

ANNOTATIONS FROM THE LITERATURE

CONTINENTAL DRIFT

Bowen BW, Meylan AB, Avise JC. 1989. An odyssey of the green sea turtle: Ascension Island revisited. *Proceedings of the National Academy of Sciences (USA)* 86:573-576.

Summary. Green turtles that breed on Ascension Island, in the Atlantic Ocean, feed off the coast of Brazil. One explanation proposed for this migratory behavior has been the suggestion that Ascension Island was originally closer to South America, and has drifted away over long ages. In this scenario, the turtles maintained their presence on Ascension Island by migration, the result being the present behavioral pattern. This hypothesis was tested by comparing mitochondrial DNA of green turtles from breeding populations on several different islands. The results showed that differences among the populations are minor, and much too small to be consistent with the hypothesis of migration as a result of continental drift. Colonization of Ascension Island by green turtles has probably occurred recently.

DIRECTED MUTATION (?)

Hall BG. 1989. Adaptive evolution that requires multiple spontaneous mutations. I. Mutations involving an insertion sequence. *Genetics* 120:887-897.

Summary. Evolutionary biologists have assumed that spontaneous mutations occur randomly and that separate mutations occur randomly, and that separate mutations are independent and unrelated. These assumptions are challenged in this study of bacterial response to nutritional conditions.

The intestinal bacterium, *E. coli*, possesses a set of genes (an operon) to utilize the sugar salicin, although the genes are not usually expressed. Expression cannot occur unless a mutation activates the operon. In the bacterial strain used, a second mutation — removal of an insertion sequence — is required for salicin utilization. The mutation rate at the activation site has been measured as about 4×10^{-8} per cell division, and the mutation rate for removal of the insertion sequence has been estimated as less than 2×10^{-10} per cell division. From the

individual mutation rates, the expected appearance of salicin-utilizing bacteria would be about 10^{-17} . However, under certain conditions, the actual rate of appearance of salicin-utilizing bacteria is about 10^{-8} , which is many orders of magnitude greater than expected. It appears that mutants caused by loss of the insertion sequence occur at an unexpectedly high rate when salicin is present but other nutrients are not available.

The experiments described in this paper suggest that mutations are not entirely random, but may be influenced by environmental conditions, and that the incidence of two mutations occurring together may be greater than expected on the basis of their separate mutation rates. Since insertion sequences may be responsible for a majority of mutations, the conclusions here may have general application. This calls into question the common assumption that shared derived traits indicate common ancestry, and also undermines the theoretical basis for the purported molecular clock.

DNA HYBRIDIZATION CRITICIZED

Sarich VM, Schmid CW, Marks J. 1989. DNA hybridization as a guide to phylogenies: a critical analysis. *Cladistics* 5:3-32.

Summary. DNA-DNA hybridization has been used extensively in the study of hominoid and avian phylogenies, and has been used as the basis for a revised classification of birds.¹ The results have been somewhat controversial, and have generated several critical papers, this paper being one of the more important. Sarich et al. conclude that the most commonly used statistic (T50H) is unreliable as a measure of phylogenetic relationships, and claim the superiority of a less commonly used statistic (Tmode). They criticize the published phylogenies based on DNA hybridization, particularly where it has been used to distinguish nodes separated by small DNA distances. Examples are also given for which the published results seem to be different from the actual data collected.

The most important criticism of the DNA hybridization method involves the lack of publication of original data, making it very difficult to evaluate the conclusions of those using the technique. Some data is published in this article. By showing the entire melting curve profile, the authors reveal that two species may have the same modal melting temperature but have quite different melting profiles. This fact calls

into question all the published results of the DNA hybridization technique. The usefulness of the DNA hybridization technique and the criteria for its use must be reevaluated.

ENDNOTE

1. Sibley CG, Ahlquist JE, Monroe BL. 1988. A classification of the living birds of the world based on DNA-DNA hybridization studies. *Auk* 105:409-423.

ISLAND BIOGEOGRAPHY

Thornton IWB, Zarin RA, Rawlinson PA, Tidemann CR, Adikerana AS, Widjaya AHT. 1988. Colonization of the Krakatau Islands by vertebrates: equilibrium, succession, and possible delayed extinction. *Proceedings of the National Academy of Sciences (USA)* 85:515-518.

Summary. Krakatau erupted in 1883, destroying all life on the island and on two adjacent islands. Most of the island was blown away, leaving a southern remnant of perhaps one-third the original area. In 1930, a new island appeared in the northern area of the former island of Krakatau. Additional eruptions have occurred, notably in 1952. McArthur and Wilson calculated that the number of bird species on the islands had approached equilibrium by about 1908-1919. However, further censuses show that colonization is continuing, and the number of species is increasing, although more slowly than during the early years after the major eruption.

MOLECULAR EVOLUTION

Field KG, Olsen GJ, Lane DJ, Giovannoni SJ, Ghiselin MT, Raff EC, Pace NR, Raff RA. 1988. Molecular phylogeny of the animal kingdom. *Science* 239:748-753.

Summary. Sequences of ribosomal RNA were compared for representatives of 22 classes in 10 animal phyla. The most conservative portions of the RNA molecules were used. Results showed that coelenterates are closer to plants, fungi and ciliates than to flatworms and other animal phyla. The placement of the root of the phylogenetic tree varies according to which nucleotides are included in the comparisons.

Among the "coelomates", arthropods and annelids are usually grouped close to each other, and chordates and echinoderms are likewise grouped close to each other. The ribosomal sequences indicate

separate lineages for each of these groups, without any special relationship between any two of the groups. Diversity among the arthropods is comparable in magnitude to that of the rest of the coelomates (annelids, chordates, echinoderms and brachiopods). An unusual result suggested by the ribosomal RNA is the grouping of molluscs, polychaete annelids, brachiopods, sipunculans, and the vent worm *Riftia*.

The authors conclude by pointing out some of the problems in using molecules to infer phylogeny. There is no simple measure of the reliability of branch points. The location of a group on a phylogenetic tree can be affected by differences in rates of substitution, or by polyphyly, and clustering of species may differ with different sets of organisms being compared.

Comment. The results of this study serve to demonstrate the highly speculative nature of phylogenetic reconstructions of taxa of high categorical rank. Perhaps the best interpretation of the data is that living things are derived from many different ancestors, rather than having a single common ancestry.

MOLECULAR EVOLUTION AND PLANTS

Gray MW, Cedergren R, Abel Y, Sankoff D. 1989. On the evolutionary origin of the plant mitochondrion and its genome. *Proceedings of the National Academy of Sciences (USA)* 86:2267-2271.

Summary. Green plants contain genetic material in three organelles: nucleus, chloroplast and mitochondrion. Ribosomal RNA (rRNA) sequences are encoded in the genomes of each of these organelles. Phylogenetic hypotheses based on chloroplast rRNA sequences suggest that green plants and green algae are most closely related to each other, and as a group most closely related to eubacteria. Proposed relationships based on nuclear rRNA are similar to those based on chloroplast rRNA.

In contrast, phylogenetic hypotheses based on mitochondrial rRNA sequences suggest that green algae share a more recent ancestry with animals than with plants, and that green plants are more closely related to purple bacteria ("blue-green algae"). The explanation offered by the authors for this seeming contradiction with evolutionary theory is that mitochondria are evolved from purple bacteria which were incorporated into ancestral plant cells as endosymbionts, and that this occurred twice during the evolution of the line leading to green plants. The first endosymbiotic event occurred early in the ancestry of eukaryotes,

while the second event occurred after the green plants diverged from other groups.

Comment. Such ad hoc explanations are purely speculative, and should be abandoned in favor of the more parsimonious explanation of separate ancestries.

Martin W, Gierl A, Saedler H. 1989. Molecular evidence for pre-Cretaceous angiosperm origins. *Nature* 339:46-48.

Angiosperms are not known as fossils in layers below the Cretaceous. Yet molecular evidence shows angiosperms to be quite different from other organisms in the nucleotide sequences for the enzyme glyceraldehyde-3-phosphate dehydrogenase (GAPDH). DNA sequences from nine animals, one yeast, and six plants were compared. The extent of difference at nonsynonymous sites is roughly proportional to the estimated time since divergence from a common ancestor. This was interpreted as supporting the existence of a constant mutation rate (molecular clock) in plants. According to the molecular clock hypothesis, the angiosperms should have diverged from some ancestral line in the Carboniferous. The absence of fossils from layers below the Cretaceous leaves a supposed gap in the fossil record of some 200 million years in which angiosperms were presumably present on earth, but were not fossilized.

Comment. The origin of angiosperms has been an evolutionary enigma since the days of Charles Darwin. This recent data merely emphasizes that the problem is still unresolved.

Syvanen M, Hartman H, Stevens PF. 1989. Classical plant taxonomic ambiguities extend to the molecular level. *Journal of Molecular Evolution* 28:536-544.

Summary. The amino-acid sequences of cytochrome c molecules from various species of animals have been used to prepare a similarity tree that successfully groups many vertebrate species in ways similar to accepted taxonomic groupings. Attempts to group plant families by conventional means has not given satisfactory results, and it was hoped that cytochrome c sequences might resolve this problem. Amino-acid sequences from 20 species of dicots and 5 species of monocots were compared, and a similarity tree was prepared using the computer program PAUP. Results varied according to the way in which information was given to the computer program, and no consensus tree could be derived. None of the trees seemed reasonable biologically. It appears

that cytochrome c sequences in plants are not useful in estimating supposed evolutionary relationships among plant families.

Wolfe KH, Gouy M, Yang Y-W, Sharp PM, Li W-H. 1989. Date of the monocot-dicot divergence estimated from chloroplast DNA sequence data. *Proceedings of the National Academy of Sciences (USA)* 86:6201-6205.

Summary. Angiosperms comprise two separate groups, monocots and dicots. The earliest reliable angiosperm macrofossils are estimated to be about 120 million years (Ma) old. Monocots and dicots are both found as far back as the record extends. Using chloroplast DNA sequences and assuming a reasonably constant mutation rate for chloroplast DNA, the authors calculated that monocot and dicot lineages diverged approximately 200 Ma before present.

Comment. This leaves the unsolved problem of why there is no fossil record of angiosperms for the purported 80 million years or so preceding their first known fossil occurrence.

PROBLEMS WITH EVOLUTION

Wilder-Smith AE. 1987. *The scientific alternative to Neo-Darwinian evolution theory.* Costa Mesa, CA: TWFT Publishers. 132 p.

Summary. Dr. A. E. Wilder-Smith has written some 30 books on the question of origins. This volume addresses in a scientific perspective the major issues he has considered in the past. The primary focus is on the difficulty of originating complex systems, both organic and inorganic, without external information. Information theory is used to substantiate the necessity of external design. The author uses his breadth of information, which is reflected in many historical and philosophical implications, to illustrate his points. Complex challenges, especially in the biological realm — and there are many — are carefully explained. The implication of his discourse is that one has to look beyond science to explain the reality we see around us. This is an important book.

TEACHING CREATION AND EVOLUTION

Skehan J. 1986. *Modern science and the book of Genesis.* Washington DC: National Science Teachers Association Science Compacts. 30 p.

Summary. This booklet, published by the National Science Teachers Association, is designed to help teachers handle the issue of creationism

in the classroom. The basic thesis is that science is factual and Genesis is allegorical; hence, there is no conflict between the two. A feeble attempt is made to explain why the authors of Genesis did not intend their statements to be taken literally.

One of the concluding remarks by the author states, “Let me suggest that our educational systems may very well be on the threshold of a new and even gloomier Dark Age of the 20th and 21st centuries, unless the anti-intellectualism and confused thinking creationist’s produce is overcome.”

Evidence within this publication would indicate that creationists may not be the only ones who are confused: 1) Fishes are stated to first appear in the Ordovician, while they are found in the Cambrian (Science 200:529, 1978); 2) An argument that Noah’s ark was too small ignores the variability in organisms recognized by creationists; 3) Uniformitarianism is lauded as based on “overwhelming evidence”, while the new trend towards catastrophism in geology is not even mentioned; 4) A definition of science that includes the necessity of testing by experimentation would seem to exclude from science much of cosmological, paleontological, and evolutionary thinking.

Comment. While one can generate sympathy for this attempt to solve the classroom evolution-creation problem, it is doubtful that this publication will have much impact on the knowledgeable reader. It may have significant impact on the unwary student.

American Scientific Affiliation. 1986. Teaching science in a climate of controversy. Committee for Integrity in Science Education. Ipswich, MA: American Scientific Affiliation. 48 p.

Summary. This is a well-prepared document that is both factual and interesting. It is designed to help the teacher cope with the creation-evolution controversy and has an attractive format suitable for student use. Its most basic themes are that there are many unanswered questions about origins and that science is limited in its scope of expertise. In general the book takes a guarded, sympathetic view of the general concept of creation, while at the same time presuming that life developed over eons of time. In this respect, the book will do little to help solve the problems faced by the student who believes in a recent creation. Specific themes covered are: classroom guidelines, the origin of the universe, the origin of life, the origin of basic kinds of animals, and the origin of man. In all these themes a gratifying sensitivity to various views is exhibited.