

ANNOTATIONS FROM THE LITERATURE*

ECOLOGY: OCEANIC BIODIVERSITY ENHANCES PRODUCTIVITY

Worm B, Barbier EB, Beaumont N, Duffy JE, Folke C, Halpern BS, Jackson JBC, Lotze HK, Michelik F, Palumbi SR, Sala E, Selkoe KA, Stachowicz JJ, Watson R. 2006. Impacts of biodiversity loss on ocean ecosystem services. *Science* 314:787-790.

Summary. Oceans provide useful services to humans, such as supporting fisheries and other sources of food, and improving water purity through filtering and detoxifying activities. Loss of diversity results in reduced quality of services. In areas where diversity has been depleted, establishment of reserves and closure of fisheries has increased biodiversity an average of 23%, based on study of four fishery closures and 44 marine reserves. Preservation of biodiversity is needed if the oceans are to continue to serve humanity as they have in the past.

Comment. Conservation involves more than merely preserving species for sentimental reasons. Biological productivity helps sustain human needs, and this productivity is negatively impacted by reductions in biodiversity. Christian stewardship includes the obligation that our interactions with our environment, including other species, be guided by informed and responsible principles.

GENETICS: PSEUDOGENES

Mira A, Pushker R. 2005. The silencing of pseudogenes. *Molecular Biology and Evolution* 22:2135-2138.

Summary. Pseudogenes fall into several different classes. This paper deals with what were once clearly functioning bacterial genes which are currently nonfunctional as a result of mutations. While these specific pseudogenes may be nonfunctional in one strain of a bacterial species, they are functional in others. The authors concentrated on sequences essential for transcription and translation of genes and found evidence of selection for mutation of pseudogene control sequences which prevent their expression as truncated proteins. This evidence is particularly strong in the Shine-Dalgarno sequence, a nucleotide sequence on mRNA that

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signals for ribosome attachment and thus translation of the sequence that follows it.

Comment. Pseudogenes have been presented as evidence of common ancestry. For example, the L-gulonogamma-lactone oxidase (GLO) gene, essential for production of vitamin C is a pseudogene in humans, primates and — strangely — guinea pigs, but not in other vertebrates. Darwinists interpret this as a synapomorphy connecting humans and apes to a common ancestor with a mutated GLO gene. However, evidence is mounting for functionality which may be selected for in some pseudogenes¹ and that at least some similar mutations may be the result of a mechanism of some kind and not simply random.

The theory that specific mutations may be “targeted” in some way or that specific mutations may be selected for appears to be well supported in this paper. Caution is warranted in comparing bacterial pseudogenes with eukaryotic pseudogenes, but clearly some portions of bacterial pseudogenes do not reflect the actions of random mutations alone. Whether this is because of positive selection — as suggested in this paper — or some other mechanism remains to be determined, but one thing is certain, bacteria possess elaborate mechanisms to mitigate the impact of damaged genes. These mechanisms include a tagging system to remove truncated gene products from pseudogenes should they be produced.² It is not unreasonable to expect similarly elegant mechanisms in eukaryotic cells and thus that some mutations interpreted as a product of common ancestry may be better explained as the product of mechanisms designed to minimize the impact of broken genes. (TGS)

ENDNOTES

1. Woodmorappe J. 2003. Pseudogene function: more evidence. *Technical Journal* 17:15–18.
2. Withey JH, Friedman DI. 2003. A salvage pathway for protein structures: tmRNA and trans-translation. *Annual Review of Microbiology* 57:101-123.

GEOLOGY: TRENDS IN SEDIMENTATION

Peters SE. 2006. Macrostratigraphy of North America. *Journal of Geology* 114:391-412.

Summary. Gaps in deposition mark boundaries between sedimentary rock packages that have histories of continuous deposition. Such gap-bound rock packages have distinct starting and ending points, with specific lithologies, fossil content, etc. A total of 4,173 such packages were identified from charts produced by the American Association of Petroleum Geologists.

Analysis of these rock packages can provide information useful in reconstructing the depositional history of North America. The study revealed a number of interesting trends. The number of rock packages is highest in the Neogene and lowest at the Permo-Triassic boundary. Other peaks occur in the Upper Cambrian, the Middle Ordovician, the Upper Devonian, the Upper Carboniferous, and the middle Cretaceous. Another interesting pattern is the shift from carbonates dominant in the Paleozoic to mostly terrestrial sediments in the Cenozoic. Evaporites are confined to the interval from the Silurian to the Cretaceous, with a peak in the Permian. A dramatic increase in terrestrial sediments occurs in the Cenozoic. There is a major discontinuity in deposition between the Paleozoic and the Mesozoic. Paleozoic basins are slowly subsiding while Mesozoic basins are more rapidly subsiding. Paleozoic volcanics are mostly submarine, while Cenozoic volcanics are most terrestrial.

Comment. Compilations such as this one may be useful in efforts to reconstruct Earth history within a shorter time frame than normally considered. Continental-based compilations are likely to be more useful than global compilations, because global compilations do not distinguish between potentially different histories on different continents. Conceptual models of the Biblical flood typically assume a worldwide transgressive sea and then a worldwide regression. A worldwide transgression would cause mainly marine sedimentation, including carbonates, whereas a worldwide regression would cause large amounts of terrestrial deposits to accumulate in inland basins. These expectations fit with the general patterns reported here.

PALEOBIOGEOGRAPHY: EUROPEAN BIRDS

Mayr G. 2005. The Paleogene fossil record of birds in Europe. *Biological Reviews* 80:515-542.

Summary. The fossil record of birds in the Paleogene of Europe is summarized. Although perching birds comprise somewhat more than half of living species, they are not found in sediments below the Oligocene in Europe. All pre-Oligocene birds appear to be on different evolutionary branches from the living members of any of the modern families of birds. Several European Paleogene fossil birds are now restricted, or nearly so, to Central and South America. These include the probable ancestors of the seriemas, potoos, hummingbirds, motmots, and New World vultures. Other biogeographic anomalies include frogmouths and possibly magpie geese, now found only in the Australian region, and mousebirds and secretary birds, now restricted to Africa. Several modern groups, including

grebes, falcons, doves and cuckoos are not found in the European Paleogene.

Comment. Creationist theory includes the proposition that all terrestrial vertebrates dispersed from southwestern Asia after the flood. Restriction of several families of terrestrial vertebrates to distant regions such as Australia and South America is a biogeographical problem that has been much discussed but not resolved. Identification of several bird families that are presently restricted to Australia or South America may indicate that the fossil record of birds is not sufficiently complete to enable us to trace the history of dispersal of terrestrial vertebrates after the flood.

PALEONTOLOGY: COMPLETENESS OF THE FOSSIL RECORD OF BIVALVES

Valentine JW, Jablonski D, Kidwell S, Roy K. 2006. Assessing the fidelity of the fossil record by using marine bivalves. *Proceedings of the National Academy of Sciences (USA)*103:6599-6604.

Summary. Many studies of trends in the fossil record depend on the completeness of the fossil record. It is not possible to measure the completeness of the fossil record when the total number of taxa for the source area is not known. For living bivalves, the number of living genera is reasonably known, and includes 1,292 living genera and subgenera. Of these, 308, or 24%, are not known as fossils. Most of the missing genera have one or more of the following properties: small size (less than 1 cm in length); aragonitic shell (as opposed to calcitic); restricted to deep sea (>200 m); or live within the substrate instead of upon it. Studies of fossil bivalves should take into account the nature of the taxa in the study in order to estimate the potential effects of missing taxa.

Comment. Completeness of the fossil record has significant implications for theories of common ancestry. Estimates of completeness based on the proportion of living taxa known as fossils seem superior to other methods of estimating completeness. If the fossil record of bivalves is 76% at the generic level, one would expect to be able to find roughly 76% of all the genus-level evolutionary steps in purported bivalve lineages. Similar statements could be made for other taxa with good fossil records.

PALEONTOLOGY: DINOSAUR TRACKS AND POSSIBLE POLYPHYLY OF DINOSAURS

Thulborn T. 2006. On the tracks of the earliest dinosaurs: implications for the hypothesis of dinosaurian monophyly. *Alcheringa* 30(2):273-311.

Summary. Dinosaurs are widely believed to be monophyletic. Numerous synapomorphies have been proposed as evidence for their monophyly, but nearly all of them are dubious or equivocal, according to recent studies. The best, and perhaps only, remaining proposed synapomorphy is the fully perforated acetabulum. Evidence from dinosaur tracks and foot structure are more easily explained by proposing separate ancestries for each of three dinosaurian clades: theropods; sauropods; and ornithischians. Each of these clades has an arrangement of bones in the foot that is not readily derivable from a single common ancestor, but is more readily explained as evolving independently from three separate ancestors. If true, this would make dinosaurs polyphyletic, and require that the term “dinosaur” be expanded to include some archosaur fossils that are currently classified as thecodonts.

Comment. The term, “dinosaur,” has become so familiar to everyone that it would take some adjustment to either replace it with three separate names, or to include some fossils that are obviously different from anything now called a dinosaur. Yet there is no a priori reason to assume that dinosaurs must derive from a single common ancestor, and splitting them into three groups might stimulate additional study to determine whether each of these three groups is truly a natural group, or whether there might be additional separate ancestries represented. Dinosaurs appear in the fossil record fully formed, without any known ancestors, and there is no actual physical evidence either for monophyly or for three lineages.

PALEONTOLOGY: MORPHOLOGICAL STASIS IN LAMPREYS

Gess RW, Coates MI, Rubidge BS. 2007. A lamprey from the Devonian period of South Africa. *Nature* 443:981-984.

Summary. A fossil lamprey found in Devonian sediments of South Africa is the geologically oldest lamprey fossil known. It shares many similarities with living species of lampreys, more so than other Paleozoic lampreys. Although the fossil record includes greater morphological diversity than seen among living members of the group, lampreys much like living species have been in existence as far back as their fossil record extends. Lampreys can rightly be called “living fossils.”

Comment. Fossil lampreys seem to be morphologically more diverse than living lampreys, with living species representing only a remnant of the former diversity. The living lampreys represent another example of morphological stasis, and could suggest that lampreys have an ancestry separate from other groups.

PALEONTOLOGY: STASIS IN MICROBES

Schmidt AR, Ragazzi E, Coppelotti O, Roghi G. 2006. A microworld in Triassic amber. *Nature* 444:835.

Summary. Triassic amber found in Italy contains fossil bacteria, fungi, algae and protozoans. Some of these amber fossils are identifiable as genera still living. These include desmids similar to the living genus *Cosmarium*, ciliate protozoans of the genus *Coleps*, and testate amoebae identical to *Centropyxis hirsuta*. The amber is thought to come from conifers in the extinct family Cheirolepidiaceae.

Comment. Microorganisms, because of their simple structure and short life-span, might be expected to be subject to relatively rapid changes in morphology over long periods of time. The persistence of genera, and perhaps even species, since the Upper Triassic seems remarkable, and suggests either that there has been much less time since the Upper Triassic than is generally believed, or that protozoa may be more resistant to morphological change than is generally believed, or both.

SPECIATION: GENES CAUSING HYBRID STERILITY IN *DROSOPHILA*

Brideau NJ, Flores HA, Jun Want, Maheshwari S, Xu Wang, Barbash DA. 2006. Two Dobzhansky-Muller genes interact to cause hybrid lethality in *Drosophila*. *Science* 314:1292-1295.

Summary. Dobzhansky and Muller independently proposed that hybrid sterility might result when two species experienced different mutations in genes that functionally interact. This would cause hybrid sterility due to failure of the two gene products to interact appropriately. This seems to have happened in two species of *Drosophila*. The gene, Lethal hybrid rescue (Lhr) produces a protein that interacts with the protein produced by the gene Hybrid male rescue (Hmr). Mutations of the first gene have occurred in *D. similans* and mutations of the second gene have occurred in *D. melanogaster*. The result is that hybrids receive a combination of genes that no longer can work together, and the resulting hybrid are not viable. Genetic changes such as this could create a barrier to reproduction and produce a new species.

Masly JP, Jones CD, Noor MAF, Locke J, Orr HA. 2006. Gene transposition as a cause of hybrid sterility in *Drosophila*. *Science* 313:448-1450.

Summary. The gene JYAlpha is necessary for male fertility in *Drosophila*. This gene is located on chromosome four of *D. melanogaster*, but on chromosome 3 of *D. simulans*. This difference sometimes results in a lack of the JYAlpha gene in some hybrid individuals, which are then sterile. The resulting reduction in fertility can lead to speciation without any change in nucleotide sequence of the gene.

Comment. Speciation occurs when two or more populations become reproductively isolated, which means they lose the ability to interbreed with each other due to genetic changes. Many different genetic changes may produce reproductive isolation, and it has been difficult to isolate which factors might be responsible. The two studies reported here offer two different mechanisms whereby reproductive isolation may be established, or strengthened: divergence of interacting genes in different populations, or changes in chromosomal location of the same gene in different populations. Speciation is consistent with creation theory, and these studies show that it can result from relatively minor genetic changes.