

ANNOTATIONS FROM THE LITERATURE*

BIOLOGY: FRAGILE PHYLOGENY

Kristensen NP, Hilton DJ, Kallies A, *et al.* 2015. A new extant family of primitive moths from Kangaroo Island, Australia, and its significance for understanding early Lepidoptera evolution. *Systematic Entomology* 40:5-16.

Summary. A new species of moth discovered on Kangaroo Island, Australia, has resulted in major changes in the theoretical relationships among moths and butterflies. The newly described species, *Aenigmatinea glatzella*, belongs to a group of moths with similar venation in forewings and hindwings (“homoneurous”). The new species has an unexpected combination of morphological traits, including degenerate mouthparts. However, genetic evidence and some morphological evidence indicate it should be classified with the tongue moths (Glossata). This analysis causes changes in the arrangement of some other families in the classification, and implies loss (reversals) or parallel gains (convergences) of several traits thought to be reliable indicators of phylogenetic relationships. It also indicates that the “Myoglossata” are not monophyletic.

Comment. The observation that the addition of a single new species caused major changes in the hypothesis of the interrelationships of moths indicates the rather fragile basis of postulating evolutionary relationships in these groups, especially at taxonomic levels above the family. The fact that morphological data are usually the only kinds available in studying fossils should suggest caution when evaluating claims of evolutionary relationships among fossil groups.

BIOLOGY: GENETICS OF GALAPAGOS FINCH BEAKS

Lamichhaney S, Berglund J, Almen MS, *et al.* 2015. Evolution of Darwin’s finches and their beaks revealed by genome sequencing. *Nature* (19 February) 519:371-375. doi:10.1038/nature14181.

Summary. The Galapagos Islands are inhabited by a group of 14 species of finches, known as “Darwin’s finches” in honor of his visit there. A fifteenth species inhabits Cocos Island, some 400 miles distant. All 15 species are believed to have descended from a common ancestor from South America. Whole-genome sequencing was conducted on 120 individuals representing all fifteen species. Results showed evidence of extensive interbreeding among the different “species,” and indicate that some “species” are the result of

hybridization. The “species,” *Geospiza difficilis*, present in the highlands of six islands, appears to be three separate “species,” each of which is more closely related to other species than to other populations of *G. difficilis*. A similar situation obtains for the species, *Geospiza conirostris*. The population on Genovesa Island is more similar to a different species than to the population on Española Island. Darwin’s finches are distinguished phenotypically largely by the shape of their beaks. The genetic basis of beak shape is not well known, but a gene, *ALX1*, is correlated with beak differences and thought to be an important genetic factor in determining beak shape.

Comment. Interbreeding, hybridization and speciation among Darwin’s finches may provide a small window into the kind of diversification of species into different habitats after the flood. As species dispersed from the ark, they would encounter different environmental conditions, and would have to adapt or go extinct. Undoubtedly, many did go extinct, but many others spread out across the earth, moving into and adapting to different habitats and developing morphological differences. The results may be seen in the frequent examples of clusters of similar species in different areas, collectively inhabiting whatever portion of the earth’s surface they were able to colonize and survive in.

BIOLOGY: PSEUDOGENES, RETROTRANSPOSONS AND GENE REGULATION

Watanabe T, Cheng E-c, Zhong M, Lin H. 2015. Retrotransposons and pseudogenes regulate mRNAs and lncRNAs via the piRNA pathway in the germline. *Genome Research* 25:368-380.

Summary. Eukaryotic protein-coding sequences are often separated by sequences of unknown function, such as pseudogenes, transposons and repetitive sequences. These sequences are transcribed into long non-coding RNAs (lncRNAs) and Piwi-interacting RNAs (piRNAs), but the function of these RNAs, if any, has been mostly unidentified. This study reports that piRNAs produced from pseudogenes and transposons regulate the degradation of mRNAs and lncRNAs in mouse spermatocytes. Regulation of mRNA stability by piRNAs means that these pseudogenes are part of a complex network of RNA sequence regulation.

Comment. Because no function had been identified for pseudogenes and repetitive sequences, evolutionary theorists postulated them to be evolutionary remnants of ancient genes no longer needed (“junk DNA”). Proponents of Intelligent Design, including creationists, suspected they were functional in some way not yet discovered, possibly relating to gene regulation. Several pseudogenes have been shown to have functions, but

the mechanisms of gene regulation are still not well understood. This report adds to our understanding of how pseudogenes are involved in regulating RNA levels in the cell during spermatogenesis in mice, and suggest that other such examples should be sought.

BIOLOGY: SCRUB JAY BEAKS VARY WITH HABITAT

Langin KM, Sillett TS, Funk WC, *et al.* 2015. Islands within an island: Repeated adaptive divergence in a single population. *Evolution* 69(3):653-665. doi:10.1111/evo.12610

Summary. A species of scrub jay, *Aphelocoma insularis*, is endemic to Santa Cruz Island, about 30 miles off the California coast. The island is mostly covered with oak woodland, with three relictual patches of Bishop pines. Jays living in the pine habitats have longer, shallower bills than jays living in the oak habitat. These differences are similar to those in mainland scrub jay populations that inhabit different habitats, but it is somewhat surprising to find such differences within a single population. This observation suggests the possibility of finding more examples of small-scale environmental variation in species, and may provide insights into the possibility of sympatric speciation.

Comment. The potential for minor morphological variation within a species is a useful concept in creationist thinking. Such variation is necessary for species to survive changes in environmental conditions during dispersal from the ark and during changes in climate since the flood.

BIOLOGY: SYNTHETIC CHROMOSOME WORKS IN YEAST

Annaluru N, Muller H, Mitchell LA, *et al.* 2014. Total synthesis of a functional designer eukaryotic chromosome. *Science* 344(4 April):55-58. doi: 10.1126/science.1249252.

Summary. The yeast *Saccharomyces cerevisiae* is used in baking and winemaking, and as a model laboratory organism. It has been studied extensively, and was the first eukaryotic organism to have its complete genome sequenced. It has 16 chromosomes, with around 6,000 genes. The third smallest chromosome has 316,617 base pairs and probably around 200 genes. Scientists have constructed an artificial chromosome, called synIII, consisting of 272,871 base pairs, and have shown that it is functional in a living yeast cell. The artificial chromosome lacks some portions of the native chromosome, and has certain additions that enable scientists to disable specific genes in experiments. This will permit scientists to determine which genes and gene combinations can be deleted and which are essential.

Future plans include construction of an entire yeast artificial genome with provision for manipulation of individual genes to facilitate determining their functions and gene interactions, and the eventual ability to design and engineer synthetic organisms.

Comment. The ability to manipulate gene activity continues to increase, and we are now approaching the technical ability to design organisms for specific purposes, and even to “create” new kinds of organisms. At least three issues arise from this situation. First, some creationists have held the belief that God would not permit humans to “create” new forms of life. This belief needs to be reconsidered. It appears to be within human technological capacity to modify organisms intentionally. Second, some creationists have insisted that God would not permit Satan to genetically modify (or “create”) new types of organisms. The ability of humans to do this should put to rest such notions. Third, underlying all these concerns is the question of bioethics. To what extent is it ethical for humans to manipulate the genomes of the Creator’s handiwork?

GENETICS – GENES OUT OF PLACE

Crisp A, Boschetti C, Perry M, Tunnacliffe A, Micklem G. 2015. Expression of multiple horizontally acquired genes is a hallmark of both vertebrate and invertebrate genomes. *Genome Biology* 16(50):1-13.

Summary. As more species genomes are sequenced, more genes are discovered that do not appear to be the result of normal “vertical transmission” of genes from one generation to the next. Two main explanations have been offered for these anomalies: multiple gene loss or horizontal gene transfer.

Multiple gene loss occurs when a gene is lost from some species but retained in other species sharing the same common ancestor. It is identified when the phylogenetic pattern of gene presence and absence appears to indicate multiple independent events. Horizontal gene transfer (HGT) occurs when a gene is transferred from one species to another, and is identified when the phylogenetic pattern of gene presence and absence is readily explained by a single, or a few, gene gains. Multiple gene loss is considered more likely than multiple gene gain by HGT.

Three groups of species were studied in this report, the nematode genus *Caenorhabditis*, the fly genus *Drosophila*, and the order of primates. Gene sequences from these three groups were compared with sequences from other groups, including non-metazoan groups such as bacteria, protists and fungi. Genes from the study groups that aligned better with non-metazoans than with other metazoans were interpreted as “foreign” genes that most likely were acquired by HGT.

Horizontal gene transfer appears to be common among bacteria, and a few examples have been described in metazoans, but claims of HGT in humans have been controversial. This study reported a much higher incidence of HGT than previously recognized. *Caenorhabditis* species have an average of 173 “foreign” genes for which HGT is a potential explanation. *Drosophila* species have an average of 40 such genes, while the primate species studied averaged 109 genes of this type.

Comment. While the evidence suggests that HGT is a real phenomenon, the authors failed to consider the possibility that some genes may be present in different groups because of design. If different taxonomic groups were created for particular environments, one would expect them to have the genes needed for those environments, regardless of whether the genes were present in some other group. “Foreign” genes are actually genes that do not fit the conventional ideas of evolutionary ancestry, and could readily be interpreted as evidence against common ancestry. In addition, numerous “orphan” genes have been identified that appear to be restricted to a single species or group of closely related species. These cannot be due to HGT if they are absent in all other species, as appears to be the case. Genes that do not fit phylogenetic hypotheses may be indicating separately created origins.

PALEONTOLOGY: JURASSIC SNAKE FOSSILS

Caldwell MW, Nydam RL, Palci A, Apesteguia S. 2015. The oldest known snakes from the Middle Jurassic-Lower Cretaceous provide insights on snake evolution. *Nature Communications* 6(27 January):5996. doi: 10.108/ncomms6996.

Summary. Newly identified fossil snakes are the oldest yet discovered. Four new snake species are described in this article. All of them are based on fragmentary fossil material that was not recognized as belonging to snakes. Three species are from Jurassic sediments. The oldest is named *Eophis underwoodi*, collected in a quarry in England (Middle Jurassic, Bathonian). *Portugalophis lignites* was recovered from coal deposits in Portugal (Upper Jurassic, Kimmeridgian). A third species, *Diablophis gilmorei*, was discovered in Colorado (Upper Jurassic, Kimmeridgian). The fourth fossil snake, *Parvivraptor estesi*, was found in England, in the Purbeck Limestone Formation (Lower Cretaceous, Berriasian). It was originally identified as a type of lizard (anguimorph). Before this study, the oldest known snake was *Najash rionegrina* from Argentina (Upper Cretaceous, Cenomanian).

Comment. The material is quite fragmentary, leaving room for caution in interpretation, but the discovery of fossil snakes in Jurassic sediments should not be a surprise. Whether the snakes had vestigial legs or were en-

tirely legless is difficult to determine from skull fragments, so reports that these snakes had legs should be considered with caution. The oldest fossil snake known before these newly identified species, *Najash rionegrina*, did have tiny but functional hindlimbs. Vestigial hindlimbs are present in some living boas and pythons, but are too small to be of use in locomotion.

PALEONTOLOGY: STASIS IS EVOLUTION?

Schopf JW, Kudryavtsev AB, Walter MR, *et al.* 2015. Sulfur-cycling fossil bacteria from the 1.8-Ga Duck Creek Formation provide promising evidence of evolution's null hypothesis. *Proceedings of the National Academy of Sciences (USA)* 112(7):2087-2092. doi: 10.1073/pnas.1419241112

Summary. Sulfur-cycling bacterial communities are known from the modern deep sea off the west coast of South America. Similar fossil communities have been discovered in Paleoproterozoic sediments in Western Australia. A community dated at 1.8 billion years was previously described, and this report adds a second fossil community, dated at 2.3 billion years in the Duck Creek Formation. Comparison of cellular morphology, community structure and chemical analyses in fossil and modern communities supports identification of the Duck Creek fossils as a sulfur-cycling bacterial community, and shows no evidence of evolutionary change. This is a remarkable example of stasis, and may be attributed to the physical stability of such sub-seafloor environments. More such fossil communities should be sought in order to evaluate the conclusions made here. Cyanobacteria involved in stromatolite formation also show stasis, but probably due to different factors. Cyanobacteria evidently have sufficient genetic plasticity to be ecologically flexible and adapt to many different habitats.

Comment. Stasis – the lack of morphological change – is a common feature of the fossil record. Stasis at the species level was the basis for the “punctuated equilibria” model famously proposed by Eldredge and Gould. This observed fossil pattern is directly contrary to Darwin’s predictions that every geological stratum should show evidence of slow, gradual changes revealing the course of evolution. These sulfur-cycling bacteria, along with the cyanobacteria to which they are compared, are striking examples of the failure of Darwin’s prediction. This point is not deflected by the proposed explanation that one group of bacteria (sulfur-cyclers) shows stasis because its environment is stable, while another group of bacteria (cyanobacteria) shows stasis despite the fact it inhabits many different environments because it has “genetic plasticity.” The appeal to search for more sub-seafloor communities throughout the geologic record may have interesting implications. We can predict that such sub-seafloor communities should be expected in

pre-flood rocks and in the modern environment, but are unlikely to be found within sediments deposited by the flood.

PALEONTOLOGY: SWIMMING TRACES CONCENTRATED IN THE TRIASSIC

Thomson TJ, Droser ML. 2015. Swimming reptiles make their mark in the Early Triassic: Delayed ecologic recovery increased the preservation potential of vertebrate swim tracks. *Geology* 43:215-218. doi: 10.1130/G36332.1

Summary. Tetrapods such as reptiles or mammals may leave marks in the sediment while swimming, as their feet contact the substrate. Fossil traces made by swimming tetrapods are found throughout the world, from the Carboniferous to the Pleistocene. This study is based on a compilation of 143 localities in some 61 geologic formations (supplementary material with the article). Tetrapod swimming traces are not evenly distributed throughout the stratigraphic record, but spike in Lower Triassic sediments, even when corrected for area of outcrop. This may be explained by the lack of bioturbation in Lower Triassic sediments, perhaps due to the destruction of bioturbating organisms in the end-Permian mass extinction event.

Comment. Patterns in the fossil record can be of great value in interpreting the processes involved in deposition of the geologic column. In the context of a global catastrophic flood, the abrupt change in the kinds of fossils at the Permian-Triassic boundary might be interpreted as due to a change in source area, bringing in new types of organisms from different habitats. A spike in swim traces might be consistent with a change in water currents associated with a change in source area. However, the Lower Triassic spike in swim traces is the result of a large number of such traces in the Moenkopi Formation of Utah (32 of 40, supplementary material), so the pattern may not apply globally. Lack of bioturbation might reflect either the lack of bioturbators or the deposition of sediments at rates faster than bioturbators could disrupt. More effort should be put forth to identify and interpret patterns in the fossil record and interpret them in a biblical context.

PALEONTOLOGY: TREND TOWARD INCREASING HABITAT DIVERSITY

Knope ML, Helm NA, Frishkoff LO, Payne JL. 2015. Limited role of functional differentiation in early diversification of animals. *Nature Communications* 6(4 March):6455. doi:10.1038/ncomms7455.

Summary. The Cambrian Explosion is a well-known pattern in the fossil record, whereby all the major body plans were present, either as fossil or

inferred on the basis of theory. The question pursued here is to what extent Cambrian fossils occupied most “ecological modes,” or only a small subset. To answer this question, 18,621 marine animal genera were assigned to different ecological modes, based on their position in the water column or sediment, mobility, and feeding strategy. Diversity of ecological mode, termed “functional differentiation,” was found to be low for Cambrian organisms, increasing in the Ordovician, and with large increases after the end-Permian and end-Cretaceous mass extinctions. Thus, although the Cambrian Explosion involved many different phyla and classes, most of them represent a relatively small number of ecological functions.

Comment. How might a creationist interpret these results? One possibility might be that animals were created in numerous body plans, which were designed with variation for different habitats. For example, the phylum Mollusca is characterized by similarities in body plan, but different mollusks inhabit different ecological zones, from the seafloor to the shoreline, and even in terrestrial settings. With such a system, a small sample, such as the Cambrian fauna, would contain a large sample of the body plans (mollusks, echinoderms, arthropods, etc), but a relatively small sample of the ecological diversity. Increasing the size and stratigraphic range of the sample would probably increase the ecological diversity represented in the record. Mass extinctions could be interpreted as changes in sources of fossils and sediments. Jumps in ecological diversity would be expected after mass extinctions, as new sources, and new habitats, were added to the stratigraphic column. A global catastrophe, in which different habitats are sequentially destroyed and buried, might produce a pattern similar to that reported in this paper. This explanation admittedly has a significant speculative component, but it hopefully will suggest new possibilities for interpreting patterns in the fossil record from a creationist perspective.

*Other annotations are available on our website: www.grisda.org