheless, the immense conceptual gap between life and non-life is neither recognized nor admitted by many evolutionary theorists. A 1978 review entitled "Chemical evolution and the origin of life" begins with these words: "Perhaps the most striking aspect of the evolution of life on earth is that it happened so fast."<sup>4</sup> More recently, the first chapter of a college textbook on the molecular biology of the cell contains this summary statement: "Living cells probably arose on earth by the spontaneous aggregation of molecules about 3.5 billion years ago."<sup>5</sup>

Regardless of their degree of optimism or enthusiasm, evolutionary theorists are forced to propose explanations for the spontaneous generation of life from non-living matter. In order for biological evolution to begin, some starting material is necessary. This need is met by the postulates of chemical evolution.

When the outlines of modern theories of chemical evolution (the natural processes on a “pre-biotic earth” which gave rise to the first living matter) were formulated by A.I. Oparin and J.B.S. Haldane in the 1920s,<sup>6</sup> very little was known about the biochemical intricacies of living matter. Consequently, there was plenty of freedom to postulate mechanistic processes by which organisms could come into existence.

Modern theories of chemical evolution found in current monographs and textbooks developed over a span of approximately 60 years. They suggest that early Earth was covered largely with a warm, slightly alkaline ocean. Though rich in carbon monoxide, carbon dioxide, ammonia, methane, hydrogen, and nitrogen, the atmosphere definitely did not contain atomic or molecular oxygen. Ultraviolet light from the sun, geothermal energy from volcanoes, shock waves from thunder, and cosmic radiation acted upon gases of the primitive atmosphere causing the formation of biomonomers such as amino acids, sugars, purines, pyrimidines, and fatty acids. These substances polymerized to form the proto-types of more recent proteins, nucleic acids and cell membranes. In time they coalesced to form the first proto-cell, a collection of polymers enclosed in a membrane. Eventually these protocells became increasingly complex, until the first true living cell was born.

### **LABORATORY SIMULATIONS OF CHEMICAL EVOLUTION**

The year 1953 was a banner year for chemical evolution. Stanley Miller, a graduate student working with Nobel prize winner Dr. Harold Urey, published his experiments on the synthesis of amino acids in a simulated primitive-earth environment.

He built a glass apparatus, in which circulating ammonia, methane, hydrogen and water vapor were exposed to electrical spark discharges for one week. Molecules forming in the vapor phase were trapped in water and analyzed. Among the 35 diverse substances identified, 9 were amino acids, almost half of the 20 different kinds found in proteins!<sup>7</sup>

Miller’s paper signaled an onslaught of experiments by numerous investigators who varied the starting materials, the source of energy and other experimental parameters. Their efforts yielded 19 of the 20 amino acids, all 5 nitrogenous bases which are crucial to nucleic-acid formation, and a number of important sugars as well.<sup>8</sup>

These results serve as a pillar on which chemical evolutionists build their theoretical edifices. Apparently it is indeed possible to envision hypothetical situations where at least the most important metabolic biomonomers may come into existence.



The evolutionary scenario requires the continual accumulation of biomonomers in the primordial ocean until it becomes an “organic soup.” The next necessary step on the chemical evolutionary ladder is to link biomonomers into polymers, especially proteins and nucleic acids. This involves the removal of a molecule of water from two biomonomers in order to form a chemical bond between them.

One of the postulates proposed for polymerization assumes that high concentrations of various amino acids accumulated at the rim of volcanoes, where the high temperatures drove off the water molecules, leaving proteins behind. Sidney Fox, the chief proponent of this theory, demonstrated that mixtures of amino acids heated at 200°C for 6 or 7 hours indeed formed protein-life polymers which he called “protenoids.” These polymers show weak catalytic activities partially resembling enzymes. When protenoids cool, they form “microspheres” supposedly resembling primitive cells morphologically.<sup>9</sup> These structures can “grow” under favorable conditions and “divide” by budding. Interesting as these experiments are, their results reveal serious deficiencies when they are used to support a scenario for chemical evolution.

### **DEFICIENCIES OF LABORATORY SIMULATIONS OF CHEMICAL EVOLUTION**

The success of the Miller-Urey type experiments depends on the types of gases introduced into the experimental systems. Early models of chemical evolution assumed a primordial atmosphere rich in methane, ammonia and molecular hydrogen, and these gases were used with considerable success. More recent models of the early Earth atmosphere, based on data from numerous space-probes, see the primordial atmosphere resulting mainly from the release of volatile materials trapped by solid particles during the formation of the planet. Thus the composition of an early atmosphere would have resembled the contents of present-day volcanic fumes. These are rich in carbon dioxide and water and have minor amounts of nitrogen, hydrogen sulfide and sulfur dioxide. Pre-biotic simulation experiments using gas mixtures of nitrogen, carbon dioxide and water vapors produced mostly ammonia and nitric acid in the hands of one investigator and formaldehyde in another laboratory.<sup>10</sup>

Whatever the composition of the primordial atmosphere may have been, evolutionary theorists agree that it could not have contained atomic or molecular oxygen. All postulated processes of chemical evolution would cease in the presence of oxygen, for oxygen would quickly react with organic compounds formed in the atmosphere, oxidizing them to carbon dioxide and formic acid.

Our present-day atmosphere contains 20% oxygen. A small portion of this gas is converted to the ozone layer of the upper atmosphere which shields us from high-energy ultraviolet radiation of the sun. A primordial earth, covered with an oxygenless atmosphere, would have been subject to the sterilizing effect of ultraviolet radiation. If, on the other hand, there was a primordial ozone shield, then oxygen also had to be present at concentrations of at least 1-10% of the current amount.

A potentially important source of pre-biotic oxygen could have been the photo-dissociation of water by ultraviolet rays. Calculations of theoretical levels of oxygen in a primordial atmosphere range from essentially nil to 25% of present levels.<sup>11</sup> Support for high rate of oxygen production by dissociation of water vapors comes from data collected during the Apollo 16 mission, where pictures of Earth were taken from the moon, using ultraviolet sensitive films. These pictures showed that a gigantic cloud of hydrogen, extending 40,000 miles into space, surrounded the earth. The source of this hydrogen could only be water vapor, bombarded by high-energy ultraviolet rays above the ozone layer

Scientists have examined uranium and iron-containing minerals from the earliest available sediments, hoping to learn whether the early atmosphere was oxidizing or reducing. The results were equivocal. We now believe that the existence of reduced minerals in sediments does not necessarily signify the existence of a reducing atmosphere and an oxidizing atmosphere does not always produce oxidized minerals. The relationship between a sediment and its environment cannot be established unless the actual rates of oxidation or reduction are known.

Two further observations should be made about the significance of the Miller-Urey type organic-soup-producing experiments. First, a consideration of yields. Even with the removal of products during experimentation by the use of traps, pre-biotic simulation experiments generate fairly small amounts of usable products. Assuming no destruction of molecules in the atmosphere, optimistic estimates ranged as high as 0.001 M concentration in the primitive ocean. However, when the destructive effect of ultraviolet radiation on amino acids is taken into account, the upper limit has been given at one ten millionth molar in the primitive sea, which happens to be the actual concentration of amino acids in the North Atlantic Ocean!<sup>12</sup>

Such low concentrations of biomonomers would have been inadequate to polymerize into macromolecules. Though it has been suggested that chemical evolution could have proceeded in smaller pools where the precursor substances would have been concentrated, there is no geologic evidence for large deposits of organic substances. Moreover, if concen-

tration had occurred, undesirable impurities likely would also accumulate and interfere with polymerization, the next step in chemical evolution.

The second observation is that synthetic reactions outside a cell produce equal amounts of optical isomers of amino acids and sugars. Therefore the primordial ocean would have contained a racemic mixture of biomonomers. Since known biopolymers exclusively utilize only one of the two or more possible isomers in the case of sugars and amino acids, it is totally incomprehensible how such an arrangement could develop from a 50-50 mixture of optical isomers.

Thus it is highly unlikely that chemical evolution could have taken place by the organic-soup mechanism. Among the factors against this mechanism are the great likelihood of substantial oxygen content in the primitive atmosphere and the small yields of biologically significant substances which would be present as equal amounts of optical isomers.

The “volcanic rim” approach of Sidney Fox assumes a primordial earth covered with an organic soup. It addresses the next difficulty — the polymerization of biomonomers — by splitting out the water in an aqueous environment, which, in terms of thermodynamics, is essentially impossible! However, by postulating a heat source, he dries up the environment and succeeds in the polymerization. But Fox pays for his success dearly.

The resulting protenoids have only a superficial resemblance to true proteins, in that the resulting peptide bonds are predominantly of the beta, gamma and epsilon variety, rather than the naturally occurring alpha bonds. The amino acid sequences are generated entirely by random means, and there is no mechanism to ensure any reproducibility. If by chance a biologically useful molecule is formed, how will its subsequent production be ensured?

When protenoids cool, they form microspheres which, according to Fox, grow and divide. True growth, however, requires numerous metabolic steps and incorporation of small molecules into the polymer structure of the cell. In Fox’s experiment, “growth” results from the physical attraction of opposite charges, and “budding” refers to the breaking up of microspheres due to changes in acidity or heat.

Since, according to this theory, all this is taking place on the surface of the earth, one must consider the destructive effect of ultraviolet radiation on any biologically active structure.

Clearly, the volcanic-rim theory does not advance the cause of chemical evolution, for it represents a dead-end approach to the problem.

## WHICH CAME FIRST, THE CHICKEN OR THE EGG?

All chemical evolutionary scenarios require the pre-biotic production of informational macromolecules. An important question to decide, however, is which type of information biopolymer evolved first, protein or nucleic acid? Proteins are the catalysts of biochemical processes, whereas nucleic acids contain the genetic information for specifying the sequence of amino acids in molecules. In living matter nucleic-acid formation occurs by enzyme catalysis, and protein synthesis is impossible without nucleic acids. Therefore, evolutionists have to solve a puzzle which resembles the question, "Which came first, the chicken or the egg?"

Until recently some theoreticians favored the notion that protein molecules were replicated directly in the absence of nucleic acids, until proteins "invented" nucleic acids. Others felt that nucleic acids were the first biopolymers formed, and they in turn "developed" protein synthesis. A third approach suggested that proteins and nucleic acids co-evolved independent of one another.

These alternatives do not explain satisfactorily the origins of protein and nucleic-acid duplicating systems. For this reason, the discovery that certain types of ribonucleic acids had enzymatic activity was quickly adopted into the chemical evolutionary scenario.<sup>13</sup>

In eucaryotic cells, processing of ribonucleic acids often includes the removal of specific intervening nucleotide sequences called "introns" from the RNA molecules. It was found that the intron sequences in the ribosomal RNA of the organism *Tetrahymena thermophila* spliced themselves without the cooperation of any protein. Moreover, this piece of RNA molecule exhibits true enzymatic activity in that it catalyzed the sequence-specific hydrolysis of certain pieces of other RNA molecules. Introns in fungal mitochondria and in nuclear RNA of higher animals have been also found to self-splice.

Enzymatically active RNAs are called "ribozymes." Their properties combine the most desirable elements of both proteins and nucleic acids. It is not surprising that ribozymes are rapidly taking the center stage among evolutionists as potentially the most likely biomolecules to have been the precursors of living matter, or in other terms, to be both "the chicken and the egg" at the same time.

The difficulties with the ribozyme hypothesis are manifold. Before the existence of RNA in a pre-biotic environment can be postulated, a supply of ribonucleotides — the monomers of RNA — is needed. Pre-biotic synthesis of ribose can only occur from the polymerization of fairly high concentrations of formaldehyde (0.01 M or greater) in alkaline

conditions. This reaction yields a mixture of different sugars, ribose being a minor component.

Condensation of ribose with adenine or guanine in the absence of enzymes yields a mixture of unnatural nucleosides.<sup>13</sup> Phosphorylation of nucleosides to nucleotides under pre-biotic conditions has not been demonstrated. Condensation of ribonucleotides to oligoribonucleotides in a pre-biotic environment has difficulties similar to those found for the condensation of amino acids to form peptide bonds, with the added problem of having to form 3' to 5' phosphodiester linkages. (There are nine different ways that two ribonucleotides can be linked by a phosphodiester linkage. Only one of these linkages is 3' to 5'.)

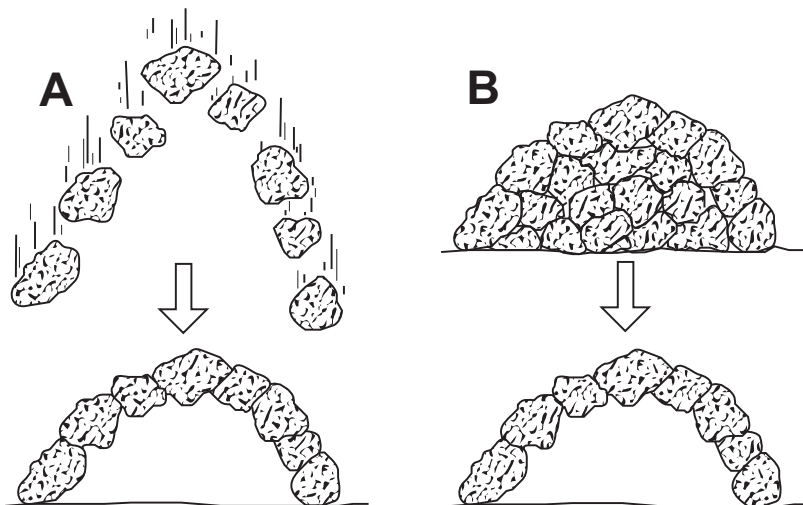
### **ALTERNATIVE CHEMICAL EVOLUTIONARY SCENARIOS**

Some evolutionists have recognized many of the difficulties mentioned above. They observe the high degree of complexity of contemporary organisms and admit the seemingly impossible task of offering a plausible explanation. However, since life is present on Earth, and some sort of mechanistic explanation for its existence is demanded, they continue to search for satisfactory theories.

Dr. Cairns-Smith, a proponent of a new approach to the problem of chemical evolution, points to a seemingly impossible formation in nature, such as an arch of stones (Figure 2). How such an arch could have formed one stone at a time requires a great deal of explaining. But if we assume that it was the top layer of stones of a round pile, and somehow the “scaffolding” below the top layer was selectively removed, then we have a reasonable explanation.

Attention is called, for example, to crystals of kaolinite (made of layers of aluminum atoms bound in a network of oxygen and silicon atoms). In any given region, the aluminum atoms are positioned in one of three possible arrangements. Such a structure could hold immense amounts of information, which could even be replicated if the relative position of the aluminum atoms is reproduced in each succeeding layer. These structures could behave as “clay genes” which carry genetic information and which, according to Dr. Cairns-Smith, could act as a scaffolding on which present-day biomolecules of RNA and DNA could form.<sup>14</sup>

The scaffold theory bypasses the nitty-gritty details of how a living cell can come into existence. It tries to show a way by which information may be transferred in the absence of a biological transfer system. It does not answer where or how the information originates, neither does it attempt to answer the most obvious question of how the process from inorganic



**FIGURE 2.** Two possible ways to form a stone arch. **A** illustrates an extraordinarily fortuitous set of circumstances. **B** suggests how such an arch might result from the aggregation of units and subsequent removal of the underlying scaffold. This illustrates how “clay genes” might act as the scaffolding for biomolecules (arch). Figure based on Cairns-Smith (1985).

clay to organic polymers occurs. It is essentially an armchair exercise, devoid of experimental support.

A group of evolutionists who cannot envision the evolution of living matter on Earth proposes that life evolved elsewhere in the universe and was imported accidentally or purposefully from outer space. Panspermia was proposed last century as an explanation for life after Pasteur disproved the spontaneous generation of life. It remained quite popular,<sup>15</sup> until the organic-soup theory took over in the 1950s. With a fuller appreciation of the difficulties of the organic-soup theory, panspermia is again gaining in popularity.

This theory is essentially an admission of failure to give a convincing naturalistic account for the origin of life on Earth. It pushes the problem out of the realm of experimentation and gives up on suggesting how life could have come about.

Max Delbruck, a confirmed evolutionist, has observed:

*In recent years various theories have outlined the possible connections between molecular selection, natural selection, and irreversible thermodynamics in this prebiotic biochemical trial process. While all these theories seem quite plausible and very*

*intelligent, in my opinion they tell us very little about the origin of life. I have made it my rule not to read this literature on prebiotic evolution until someone comes up with a recipe that says 'do this and do that, and in three months, things will crawl in there.' When someone is able to create life in a shorter time than was originally taken by nature, I will once more start reading that literature .<sup>16</sup>*

## **WHY LIFE CANNOT ARISE SPONTANEOUSLY**

Some general considerations take the topic of the origin of life beyond listing various theories of chemical evolution and a discussion of their inadequacies. First, there is the tacit assumption by evolutionists that matter possesses some sort of internal drive which pushes it to self-organize into living structures. It is as if molecules constituting biopolymers would confer some sort of benefit to their constituent atoms.

There is no evidence that this is the case. Atoms and molecules respond to only one type of drive; that is, to exist in the lowest possible state of energy. Biomolecules are examples of exactly the opposite; they are complexes of atoms in a high energy state. If atoms had a choice, they would rather get out of being part of the high energy configurations called proteins and nucleic acids.

All mechanistic explanations of origins have two deficiencies. One difficulty is in explaining the source of biological information, which ultimately dictates the structure and function of biopolymers. It is clear that chance cannot provide this information.

A second consideration which renders all mechanistic explanations invalid is that life processes are non-equilibrium events. If by chance all necessary biopolymers and small metabolites could have been produced in the primordial environment, brought together and enclosed in a membrane, a non-living cell would be the result. In the very process of assembly, reactants and their catalysts would be brought together, providing opportunity for individual chemical reactions to reach equilibrium.

There is such a concentration of living organisms on Earth's surface that it is difficult to locate any area that is sterile. Obviously, life had to start somehow. The existence of a supernatural Intelligence who is capable of designing and creating the various living organisms found on Earth is inconceivable to the modern secular mind which is accustomed to explaining all phenomenon by natural processes. But this is precisely the lesson to be learned from our chemical evolutionary efforts. Our inability not only to create living matter but even to suggest how such could come into existence forces us to admit that the existence of life demands the existence of a Creator.

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# NEWS AND COMMENTS

## THE U.S. SUPREME COURT RULES AGAINST CREATION-SCIENCE

On June 19, 1987, by a vote of 7-2, the justices of the U.S. Supreme Court struck down the Louisiana Balanced Treatment of Creation-Science and Evolution-Science Act. Previous issues of *Origins* (12:38-40; 13:36-37, 86-87) have discussed the legal battles over this 1981 Act which required the equal presentation of scientific evidence for creation whenever evolutionary ideas concerning origins are presented in public-school science classes.

The justices did not rule on the validity of scientific evidence for creation; rather, they rejected the Louisiana law's pre-eminent purpose, which they perceived to be "clearly to advance the religious viewpoint that a supernatural being created humankind." Representing the majority opinion, Justice William J. Brennan, Jr. stated that the law's purported neutrality was a sham and that its actual purpose "advances a religious doctrine by requiring either the banishment of the theory of evolution from public school classrooms or the presentation of a religious viewpoint that rejects evolution in its entirety." Rather than advancing academic freedom, Brennan said, "The act actually serves to diminish academic freedom by removing the flexibility to teach evolution without also teaching creation science."

Walter Slocombe, an attorney who had filed a brief representing 72 Nobel-Prize winning scientists and 17 state academies of science who opposed the Louisiana law, applauded the verdict: "This decision tells lower courts and responsible state legislatures that simply relabeling religious dogma as pseudoscience won't do."

In a 31-page dissenting opinion, Justice Antonin Scalia and Chief Justice William H. Rehnquist argued that the merits of the law had not been fully considered by the lower courts and that it should have been returned to the appeals courts for a trial that would have given definition to "creation science." The two justices compared the ruling to the 1925 Scopes Trial:

*In this case ... the Court's position is the repressive one. The people of Louisiana, including those who are Christian fundamentalists, are quite entitled, as a secular matter, to have whatever scientific evidence there may be against evolution presented in their schools, just as Mr. Scopes was*

*entitled to present whatever scientific evidence there was for it... Yet that illiberal judgment, that Scopes-in-reverse, is ultimately the basis on which the Court's facile rejection of the Louisiana Legislature's purpose must rest.*

Although the Supreme Court ruling apparently killed further attempts to enforce the teaching of creation-science through state laws, the creation movement is not dead. Arthur J. Kropp of People for the American Way predicted that “the battle to stop this thinly veiled fraud isn’t over.” Louisiana Attorney General William Guste observed that teachers should be able to present evidence favoring creation, because the Supreme Court recognizes that teachers “already possess” the “flexibility to teach *all* the scientific evidence about the origins of life.” The monitoring of state textbooks and science curricula is expected to continue, along with individual lawsuits by teachers who are punished or prohibited from teaching a variety of theories, including creation-science.

Katherine Ching

# ANNOTATIONS FROM THE LITERATURE

## ANIMO-ACID DATING

Kimber RWL, Griffin CV. 1987. Further evidence of the complexity of the racemization process in fossil shells with implications for amino acid racemization dating. *Geochimica et Cosmochimica Acta* 51:839-846.

*Summary.* In their 1987 report Kimber and Griffin present a detailed analysis of amino acid racemization associated with accelerated aging of modern and fossil mollusc shells. They produced accelerated aging by maintaining powdered shell in 110°C water for 1, 2, 4, 8, 16, 32, and 64 days. Their results clearly show that after 4-16 days of such accelerated aging the D/L ratio of some molecular subfractions and of some total hydrolysates may actually decrease with further processing which is the opposite of what would be expected with aging.

This surprising observation can be accounted for by differing molecular stabilities, i.e., differing chemical breakdown rates during aging, among the peptide components of the shell. If the amino acid sites in these various peptide molecules have differing racemization rates, the average chemical composition later in the aging process could contain a higher representation of sites at which the racemization curve [D/L ratio versus time] departs from the ... ideal ... sites in a peptide chain racemize more slowly than those at external sites, the authors say, "In theory, the degree to which the racemization curve [D/L ratio versus time] departs from the ... ideal ... should reflect the number of the stable amino acids remaining in internal positions during the aging process." In what may appear to be a contradictory statement, they also say, "... valine, isoleucine, and leucine all display ... curves ... indicating a slow initial racemization (epimerization) followed by more rapid rates."

There is no uncertainty regarding their conclusion "that considerable research is still required to understand fully the complexities of the amino acid racemization process in fossil materials and that this may have implications for accurate quantitative dating."

## CREATIONISM

Gange RA. 1986. *Origins and destiny*. Waco, TX: Word Books. 193 p.

*Summary.* Gange presents a fresh approach to the argument for design from the viewpoint of a physical scientist. The author argues

that the fitness of the environment of our earth for life is unique and beyond happenstance, that the origin of life demands intelligent design, and that man has characteristics above the level of naturalistic explanations. The book is well written in a style that avoids technical details, which are relegated to an appendix.

Geisler NL, Anderson JK. 1987. *Origin science: a proposal for the creation-evolution controversy*. Grand Rapids, MI: Baker Book House. 198 p.

*Summary.* The authors analyze the creation-evolution controversy in the context of its historical background. This book gives much-needed breadth to an often oversimplified argumentation. The authors, who are creationists, emphasize the religious roots of modern science and the inadequacies of naturalistic explanations, as well as the scientific evidence in favor of creation.

Huse SM. 1983. *The collapse of evolution*. Grand Rapids, MI: Baker Book House. 178 p.

*Summary.* This book is a general, non-technical account of the standard arguments used by creationists against evolution. Unfortunately, it suffers from a lack of critical judgment, with both good and bad arguments being used. Use of this book is recommended only in conjunction with supplemental material that evaluates the various arguments. Given the lack of information in certain specific areas, it will do little to convince the knowledgeable individual about the general validity of creation. An appendix includes a glossary and the names and addresses of 73 creationist organizations.

## **CRETACEOUS-TERTIARY EXTINCTIONS**

Officer CB, Hallam A, Drake CL, Devine JD. 1987. Late Cretaceous and proxysmal Cretaceous/Tertiary extinctions. *Nature* 326:143-149.

*Summary.* The impact hypothesis is unsatisfactory as an explanation for the end-Cretaceous extinctions for several reasons. No crater has been found for the proposed impact, the extinctions appear to have occurred over too long a period of time, multiple iridium anomalies exist, the clay layer is of different chemical composition in different regions, and the extinctions are too selective. These features are better explained as the result of intense global volcanic activity over a moderately extended period of time, combined with a major sea level regression. The geologic and biological evidence at the Cretaceous-Tertiary boundary is more consistent with such a scenario than with the impact of an extraterrestrial body.

## EVOLUTION

Dawkins R. 1986. *The blind watchmaker*. NY: W.W. Norton & Co. 332 p.

**Summary.** This is one of the most challenging books to creation in this decade. *The Blind Watchmaker* addresses what is considered by many to be the most convincing argument for creation, namely, the argument for intelligent design. The book derives its title from William Paley's argument that, since a watch must have a watchmaker, the complexities of living organisms must have a Creator. To Dawkins the "blind watchmaker" is natural selection and other naturalistic explanations for both the origin and evolution of life. The last part of the book is devoted to a discussion of controversies within evolutionary thought, including a chapter criticizing punctuatedism, entitled "Puncturing Punctuatedism."

**Comment.** Dawkins is an excellent writer and argues quite convincingly as he attempts to bring all of reality down to his understanding of it. The book is a beautiful package of assumptions built on assumptions which the unwary reader would be ill-advised to take for granted. Nevertheless, in this book — which is worthy of study — the argumentation is comprehensive and embellished with many examples.

Lewin R. 1987. The surprising genetics of bottlenecked flies. *Science* 235:1325-1327.

**Summary.** Genetic bottlenecks (in which the size of a breeding population is reduced to a very few individuals) are believed to play an important role in speciation. According to conventional wisdom, the gene pool would be reduced in size, resulting in a decrease in genetic variance. This would be true if genetic variance is simply additive, but the results of experiments by E.H. Bryant et al. suggest the situation is not so simple. When fruit-fly populations were passed through bottlenecks of 1, 4, or 16 breeding pairs, genetic variance actually increased in the new populations, especially those started from 4 or 16 pairs.

**Comment.** This study has important implications for creation theory concerning speciation in small populations after the flood.

Opadia-Kadima GZ. 1987. How the slot machine led biologists astray. *Journal of Theoretical Biology* 124:127-135.

**Summary.** This article challenges the concept that chance mutations produced a new enzyme preadapted to new conditions. Instead, the author argues for post-adaptational mutations, which he describes as more Lamarckian than Darwinian. His conclusion is based on his review

of all the new enzymes he could find reported in the literature — a total of two. Both enzymes were detected in strains of *Escherichia coli* having a deletion for the beta-galactosidase gene. On further examination, the two enzymes were found to be identical, so there is really only one example, which has arisen twice. But preadaptation was not a factor in either case. The new enzyme appeared only in the presence of lactose, and in all cases studied was regulated by the presence of lactose. Never has any colony of lactase-deleted *E. coli* produced a new enzyme without exposure to lactose. These results have two important consequences to evolutionary theory. First, preadaptation appears to be absent, with adaptative mutations occurring only after environmental stress. This is directly contrary to conventional neo-Darwinism. Second, the new enzyme showed no evidence of being produced by a random process. The same enzyme was produced by the single strain in one experiment and each of the 34 strains in the second experiment. This suggests that *E. coli* bacteria possess the capacity to produce a new enzyme under the appropriate conditions.

**Comment.** One cannot help wondering whether the “new” enzyme is not truly new to the cell, but is a pre-existing enzyme with low affinity for lactase, being produced in abnormally large quantities due to a change in regulatory processes.

## HISTORY

Lindberg DC, Numbers RL, editors. 1986. God and nature: historical essays on the encounter between Christianity and science. Berkeley: University of California Press. 516 p.

**Summary.** This volume contains papers presented by church historians and historians of science at an international conference on the historic relations of Christianity and science. The eighteen essays provide a comprehensive view of the relation between science and religion from the time of the early church to the present.

**Comment.** This book is not a polemic, neither does it “set up” an adversarial relationship between science and religion, as has been the custom in previous treatises on the subject. It is a good reference that is sure to remain a classic in this area.

## PALEOBIOGEOGRAPHY

Case JA, Woodburne MO. 1986. South American marsupials: a successful crossing of the Cretaceous-Tertiary boundary. *Palaios* 1:413-416.

**Summary.** The North American fossil record of marsupials shows a dramatic decrease across the Cretaceous-Tertiary boundary, with

only one genus continuing through to the Paleocene. The South American fossil record, although not so well known, shows a different trend. The number of fossil marsupial taxa increases across the Cretaceous-Tertiary boundary, with four taxa at or near the genus level found both above and below the boundary.

**Comment.** This paper provides an illustration of the pitfalls of using the data from one continent to extrapolate conditions for the whole world. It also shows that the end-Cretaceous impact hypothesis has some serious problems.

Hendrickson, D.A. 1986. Congruence of bolitoglossine biogeography and phylogeny with geologic history: paleotransport on displaced suspect terranes. *Cladistics* 2:113-129.

This paper examines the relationships of a group of New World plethodontid salamanders to the geologic history of their areas of distribution. Most species in the group are found on suspect terranes, which are believed to have accreted to the North and South American continents at various times, beginning during the Cretaceous. The historical and geological relationships of the terranes are compared with previously proposed phylogenetic relationships among the salamanders. The results were suggestive, but not compelling, that these salamanders may have drifted onto the Pacific Coast on microplates from a distant source. The author suggests the possibility that other groups may have arrived in South America via drifting microplates. This might explain the presence of various groups of "island hoppers" in South America before the Late Pliocene land bridge was established.

Houde P. 1986. Ostrich ancestors found in the Northern Hemisphere suggest new hypothesis of ratite origins. *Nature* 324:563-566.

**Summary.** The large flightless birds of the southern continents are known as the ratite birds and are believed to be related to each other. Their distribution on the southern continents is often explained as the result of an ancestral Gondwanan distribution, with subsequent fragmentation and divergence as a result of continental drift. The fossil record does not support this scenario. The only fossils of living families are restricted to the Neogene, long after the conventional date for the breakup of Gondwanaland. This paper identifies a Paleogene European fossil as an ostrich, placing the ancestry of the family in the Northern Hemisphere. Other fossils believed to be ancestral to the ratites are known from the Paleogene of both Europe and North America, but none have been found from any of the southern continents. This conclusion challenges the relationships among the ratites, and also the

basis for calibration of the DNA molecular clock (see: Sibley CG, Ahlquist JE. 1981. In: Scudder GGE, Reveal JL, editors. *Evolution Today*. PA: Carnegie-Mellon University).

Shaw CA, McDonald HG. 1987. First record of giant anteater (*Xenarthra*, *Myrmecophagidae*) in North America. *Science* 236:186-188.

**Summary.** One of the most frustrating problems in historical biogeography is dealing with negative evidence. If no fossils of a species are found in an area, does that mean the species was never present in the area? A bone from a giant anteater has been found in northwestern Sonora, Mexico, more than 3000 km north of its present range. Because anteaters are considered to be tropical animals, this finding was unexpected. Evidently, either climatic conditions or anteater ecology, or both, have been different in the past. The fossil locality is considered to be early Pleistocene (Irvingtonian).

## PALEONTOLOGY

Rose KD. 1987. Climbing adaptations in the Early Eocene mammal *Chriacus* and the origin of Artiodactyla. *Science* 236:314-316.

**Summary.** Orders of living mammals are often hypothesized to have their origins in generalized Paleogene mammalian ancestors, which may be represented by fossil remains or may be hypothetical. Typically, dental morphology forms the basis for postulating such relationships. *Chriacus* belongs to the family Arctocyonidae, of the extinct Order Condylarthra, and has been proposed as being near the ancestry of the artiodactyls (even-toed, hoofed mammals such as deer, cattle, camels, etc.). However, the recent discovery of a nearly complete skeleton shows that *Chriacus* was adapted for climbing trees, and could not have been ancestral to artiodactyls.

**Comment.** This article illustrates the difficulty of trying to reconstruct the habits and relationships of an extinct type of mammal from its dental morphology, as well as the uncertainties in determining the ancestries of living mammals.



## LITERATURE REVIEWS

*Readers are invited to submit reviews of current literature relating to origins. Mailing address: ORIGINS, Geoscience Research Institute, 11060 Campus St., Loma Linda, California 92350 USA. The Institute does not distribute the publications reviewed; please contact the publisher directly.*

### A NEW GENERAL REFERENCE ON CARBON-14 AGE DATING

RADIOCARBON DATING: AN ARCHAEOLOGICAL PERSPECTIVE.  
1987. R.E. Taylor. Orlando, FL: Academic Press, Inc. 212 p.

*Reviewed by R.H. Brown, Geoscience Research Institute*

As the title implies, this book was written for individuals who wish to understand radiocarbon dating, but do not have a strong background in physical science. The author is eminently qualified to provide both breadth and depth in a treatment of radiocarbon dating. He is currently professor of anthropology and director of the Radiocarbon Laboratory, Institute of Geophysics and Planetary Physics, at the University of California, Riverside. While a graduate student at the University of California, Los Angeles, he served as a research assistant in the isotope laboratory established by the late Willard F. Libby who developed the radiocarbon dating concept and pioneered the associated laboratory techniques.

The text is amply illustrated and written in a clear, easily readable style. There is a broad discussion of techniques, as well as of the basic principles on which these techniques are based. Explanations from elementary principles are provided for readers who wish to understand the technical details. Extensive references provide easy access to the original literature. A reader who goes through the book rapidly will notice some repetition — repetition that provides for ease of understanding when interest may be limited to only a particular section or chapter.

Throughout the book, particularly in Chapter 5 (“Evaluation of Radiocarbon Data”), Dr. Taylor gives a thorough discussion of the difficulties and uncertainties in the translation of a C-14 measurement into an estimate of real-time calendric age. In Chapter 2 (p 16) he states, “The minimum overall level of uncertainty for an individual C-14 age estimate for middle and late Holocene [less than 6000 years old] samples is about 200 years.”

For many individuals these discussions are worth more than the cost of the entire book.

The final chapter (No. 6) gives a highly interesting history of the development of radiocarbon dating from the first suggestion concerning the existence of C-14 that was made in 1934 to the death of Willard Libby in 1980.

The author and publisher are to be commended for a first edition remarkably free of errors. I can cite only two of any significance. In Figure 2:12 on p 33 the lower horizontal line designated "ca. 410 yrs" should extend to the extreme right vertical dashed line, not only to the vertical solid line at which the "ca. 265 yrs" horizontal line terminates. In each of the first two examples on p 138 the last line above "Age range" should be "years B.C.", not "years B.P."

Dr. Taylor's book meets a long-standing need for an up-to-date, comprehensive, authoritative and succinct treatment of radiocarbon dating.

# LITERATURE REVIEWS

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## TWO SIDES OF SEVERAL QUESTIONS

THE GENESIS DEBATE. 1986. Ronald Youngblood, editor. Nashville, TN: Thomas Nelson Publishers. 250 p.

*Reviewed by R.H. Brown, Geoscience Research Institute*

Ronald Youngblood, professor of Old Testament at Bethel Seminary West, San Diego, and editor of the *Journal for the Evangelical Theological Society*, has brought together a unique collection of 22 essays on the most frequently debated topics concerning the interpretation of the first eleven chapters of Genesis. The essays are organized under chapter headings in a question format.

1. Were the days of creation twenty-four hours long?
2. Are the events in the Genesis creation account set forth in chronological order?
3. Was the Earth created a few thousand years ago?
4. Was evolution involved in the process of creation?
5. Is the doctrine of the Trinity implied in the Genesis creation account?
6. Was Cain's offering rejected by God because it was not a blood sacrifice?
7. Were there people before Adam and Eve?
8. Did people live to be hundreds of years old before the Flood?
9. Are the "sons of God" in Genesis 6 angels?
10. Did Noah's flood cover the entire world?
11. Does Genesis 9 justify capital punishment?

For each of the eleven topics there is a YES response, printed in the upper portion of the page, and a NO response, printed with contrasting boldface type in the lower portion of the page. Extensive footnotes and references for both YES and NO essays are given at the end of each chapter.

The principal professional association of each of the 22 authors of these essays is given with the list of contributors in the introductory section of the book.

Any collection of essays by 22 authors on a range of controversial topics would not be expected to be of uniform quality. Editor Youngblood is to be commended for his accomplishments in securing competent writers and obtaining lucid presentations. Regardless of previous bias, the careful reader may expect to gain fresh insights from both the YES and the NO responses.

It is unfortunate that the YES response in Chapter 3 was written by a theologian and biblical scholar whose scientific competence appears to have been obtained from an uncritical reading of creationist literature, rather than by a broadly competent scientist who has confidence in the historical validity of the events described in Genesis 1-11.

According to my assessment, many readers would find Chapter 4 both more pleasing and more useful if the NO response had been principally analytical and less polemical.

Neither the YES nor the NO response in Chapter 7 makes a contribution to a careful grammatical-historical reading of Genesis 1-11. The cavil “Three people do not make a city” ignores the possibility that Moses may have referred to a city built by Cain during his later years, hundreds of years after the death of Abel.

The NO essay in Chapter 8 presents numerical patterns in the patriarchal age data of Genesis 5 and 11 that some readers will find intriguing. It would be unfortunate for a reader of the YES essay in Chapter 10 to be left with the impression that tsunamis offer the best available explanation for a universal inundation of the continents. Tsunamis probably contributed to the universal devastation described in Genesis 7, but the major factor most likely was continental subsidence and ocean floor uplift that returned the planetary surface to a condition similar to that which existed before Day Three of Creation Week.

The outlines of thought and evidence given in these 22 essays, together with their accompanying references, make *The Genesis Debate* a valuable addition to the library of anyone interested in a correct understanding of the first eleven chapters of the Hebrew-Christian scriptures.

# GENERAL SCIENCE NOTES

## OF DINOSAURS AND MEN

*By Arthur V. Chadwick, Professor of Biology & Geology,  
Southwestern Adventist College, Keene, Texas*

### WHAT THIS ARTICLE IS ABOUT

*The riverbed of the Paluxy of central Texas has been a source of extensive discussion between evolutionists and creationists, and likewise among creationists. The interest stems from reports that both human and dinosaur tracks occur in the same Cretaceous limestones. This would mean that men and dinosaurs lived at the same time — a point that would support the creation model and severely challenge the evolutionary time scale which places the development of man about 100 million years after the dinosaurs.*

*Dr. Chadwick, who has been closely associated with the Paluxy River question over the years, recounts the history of major developments. While some creationists were producing films and writing articles supporting the humanness of the tracks, Dr. Berney Neufeld (Origins 2:64-76, 1975) raised serious questions regarding their authenticity. Some investigators unknowingly “reinvented the wheel” and repeated studies of the area, while others continued to claim authenticity of the tracks. Repudiation by some leading creationists has not dampened the spirit of those who still believe that authentic human tracks exist in the riverbed of the Paluxy.*

As the unofficial local scientist and “expert” on human footprints, I often receive queries regarding the happenings at Glen Rose. This past year has been no exception. In fact, the past two years have been rather remarkable for Glen Rose. But the story begins some 17 years ago.

Drs. Berney Neufeld, Leonard Brand and I were fresh out of graduate school and anxious to investigate various lines of evidence being used to support the biblical account of Earth history. Among the most prominent of these were tales of giant human tracks in the bed of the Paluxy River, near Glen Rose, Texas. These tracks were in Cretaceous limestone, supposed to be 80-100 million years old, alongside giant bipedal tracks of carnivorous dinosaurs (Morris & Whitcomb 1961, p 173-175). While we were interested in the significance of the tracks,



**FIGURE 1. Photo of the famous “Taylor trackway” which initiated the current wave of interest in the Paluxy River locality. This series of bipedal elongate tracks was identified as dinosaurian by Dr. Berney Neufeld in ORIGINS in 1975.**

we were also puzzled by the lack of careful analytical investigation. Here was a piece of evidence so important that — if correct — could turn the whole history of the Earth upside down. Why were the earth scientists not flocking to Glen Rose to investigate? Why were the creationists not carrying on a carefully orchestrated investigation to determine the nature and significance of the evidence? We had a lot to learn.

It did not take us long to organize an expedition to the river. Setting out late in the summer of 1970, we arrived at the site at an opportune time. A flurry of activity earlier in the summer connected with the work of Stan Taylor of Films for Christ had left many new tracks exposed, and piles of discarded sandbags and plastic sheets littered the banks. We were able to sandbag a section of the river and bail it dry (Figure 1). There on the floor of the river was a clear bipedal trackway unlike anything we had seen before. We made casts of the prints, photographed the site carefully, and puzzled about what could have made the trail. The tracks had a clear humanoid appearance, but lacked some of the most important characteristics. There were no clear pentamerous feet, and the profile was more elongate and narrow than one would expect for a human track. A careful study revealed that several of them bore three unmistakable divisions at the anterior end, which led us to conclude that they were probably made by sauropods, perhaps walking in water too shallow for normal tracks. But they were very different from the common tridactyl trackways in the river bottom. Our initial suspicions were further heightened by a trackway on a nearby ledge. Several of the poorly defined depressions exhibited the elongate appearance of the “man tracks,” but further along they became clearly defined as dinosaurian. While we harbored some doubt as to what had made the elongate tracks in the river bottom, we were now certain that they did not provide irrefutable evidence of the coexistence of man and dinosaur.

We returned to Loma Linda University convinced that the man-like tracks in Glen Rose were not human. But another problem had to be dealt with: a number of unmistakably human footprints reported to have been dug from the Paluxy River were in circulation, complete with notarized eyewitness accounts of their origin. Could they have been carved? How could we test for carving? We devoured anything we could find that related to the tracks in the river. We needed equipment to cut the rocks, and time to check out every lead. Neufeld traveled that

summer to New York, where he interviewed archivists at the American Museum regarding the whereabouts of the field notes of the scientist who first brought these tracks to widespread attention.

In 1937, Dr. Roland T. Bird, on a fossil-collecting trip from the museum, stopped at a rock shop in New Mexico. In the window of the shop were displayed two large human footprints, in stone! Inside, the owner showed him additional fossil footprints made by a three-toed creature. Bird recognized them instantly as dinosaurian. Investigating further, he learned that the track had been excavated from the Paluxy riverbed near Glen Rose, Texas. Shortly thereafter, he arrived in Glen Rose. There in the bed of the river, he found a bipedal trackway of three-toed *Allosaurus* and, nearby, a long trackway of *Brontosaurus*, the largest animal ever to walk on the earth. It occurred to him that this trackway would be a veritable prize for the American Museum's new Hall of Dinosaurs, where a full-sized skeleton of *Brontosaurus* was being readied for display. The dinosaur trackway was quarried from the riverbed and shipped to New York where it is presently part of that exhibit.

Neufeld discovered that either Bird took no notes, or they were never archived, so whatever information he may have had regarding the man-like tracks was lost to science. Continuing his quest, he traveled to Columbia Union College in Takoma Park, Maryland, where a collection of the man-like and dinosaur tracks supposed to have been removed from the Paluxy riverbed was housed. A series of cuts in both the dinosaur and human tracks led Neufeld to conclude that both the human and dinosaur tracks were artful carvings.

On his way back to California, Neufeld stopped by Glen Rose and interviewed some of the colorful local residents. He also purchased a genuine dinosaurian track from Mr. McFall, who owns the land along the stretch of river where most of the man-like tracks occur. How did he know it was genuine? "It looked too bad to have been carved." With this track he returned to Loma Linda. There, we carefully sectioned the dinosaur track in several planes. We observed that fine laminations which could be seen in the rock bent downward in conformity to the track just as one would expect, had the animal stepped in soft mud. This was in clear contrast to the Takoma Park "footprints" which cut across the laminations of the rock without any evidence of deformation. We obtained a human and a "cat" track from Dr. Clifford Burdick, who



graciously permitted us to cut them. We were told that this human track was the same one seen by Bird in New Mexico. Unfortunately, these tracks lacked any internal laminar structure, and yielded inconclusive results. This work eventually led to the publication of the first carefully documented study of the Paluxy River tracks in 1975 in *Origins* (Neufeld 1975). This remained the only scientific treatment of the tracks for over ten years. However, it was largely ignored by creationists who did not favor its conclusions, and by evolutionists who had not yet started to be interested in the fray.

During those ten years, several events conspired to bring renewed interest in the Paluxy River trackways. Creationists became increasingly vocal concerning the tracks and their inescapable meaning to evolutionary theory, and evolutionists became commensurately uneasy about the same things. Thus it was only a matter of time until the Paluxy area came to the forefront. It happened this way (Golden 1986).

In 1980, Glen Kuban, a young computer programmer from Ohio who was intrigued with the same stories that had motivated us a decade earlier, began a series of trips to the central Texas site of the “fossil man-tracks.” Apparently unaware of Neufeld’s article, he had hopes of being able to document the tracks as evidence for creation. It was not long before he recognized problems. In fact, he soon found himself becoming increasingly annoyed by the claims that various groups were making for the tracks’ “irrefutably human” origins. He saw the need to document unequivocally that the tracks were not human.

During the next two years, he worked doggedly on the problem, mostly alone. In 1982, quite by accident he encountered Ron Hastings, a local high school physics teacher who had come to the river with quite different motives. He had been annoyed by the noises that creationists had been making and especially by what he viewed as exaggerated claims about the Paluxy footprints. The two men, ideologically divergent, but united in their desire to get to the bottom of the Paluxy story, labored on. Increasingly their work, and that of a third player in the Paluxy drama, were making local and, occasionally, national news.

That third party was Dr. Carl Baugh, a Baptist minister. Baugh had also come to Glen Rose in the early 1980s with the goal of establishing a museum of creationist evidences at the site of the most famous of all creationist evidences — the Paluxy River man tracks. Baugh was understandably anxious to find authentic evidences of the human trackways.

He was probably also disappointed by what he saw in the river. But Carl Baugh was not afraid of hard work! If finding man tracks meant digging up the riverbank, or buying riverfront property, he was game for the task. He was also out to let the world know what he was doing.

Meanwhile, all this activity could hardly escape those who had originally brought the tracks to the attention of the world. In San Diego, at the Institute for Creation Research (ICR), various leaders were being apprised of the activity of Kuban. ICR and Paul Taylor of Films for Christ accompanied Glen to the site of the tracks in late 1985. There they saw for themselves evidence that Kuban and Hastings had discovered: surrounding and superimposed on some of the “man-tracks” were discolored haloes having the unmistakable form of tridactyl sauro-pod tracks. While the origin of the discolorations was not clear, the evidence was compelling. The tracks had to be dinosaurian.

Dr. John Morris returned to ICR and published a carefully worded retraction of the positions he and the Institute had taken on the character and significance of the tracks (Morris 1986). This must have been a difficult task, in the face of his own published book on the tracks (Morris 1980). In an equally difficult decision, Paul Taylor withdrew from circulation the film “Footprints in Stone,” an elegant and compelling account of the tracks and their implications for evolution. These repudiations occurred in early 1986.

The next move was a series of articles in the Spring/Summer issue of *Origins Research* (the journalistic arm of Students for Origins Research, an informed student creationist organization currently operating from Goleta, California). This issue featured an article by Glen Kuban, a member of the society himself, and articles by Morris and Taylor, an editorial, and responses by Kuban to Morris (Kuban 1986a). This was followed by a carefully documented monograph by Kuban on his track studies (Kuban 1986b). The work of Kuban resulted in a flood of “me-too” type articles from a variety of sources (Hastings 1987). A special issue of the Humanist journal *Creation/Evolution* featured four separate articles on the tracks. A second number continued the discussion.

In retrospect, we may well ask why it took so long for the mystery of the tracks to evaporate. It is clear that the evidence was in hand in the early 1970s. The *Origins* article was certainly known to the groups participating in this drama. Informed creationists had long known of

Neufeld's work. Well-read evolutionists had also been aware of the article for years, and it was often cited in anti-creationist writings. At what cost to truth did we ignore data which were contrary to some pet theory, however interesting or inviting it may have seemed? The cost was indeed great. Creationists might have had the honor of laying aside this misconception ten years ago with little philosophical expense, as a result of their own scientific research. It has now been torn away by individuals, many of whom, unlike Kuban himself, have little regard for the cause of creationism.

Creationism does not need footprints in the Paluxy River for its support. Scientists who recognized the validity of Neufeld's findings have done quite well without human tracks in Cretaceous rocks for 15 years. Those who refused to let go of the tracks have placed in the hands of the cause of humanism a new weapon with which to attack creationists. They can with some justification now say: "As the Paluxy River data went down under careful scrutiny, so will every other piece of data put forth by the creationists." How much better the scenario that could have been!

**FIGURE 2. Dr. Carl Baugh points to a newly uncovered bipedal track in the bank of the Paluxy River, Glen Rose, Texas.**



For the future, we would do well to learn from our past mistakes, refusing to use as scientific evidence material which has not been carefully scrutinized. Note also that other evidences used in the past as support for creationism made no sense in context: “human footprints” in deep marine sediments (Delta, Utah — was man walking on the floor of the ocean?), pollen in Precambrian deposits (Grand Canyon — how do you account for these?), and out-of-order fossils (Heart Mountain and Lewis Overthrusts — how do you explain the reverse order?), to name a few. Creationists and evolutionists alike would be well advised to pay particular attention to all of the creation literature, where other so-called “evidences” for creation have been investigated and reported, before waging an unnecessary and costly battle again.

Meanwhile, the story is not yet over in Glen Rose. The undaunted Carl Baugh recently announced a new site with new tracks (Figure 2), this time so incredible that you had to see them to believe them! The news coverage was back, this time a little older and wiser, but eager for anything that would produce a new headline. The authenticity of the tracks was attested by forensic experts from Dallas, a professor of anthropology, and the list goes on. Maybe, someday soon, if I have a little spare time, I will take a run down there just to satisfy my curiosity, you understand....

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# EDITORIAL

## CLICHÉS

“Today is the first day of the rest of your life.” This seemingly profound statement implies that tomorrow will be the second day of the rest of your life, and the day after tomorrow will be the third day of the rest of your life. Yesterday was probably not special, because yesterday was only the last day of the past of your life, and likewise for the day before yesterday which was the next to the last day of the past of your life. On the other hand, today is apparently special, because it is the first day of the rest of your life. However, by tomorrow, tomorrow will be the first day of the rest of your life, and today will be yesterday. By the time you reach the day after tomorrow, that will also be the first day of the rest of your life, and by then tomorrow will be yesterday. It turns out that every day of your life is the first day of the rest of your life.

Another cliché tells us that we “love tomorrow” because it “is only a day away.” To be consistent, we should also love yesterday because it, too, is only a day away. We probably should also love the day after tomorrow, because it is always two days away, even if it happens to be Monday, and the day after the day after tomorrow is always three days away, and that should also evoke love, even if it happens to be the day that taxes are due. However, by tomorrow, or the day after tomorrow, or the day after the day after tomorrow, we will be faced with today, and it won’t be a day away.

Then consider what happens when you cross the international dateline going west and suddenly today becomes tomorrow, and when going east, today becomes yesterday. Today is not special of itself, neither is tomorrow or yesterday. Yesterday does not deserve any more love than tomorrow, because tomorrow will be the third day of the rest of your life, if you begin counting from yesterday.

Seriously, clichés are often trivial, misleading, and unfortunately, very influential. In our efforts to be analytical and cautious, clichés deserve more critical attention than they receive. Their modicum of acceptance can cause unconscious incorporation into our thought matrix. This must be avoided. Clichés often reflect accepted thinking that represents over-generalizations that become an unrecognized danger to our task of finding truth. They stereotype by giving stock images that too

often distort reality. Their varied approaches, be it from speeches, songs, television, conversation, writing, or pictures, impinge on most areas of thought. The arena of political activity is prime turf for clichés that are suspect but that we hear so often we come to accept. In national and international conflicts such as the fulminating Middle East crises, we often suggest simple popular solutions that seldom reflect an understanding of the concerned factions. In theology, the cliché “facts are not significant, meaning is” can provide an open field for almost any idea, as long as it is considered meaningful. However, meaning based upon erroneous concepts should be suspect, and a knowledge of the facts is highly essential. Unfortunately, there is no shortage of unreliable clichés.

Some examples of erroneous clichés that are pertinent to the question of origins follow.

“Evolution is fact” — however, major changes in organisms have not been demonstrated.

“Creation is science” — this depends on one’s definition of science, and only some aspects of creation quality.

“Evolution is religion” — this depends on one’s definition of religion.

“Creation is religion” — concepts of creation *per se* do not mandate the commitment associated with religion.

Many clichés turn out to be oversimplified and unwarranted conclusions that will only isolate us from the unavoidable complexities of reality. The remedy is more thorough study today, tomorrow, the day after tomorrow . . . every day.

Ariel A. Roth

# ARTICLES

## DO DNA DISTANCES REVEAL AVIAN PHYLOGENY?

L. James Gibson

*Geoscience Research Institute*

### WHAT THIS ARTICLE IS ABOUT

*DNA normally exists in double-stranded form, each strand composed of molecular subunits called bases. The strength of attraction between the two strands depends on proper matching of their bases. The better the matching, the stronger the attraction, and the higher the temperature required to melt them (separate the strands). DNA distance is a measure of the extent of base matching of DNA strands from different species, and can be estimated from the effect of base mismatching on the melting temperature. One unit of DNA distance is equivalent to a melting point depression of 1°C.*

*DNA distances have been used to estimate the degree of genetic similarity between species. "Family trees" have been constructed from DNA distances for most families of songbirds. Species classified as closely related usually cluster together in a distinct group with DNA distances of less than about 5 to 7. Species groups often are separated from other such groups by distances of 10 or more units. At distances more than about 8 to 10, branches tend to be so close together that the relationships among groups may be difficult to interpret. In addition, the branching pattern at greater DNA distances often conflicts with branching patterns derived from other methods of classification, leaving one to wonder which system is best.*

*The clustering of species into distinct groups suggests they may be related by common ancestry. DNA distances seem to be useful in grouping species into higher taxonomic categories. The method sometimes suggests hypotheses of relationship between groups of species, or for unique species, that may not have been seriously considered previously. This is interesting, but, as with other methods of systematics, difficulties remain. One important question is the limit of resolution of the method. It seems likely that the reliability of the method decreases as DNA distance increases, and the method is probably best used for grouping species rather than determining relationships among such groups. Nevertheless, DNA distance, along with other methods of comparing species, will continue to be of interest to all who are interested in the relationships among living organisms.*

## INTRODUCTION

Two goals of evolutionary studies are to determine the relationships among organisms and the mechanisms by which change occurs (Sibley & Ahlquist 1986). For various reasons, both goals have been elusive. Relationships among species are often difficult to establish, especially because different methods of comparison may give different results. Such conflicting results are attributed to convergence, parallelism, reversals, and unequal rates of change. These problems are usually explained as the result of natural selection. By this reasoning, the best method for determining phylogeny would be to use some feature not controlled by selection.

If, as has been suggested (Kimura 1968), most point mutations are neutral to selection, such mutations could provide a record of ancestry. It should be possible to identify mutations and determine relationships by comparing DNA sequences. Several methods of estimating DNA differences have been devised. Comparison of amino-acid sequences gives an estimate of the corresponding differences in DNA sequence for relatively small amounts of DNA. Actual sequencing of entire genomes is not yet practical. Restriction framing mapping may be the most efficient molecular method of phylogenetic estimation at the present time. Discussion of these methods is beyond the scope of this article. DNA/DNA hybridization is a very crude method of estimating sequence differences, but is the subject of this paper because of the large amount of published data for birds, and especially the single order of perching birds. In this paper, the term DNA distance is used only to refer to results of the DNA/DNA hybridization technique.

**Neutral Mutation Theory.** Based on calculations of the rate of mutations thought to be needed to explain amino-acid differences in proteins from different species, Kimura (1968) proposed that most point mutations must be nearly neutral to selection in order to explain their apparently rapid rate of fixation (see also Kimura 1979). The suggestion that mutations might be neutral led to the development of a theoretical explanation for their neutrality.

Mutations may be neutral either because they occur in DNA that is non-functional or because the mutation does not alter the function of the sequence. In many organisms from 20% to 50% of the genome may consist of highly repetitive DNA (Britten & Davidson 1971), most of which has no known function. In addition, it appears that most of the single-copy DNA is present as intervening sequences (introns) that are not translated (e.g., see Wozney et al. 1981). Most mutations in multiple-



copy DNA or in introns should theoretically have no effect on the organism (but see below).

Mutations may also be neutral because they do not change the function of a translated DNA sequence. Within coding sequences, many mutations in the third base of a codon do not alter the meaning of the codon (Jukes 1980). Such “silent substitutions” could account for as much as 17% difference between two functionally identical DNA sequences (McCarthy & Farquhar 1972). Also, mutations that result in substitution of an amino acid for a very similar amino acid might have no noticeable effect on the phenotype, and be essentially neutral.

The proposal that most mutations are neutral seems to have been generally accepted, although not universally (e.g., Bernardi & Bernardi 1986, Gillespie 1986). However, recent evidence shows that an active gene may be contained within an intron of another gene (Henikoff et al. 1986), and that two genes may overlap each other on opposite DNA strands (Adelman et al. 1987). Nesting and overlapping of genes are believed to be uncommon in vertebrates, but mutations in such DNA would probably not be neutral. It should be noted that the theory stressing the importance of neutral mutations in evolution was originally proposed (Kimura 1968) to explain the larger-than-expected differences in amino-acid sequences among several species of mammals assumed to have a common ancestry datable from the fossil record. If one accepts the possibility of separately created lineages the problem of explaining large differences between species disappears, and the issue of neutral mutations becomes less important.

**DNA Clock and Systematics.** There are large numbers of genes in the genome of a multicellular organism, and it has been argued that, even if mutation rates vary for different genes, the average rate of nucleotide substitution for all genes would be uniform over long periods of time (Sibley & Ahlquist 1983a, 1986). If true, the difference in DNA sequences between two species would be a function of the time since their divergence. This concept forms the basis of the purported “DNA clock”.

Sibley & Ahlquist (1983a) assert that DNA/DNA hybridization results give an accurate estimate of the overall sequence difference between any two species, and (1983a, 1986) that the resulting measurements of DNA distance provide a tool for accurately determining relationships and estimating times of origin of the species. Sibley, Ahlquist & Sheldon (1987) have suggested that DNA comparisons are more reliable than morphological comparisons in determining phylogeny because DNA sequences are not subject to convergence.

Recently it has been shown that differences in DNA sequences are not necessarily related to the supposed age of lineages (Sheldon 1987b, Catzeflis et al. 1987), thus invalidating the use of DNA/DNA hybridization distance data as a clock. However, the data show some interesting patterns and further investigation seems worthwhile.

## DESCRIPTION OF TECHNIQUES

**DNA preparation.** The following description of the technique is based on Sibley & Ahlquist (1983a, 1986). DNA is collected from red blood cells or other appropriate tissue. After purification, the DNA is sheared by sonication into fragments that average about 500 base pairs in length. These fragments are boiled to separate the strands, then the mixture is partially cooled. Since the number of copies of repetitive sequences in the mixture is much greater than those of single-copy DNA, they will reassociate faster. When the mixture is passed over a hydroxyapatite column, double-stranded reassociated fragments bind to the column, while the single-stranded fragments of single-copy DNA are collected in the effluent. This single-copy DNA is believed to contain 95-98% of the different sequences present (Sibley & Ahlquist 1983a, p 248).

The single-copy DNA to be used as the "tracer" is labeled with radioactive Iodine-125. Single-copy DNA from a second species is used as the "driver," and is not labeled. When the DNAs are mixed in the proportion of 1000 parts "driver" to one part "tracer," each "tracer" fragment will reassociate with a "driver" fragment, forming a hybrid DNA fragment.

**Measuring the DNA distance.** The two strands of a DNA duplex are held together by hydrogen bonding, which depends on correct matching of base pairs. The greater the extent of matching, the higher the temperature required to separate ("melt") them. The DNA distance is a measure of the reduction in melting temperature of hybrid DNA fragments, caused by differences in their base sequences, and is presumably a measure of the difference between the DNAs of the two species.

To determine the melting temperature of the hybrid fragments, they are first bound to a hydroxyapatite column. The temperature is then raised in increments, typically of 2.5°C, and the column is washed, removing any DNA which may have separated into single strands. The amount of DNA removed is measured by the level of radioactivity in the sample (due to the Iodine-125 labeling). The percentage of DNA removed at each temperature increment is plotted against temperature, producing a melting-point curve. In the most common procedure, the temperature is recorded

when 50% of the tracer DNA is recovered in single-stranded form. This temperature is subtracted from the temperature at which 50% of the pure “tracer” DNA melts. The result is called the “ $\Delta T_{50H}$ ” (delta T50H), and is used as a measure of DNA distance. In an alternative method, the measurements used are for only the tracer DNA fragments that form duplexes with driver DNA. This result is called the  $\Delta T_m$  (Sibley & Ahlquist 1983a, p 257). The latter method should be used only when the proportion of tracer DNA forming hybrid duplexes is greater than 80% (Sheldon 1987a).

**Normalized Percentage of Hybridization.** It seems that each species has some unique sequences, so that there is never a 100% match of the DNA fragments of two species. The normalized percentage of hybridization (NPH) is the amount of a species’ DNA that hybridizes with that of another species, standardized against the amount that hybridizes with DNA of its own species. High variances have been reported for the NPH values for comparisons of closely related species (Bledsoe 1987), which would make this measurement difficult to use in systematics. Under the experimental conditions used, the NPH is often less than 75%. Because the non-hybridizing DNA will not attach to the hydroxyapatite column, it is eliminated from the determination of the melting curve. If the NPH is small, only a small fraction of the DNA remains for study, making the results questionable.

**Delta T50H and DNA distance.** Experiments to determine the relationship between difference in DNA sequence and melting point change of DNA duplexes have shown that a change of 1°C in the melting point represents from 0.7% to 3.2% difference in DNA sequence, the best average estimates ranging from 1% (Bonner et al. 1973) to 1.6% (McCarthy & Farquhar 1972). Usually a  $\Delta T_{50H}$  value of 1°C is taken to indicate a difference of 1% in DNA sequences. Since the  $\Delta T_{50H}$  value and the percentage sequence difference are numerically the same, I will use the term “DNA distance” for  $\Delta T_{50H}$  values.

## DISCUSSION OF RESULTS

Among the numerous papers published on the topic, two groups have been selected for discussion. The study of the large flightless birds (ratites) was used to calibrate the “DNA clock”, and the studies of songbirds illustrate the complexity of the results.

**Phylogeny of the Ratites.** The ratites are a group of large flightless birds, including the ostrich, rheas, emu and cassowaries. The kiwi and

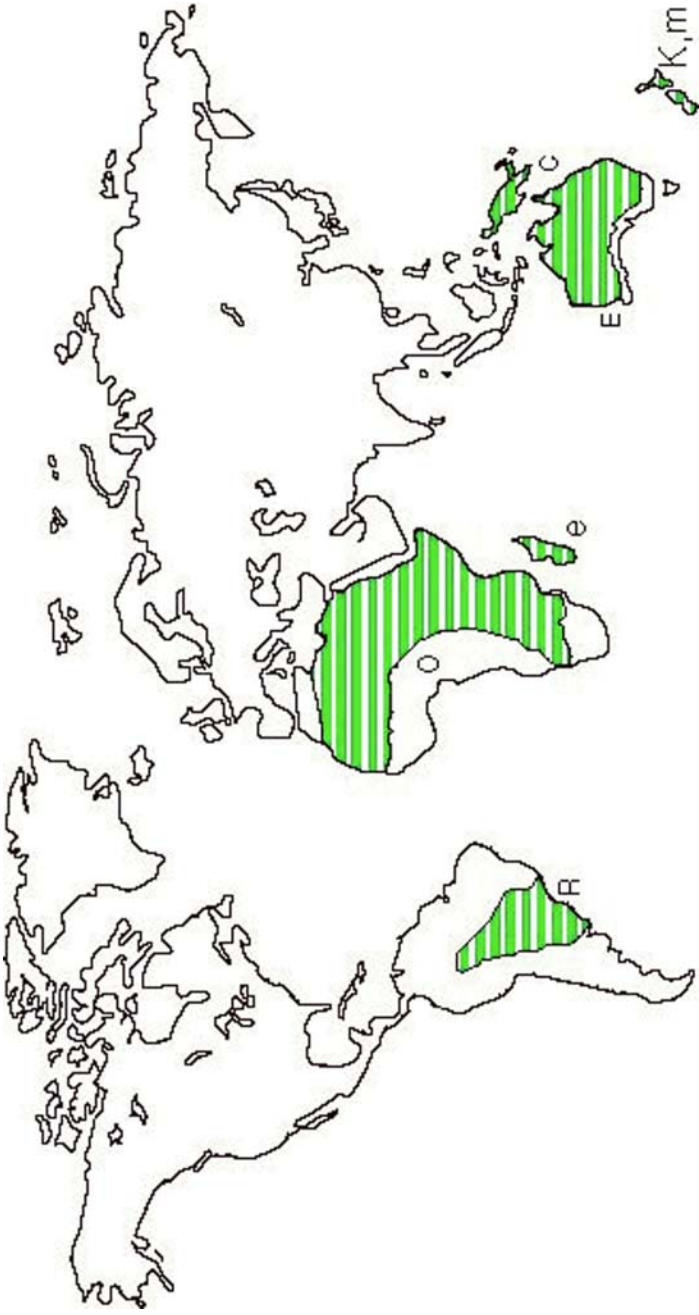


FIGURE 1. Map showing distribution of living and recently extinct ratite birds. Key: C = Cassowary; E = Emu; e = Elephant Bird; K = Kiwi; m = Moa; O = Ostrich; R = Rhea.

extinct moas are also usually included, and the extinct elephant birds and some other extinct groups are sometimes included as well (Cracraft 1974). The South American tinamous are considered to be the closest relatives of the ratites. Because all the living and recently extinct ratites are found on continental fragments of Gondwanaland (see Figure 1) and share certain skeletal features, it has been postulated that they form a natural group with a common ancestor which dispersed before the breakup of Gondwanaland.

The separation of Africa and South America due to the breakup of Gondwanaland is believed to have occurred by the Late Cretaceous, about 80 million years ago (Ma), according to conventional geological dating. This date has been used as an estimate of the time of divergence of the ostrich and rhea. These two species show a  $\Delta T_{50H}$  of about 17.4 (Sibley & Ahlquist 1985d; first calculated as 15.7, Sibley & Ahlquist 1981), indicating about a 17.4% divergence of their respective DNAs (Bonner et al. 1973). This figure was used to calibrate the "DNA clock" at about 1% divergence per 4.6 Ma.

The  $\Delta T_{50H}$  values and calculated times of divergence of the living ratites are shown in Figure 2. Since the "DNA clock" is no longer considered reliable (Catzefflis et al. 1987), the divergence times should no longer be defended. It appears that most of the ratites have extensive differences in their DNAs, and may not be related. Fossil evidence (Houde & Olson 1981, Olson 1985) has proposed that the ratites are not all related.

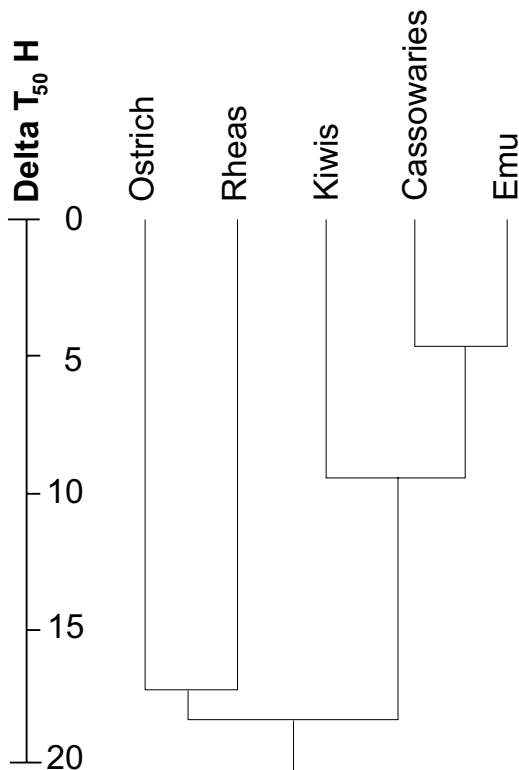
**Phylogeny of the songbirds.** The order of perching birds (Passeriformes) contains more than half the known species of birds (Bock & Farrand 1980). The New World flycatchers, ovenbirds and antbirds, and the Old World pittas and broadbills are grouped together in one or more suborders known collectively as the suboscines. The rest of the passeriforms are grouped in the suborder Passeres, or songbirds. Three main divisions of songbirds are generally recognized (Storer 1971): the corvine assemblage (crows, bowerbirds, birds of paradise, etc.), the predominantly Old World ten-primaried group (thrushes, babblers, Old World warblers and flycatchers, wrens, thrashers, etc.), and the predominantly New World "nine-primaried" assemblage (finches, woodwarblers, tanagers, blackbirds, etc.).

Sibley and Ahlquist (1985a,b,c,d and references therein) have applied the DNA/DNA hybridization technique to species representing most of the passeriform families. Based on their results, they have proposed a classification involving numerous taxonomic changes, many of which are

significant departures from more traditional classifications. They recognize (Sibley & Ahlquist 1985c) two main lineages of songbirds: a crow-like assemblage, which includes a majority of the endemic Australian species, and a second assemblage which includes the thrushes, sparrows, warblers and most other species from non-Australian groups.

The taxonomic changes proposed by Sibley & Ahlquist involve considerable re-grouping of genera, splitting certain families and joining the fragments to various other families and erection of new families from pieces of old families. The extent of the proposed changes can be illustrated by comparing the composition of their family Corvidae with the more traditional classification (see Table 1). Quite naturally, there has been a certain amount of resistance to some of these suggestions. It should,

**FIGURE 2.** DNA-distance tree for the living ratites. To determine the DNA distance between any two species, locate the point where the lines from the two species connect, and read the DNA distance from the scale on the left.



**TABLE 1**

**Comparison of classification of members of Corvidae according to Sibley & Ahlquist (1985a) with their classification in Bock & Farrand (1980).**

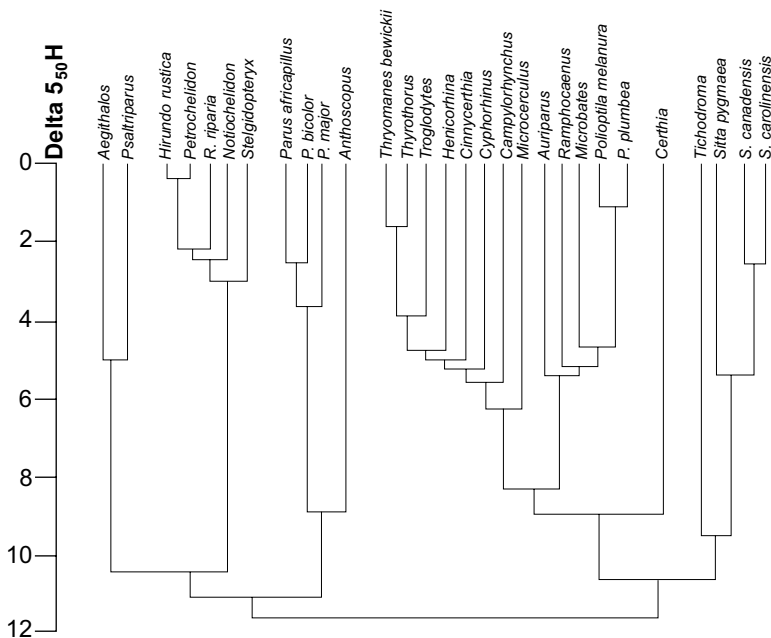
<b>Common Name</b>	<b>Old Classification</b>	<b>New Classification (Family Corvidae)</b>
cuckoo-shrikes	Family Campephagidae	Subfamily Corvinae
wood shrike	Family Laniidae Subfamily Pityriasiinae	Subfamily Corvinae
whipbird	Family Muscicapidae Subfamily Orthonynchinae	Subfamily Cinclosomatinae
silktail	Family Muscicapidae Subfamily Sylviinae	Subfamily Monarchinae
Peltops flycatcher	Family Muscicapidae Subfamily Muscicapinae	Subfamily Corvinae
monarch flycatchers	Family Muscicapidae Subfamily Monarchinae	Subfamily Monarchinae
fantails	Family Muscicapidae Subfamily Rhipidurinae	Subfamily Monarchinae
whistlers	Family Muscicapidae Subfamily Pachycephalinae	Subfamily Pachycephalinae
Australian nuthatches	Family Sittidae Subfamily Daphoenosittinae	Subfamily Pachycephalinae
figbird	Family Oriolidae	Subfamily Corvinae
drongos	Family Dicruridae	Subfamily Monarchinae
magpie-lark	Family Grallinidae Subfamily Grallininae	Subfamily Monarchinae
apostlebird	Family Grallinidae Subfamily Corcoracinae	Subfamily Corcoracinae
woodswallows	Family Artamidae	Subfamily Corvinae
currawongs	Family Cracticidae	Subfamily Corvinae
birds of paradise	Family Paradiseaeidae	Subfamily Corvinae
crows	Family Corvidae	Subfamily Corvinae

however, be pointed out that several of the genera of birds involved in the controversy have been rather puzzling taxonomically. The DNA-based classification at least provides a new approach to the problem of classifying them. Several of the challenges to the method are discussed later in this paper.

A diagram of a portion of the classification proposed by Sibley & Ahlquist (1985c) is shown in Figure 3. Note that the DNA distance between branching points is often very small. In such cases the order of branching is highly uncertain, even if the branches are statistically distinguishable. Note also that groups of species tend to form distinct clusters at lesser DNA distances, the clusters joining together in a series of closely spaced nodes at DNA distances of about 8 or greater. Some possible interpretations of these tendencies will be discussed later.

In considering the usefulness of DNA distances in classification, two aspects of systematics can be considered separately. One goal of systematics is to identify the group to which a particular species belongs. Another goal is to estimate the degree of relatedness of various species groups. Examples have been chosen from the literature to illustrate the use of DNA distances in attempting to satisfy each of these goals. The success of the technique will be evaluated by its ability to produce distinct clusters

**FIGURE 3. Partial phylogeny of songbirds. Based on DNA-DNA hybridization. To determine the DNA distance between two species, find the horizontal line joining the lines from the two species and read the DNA distance from the scale on the left of the diagram. After Sibley & Ahlquist 1985c, Fig. 16.**





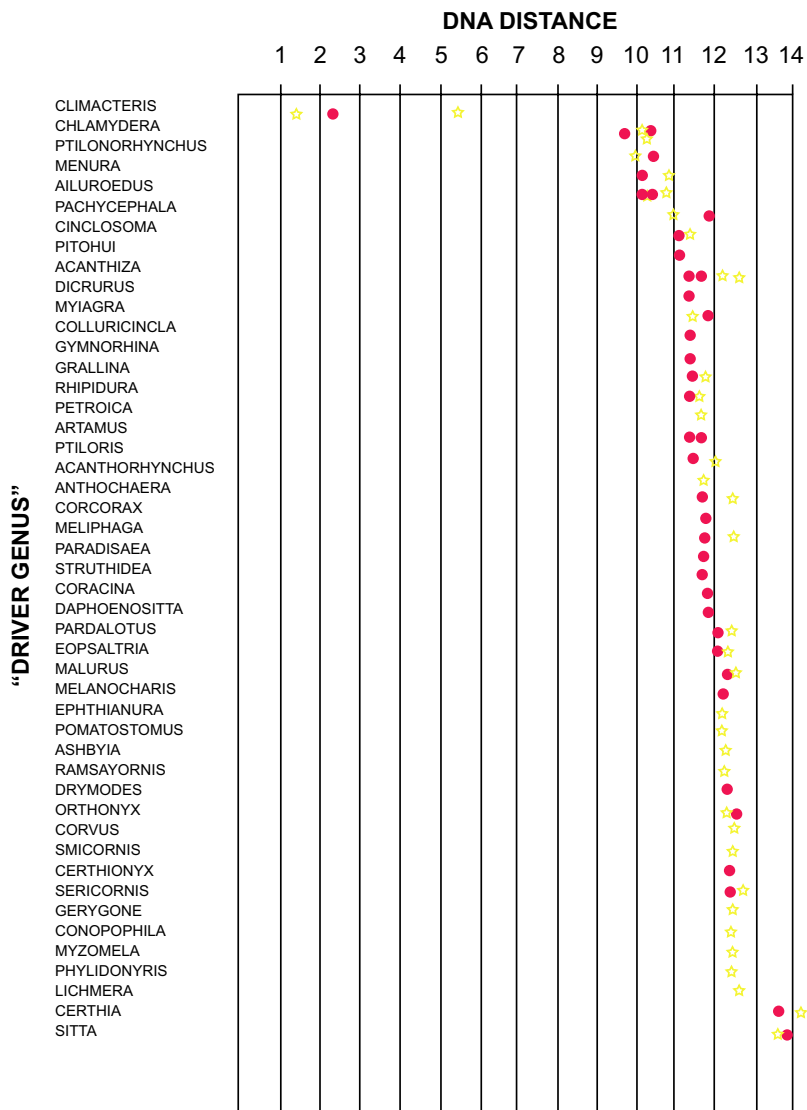
of species. Different clusters should be separated by gaps that are greater than the range of values for species within a cluster.

DNA distances for comparisons of three species of thrashers (Family Mimidae) to several species of songbirds are shown in Figure 4. Note the small distances among the thrashers, and their isolation from species in other families. One species, *Donacobius atricapillus* (see arrow in Figure 4), is classified with the thrashers in Peter's checklist (Mayr & Greenway 1960), but is far from the thrashers using DNA distances (Sibley & Ahlquist 1984b). The latter authors suggest it may be a wren, but have not measured the DNA distance involved. If *Donacobius* is truly a wren the usefulness of the DNA/DNA hybridization technique in classification would be supported.

Referring again to Figure 4, note that the starlings are grouped together, and are separated from the thrashers at DNA distances ranging from 5.0 to 6.4. Note also that the range of values within the starlings (1.4) is less than the gap (2.3) separating the family from the next closest group (Turdinae + Muscicapinae). This result suggests the surprising possibility that starlings may be the closest relatives of mockingbirds. If so, the DNA/DNA hybridization technique has been useful in the second goal of systematics mentioned above, determining which other groups are most similar to a given group of species. However, gaps between groups become less than ranges within groups for DNA distances above 8, and DNA distances between different groups run together at values over 10. This pattern of distinct clusters at values less than about 8, and joining of many clusters at values over about 8 or 10 is also seen in comparisons for several other genera (Sibley & Ahlquist 1982a,b; 1985d), and suggests that DNA distances are most meaningful for values less than perhaps about 8.

A somewhat different situation is illustrated by the DNA distances for Australian treecreepers, shown in Figure 5. Two species of treecreepers are separated by a DNA distance of 5.4, an unusually high figure for species in the same genus, leading to the suggestion they be placed in separate genera (Sibley, Shodde & Ahlquist 1984). No other family seems close to the treecreepers based on DNA distances. The closest species are bowerbirds, but the DNA distances (>10) are not sufficiently distributed to clearly indicate relationships. Thus it appears that either the treecreepers have no close relatives, or their relatives were not included in the tests, or the tests were unsuccessful in identifying them.





**FIGURE 5.** Some DNA distances for two species of Australian treecreepers, *Climacteris rufa* (☆) and *C. picumnus* (●), Family Climacteridae. Note the unusually large DNA distance of 5.4 between the two species of *Climacteris*, and the large gap separating the genus *Climacteris* from all other genera. Data from Sibley, Schodde & Ahlquist 1984.

Not all DNA distance experiments produce distinct clusters of species. DNA distances for the blue vanga of Madagascar are shown in Figure 6. No distinct clusters are seen, nor any very close relatives. A similar lack of meaningful clustering is shown by the Australian "nuthatches" (Sibley & Ahlquist 1982c). Another problematic result is illustrated in Figure 7. Here the DNA distances for the olive bush-shrike are shown. Note the lack of distinct clustering among the values. The gaps that do exist are small, and do not appear to have biological significance. In these instances, the DNA/DNA hybridization method does not seem to have given a clear answer to the question of the relationships of the species involved.

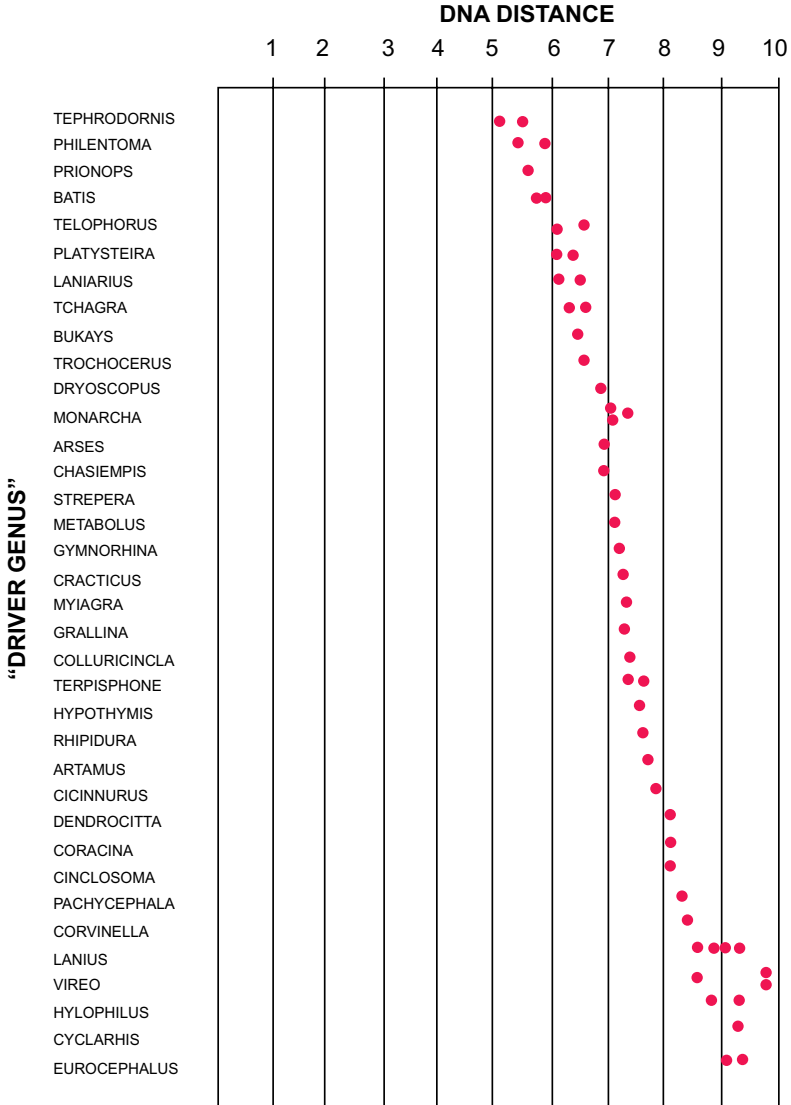
### **CRITICISMS OF DNA HYBRIDIZATION METHODOLOGY**

Several papers critical of various aspects of DNA hybridization have recently been published (Templeton 1985, 1986; Britten 1986; Houde 1986, 1987; Cracraft 1987). The criticisms may be divided into those pertaining to the assumptions, the experimental technique and the interpretation of the data (Houde 1987). I will discuss several of the criticisms that have been raised.

**Criticisms of the Assumptions of the Method.** Acceptance of the method of DNA hybridization is based on the acceptance of certain assumptions, such as that all single-copy DNA sequences have homologs with which they can hybridize, and all degrees of divergence can be detected (Sibley & Ahlquist 1983a, p 257). Another assumption is that nonhomologous sequences will not be similar enough to hybridize (Sibley, Ahlquist & Sheldon 1987, p 114). However, each of these assumptions is sometimes violated (see Templeton 1986, Zweibel et al. 1982).

The first assumption is violated because different lineages probably have unique sequences, without homologs in other lineages. If homologous sequences have diverged beyond the 75-80% matching required for duplex formation (Sibley, Ahlquist & Sheldon 1987), homology could not be detected by the method.

The second assumption is violated because not all degrees of divergence can be detected. For example, random reassociation is reported below about 45°C (Sibley & Ahlquist 1981, p 305), making analysis impossible below this temperature. To avoid this problem, the beginning temperature used experimentally is usually about 60°C. Since most homologous hybrids melt at about 80-85°C, the method can be applied only for  $\Delta T_{50H}$  values less than about 20-25 units. Even this range may be too great, as a rapid



**FIGURE 6.** DNA distances to several species of songbirds, for the blue vanga, *Leptopterus madagascarinus*, Family Vangidae. Note the lack of significant gaps in the range of values. Data from Sibley & Ahlquist 1985d.

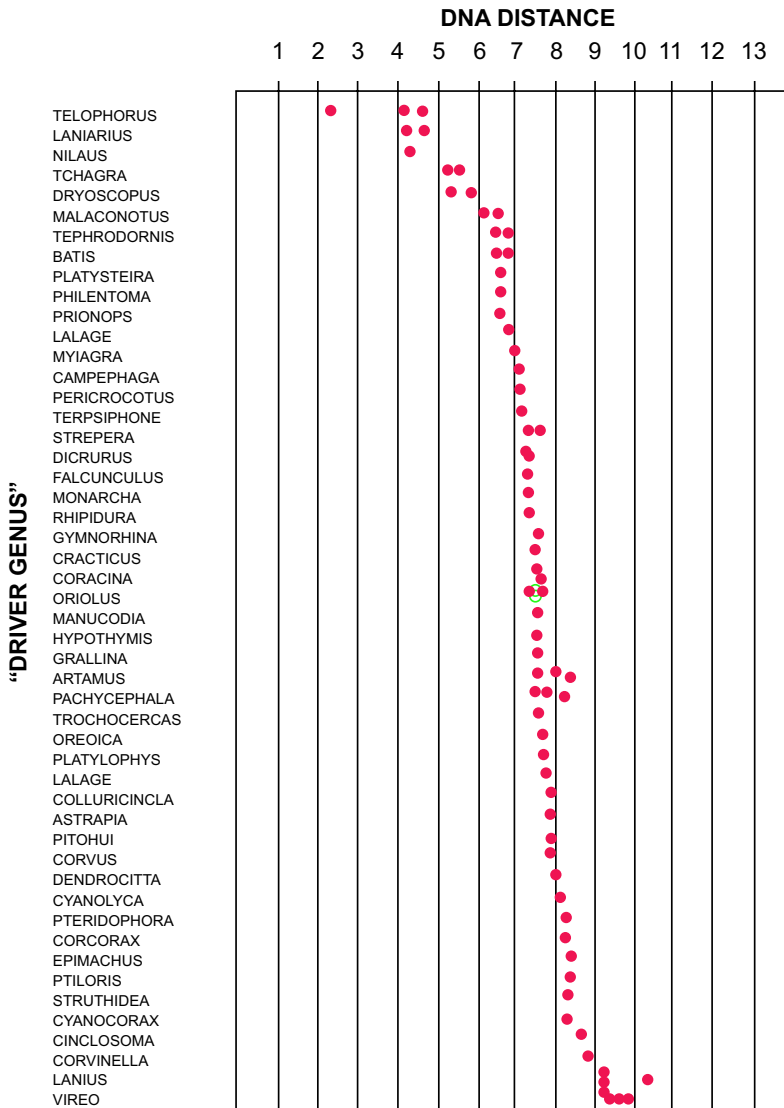
departure from a linear relationship is reported at  $\Delta T_{50H}$  greater than about 15 (Houde 1987; Sibley & Ahlquist 1985d, p 152).

The assumption that nonhomologous sequences will not form duplexes may be true in most cases, but it appears that some nonhomologous proteins do have similar amino-acid sequences (see Hill & Hastie 1987, Schwabe & Warr 1984), implying similar DNA sequences and the possibility of nonhomologous matching in duplex formation.

**Criticisms of Experimental Methodology.** The experimental methodology has been criticized on two main counts: experimental uncertainty and the nature of the DNA sequences being compared.

Variation in fragment size may cause inconsistencies in experimental results (Sibley & Ahlquist 1981, p 307; Sibley, Ahlquist & Sheldon 1987, p 104). Differences in fragment length can alter the melting temperature by 1.5 to 2.5°C (Caccone & Sbordoni 1987). Variation between individuals of a species can also affect experimental error (Cracraft 1987), and should be better analyzed. However, in hybridizations involving six species and subspecies of juncos, the maximum  $\Delta T_m$  distance detected was only 0.2 (Shields & Straus 1975). The range of  $\Delta T_{50H}$  values among 13 individuals of the American robin was 2.1 (Sibley & Ahlquist 1983a). Repeated measurements using the same material may vary by 0.6°C (Sibley & Ahlquist 1983a, p 265). Overall uncertainty has been estimated as from 0.4 (Shields & Straus 1975) to about 2 (Sibley & Ahlquist 1981, p 319) or possibly even as high as 3.1 (Sibley & Ahlquist 1983a, p 275). It appears that the total uncertainty in comparing two DNA distances based on single measurements could be large enough to cause problems in interpretation.

Another question concerns the nature of the DNA used in the experiments. The distinction between single-copy and multiple-copy DNA depends on experimental conditions (McCarthy & Farquhar 1972). If DNA from different species reacts in different ways, it seems possible that the DNA samples from the two species might not be equivalent qualitatively or quantitatively. How well the technique separates the single-copy DNA is not clear (see Sibley & Ahlquist 1981, p 319), nor is it certain that the single-copy DNA contains the sequences that distinguish species. Species differences may be determined by developmental control sequences, which may be found among the moderately repetitive sequences. The sometimes considerable differences between phylogenies based on DNA distances and those based on morphology raise the question of whether the appropriate data are being collected. (For further discussion



**FIGURE 7.** DNA distances to several species of songbirds, for the olive bush-shrike, *Telophorus olivaceus*, Family Laniidae. Note the lack of significant gaps in the distribution of the values. Data from Sibley & Ahlquist 1985d.

of this point, see below under section titled “DNA distance and relationships.”)

**Criticisms of Data Interpretation.** The most severe criticisms of the DNA distance method have been directed against the method of tree construction and the accuracy of the “DNA clock.”

The validity of using a single distance figure to construct phylogenetic trees is open to question. DNA distance may not be an accurate indicator of branching order if it is not well correlated with time. This is because the DNA distance is the sum of the differences between two species. Species that diverge slowly might have smaller DNA distances than species that diverged rapidly, regardless of time since divergence. Simply showing that two measurements are statistically different (e.g., Sibley & Ahlquist 1987) does not necessarily indicate their order of branching. Since it has been shown that rate differences exist (Catzefflis et al. 1987, Houde 1987, Sheldon 1987b), trees based solely on DNA distance should be checked against other methods.

Another problem with the method of tree construction is that branching points within a tree are often separated by less distance than the experimental uncertainty (usually estimated at about 1.0, but possibly up to 3.0 units, Sibley & Ahlquist 1983a, p 275). Branches of a tree should be separated by distances greater than the experimental uncertainty if the data are to be used to determine the order of branching.

Another criticism of the method of tree construction is that it is not cladistic, that is, the DNA hybridization method makes no distinction between “shared derived” sequences and “shared primitive” sequences. Instead, it is simply an attempt to sum the unique (autoapomorphic) sequences of two species. In addition, Houde (1987) has pointed out that the branching pattern of a DNA distance tree depends on the clustering method used, and Lanyon (1985) has shown that omission of a single taxon can affect the branching order of the remaining taxa. This lack of stability of some DNA trees under differing conditions weakens confidence in the method.

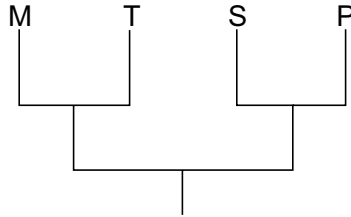
Phylogenetic trees based on DNA distance often conflict with trees based on other types of data (e.g., Sibley & Ahlquist 1984a, 1985a,b,d; Lanyon 1985). Agreement of DNA distance data with morphological data is good when species are morphologically similar, but declines as morphological differences increase, such as at the levels of family and order (Sibley & Ahlquist 1983a, p 278). Three phylogenies of the superfamily Tyrannoidea, each based on a different database, were compared by Lanyon



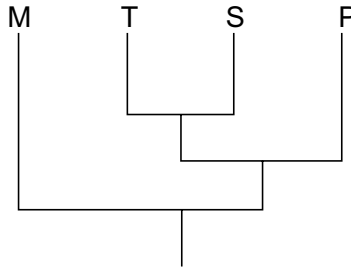
(1985). The three databases were based respectively on morphology, protein electrophoresis, and DNA/DNA hybridization (see Figure 8). Each phylogeny was different, with no agreement of all three methods on any relationships at the family or subfamily levels. Lanyon (1985) suggested that the three groups may all have arisen at essentially the same time. The lack of agreement between different methods may suggest the existence of separate lineages. On the other hand, it might be that the three groups are descended from a common ancestor with a high degree of genetic

**FIGURE 8.** Comparison of trees for four species of suboscines. Based on three different data sets M = *Myiarchus*, S = *Schiffornis*, T = *Tityra*, P = *Pipra*.

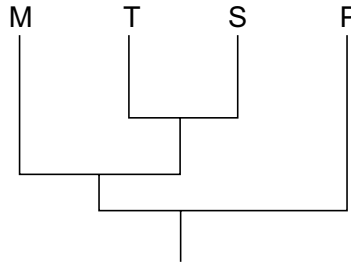
**A.** Cladogram based on electrophoretic data. Adapted from Lanyon 1985, Fig. 4.



**B.** Cladogram based on morphological data. Adapted from McKittrick 1985, Fig. 1A.



**C.** Phenogram based on DNA distance data. Adapted from Sibley & Ahlquist 1985b, Fig. 1.



variability, or that point mutations are not the only factor affecting measurements of DNA distance.

**Some Comments on the DNA Clock.** Although Sibley & Ahlquist have backed away from their earlier insistence that their method is clock-like (Catzefflis et al. 1987), the idea is still considered useful (Sibley & Ahlquist 1987) and a few comments concerning the “clock” are given below.

The theoretical basis for the DNA distance clock rests on the assumption of the importance of neutral mutations. Yet the method is designed to eliminate most of the DNA in which mutations seem most likely to be neutral, the repetitive DNA. Mutations in translated sequences of the single-copy DNA may be subject to natural selection to a significant extent. If true, different branches of a lineage might diverge at different rates, making it impossible to reconstruct the order of branching from the distance data. The importance of this effect would depend on the relative proportions of translated DNA and non-translated intervening sequences. Mutation rate differences of 25-50% have been reported among herons (Sheldon 1987b) and primates (Fitch 1986; Bonner, Heinemann & Todaro 1980). Catzefflis et al. (1987) estimated the rate for rodents to be ten times the rate for hominoid primates. These estimates are based on evolutionary assumptions concerning the time since divergence from a hypothetical common ancestor, and show that the proposed clock is not consistent with the evolutionary assumptions.

It is difficult to compare estimates of time since divergence based on DNA distances, with estimates based on the fossil record. Fossil songbirds are not abundant and are difficult to identify even to family. However, no fossil songbirds are known before the Miocene (Brodkorb 1987, Olson 1985), while the proposed DNA distance clock suggests divergence of most families by the end of the Eocene (Sibley & Ahlquist 1985c). This difference has not been resolved satisfactorily.

The reason for differences in mutation rates is not yet known. It has been suggested (Britten 1986; Li, Tanimura & Sharp 1987) that mutation rate may depend on the number of DNA replications per year. This hypothesis has not been adequately studied, but does not appear to be satisfactory. Another suggestion (Britten 1986) is that differences in mutation rates are due to differences in efficiency of DNA replication and repair enzymes. Another possibility that deserves more attention is that many differences in DNA sequences may be the result of the original creation of separate lineages rather than to divergence from a common ancestor.

## WHAT DOES DNA DISTANCE MEAN?

Despite the shortcomings of the DNA/DNA hybridization method, there appear to be some interesting patterns in the results. It seems useful to attempt to evaluate the data to determine whether it can be meaningfully interpreted within a creationist philosophical framework.

**Causes of DNA Sequence Similarities.** Similarities in organisms could come about from a number of different causes (see Coyne & Barton 1988, Gibson 1986). Neither chance nor convergence seem plausible as causes of DNA sequence similarity. Sibley & Ahlquist (1985c, p 84) state that 80% homology is required to form a stable DNA duplex at 60°C. Random changes do not seem likely to create 80% similarity in a sequence of 500 base pairs, even if aided by selection. The possible importance of constraints on genetic variation as a cause of convergence is not known. Cross-species gene exchange has been suggested as a cause of DNA similarity (Syvanen 1987), but it is not well understood, and seems to be uncommon.

There are at least two other possibilities for explaining similarities in DNA sequence: common ancestry and common design. Creationists accept both factors as valid. The question of interest here is whether the DNA distance data show any pattern that might be useful to distinguish common ancestry from common design. The following sections pursue this question further.

**How Rapidly Do DNAs Diverge?** The rate of change of DNA sequences has never been measured directly, so it is difficult to estimate how much DNA divergence is plausible within 5,000 to 10,000 years. No practical method is available that detects all point mutations in an entire genome, although it is possible to clone and sequence a gene and compare genes from different species. To be meaningful, variation within a population would have to be distinguished from variation between populations. It is problematic whether the results could be extrapolated to entire genomes.

Experimentally detected spontaneous mutations appear to be rare. Most estimates of mutation rate are based on protein electrophoresis, and are minimum rates because electrophoresis detects only mutations resulting in a substitution of an amino acid having different charge characteristics. Overall mutation rates are greater by an unknown amount. Mutation rates for laboratory mice have been estimated at about  $10^{-6}$  per locus (gene) per generation (Neel, Mohrenweiser & Mesiler 1980; Russell et al. 1979;

Johnson & Lewis 1981; Johnson et al. 1985). This is about  $10^{-9}$  per nucleotide per generation (assuming an average of  $10^3$  amino acids per locus, see Table 2 in Jukes 1980). A mutation rate of  $10^{-8}$  (per nucleotide) as an average for the entire genome would suggest a rate of DNA divergence on the order of 1% per Ma, or 0.01% per 10,000 years.

The highest mutation rate known for a human genetic disease (Duchenne muscular dystrophy) is about  $10^{-4}$  (Rotter & Diamond 1987, Moser 1984). This seems a very high rate for a deleterious mutation, and suggests that there is much more to learn about mutation rates, such as the causes of mutational "hot spots". The DNA/DNA hybridization technique is probably sensitive to major differences in DNA sequence, but may not be able to distinguish small differences from experimental uncertainty. The questionable ability of the method to identify homologous sequences also weakens any confidence one might like to have in any estimate of mutation rate based on DNA distance. Since DNA distance is not considered to be linear with time (Sibley & Ahlquist 1985c, Catzefflis et al. 1987), estimates of mutation rates based on DNA distance might not be meaningful. Rough estimates are from about 0.1% per Ma to more than 1% per Ma (Britten 1986, Table 1). These estimates are based on assumptions of a hypothetical common ancestor and a datable speciation event.

Determinations of DNA distance between populations of known historical age are not available. Many historically dated introductions are known, and measurements of DNA distances among them would be of interest. If different individuals of a species may differ by more than 2 DNA distance units (Sibley & Ahlquist 1983a), it seems likely that newly formed daughter species could differ by that amount at the time of their formation.

Based on a study by Fitch & Atchley (1985), Lewin (1985) suggested that mutation rates in inbred laboratory mice may be as high as about  $5 \times 10^{-4}$  per locus, which would be about  $5 \times 10^{-7}$  per nucleotide pair per generation. The rate of DNA divergence calculated from this mutation rate would be on the order of 0.5% divergence per 10,000 years, far higher than previous estimates. However, other explanations of the data have been offered (Bishop et al. 1985, Bonhomme et al. 1987, Green et al. 1985, Johnson et al. 1985). The present interpretation (Fitch & Atchley 1987) seems to be that the original breeding stock came from a cross between two subspecies and that a high degree of heterozygosity has

been maintained in the breeding stock. Thus there seems to be no presently accepted evidence that inbred mice have high mutation rates.

**DNA Distance and Relationships.** It seems likely that all species in a genus of birds share a common ancestry. DNA distances for congeneric birds are usually less than about 3.0, although distances as high as 5.3 have been recorded (Sibley & Ahlquist 1985d). Experimental uncertainty can easily explain distances of 2.5 (see above under criticisms of methodology). Distances greater than 4 or 5 are not so easily explained by experimental uncertainty, and another explanation should be sought.

Differences in DNA among genetically related species may not be due exclusively to point mutations. Viruses, movable elements, and chromosomal deletions and rearrangements may affect comparisons of DNA sequences. The effects of these factors should be investigated. Natural selection may also affect DNA sequences greatly enough to affect DNA distances. If most mutations are subject to natural selection rather than being neutral, it will be necessary to reevaluate the use of DNA sequence comparisons in estimating mutation rates and in estimating the importance of neutral mutations in evolution.

On the other hand, species may have been created with a high degree of genetic variability, with many different genes acting on single traits (polygenes) and many alternative forms of genes (multiple alleles). Speciation could then result in division of the original gene pool with concomitant differences in DNA sequences without the need for mutations (see Lester & Bohlin 1984, p 168). The result would be increasing specialization and loss of adaptability, trends well illustrated in insular faunas.

The fact that DNA distance is sometimes poorly correlated with other methods of classification illustrates the difficulties in classification. The example of the groups of New World tyrant flycatchers has already been mentioned. A few other examples are described in the paragraphs below. The barbets (family Capitonidae) are believed to be related to the woodpeckers, and are found in both Africa and South America. DNA distances between species of this family are as high as 17.4 (Sibley & Ahlquist 1985d). The explanation given is that the African and South American groups are only distantly related, although they are morphologically similar.

On the other hand, the DNA distance between pelicans and New World vultures, classified in different orders, is only 9.7 (Sibley & Ahlquist 1985d). This latter figure is about the same as the DNA distance between kinglets and Old World warblers, both from the same subfamily (Sibley & Ahlquist 1985c).

Species from different subfamilies of vireos may have DNA distances of only 4.1 (Sibley & Ahlquist 1982b). Compare this with the DNA distance of 5.3 for two species in the same genus of treecreepers (Sibley, Schodde & Ahlquist 1984). One would expect species from the same genus to have smaller DNA distances than species from different subfamilies. It appears that similar DNA distance values may not have the same significance in different groups, and may not always be accurate indicators of relationships.

Although taxonomic groupings determined by DNA distances are often congruent with those determined by morphology, the number of inconsistencies is substantial. Unless some independent evidence can be found to support the relationships proposed from DNA distances, it seems reasonable to suggest that a point is reached beyond which the DNA/DNA hybridization method is not useful in determining relationships. On the other hand, if morphology is truly subject to convergence as much as is suggested by the DNA/DNA hybridization technique, classifications based on morphology need to be reevaluated. The usefulness of fossils in tracing ancestry would also be seriously challenged, since morphology is the basis for comparing fossils.

**Design Vs Ancestry.** One goal of creationism would be to search for some method of distinguishing differences in design from differences resulting from divergence from a common ancestor. It would be desirable to find a method that clusters species into separate and distinct groups. The DNA distance method seems to be able to do this for some groups of songbirds (see Figure 4) but does not do so well with others (see Figures 6,7).

Since DNA distances for songbirds seem to produce species clusters at low values, and these clusters often seem distinct at DNA distances of about 8 or less (see Figure 3), one could propose that the species within such a cluster may be truly related by ancestry. Distances greater than 8 or 10 appear to be of limited usefulness in determining relationships, either because of limitations of the technique, or because such differences are due to separate ancestries.

Additional data would be helpful in testing whether these figures are plausible. Especially interesting would be determination of DNA distances for the following: populations of known historical age, such as various breeds of pigeons or other domesticated species; similar species with greatly differing chromosomal banding patterns, such as the muntjacs; and groups with disjunct distributions, such as parrots or trogons. Complete

matrices of DNA distances for all species in a few related groups would also be of interest. Such information could significantly affect the above tentative interpretations.

## SUMMARY AND CONCLUSIONS

DNA strands are held together by hydrogen bonding between complementary bases in the DNA. The closer the matching of the two strands, the higher the temperature required to separate them. DNA distance is the number of degrees Celsius the melting temperature of a hybrid DNA duplex is lowered because of mismatching of DNA bases from the two different species. DNA distance is used as a measure of the similarities in base sequence of DNA from two species, and is used as an estimate of the closeness of their relationship. However, as the difference between two species increases, the amount of DNA able to form duplexes decreases. If the portion forming duplexes is less than perhaps 90-95% of the DNA fragments, the results may be of questionable significance.

Phylogenies based on DNA/DNA hybridization have been constructed for several groups, including ratites, herons and songbirds. Among songbirds, the following trends are noted:

1. DNA distance values using a single tracer species are typically not continuously distributed, but show gaps at values less than about 8. At values above about 10, the values become more nearly continuously distributed (Figure 4).
2. Species often tend to form clusters that are separated from other clusters at DNA distances of about 6 to 9 (Figure 3).
3. Nodes joining species clusters at distances of about 10 or more are so close together as to make sequencing of the nodes highly questionable (Figure 3).
4. DNA distances seem to be useful in assigning a species to a group for values less than about 6 or 8. Occasionally, a DNA distance value is unexpectedly high, suggesting a species has been misclassified (e.g., *Donacobius*, Figure 4).
5. DNA distances sometimes indicate a probable genetic similarity of two groups of species (e.g., mimids and sturnids, Figure 4) at values less than about 8.
6. DNA distances of the same magnitude do not necessarily have the same significance in different groups (see above discussion under DNA distance and relationship).

These trends suggest the following tentative conclusions:

1. Low DNA distances (less than 5 or 6) between species of songbirds suggest genetic similarity, and probable common ancestry if supported by other data.
2. High DNA distances (above 10) suggest genetic differences, but are not necessarily indicative of evolutionary relationships between groups. Instead, they may suggest different ancestries.
3. The results of DNA distance experiments are sometimes unclear and should not be used as the sole basis for a phylogeny.
4. Equal DNA distances in different groups do not necessarily have equivalent meaning. Results from one group should not be extrapolated to another group.

To this creationist, the DNA-distance data present interesting hypotheses that might not have been thought of without the technique. From this view, the method is interesting and stimulating. However, the method is fraught with difficulties similar to those of other methods of systematics. The ability to cluster species into groups is interesting and may be useful. Attempting to infer time since divergence or the precise order of speciation events seems to require too much from the method. More data would be of interest, especially complete matrices for family groups, and DNA distances between isolated populations of known historical age. Such data will continue to be of interest to those interested in developing a modern creationary theory of systematics.

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# NEWS AND COMMENTS

## THE LONGER LOOK

Thirty years ago it would have been unrealistic to predict what we now see in the creation-evolution controversy. The issue was essentially dead. One had to really search for the rare disparaging remarks that characterized the muffled war. Little did one realize that in two decades a plethora of books, journals, pamphlets and debates would address themselves exclusively to the issue. Both TV evangelists and popular scientific writers would indulge freely in the melee.

A few interesting facts and trends have surfaced. Creationists who thought they were a small peculiar minority have been surprised to find how common they are. A 1982 Gallup poll indicates that 44% of adults in the US believe in creation, while only 9% believe in naturalistic evolution. Recent surveys in three states indicate that about ¼ of students in college classes believe in creation, and one scholar reports that “the creationist view of science is the majority view in the United States even among the educated portions of society” (Chronicle of Higher Education, Dec. 10, 1986). Another surprise has been the acrimony that has characterized what is sometimes considered to be an intellectual battle. More than academic questions are involved. This is no doubt due in part to the fact that one’s world view affects much more than the intellectual dimensions of reality. While in general the conflict has united differing factions against a common enemy, the current controversies among biologists over the mechanism of evolution seem surprising.

Some are deploring the disarray with a strong plea for moderation, while others shout victory for their side. A significant number of scientists and theologians are taking cognizance of the argumentation and are attempting some kind of synthesis that is usually a compromise of both sides.

In view of the many unexpected changes during the last few decades, it would seem almost foolhardy to say anything about the future. Possibly longer trends could give some clues. It is not expected that the scientific community, which has now grown powerful, will easily yield to non-naturalistic explanations of origins. Neither is it expected that the Bible, which has withstood assaults for many centuries, will disappear. The many attempts to compromise naturalistic evolutionary views with creation concepts have thus far not resulted in well-defined concepts that have

cogent support. Neither naturalistic science nor the Bible can really accept such views. It does not appear that we are headed towards an easy solution, and indications are that for now at least the conflict will endure.

Ariel A. Roth

# ANNOTATIONS FROM THE LITERATURE

## CREATIONISM

Pun PPT. 1987. A theology of progressive creationism. *Journal of the American Scientific Affiliation* 39:9-19.

*Summary.* A recent article (JASA 38:11-18) discussed theological problems with theistic evolution and progressive creation. In this response, Dr. Pun outlines a theology of progressive creationism, summarized in the following three arguments: 1) God is continuously involved in His creation, using natural selection and other processes; 2) Adam and Eve are historical figures, and the Fall was an historical event; 3) God is revealed in both nature and scripture. Pun criticizes contemporary creationism for allegedly not accepting scientific evidence supporting natural selection and the antiquity of the earth, and for allegedly implying that God is no longer actively involved in His creation. Theistic evolution is faulted for not taking Genesis seriously and for not adequately explaining the origin of evil. Neo-orthodoxy is criticized for allowing God to interact with individuals, but denying His action in a historical creation.

*Comment.* By outlining some aspects of the theory of progressive creationism, Dr. Pun has made it easier to evaluate this theory. In this respect, the article is useful, although as an answer to the criticisms leveled at progressive creation it is quite unconvincing.

Van Dyke F. 1986. Theological problems of theistic evolution. *Journal of the American Scientific Affiliation* 38:11-18.

*Summary.* The author, a wildlife biologist, raises both theological and scientific objections to theistic evolution. Theological objections center around the biblical view of death. Evolution cannot operate without death and replacement of individuals. Natural selection, the generally accepted mechanism of evolution, cannot operate without competition, which requires resource scarcity, and death. Yet the biblical view of death is that: 1) it is a curse resulting from sin; 2) it was opposed by Jesus Christ; and 3) it will be abolished in the Kingdom of God. Thus it is inconsistent with the biblical record to postulate death before sin. The same argument can be applied to the theory of Pro-

gressive Creation, in which death and speciation of animals supposedly preceded the creation of man.

Scientific objections to theistic evolution concern the effectiveness of competition and natural selection. Competition itself has been somewhat controversial and notoriously difficult to demonstrate. Van Dyke argues that such a mechanism is too weak to be effective in creation of new adaptations. Natural selection is seen as opportunistic but not creative. The author ends with an appeal to creationists to conduct research within a paradigm in which natural selection operates on previously created life forms to produce variation.

Wilcox DL. 1986. A taxonomy of creation. *Journal of the American Scientific Affiliation* 38:244-250.

**Summary.** The most important conceptual difference between world views is the relationship between God and matter. Five different views of this relationship are discussed, ranging from “full theism” to “materialism.” These differences are explored from four considerations regarding matter: origin, intervention, existence, and direction. The author identifies four of the most frequently discussed positions: atheistic evolution, recent creation, progressive creation, and theistic evolution, which could also be called “continuous creation.” The problem with theistic evolution is “not that it concedes too much to materialism, but that it refuses to concede so much as the spin of a single electron.” In conclusion, Wilcox accepts the usefulness of materialistic explanations “within the limits set by their simplifying assumptions.” It is acceptable to rule out scientific explanations based on the activity of God, so long as one realizes such limitations are only a model, and not reality itself.

## EVOLUTION

Godfrey LR, editor. 1985. *What Darwin began: modern Darwinism and non-Darwinism perspectives on evolution*. Boston: Allyn and Bacon. 312 p.

**Summary.** This collection of essays embodies a discussion of Darwinian and post-Darwinian evolutionary ideas mixed with anti-creation arguments. A few of the essays are excellent; most betray an unsatisfactory degree of unsupported argumentation.

**Comment.** The book gives a good general overview of current evolutionary thought and may serve to comfort the confirmed



evolutionist, but will do little to convince one who has serious questions about evolution.

## PALEONTOLOGY

Blinderman C. 1986. *The Piltdown inquest*. Buffalo, NY: Prometheus Books. 261 p.

*Summary.* *The Piltdown Inquest* is a comprehensive review of science's "most sensational and influential hoax." The author takes the reader through a historical review of the observed and inferred complexities of the fabrication of the Piltdown skull. The fossil, which for a while gained a respectable place in man's evolutionary tree, has been found to consist of a human skull and an ape jaw. It has been facetiously described as the first human being to have false teeth. The writer also discusses at length a number of possible suspects and includes his own solution. Though the book reads like a detective story, conjecture is well-separated from the facts, which are well-documented. In his concluding section Blinderman discusses the reaction of creationists to this ingenious fabrication, as well as the merits of the recognition and correction by evolutionists. He leaves the reader with some anticipation concerning the possibility of other undiscovered falsehoods.

## LITERATURE REVIEWS

*Readers are invited to submit reviews of current literature relating to origins. Mailing address: ORIGINS, Geoscience Research Institute, 11060 Campus St., Loma Linda, California 92350 USA. The Institute does not distribute the publications reviewed; please contact the publisher directly.*

### WORKING ON THE FLOOD

THE GEOLOGY OF THE FLOOD. 1987. G.R. Morton. Dallas TX: DMD Publishing Co. 176 p.

*Reviewed by R.H. Brown, Geoscience Research Institute*

This is not a book for the individual who is looking for an effective scientific defense of the flood, chronology, or creation as presented in the first eleven chapters of Genesis. But without hesitation I classify it as an essential addition to the library of everyone who is seeking to *develop* explanations for scientific data that are pertinent to the testimony of these chapters. The massive bibliography alone justifies such classification. Of equal value are the author's critiques of the various attempts that have been made to develop a biblically supportive model for the pertinent scientific data. Since he makes his analyses from the viewpoint of sympathetic biblical literalism combined with scientific competence, some readers who have derived great comfort from a particularly narrow model of scientific creationism or flood geology will be deeply disturbed by Morton's revelations.

Not all of Morton's critiques are as thorough or as favorable as their target deserves, but in every case they contribute to the development of a more credible treatment of scientific data from a biblical perspective. In my judgment, Morton can be faulted for excessive insistence on rationalistic explanation. For example, he says that "there can be no worldwide flood" (p 83) if we cannot satisfactorily account for the source and the disposition of the water! Is our available data *that* complete, and our ability to understand *that* good?

Morton is convinced that all the pertinent scientific data from geomorphology to radioisotope age, fossil evidence for evolution of species, and astrophysics can be explained on the basis of a universal increase in permittivity (the dielectric constant of free space) during and since the year of the Noachian flood. This increase in permittivity has presumably caused the Earth to expand to double the diameter it had before the flood. The

reader who does not accept this all-encompassing explanation will nevertheless gain fresh and beneficial insights from Morton's various detailed attempts to justify it.

Morton's handling of biblical sources is questionable when he rejects a chronology based on Genesis 5 and 11 on the basis that the Gospel of Luke (ch 3, v 36) lists a Cainan who is not included in Genesis 11 (p 125). Luke merely quotes from the Septuagint, a source which was prepared over 1100 years closer to Moses than was the Masoretic text on which our English translations are primarily based and which *does* give chronologic data for the extra Cainan. It is quite probable that both the Septuagint and the Masoretic give abbreviated name lists in Genesis 5 and 11. Omission of the names of some intervening individuals in no way renders meaningless the time intervals specified between those who are listed.

In order to make his increasing permittivity model consistent and reasonable, Morton places creation not less than about 125,000 years ago, and not more than about 14 million years ago (p 126). If one abandons the less-than-10,000-years constraint from Genesis 5 and 11, why not accept the conclusions of the overwhelming majority of scientists that the universe as presently observed is the product of processes that have been in operation for probably in the order of 15 billion years, and that the Solar System has been in existence for about 4.56 billion years?

*The Geology of the Flood* is spiralbound and printed at 17 characters per inch with a dot-matrix printer. It contains frequent typographical errors, a few of which impede the reader's comprehension of the author's thought. The most notable example is on page 144, paragraph 2, line 1, in which "was deposited rapidly, the shell" evidently has been omitted following "If the sand" and preceding "would not have time to wear away...." There is a good index of topics and proper names that appear in the text, along with a helpful index of the 51 figures and 21 tabulations it contains.

In conclusion I wish to reemphasize the first four sentences of this review.

# GENERAL SCIENCE NOTES

## FOSSIL BINDING IN MODERN AND ANCIENT REEFS

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### WHAT THIS ARTICLE IS ABOUT

*Fossil reefs are reported from many parts of the world, especially for the Paleozoic era. While binding of reef components by carbonate-secreting organisms is an undisputed fact for modern reefs, such binding for Paleozoic reefs is not generally observed. Other major differences include the size, taxonomy and abundance of reef-building organisms and the composition and coarseness of matrix material. Such differences make use of the term "reef" for the Paleozoic structures highly controversial.*

An extended period of time is necessary for organisms to build a modern reef. The same would seem to apply to ancient reefs described in the geologic record of the past. Are these ancient reefs true reefs that took a long time to develop? We shall consider some comparisons between modern and ancient reefs.

### A. GREAT LAKES FOSSIL REEFS

The geological literature states that fossil reefs are found in many parts of the world. Many reefs are reported from the Paleozoic era which includes the Silurian and Devonian periods. The fossil reefs of the Great Lakes region in Silurian and Devonian rocks have been studied fairly intensively for about 60 years. These Great Lakes reefs are composed of a central mound or core of massive dolostone (Silurian) or limestone (Devonian), surrounded by flank beds which dip away from the central core. The cores may be a few feet to many hundreds of feet across. Parts of such reef complexes can be observed in limestone quarries, roadcuts, and outcrops.

When the average person thinks of a reef, he envisions a beautiful, colorful, underwater scene with rock-like coral and algal growth, fish, and other marine plants and animals. He might then expect that corals and other calcareous rock-forming organisms would be essential and

important parts of the fossil reefs which now are found elevated on dry land, and assumed to have grown in the ocean. This expectation is in fact the case for “modern” fossil reefs now found in such places as the Florida Keys, Jamaica, and Barbados. But what of the fossil reefs of the Great Lakes region? Are they composed largely of a framework of corals and other calcareous binding fossils?

To the contrary, a casual inspection of the outcrops of fossil reefs of Silurian and Devonian age indicates that they are generally devoid of

larger, framework-type fossils. Only small portions of some of these outcrops appear to be very fossiliferous or moderately so. Figure 1 is a photograph of an atypical, very fossiliferous zone in a Devonian reef near Formosa, Ontario, Canada. From an inspection of outcrops of many reef, reef flank and interreef localities in the Great Lakes region, the outcrop areas with an obviously significant content of binding fossils are estimated to be considerably less than 10% of the total area of the outcrops. Most rock surfaces (over 90%) have no obvious larger fossils or only scattered fossils. Figure 2 is a photograph of a “baby reef” in a “reef” complex at Richvalley, Indiana, which is nearly devoid of frame-



**FIGURE 1. Very fossiliferous zone in a bioherm in the Formosa reef limestone near Formosa, Ontario. Laminar stromatoporoids, rugosan corals and crinoids are abundant. Such fossil abundance is atypical in Silurian and Devonian reefs.**

building fossils. One could argue that most of the original fossil material has undergone dissolution, replacement by dolomite, or other obscuring processes. While some dissolution and replacement have undoubtedly occurred, the fossils presently seen in the fossil reefs are quite well-preserved in many cases and can be identified often to species level. These fossils are not generally observed to be partially dissolved or replaced to a significant degree, also suggesting that fossil dissolution and replacement are not pervasive.

Laminar and globular stromatoporoids, stromatolites, tabulate corals, etc., are probably useful as fossil framework and binding agents in those areas with some fossil abundance. However, even where fossils occur in some abundance, the actual area of the outcrop covered by framework fossil material is generally less than 10% except for a few isolated cases. For all the reef core and flank areas studied in the Silurian and Devonian, the actual rock surface area covered by larger fossils is roughly estimated to be in the 1% range. This does not build a convincing case for the fossil reef interpretation of these limestones and the presence

**FIGURE 2. A “baby reef” occupies the central portion of this photograph from a long railroad cut in a reef complex near Richvalley, Indiana. The baby reef and surrounding rock are nearly devoid of larger fossils such as corals. This is typical of most reef outcrops in Silurian and Devonian rocks.**



of fossil framework as an essential binding agent for these so-called reefs.

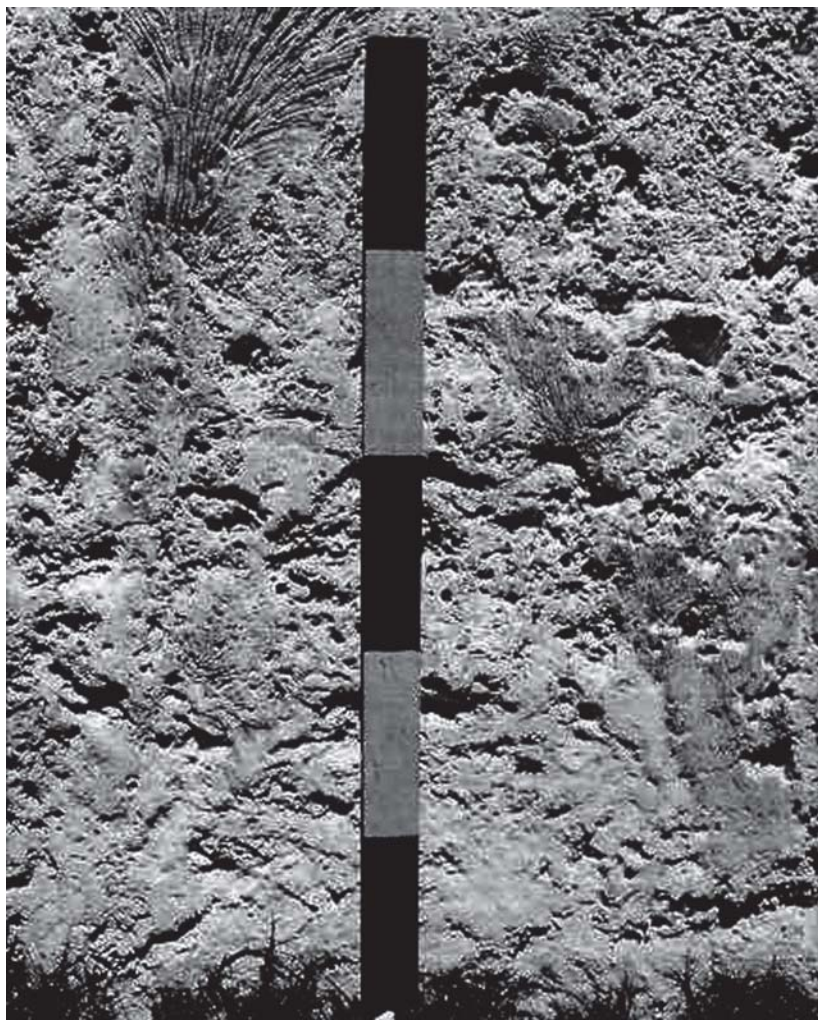
Finally, a look at the matrix (the finer-grained portion of the rock surrounding the fossils) of the Silurian and Devonian reef rocks indicates that in most places, the matrix is primarily lime mud and/or cement, rather than sand-sized grains. (I am not making a distinction here between dolomitic mud and lime mud.) At most reef sites the mud-sized fraction of the matrix greatly dominates over the sand-sized fraction. Because mud grains are silt or clay-sized, that is, fine-grained, their origin (fossil or other) is not usually determinable.

## **B. FLORIDA — THE KEY LARGO LIMESTONE — A MODERN REEF**

The above-noted paucity of fossils in the Silurian and Devonian reefs is in contrast to the Pleistocene Key Largo Limestone of the Florida Keys, which I found to be abundantly fossiliferous in framework-binding corals such as *Montastrea annularis* and *Diploria* at 4 sites. Figure 3 is a photograph of the coral-covered wall in the Windley Key quarry. This is typical of the rock surfaces at all sites. There are no significant outcrop areas at these sites where corals are not present. This is in sharp contrast to the situation in the Silurian and Devonian reefs.

The coral content of the Key Largo Limestone on a vertical outcrop wall in a quarry on Windley Key was studied in detail by Pasley (1972). Pasley measured the percentage of rock surface covered by various species of coral on a section of quarry wall 6 feet in height by 41 feet in width, an area of 246 square feet. He also made a map of the wall outlining the coral on the wall by species. Coral covered 30.7% of the study area, almost one-third. Of the coral-covered area, 50% was covered by *Montastrea annularis*, which often has a large multi-lobed growth form a meter or more in diameter. *Diploria* (four species) made up 23% of the coral area. *Diploria* also often has large heads, but not quite as large as the largest *Montastrea* heads. *Porites* (two species) covered 20% of the coral area. *Porites* are smaller corals but are also good rock-binding corals. Other species of corals made up the remaining 7% of the coral-covered area.

Earlier, Stanley (1966) reported on a similar study of the same Key Largo Limestone, but did not give as much detail on the coral. He did, however, give fossil information on the matrix portion of the rock. Stanley



**FIGURE 3.** Typical coral-covered wall in the Key Largo Limestone at Windley Key Quarry, Florida. Two large corals are a *Diplora labyrinthiformis* at the upper left and a *Siderastrea siderea* at the lower right. Scale rod is 5 feet (1.52 meters).

found that 31 % of the rock was composed of coral framework, with *Montastrea annularis* the principal frame builder, forming 17% of the rock. This was followed by *Diploria* at 10% and *Porites astreoides* at 4%. The sand-sized portion (calcarenite) of the interstitial matrix made



up 41% of the rock, with the following fossil composition (percentages relative to all the rock): *Halimeda* 17%, mollusks 7%, coral fragments 4%, red algae 3%, forams 2%, and minor and unidentified 8%. Note that the coarser matrix (calcarenite) is essentially a fine fossil “hash.” Calcilutite (lime mud) made up 28% of the rock. The mud itself may in part be composed of silt and clay-sized fossil debris. Thus the Key Largo Limestone is composed of a minimum of 72% fossil material.

In summary, it is clear that the binding-fossil content of the Pleistocene Key Largo Limestone is much greater and much more significant for binding than that of the Silurian and Devonian reefs of the Great Lakes region. The fossil content and the grain-size distribution of the matrix of these rocks are also in sharp contrast. Similar conclusions are found on p 447 in the well-known text on sedimentary rocks by Blatt, Middleton and Murray (1980), where they state:

*Closer inspection of many of these ancient carbonate ‘reefs’ reveals that they are composed largely of carbonate mud with the larger skeletal particles ‘floating’ within the mud matrix. Conclusive evidence for a rigid organic framework does not exist in most of the ancient carbonate mounds. In this sense, they are remarkably different from modern coral-algal reefs.*

Similar conclusions may be reached concerning the world-famous Permian Capitan reef complex of southeastern New Mexico and western Texas in the Guadalupe Mountains. Hayes (1964) states:

*The massive member of the Capitan Limestone is interpreted to be a reef deposit made up of the remains of marine organisms; however, upon cursory examination it seem to be only sparsely fossiliferous at most places.*

Hayes (1964) goes on to state: “Small profusely fossiliferous patches of rock can be found, however.” This general lack of framebuilding fossils and the presence of small very fossiliferous patches is exactly the situation noted above for the Great Lakes “reefs.” Dunham (1970) states that binding at the Capitan reef is wholly or largely inorganic (i.e., lime cement), and concludes that the Capitan reef is not an ecologic reef. This means that it is not a reef in the sense that modern reefs are.

### **C. GREAT LAKES REEFS — CARBONATE MUD MOUNDS?**

We have noted the contrast between the framebuilders and matrices of the Great Lakes Paleozoic reefs and the Florida Pleistocene reefs.

Recently there has been less of a tendency to call the Paleozoic reefs of the Great Lakes region reefs in the modern sense. That is, these structures are less likely to be characterized as wave-resistant, organic-framework reefs. Currently, there is a trend to identify these reefs as carbonate mud mounds, implying that binding fossil framework and the resulting wave-resistance are not characteristic, but that carbonate mud is the dominant feature (Textoris 1966). After visiting many of these Paleozoic mounds, I concur. Rather than originating in the shallow surf zone, Pratt (1982) thinks the Paleozoic mounds originated in moderately deep water, occasionally at depths of 100 meters or more. Pratt attributes the binding in these mounds to types of bluegreen algae (non-calcareous) and cement. Earlier, Coron and Textoris (1974) dissolved 75 rock samples from the classic Silurian reef at Wabash, Indiana, in acid. The residues in some cases contained filaments resembling various kinds of non-calcareous algae. In both the Pratt (1982) and Coron and Textoris (1974) papers, the emphasis was on non-calcareous algae, rather than the encrusting, framebuilding calcareous algae, associated with modern, shallow-water reefs.

While noting the lack of wave-resistant framebuilders in the Paleozoic reefs, a paper by Hodges and Roth (1986) shows that coral-bearing Paleozoic mounds, while relatively sparse in coral content, are not disordered piles of debris, especially in the central core region. Corals in the core are primarily upright in position, suggesting that either the cores are in their original position, with upright coral growth, or have been transported with no appreciable tilting.

In conclusion, it is clear that the Paleozoic reefs of the Great Lakes region are markedly different in many respects from the modern-appearing Pleistocene reefs of Florida. Still, relatively little is known about the origin and ecology of the Paleozoic reefs of the Great Lakes region and their fascinating, important, and often-controversial role in deciphering Earth's history.

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