

ANNOTATIONS FROM THE LITERATURE

EVOLUTION

Brooks DR, McLennan DA. 1993. Macroevolutionary patterns of morphological diversification among parasitic flatworms (Platyhelminthes: Cercomeria). *Evolution* 47:494-509.

Summary: Parasites have traditionally been considered to exhibit morphological degeneration. Brooks and McLennan challenge this interpretation for parasitic flatworms (flukes and tapeworms). Cladistic methodology was used to analyze character transformations in parasitic flatworms. Free-living flatworms were not included in the analysis. Results of the study indicated that character loss amounted to slightly more than 10% of the inferred character transformations. The conclusion was that these parasitic flatworms are not unusually degenerate, but are better described as specialized.

Comment: The conclusions in the study are based on the assumption of common ancestry for all parasitic flatworms, a conclusion that should be independently investigated. The authors suggest that some parasitic flatworms may actually be more complex than some free-living flatworms. This may raise the possibility that these parasites are not simply degenerate derivatives of free-living flatworms, but may be designed to be parasites or commensals. The addition of free-living flatworms to the study would add interest to the results.

Carroll RL, Currie PJ. 1991. The early radiation of diapsid reptiles. In: Schultze H-P, Trueb L, editors. *Origins of the higher groups of tetrapods*. Ithaca and London: Comstock Publishing, p 354-424.

Summary: Species are classified into groups on the basis of uniquely shared characteristics. Shared characteristics may be interpreted as due to common ancestry or to convergence. Convergence is inferred when two groups share a similar characteristic that is thought to be not due to common ancestry. Convergence confuses the evolutionary interpretation of shared features, causing inconsistencies in the pattern. But convergence is a common problem in evolutionary

studies, often producing numerous inconsistencies in proposed evolutionary trees.

Comment: Reptiles have been divided into subgroups, one of which is Diapsida. This group includes lizards, snakes, crocodylians, sphenodontids, dinosaurs, and several other extinct groups. Diapsids first appear in Upper Carboniferous strata, but are relatively rare in Paleozoic sediments. The number of groups of diapsid fossils increases as one moves upward through the geologic column. As additional groups are included, the number of uniquely shared characteristics decreases, apparently due to convergence. Another pattern resulting from including additional groups of fossils is the increasing difficulty of comparing structures (determining homology). Carroll calculated that 70% of the character traits examined in his study exhibited convergence. This means that only a minority of character traits show patterns consistent with the hypothesis of common ancestry for this group.

Dawson A, McNaughton FJ, Goldsmith AR, Degen AA. 1994. Ratite-like neoteny induced by neonatal thyroidectomy of European starlings, *Sturnus vulgaris*. Journal of Zoology, London.

Summary: Ostriches and several other types of large flightless birds are collectively known as “ratites.” In addition to being large and flightless, ratites share certain other morphological traits, such as features of the palate, unfused skull sutures, persistence of downy, juvenile type feathers, and an unkeeled sternum. These shared features are similar to those seen in juvenile birds, and it has been suggested that some of the ratites may have independent ancestries.

In the experiment reported in this article, the thyroid glands were removed from hatchling starlings at the age of four days. The affected birds showed delayed maturation, including slowed sternum growth, slowed development of feathers, undeveloped palatine bones and unfused skull sutures. In contrast to ratites, the affected birds did not grow as large as normal. Sexual maturation was accelerated, resulting in neoteny (the retention of early features into adulthood). Future studies will examine thyroid function in ratites.

Comment: In their present distribution, ratites are confined to the southern continents. This has often been interpreted to support the plate tectonics model of biogeography. However, some paleontologists have expressed doubts that ratites are related. If the ratites are simply neotonous forms lacking a common ancestry, the biogeographical

argument is invalid, as is suggested by some fossil and molecular evidence.

GENETICS

Farabaugh PJ. 1993. Alternative readings of the genetic code. *Cell* 74:591-596.

Summary: The genetic code has been known for twenty years or so. The code is based on groups of three DNA nucleotides (a codon), which either codes for a specific amino acid or is a start or stop signal. By determining the DNA sequence of a gene, one is theoretically able to predict the amino acid sequence of its product. There are some complications to this standard scenario. Intervening sequences (introns) are well-known, in which portions of the messenger RNA are spliced out before decoding and protein synthesis begins at the ribosome.

Comment: There are other rare phenomena that indicate the potential for altering the conventional message of a DNA sequence during the process of decoding. For example, termination codons are sometimes ineffective in stopping the cell from continuing to add amino acids to the protein being manufactured. Thus a codon that appears to be a stopping point may not function as a stopping point. Another unusual observation is frameshifting. In this situation, the predicted grouping of nucleotides into codons is altered so that the message is read in a completely different way. A third type of alteration is hopping, in which large DNA segments may simply be skipped. These observations indicate that the operation of the genetic system is much more complex than a simple understanding of the genetic code would indicate.

Hall BG. 1994. On alternatives to selection-induced mutation in the Bgl operon of *Escherichia coli*. *Molecular Biology and Evolution* 11:159-168.

Summary: The assumption that mutations were random was challenged in 1988 by experiments that appeared to show that mutations occurred more rapidly than expected under conditions favoring the mutant phenotype. The suggestion that mutations might somehow be directed touched off a controversy that has not yet been resolved. Other researchers challenged the conclusion that mutations may be directed, reporting tests that explained the previous results without recourse to directed mutation.

Comment: In this paper, Hall expands the experimental protocol to include tests of his own previous interpretations as well as those of his challengers. The mutation in question involves excision of a movable element, resulting in the ability of the cell to utilize the sugar salicin. Hall provides an explanation for his own previous results, his present results, and those of his challengers that involves directed mutation, and concludes that mutations may be directed, contrary to conventional wisdom.

GEOLOGY

Armitage MH. 1993. Internal radiohalos in a diamond. *American Laboratory* 25:28-30.

Summary: Radiohalos are cross-sections of spheres of crystal damage caused by radioactive decay. Over 75 radiohalos are visible in a small (0.012 g) diamond at magnifications of 125x - 250x. Since most diamonds are not examined at such high magnifications, it is uncertain to what extent radiohalos are found in other diamonds. The radiohalos have up to four visible rings, corresponding to the U-238 decay series. The U-238 ring itself is missing in all these halos. The visible rings include those of Ra-222, Po-218, Po-214 and Po-210. All of these isotopes have short half-lives, on the order of days or minutes. This suggests that either the diamond formed rapidly or was penetrated by a fluid containing radioactive atoms. The formation of diamonds is still not well understood, a situation made more complicated by the discovery of these radiohalos.

Comment: The origin of the radiohalos in these diamonds is another issue of interest. The radiohalos are similar to those often associated with uranium-bearing granitoid rocks. Their origin has been the subject of controversy, but may be the result of high-pressure transport of fluids containing products of uranium decay.

MOLECULAR PHYLOGENY

Amemiya CT, et al. 1993. VH gene organization in a relict species, the coelacanth *Latimeria chalumnae*: evolutionary implications. *Proceedings of the National Academy of Sciences* 90:6661-6665.

Summary: The coelacanth is sometimes considered to be the closest fish relative to land animals. Many have hoped that the characteristics

of this lobe-finned “living fossil” might provide some insight into the evolution of the tetrapods. However, this hope has not materialized. The arrangement of immunoglobulin genes in the coelacanth differs from that in any other known group. Like sharks and skates, the V_H (variable-chain heavy region) and D (diversity) elements are adjacent. Like bony fishes and mammals, the coelacanth has a V_H transcriptional octamer, V_H elements close together, and presumably many pseudo-genes.

Comment: In an evolutionary scheme, these characteristics would indicate that tetrapods are more closely related to teleost fishes than to the coelacanth, contrary to the most popular hypotheses of evolutionary relationship.

Janke A, Feldmaier-Fuchs G, Thomas WK, von Haeseler A, Paabo S. 1994. The marsupial mitochondrial genome and the evolution of placental mammals. *Genetics* 137:243-256.

Summary: The entire mitochondrial genome of the American opossum has been sequenced. Two major differences with placental genomes are noted. First, the sequence of five tRNA genes is different. Second, the aspartic acid tRNA has an anticodon not normally found in the mitochondrion. Eight of thirteen mitochondrial genes are said to exhibit clocklike divergence rates. Lineage divergences based on these genes and calibrated against the geologic time-scale indicate a date of 35 Ma for the divergence of the closely related rat and mouse, compared with 41 Ma for divergence of cow and whale.

Comment: These results reveal a large discordance between morphological and molecular measures of similarity. Rats and mice are classified in the same Family, while cows and whales are classified in different Orders. Perhaps molecular sequences are not necessarily giving us an accurate picture of ancestry.

ORIGIN OF LIFE

Barbier B, Visscher J, Schwartz AW. 1993. Polypeptide-assisted oligomerization of analogs in dilute aqueous solution. *Journal of Molecular Evolution* 37:554-558.

Summary: The source and polymerization of nucleotides is a major unsolved problem for origin-of-life models. One proposal is that a series of chemical reactions developed into a self-sustaining cycle of

nucleic acid production. In this hypothetical autocatalytic cycle, template nucleic acid molecules would form a pattern which would be copied by a replicate nucleic acid molecule. This hypothesis has been bolstered by the production of purine polynucleotides up to 40 units in length, using a poly-C template. However, pyrimidine polynucleotides, such as the poly-C template itself, are more difficult to produce. Because of this, a purine-dominated template would not be a suitable template for the cycle to continue. This problem effectively prevents an autocatalytic system from forming. Without a preformed template, polymerizations produce very low yields. The authors attempted to get around this problem by adding polypeptides of leucine and lysine, rather than using a nucleotide template. This procedure increased the yield and oligomeric length of DNA nucleotide polymerization substantially.

Comment: This experiment advances our understanding of chemistry, but does not help explain the origin of life. The idea that ribonucleotides could somehow form in a primordial ocean full of chemical contaminants is highly implausible to begin with. No plausible source is identified for the polypeptides used in the experiment. In addition, the experimental conditions are implausible in a prebiotic world.

PALEONTOLOGY

Aberhan M. 1993. Faunal replacement in the Early Jurassic of northern Chile: implications for the evolution in Mesozoic benthic shelf ecosystems. *Palaeogeography, Palaeoecology, Palaeoclimatology* 103:155-177.

Summary: Differing geologic strata have different types of fossils. Paleontologists typically interpret such stratigraphic differences as the result of either evolution or migration. Evolutionary replacement would occur as newly evolved species replace their more poorly adapted ancestors. Ecological replacement would occur as environmental conditions changed, favoring migration of species from other areas.

Aberhan reports that ecological replacement is characteristic of Lower Jurassic benthic shelf faunas from northern Chile. His survey of the literature showed that ecological replacement is a common and widespread feature of Mesozoic benthic shelf fossil assemblages. "Evolutionary replacement" seems limited to restricted basins. Within-habitat species replacement seems controlled by "sea level fluctuations."

Comment: How would these patterns be interpreted in a flood model? Patterns interpreted as “ecological replacement” might result from a change in source area, or from taphonomic sorting. A sequence produced by such activity could produce a fossil sequence in which successive layers did not appear to have ancestral-descendent characteristics. Patterns interpreted as “evolutionary replacement” might be produced if the same source habitat or area were sampled in successive layers. Similar species generally live in proximity to each other, providing the potential for successive fossil samples to be closely related. Differences could be due to taphonomic sorting, morphological gradients across a region, or ecological gradients across a region.