

ANNOTATIONS FROM THE LITERATURE

MASS EXTINCTIONS

Erwin DH. 1989. The end-Permian mass extinction: what really happened and did it matter? *Trends in Ecology and Evolution* 4:225-229.

Summary. This paper reviews the end-Permian extinction event, which is considered to be the largest known extinction in earth history. Of Permian marine taxa, about 80% of the genera and an estimated 95-96% of the species are not found in strata above the Permian. Significant extinctions also occurred among terrestrial plants and tetrapods, especially in amphibians. There is no global iridium enrichment or other evidence for an impact at the Permo-Triassic border, and the cause of the extinctions is not clear. Global cooling has been suggested, but terrestrial fossils indicate a warming trend.

Comment. The authors state that Paleozoic marine fossil assemblages are dominated by largely sessile groups, such as articulate brachiopods, bryozoans and stalked echinoderms. Mesozoic fossil assemblages are dominated by groups that were more mobile than those predominant in the Paleozoic strata. Further study of general differences in mobility of Paleozoic and Mesozoic fossil organisms might prove useful in efforts to refine Ecological Zonation Theory.

MOLECULAR PALEONTOLOGY

Golenberg EM, Giannasi DE, Clegg MT, Smiley CJ, Durbin M, Henderson D, Zurawski G. 1990. Chloroplast DNA sequence from a Miocene *Magnolia* species. *Nature* 344:656-658.

Summary. An 820 base pair length of chloroplast DNA was extracted from a well-preserved Miocene fossil leaf of an extinct species of *Magnolia*. This DNA was sequenced and compared with an extant species of *Magnolia*, and some other close relatives. Compared with the living species, there were 17 differences (substitutions) in the DNA, 4 of which were non-synonymous (changed the amino acid being coded for).

Comment. The successful extraction and sequencing of DNA from a fossil leaf suggests it may be possible to determine DNA sequences

from other well-preserved fossils, as well as old museum skins. Results of such studies may provide information about mutation rates and may contribute to other comparative studies.

MOLECULAR PHYLOGENY

Devereux R, Loeblich AR, Fox GE. 1990. Higher plant origins and the phylogeny of green algae. *Journal of Molecular Evolution* 31:18-24.

Summary. Higher plants are believed to be derived from green algae. This paper reports ribosomal RNA (5S rRNA) sequences from three species of green algae. These 5S rRNA sequences have been criticized as being too short to be reliable, because they gave anomalous results. Devereux et al. state that they should be taken seriously, but not over-interpreted. In this study, higher plants should be grouped with charophytes (stoneworts). Chlorophytes (green algae) form a second group, in agreement with recent taxonomic thinking. However, one group of green alga-like organisms, the chlamydomonads, form a third, more remote group. This result differs from present theories. The *Spirogyra* sequence reported here is greatly different from that reported earlier, prompting the authors to question whether the other form was truly a *Spirogyra*.

Hedges SB, Moberg KD, Maxson LR. 1990. Tetrapod phylogeny inferred from 18S and 28S ribosomal RNA sequences and a review of the evidence for amniote relationships. *Molecular Biology and Evolution* 7:607-633.

Summary. Similarities in ribosomal RNA sequence were investigated for 15 species of amphibians, 4 species of reptiles, and 2 species of birds. These were compared with published sequences for one species of amphibian and four species of mammals. Results showed birds more similar to mammals than to reptiles, contrary to expectations based on the fossil record. The authors cite other literature supporting this result, involving the amino acid sequences of beta-hemoglobin and myoglobin. Birds are most often grouped closest to crocodylians, a grouping supported by histone H2B sequences. Alpha-hemoglobin sequences group birds with either crocodiles or mammals, depending on the method used. Alpha-crystallin A groups birds with either crocodylians or lizards, depending on the method. Cytochrome c sequences join birds with lizards, not with mammals. Insulin sequences show some birds to be closer to alligators than to some other birds.

Comment. If these results are reliable, one may question the utility of molecular sequences for determining relationships among higher taxa of tetrapods.

Li W-H, Gouy M, Sharp PM, O'hUigin C, Yang Y-W. 1990. Molecular phylogeny of Rodentia, Lagomorpha, Primates, Artiodactyla, and Carnivora and molecular clocks. *Proceedings of the National Academy of Sciences (USA)* 87:6703-6707.

Comment. Analysis of DNA sequences from more than 30 gene portions were used to determine similarities among five orders of mammals. Rodents were determined to be the most distant from the other four orders, although the data contains considerable inconsistencies. Artiodactyla and Carnivora grouped together, but the branching diagram was bush-like for the four orders other than Rodentia and the branching sequence was uncertain. The number of differences is greater in the rodents than in the other groups, indicating the "molecular clock" does not have the same rate in all lineages.

Sogin ML, Gunderson JH, Elwood HJ, Alonso RA, Peattie DA. 1989. Phylogenetic meaning of the kingdom concept: an unusual ribosomal RNA from *Giardia lamblia*. *Science* 243:75-77.

Summary. *Giardia lamblia*, a flagellated protozoan, lacks mitochondria, endoplasmic reticulum, or Golgi bodies. The sequence of 16S-like ribosomal RNA is so different that it is interpreted to represent the earliest-diverging lineage of eukaryotes. The extent of divergence is said to be sufficient to justify a separate kingdom, but the authors do not recommend this. Either eukaryote ribosomal RNA is more rapidly evolving, or eukaryotes are as ancient as eubacteria and archaeobacteria. Ciliated protozoa are genetically as diverse as the plant or animal kingdoms.

PALEOBIOGEOGRAPHY

Sues H-D, Olson PE. 1990. Triassic vertebrates of Gondwanan aspect from the Richmond Basin of Virginia. *Science* 249:1020-1023.

Comment. Fossil vertebrates from Upper Triassic sediments in southern continents are generally dissimilar from any found in the northern continents. This has been interpreted as indicating a geographical separation of the southern continents (Gondwana) from the northern continents (Laurasia). Recently studied material from Virginia,

USA, includes reptiles similar to those found in Upper Triassic deposits from southern continents. This new evidence suggests that previously known Upper Triassic faunal differences between Gondwana and Laurasia may have been due to different strata being present rather than to geographical distance.

PALEONTOLOGY

Beard KC. 1990. Gliding behaviour and palaeoecology of the alleged primate family Paromomyidae (Mammalia, Dermoptera). *Nature* 345:340-341.

Kay RF, Thorington RW, Houde P. 1990. Eocene plesiadapiform shows affinities with flying lemurs not primates. *Nature* 345:342-344.

Summary. Two papers have presented evidence that fossils of the extinct mammal family Paromomyidae have been misclassified. The first paper reaches this conclusion based on a study of post-cranial bones of two genera of these Eocene fossils. The second paper reaches a similar conclusion based on a study of a recently found skull. Paromomyids had previously been classified as primates on the basis of their teeth. Both papers concluded that paromomyids are more similar to living colugos than to primates. (Colugos are nocturnal gliding mammals living in the Philippines and Southeast Asia.)

Coates MI, Clack JA. 1990. Polydactyly in the earliest known tetrapod limbs. *Nature* 247:66-69.

Summary. Conventional evolutionary wisdom has held that vertebrates descended from an ancestor having five digits on each limb. It came as a surprise to discover that the earliest known tetrapod limbs have more than five digits. Limbs are now known from three genera of Devonian tetrapods. The number of digits varies from six in the genus *Tulerpeton*, to seven in the hindlimb of the genus *Ichthyostega* to eight in the forelimb of *Acanthostega*. The number of elements and their pattern cannot be accounted for on the basis of homology with any known fish fin, but a recent morphogenetic model is said to compare favorably with the newly discovered pattern of limb structure.

Dodson P. 1990. Counting dinosaurs: how many kinds were there? *Proceedings of the National Academy of Sciences (USA)* 87:7608-7612.

Summary. Dinosaurs have always had a special attraction, and interest in them has increased in the past decade, due to new discoveries and the controversy over the cause of their demise. Now we have a

better idea of how many different kinds of dinosaurs there were. Dodson reduces the number of genera from 540 to 285, with 336 species. A little less than half these genera are each represented by single specimens, and skulls are unknown for about the same proportion. The most common dinosaur fossil seems to be *Maiasaura*, a hadrosaur (duck-billed dinosaur), with over 200 specimens. More than three-fourths of the genera are restricted to a single country, with the United States having the greatest number: 64 genera. Dodson estimates that the fossil record of dinosaur genera is about 25% complete, and the total number of dinosaur genera may have been between 900-1200.

PHILOSOPHY OF SCIENCE

Mills GC. 1990. Presuppositions of science as related to origins. *Perspectives on Science and Christian Faith* 42:155-161.

Summary. The importance of presuppositions in doing science is the subject of this paper. Mills lists four presuppositions that seem to be accepted by most scientists. These are:

1. Nature has an underlying order that can be discovered.
2. There is uniformity in nature (repeatability).
3. Sense perceptions are valid.
4. All events can be explained in terms of natural processes.

Mills accepts the first three points, but takes exception to the last one. The origin of the universe and the origin of life have not been satisfactorily explained by natural processes, and in fact appear to require processes different from those observed at present. Because of this, Mills would substitute two other presuppositions for the fourth point listed above. These two points are:

1. An intelligent cause was involved in cosmological and biological origins.
2. Nearly everything else can be explained in terms of natural processes.

Comment. Mills' suggestion undoubtedly represents an improvement over the original statement that all events can be explained in terms of natural processes. However, there is plenty of room for discussion about what events might be included in the phrase "nearly everything else."

RADIOCARBON DATING

Stafford TW, Hare PE, Currie L, Jull AJT, Donahue D. 1990. Accuracy of North American human skeleton ages. *Quaternary Research* 34:111-120.

Summary. This paper strikes a blow in the lively debate over the age of human occupation of North America. The paper presents evidence that counters the results of carbon-14 dates which indicate a shorter human occupation. According to the authors, the accuracy of radiocarbon dating of fossil bones depends on the state of preservation of the bones. Fossil bones vary widely in state of preservation, so carbon-14 dates vary widely in their accuracy. Recent AMS dates showing no human fossils in North America before 11,000 yrs BP are therefore not reliable, in this view. Only collagenous fossils give reliable ages; non-collagenous bones give underestimates of ages. The authors suggest applying radiocarbon dating to isolated amino acid fractions from collagenous bones to improve accuracy.

SPECIATION

Meyer A, Kocher TD, Basasibwaki P, Wilson AC. 1990. Monophyletic origin of Lake Victoria cichlid fishes. *Nature* 347:550-553.

Summary. Approximately 200 endemic forms of cichlid fishes inhabit Lake Victoria and its satellite lakes. These forms have been variously considered to represent a small number of species with different morphs, or a large number of species, some of which are more closely related to morphologically similar species in other East African lakes. The authors report on a comparison of mitochondrial DNA sequences from fourteen Lake Victorian species, as well as species from other areas of Africa. Their results are interpreted as showing that the Lake Victorian fish are separate species, all of which have a recent common ancestor. In addition, the Lake Victorian fish are more similar to fish from Lake Malawi than to fish from Lake Tanganyika. The amount of variation in mitochondrial DNA sequence is less than is found within the human species.

TAPHONOMY

Cutler AH, Flessa KW. 1990. Fossils out of sequence: computer simulations and strategies for dealing with stratigraphic disorder. *Palaios* 5:227-235.

Summary. Fossil sequence can be disturbed by mixing or by reworking. Mixing occurs primarily by bioturbation, where sediments are moved by burrowing animals. Reworking occurs when sediments are eroded and redeposited. Reworking can produce a deposit containing both young and old fossils, mixed together in random order. Computer simulations were run to compare the effectiveness of mixing and reworking on fossil sequence. Mixing was found to be quite ineffective in obliterating the original fossil sequence. In contrast, reworking was found to be highly effective in destroying the order of the fossil sequence. Reworking can obliterate the fossil sequence in a deposit even if more than half the fossils are in situ and less than one-half are reworked from another deposit. Increasing sample size improves sequence accuracy after mixing, but not after reworking. Thus reworking is potentially a significant source of disorder in the fossil record.

Meldahl KH. 1990. Sampling, species abundance and the stratigraphic signature of mass extinction: a test using Holocene tidal flat molluscs. *Geology* 18:890-893.

Summary. Inferences of the geologic causes of mass extinctions in the fossil record rely heavily on the suddenness of the mass extinctions. The most notable example is the mass extinction that occurred at the Cretaceous-Tertiary boundary. This paper attempts to use tidal flat molluscs to discover differences in extinction patterns for sudden extinction, stepped extinction, or gradual extinction.

The depths of 45 species of tidal flat molluscs were recorded to the nearest cm, and "last appearances" plotted for each species. "Last appearances" showed a gradual loss of species, with only ten of the 45 species having last appearances at the surface. About half the species had "last appearances" lower than 15 cm below the surface.

Gradual and stepped extinctions were simulated by eliminating all biostratigraphic occurrences above certain levels. The resulting patterns were compared. A graph of stratigraphic abundance vs depth of "last appearance" showed a hollow curve for sudden extinctions. For gradual extinctions, the graph was roughly flattened and without nodes. Stepped extinctions showed a series of hollow curves, each similar to the sudden

extinction graph. One conclusion is that “last appearances” are not accurately recorded in this situation unless the species is present in at least 15% of the stratigraphic sections. Another conclusion is that a sudden mass extinction would appear gradual stratigraphically, but the extinction event might be identifiable from the pattern of the distributions of stratigraphic last appearance and stratigraphic abundance.