

ANNOTATIONS FROM THE LITERATURE

BIOGEOGRAPHY: FROGS LINK SEYCHELLES WITH INDIA

Biju SD, Bossuyt F. 2003. New frog family from India reveals an ancient biogeographical link with the Seychelles. *Nature* 425:711-714.

Summary. A new species of frog discovered in western India represents a previously unknown family of burrowing frogs. Based on DNA sequence comparisons, the new family, Nasikabatrachidae, is most closely related to the Sooglossidae of the Seychelles Islands. However, the two groups of frogs are quite distinct genetically.

Comment. Geologic evidence links India with Madagascar and the Seychelles during the Mesozoic. This discovery is consistent with the idea that India and the Seychelles were once linked, although there is no fossil evidence to test the idea. However, the biogeography of India presents many anomalies. The fossil record of India shares as many or more families of land vertebrates with the northern continents than with the southern continents. This is true even for sediments deposited when India was supposedly attached to the southern continent of Gondwana and separated from the northern Laurasian continent. The paleobiogeography of India remains enigmatic.

BIRD PHYLOGENY: FEWER MOAS

Huynen L, Millar CD, Scofield RP, Lambert DM. 2003. Nuclear DNA sequences detect species limits in ancient moa. *Nature* 425:175-178.

Summary. Moas were large ostrich-like birds that lived in New Zealand, becoming extinct several hundred years ago. The number of species that actually lived in New Zealand has been a question of interest. The first describers of moa skeletons named at least 64 species in about 20 genera. Over the past 25 years, the number of species has been reduced to 11, on the basis that moas were sexually dimorphic and highly variable in size. Nuclear DNA recovered from moa bones indicates that the three “species” in the genus *Dinornis* actually repre-

sent only two groups, one from the North Island and one from the South. This further reduces the number of moa species by one species, and suggests the possibility that further reduction might be justified.

Comment. Moas may have been more highly variable morphologically than modern bird species. To what extent this tendency applies to the rest of the fossil record remains unknown. Another problem is the tendency among paleontologists to give a separate name to specimens that are only slightly different, especially if they are found at different fossil localities. Both these points show the need for caution in interpreting patterns of evolutionary relationships based only on skeletal material.

BIRD PHYLOGENY: WHERE DOES THE HOATZIN FIT?

Sorenson MD, Oneal E, Garcia-Moreno J, Mindell DP. 2003. More taxa, more characters: the hoatzin problem is still unresolved. *Molecular Biology and Evolution* 20:1484-1499.

Summary. The hoatzin is a South American bird with unique traits that make it difficult to classify. Previous reports have allied the hoatzin with cuckoos, pheasants, or turacos. Comparisons of nuclear DNA rule out any relationship with pheasants, and make highly unlikely any relationship with pheasants or cuckoos. Some weak support was discovered for relationship with falcons or doves, but the hoatzin appears not to have any identified close relatives. Previous reports of hoatzin affinities with turacos were based on sequences of mitochondrial DNA with numerous errors.

Comment. The hoatzin is a bird of enigmatic affinities, restricted to South America, and without known fossil ancestors. The significance of the previous identification as a turaco was commented on in *Origins* 52:42.

CREATION AND “MAGIC BULLETS”

Ham K. 2003. Searching for the “magic bullet.” *Creation* 25(2):34-37.

Summary. Creationists have a history of uncritical acceptance of claims that tend to support creation. Several of these spurious claims have been refuted by creation scientists, much to the dismay of the

laity. Creationists should be eager to learn which arguments are sound and which are not, but too many seem eager to find some “magic bullet” that will prove creation and refute evolution once and for all. This is not likely to happen, and is not even necessary. We will never have all the answers, and it is more important to know the limitations of our knowledge than to be able to out-debate someone with views different from our own. Everyone has the same evidence available to him; creationists must learn to interpret the evidence within the Biblical view of earth history.

Comment. This is a refreshing statement that should be thoughtfully read by all creationists. If put into practice, the result would surely be an advance in our collective understanding, and an increase in respect among those with whom we disagree.

DESIGN: IRREDUCIBLY COMPLEX CONVERGENCE

Kesel AB, Martin A, Seidl T. 2003. Adhesion measurements on the attachment devices of the jumping spider *Evarcha arcuata*. *Journal of Experimental Biology* 206:2733-2738; and Kesel AB, Martin A, Seidl T. 2004. Getting a grip on spider attachment: an AFM approach to microstructure adhesion in arthropods. *Smart Materials and Structures* 13:512-518.

Summary. The cuticle or exoskeleton of arthropods is composed of a polysaccharide, chitin, complexed with proteins and lipids. This material is notable for its low adhesion to surfaces and yet many arthropods are capable of walking on smooth vertical surfaces like glass windows or painted walls. In at least some insects, the ability to attach to smooth surfaces is known to be mediated by an oily fluid.¹ In these two almost identical papers, Kesel et al. show that a different mechanism involving van der Waal’s forces is used by the jumping spider *Evarcha arcuata*. Thousands of tiny fibers, setule, on the feet of these spiders interact with surfaces they contact taking advantage of the weak intermolecular van der Waals’ force. Added together, the estimated 624,000 setule on each jumping spider have the potential to exert a force sufficient to hold 160-173 times the mass of *E. arcuata*.

Comment. Geckos are known to use a system for attachment almost identical to that reported for spiders by Kesel et al.² In their words, “The attachment systems of spiders and geckoes show astounding similarities.”³ This is remarkable given the profoundly differ-

ent surface materials found on arthropods and reptiles: chitin and keratin respectively. Presumably, arriving at these similar solutions to the problem of attachment would require very different genetic, developmental and biochemical mechanisms given the profound differences between arthropods and vertebrates.

Explaining morphological similarities in the feet of geckos and jumping spiders as a dramatic example of convergent evolution seems implausible given the mechanism by which attachment occurs in both taxa. The problem is that van der Waals' forces only act over very short distances. In addition, they are relatively weak. To take advantage of these forces requires both very small hairs and a large number of them. No gradualistic path to what is seen in jumping spider and gecko feet is evident, as gradual reduction in hair size on feet will achieve nothing until size falls below a very small threshold. In addition, even given small hairs already present on the feet, they must exhibit appropriate mechanical properties including elasticity and flexibility to allow efficient surface contact. If they are to achieve sufficient force to hold spiders or geckos on smooth surfaces these hairs must be present at very high densities.

Perhaps it could be argued that a few small hairs on the feet could increase traction with more producing greater traction. Thus natural selection could select for those individuals with more hairs on their feet. This scenario relies on some chance process to produce the very small hairs in the first place and assumes that fewer larger hairs would not be a superior solution to the traction problem. In addition, traction generated using this mechanism has the disadvantage of requiring significant force to detach feet from a surface, something presumably achieved via a modification in how feet are peeled off a surface. Thus the cost of having "sticky feet" that are not sticky enough to allow climbing on smooth surfaces may outweigh the advantages.

Use of tiny hairs to take advantage of van der Waals' forces when attaching to smooth surfaces appears to be a complex yet elegant solution to a difficult problem. This solution can logically and reasonably be explained within the context of intelligent causes, but presents difficulties when invoking chance modifications coupled with natural selection. The fact that this mechanism is now known in two very different taxa compounds this problem, as no obvious common ancestor could have provided this engineering solution as a genetic heritage and thus it must have evolved multiple times. On the other

hand, an Intelligent Designer would be free to employ the same solution in multiple organisms. (TS)

ENDNOTES

1. Walker G. 1993. Adhesion to smooth surfaces by insects – a review. *International Journal of Adhesion and Adhesives* 13,3 -7.
2. Autumn K, Liang YA, Hsieh ST, Zesch W, Chan WP, Kenny TW, Fearing R, Full RJ. 2000. Adhesive force of a single gecko foot-hair. *Nature* 405:684-688.
3. Kesel AB, Martin A, Seidl T. 2004. Getting a grip on spider attachment: an AFM approach to microstructure adhesion in arthropods. *Smart Materials and Structures* 13:512-518.

GENE DUPLICATION AND PROTEIN EVOLUTION

Behe, MJ, Snoke DW. 2004. Simulating evolution by gene duplication of protein features that require multiple amino acid residues. *Protein Science* 13:1-14.

Summary. A common explanation for the origin of new genes involves duplication of an already functional gene followed by modification of one copy to produce a novel function. Behe and Snoke examine this concept using mathematical modeling and published rates of gene duplication and mutation. Their model assumes the simplest route to production of new gene function: a duplicated gene free from purifying selection and subject to point mutation, but not recombination. In addition, they consider a biologically relevant number of modifications that must be made in the gene to create a novel function. Because the minimum number of changes necessary for most new functions appears to be greater than one altered amino acid and the number of changes needed in DNA for each altered amino acid varies between 1 and 3, making definitive estimates is difficult, but any reasonable estimate is useful when evaluating the validity of the duplication-mutation model; especially given its widespread acceptance.

Behe and Snoke show that, given liberal estimates, fixation of features requiring changes in multiple residues requires population sizes and numbers of generations that “seem prohibitive.” They thus conclude that gene duplication coupled with point mutations does not appear to be a promising mechanism for producing novel functions in proteins that require more than a single point mutation.

Comment. This paper does not exclude the possibility that other more complex mechanisms involving larger mutations and/or selection of intermediate states acting on duplicated genes may serve as engines of new gene production. The problem is that these other mechanisms appear to be even more complex and thus less probable than the conceptually simple duplication-point mutation model Behe and Snoke examined. While their paper suggests that other potential mechanisms should be rigorously examined before discarding gene duplication and modification as a potential mechanism of evolution, it clearly demonstrates that even the most superficially reasonable sounding Darwinian mechanisms should be carefully evaluated before they are accepted as truly reasonable. (TS)

ECOLOGY: SNAILS REJECT BERGMAN'S RULE

Hausdorf B. 2003. Latitudinal and altitudinal variation among north-west European land snail species. *Global Ecology and Biogeography* 12:389-394.

Summary. Body sizes of land snail species in northwestern Europe are generally larger in lower latitudes and smaller in higher latitudes. This is the opposite of the relationship observed in many birds and mammals and summarized in Bergman's Rule. Bergman's rule states that species tend to be larger at higher latitudes; a similar pattern has also been noted with higher elevation. No pattern of species size was observed in the Alps, but individuals within a species tended to be smaller at high elevations. The reason for the smaller species in northern latitudes seems to be that the northern snails are generally from families with small body size, while southern snails are largely from families with larger body size. When the effects of phylogeny are removed, no pattern is discernable in body sizes of land snail species.

Comment. Ecological "rules" that apply to some taxonomic groups may not apply to other groups. Differences in body size of European land snails may reflect historical factors such as the body size of the first colonist, rather than due to natural selection acting in parallel ways in independent lineages.

GENE DUPLICATION: A SOURCE OF NEW INFORMATION?

Zhang J. 2003. Evolution by gene duplication: an update. *Trends in Ecology and Evolution* 18:292-298.

Summary. Gene duplication and subsequent divergence is thought to be the source of new genetic information needed for increasing complexity during evolution. Duplication of genetic material was observed as long ago as 1936. The proportion of duplicated genes in an organism's genome is estimated to range from 17% in certain bacteria to 65% in the plant, *Arabidopsis*. This is probably an underestimate, because many purported gene duplicates have diverged so much that the sequences no longer appear similar. Gene divergence occurs through random mutation, and the longer two gene sequences have been isolated, the greater the differences in sequence. One gene copy may remain functional, while the other copy accumulates mutations freely. Many duplicated genes become degenerate, non-functional pseudogenes, although some pseudogenes may have a function. Pseudogenes are abundant — mammals have one pseudogene for about every two functional genes. Some gene copies may remain functional and diverge very little. Still other duplicated genes may lose part of their function and become specialized, such as being expressed in different tissues. In rare cases, a new function may evolve, as in the case of the douc langur monkey. This monkey has two copies of a gene for an RNA-degrading enzyme, while other monkeys have only one copy. The extra copy aids the langur digest its specialized diet of leaves. Positive natural selection is thought to be an important factor in creating new gene functions for duplicated genes. Duplicated genes may help provide functional redundancy, which protects organisms against the potentially harmful effects of gene degeneration.

Comment. Genes may become duplicated, but it is not so clear that new functions may arise for gene copies. If most genes have been subject to natural selection so that they are functioning efficiently, it is easy to suppose that random mutations accumulating in a redundant gene copy would tend to reduce the functional efficiency, and would be selected against. This would prevent a new function from evolving. If the duplicate copy could mutate free of selection, it seems far more likely to become a non-functioning pseudogene. The chances of a duplicated gene somehow accidentally acquiring a new

function without disrupting other gene interactions seem remote indeed. The high incidence of pseudogenes, and the tendency of genetic systems to degenerate in the absence of natural selection, cast serious doubts on claims that gene duplication serves as the source of new genetic information.

GEOLOGY: DEEP-WATER LAGERSTÄTTEN ONLY IN THE CAMBRIAN?

Orr PJ, Benton MJ, Briggs DEG. 2003. Post-Cambrian closure of the deep-water slope-basin taphonomic window. *Geology* 31:769-772.

Summary. Fossil localities with exceptional preservation of soft-tissued organisms (Konservat-Lagerstätten) are over-represented in the Cambrian and Jurassic. The high incidence of Konservat-Lagerstätten in the Cambrian seems to be associated with a relatively low incidence of deep bioturbation. Cambrian sediments have similar numbers of types of fossil traces, compared to other Paleozoic sediments, but have relatively low levels of traces left by active feeders. Cambrian Konservat-Lagerstätten are mostly found in sediments interpreted as deep water, and their over-representation in the fossil record may be due to a reduced number of active feeders in Cambrian fossil communities.

Comment. There may be a pattern in the sequence of depositional environments in which exceptional faunas (Konservat-Lagerstätten) are preserved in the fossil record. Cambrian examples are mostly from sediments interpreted as deep water slope or basins; Upper Paleozoic and Triassic examples are mostly from sediments interpreted as broad coastal delta plains; Jurassic examples are mostly from sediments interpreted as restricted, oxygen-deficient marine basins (Allison and Briggs, *Geology* 21:527-530). These interpretations should be taken into consideration by those working to model the flood. The abundance of Cambrian lagerstätten may suggest they formed during the onset of the Genesis flood, and that this event might have begun as a deep-water catastrophe.

GEOLOGY: DEVONIAN MASS-EXTINCTION LINKED TO IMPACT

Ellwood BB, Benoist SL, El Hassani A, Wheeler C, Crick RE. 2003. Impact ejecta layer from the Mid-Devonian: possible connection to global mass extinctions. *Science* 300:1734-1737.

Summary. Evidence of a mid-Devonian extraterrestrial impact has been discovered in the Anti Atlas desert of Morocco. The evidence includes shocked quartz, anomalous concentrations of heavy metals, a large negative carbon isotope shift, and microspherules. This discovery is of special interest because it coincides with a global mass extinction that may have destroyed up to 40% of genera of marine animals.

Comment. No known impact crater is associated with this stratigraphic level. Despite the success of the end-Cretaceous impact hypothesis, scientists have not yet successfully linked any other mass extinction to an extraterrestrial impact. The causes of mass extinctions are still not well understood.

GEOLOGY: METEORITE FRAGMENTS AT THE P/T BOUNDARY

Basu AR, Petaev MI, Poreda RJ, Jacobsen SB, Becker L. 2003. Chondritic meteorite fragments associated with the Permian-Triassic boundary in Antarctica. *Science* 302:1388-1392. Comment, *Science* 302:1314-1316.

Summary. The greatest and most dramatic change in fossil content occurs at the transition of the Upper Permian and Lower Triassic. Much speculation has transpired concerning the cause of the greatest of the “mass extinctions,” with recent discussion focusing on the possibility of an extraterrestrial impact. This possibility is strengthened with the discovery reported here, of dozens of meteorite fragments in end-Permian sediments at the base of the Fremouw Formation at Graphite Peak in Antarctica. Associated geochemical evidence, along with shocked quartz also suggests an extraterrestrial impact. Metal grains are present, similar to those found in end-Permian sediments in China and Japan. However, the lack of a suitable impact crater at the appropriate stratigraphic level causes many scientists to remain skeptical. More evidence is needed to settle the question of the cause of the end-Permian extinction.

Comment. Abrupt changes in fossil content and abundance at certain points in the fossil record are difficult to explain. The usual term, “mass extinction” is descriptive, but not explanatory. One or more catastrophic events seems indicated, but it is difficult to determine what process could destroy so many entire species and higher taxa yet leave the diversity of survivors seen in the succeeding layers. Perhaps the fossil record is not composed of a series of independent events over long ages, but is somehow tied together in a complex catastrophic process that is not yet understood.

GEOLOGY: MOVING HOTSPOTS IN THE PACIFIC

Tarduno JA, Duncan RA, Scholl DW, Cottrell RD, Steinberger B, Thordarson T, Kerr BC, Neal CR, Frey FA, Torii M, Carvallo C. 2003. The Emperor Seamounts: southward motion of the Hawaiian hotspot plume in Earth’s mantle. *Science* 301:1064-1069. Comment, *Science* 301:1059-1060.

Summary. The Hawaiian Islands form a chain that extends through the Emperor Seamounts, ending near the Kamchatka Peninsula and producing one of the most famous topographical features of the Pacific Ocean. The islands are arranged in two straight lines, subequal in length, that meet at an angle. It has long been held that hotspots are mantle upwellings that are geographically fixed, which implies that the angle between the two island chains was formed by rapid rotation of the Pacific Plate. However, it now appears that the angle is due to movement of the hotspot rather than movement of the Pacific Plate. Rocks cored from some of the Emperor Seamounts produce paleo-latitudinal measurements that indicate they were much farther north than the present-day location of the Hawaiian hotspot. If confirmed, this discovery will change our interpretation of mantle dynamics and plate motions. It may indicate that the earth’s rotation has been relatively stable, and that estimates of large amounts of true polar wander are incorrect.

Comment. It has been difficult to model how the Pacific Plate could change direction so suddenly. This problem is now replaced with the problem of understanding how a mantle upwelling could maintain a constant direction, then suddenly change direction and

maintain that direction. Perhaps there is some mechanism yet to be discovered to account for these islands chains.

GEOLOGY: TRENDS IN CARBONATES

Kiessling W, Flugel E, Golonka J. 2003. Patterns of Phanerozoic carbonate platform sedimentation. *Lethaia* 36:195-226.

Summary. Carbonate deposits in shallow marine water are known as carbonate platforms. A survey of carbonate platform characteristics through the geologic column reveals a number of trends (carbonate reefs are excluded from this study). Trends include an increase in the range of inferred paleolatitude and a decrease in the relative cover of equatorial shelves. Paleozoic carbonate platforms were generally much larger than those of the Mesozoic and Cenozoic. Platform composition also changes through the geologic column. Microbial and peloidal carbonates generally decline from the Cambrian to the present. Foraminifera became important constituents of carbonate platforms in the Carboniferous, and contributed variably upward through the sedimentary column. Echinoderms are important contributors to carbonate platforms from the mid-Paleozoic to the mid-Mesozoic, being mostly replaced by molluscs in the Upper Mesozoic and Cenozoic. Mass extinctions seem to have no predictable effect on development of carbonate platforms.

Comment. Global flood models need to account for trends in geochemical patterns and accumulation of sediments in addition to the ecological successions. Development of a global model of earth history will be facilitated by extensive data bases such as represented here.

HUMAN ANCESTRY: MITOCHONDRIAL EVE IN DOUBT

Kraytsberg Y, Schwartz M, Brown TA, Ebraldise K, Kunz WS, Clayton DA, Vissing J, Khrapko K. 2004. Recombination of human mitochondrial DNA. *Science* 304:981.

Summary. Human mitochondrial DNA (mtDNA) was once thought to be exclusively maternally inherited and thus not subject to recombination. This assumption was called into question by Adwadalla et al.¹ on the basis of apparent linkage disequilibrium evident in human and ape mtDNA. In an earlier paper Schwarts and Vissing reported

on a human with paternally inherited as well as maternally inherited mitochondria.² In this paper Kraytsberg et al. build off the earlier Schwarts and Vissing paper and demonstrate that mtDNA in this individual with a mixed population of maternal and paternal mitochondria experienced a high rate of recombination. In addition they were able to show that sites of recombination are concentrated in certain “hotspots” within the mitochondrial genome.

Comment. In 1987 Cann, Stoneking and Wilson³ created a storm of controversy after proposing that, on the basis of mtDNA all humans can be traced back to a single woman, “Mitochondrial Eve,” who lived in Africa about 200,000 years ago. Much of the controversy revolved around how their data were analyzed, but little criticism seems to have focused on the assumptions of maternal inheritance and lack of recombination in mtDNA. While biblical creationists took some comfort in the idea that science has shown that we all share a common female ancestor, they were not pleased with the date placed on “Mitochondrial Eve.” Interestingly, paleoanthropologists were equally discomfited over the dating of “Mitochondrial Eve” but for them the problem was that she was not old enough as they claimed that the last human common ancestor must have lived on the order of 1,000,000 years ago. In addition, the human evolution camp was split into two factions, one that believed humans arose from multiple origins and another that believed humans arose from a single source in Africa. Those who believed in multiple origins did not take lightly the news that molecular data supported the “out of Africa” theory.

Since publication of the Cann, Stoneking and Wilson paper, controversy has raged about the very concept that mitochondrial Eve, a single human female ancestor, could exist.⁴ What Kraytsberg et al. have shown is that much of this controversy was predicated on faulty assumptions. A careful reading of the original Cann, Stoneking and Wilson paper shows that the assumption of maternal inheritance was based on work done with cows,⁵ not humans. Kraytsberg et al. have dealt the final blow to the second assumption, that there is no genetic recombination in human mtDNA. This calls into question all papers reporting research done under this faulty assumption and serves as a cautionary tale for those who were once overly impressed by the weight of molecular data in informing human history. (TS)

ENDNOTES

1. Awadalla P, Eyre-Walker A, Smith JM. 1999. Linkage disequilibrium and recombination in hominid mitochondrial DNA. *Science* 286(5449):2524-2525.
2. Schwartz M, Vissing J. 2002. Paternal inheritance of mitochondrial DNA. *New England Journal of Medicine* 22;347(8):576-80.
3. Cann RL, Stoneking M, Wilson AC. 1987. Mitochondrial DNA and human evolution. *Nature* 325:31-36.
4. For examples see: (a) Ayala FJ. 1995. The myth of Eve: molecular biology and human origins. *Science* 270(5244):1930-6; (b) Gibbons A. 1993. Mitochondrial Eve refuses to die. *Science* 259(5099):1249-50; (c) Gibbons A. 1992. Mitochondrial Eve: wounded, but not dead yet. *Science* 257(5072):873-5; (d) Lewin R. 1987. The unmasking of mitochondrial Eve. *Science* 238(4823):24-6.
5. Olivo P, Van de Walle MJ, Laipis PG, Hausirth WW. 1983. Nucleotide sequence evidence for rapid genotypic shifts in the bovine mitochondrial DNA D-loop. *Nature* 306:400-402.

HUMAN ANCESTRY: MOST RECENT COMMON ANCESTOR

Rhode DLT, Olson S, Chang JT. 2004. Modeling the recent common ancestry of all living humans. *Nature* 431:562-566.

Summary. The number of ancestors of all living people increases at a rate of 2^n with each preceding generation where n represents the number of generations. Thus each individual has 2 parents, 4 grandparents, 8 great grandparents and so on. A similar phenomenon applies to the descendents of each generation although it is harder to model as the number of offspring from any union is difficult to predict. Given the exponential rate at which ancestors increase, if one goes back enough generations, the number of ancestors they have will approximately equal the number of living people at that time. In reality, however, there are complicating factors among which non-random mating between groups figures highly. Rhode et al. show that even given reasonable assumptions and correction for what is known about the history of human populations, the most recent common ancestor (MRCA) of all humans most probably lived in the relatively recent past and quite possibly since the time of Christ.

A differentiation is made between the most recent common genealogical ancestor of all humans and the most recent time in which all currently living people have exactly the same set of ancestors; the identical ancestors (IA) point. This IA point is more ancient than the time of the MRCA, but still surprisingly recent according to the model of Rhode et al. who suggest dates substantially lower than 6,000 years and possibly as recent as 2,158 BC.

Comment. It is possible to misinterpret the results of this paper as showing the Biblical Adam and Eve, or Noah and his wife, sons and daughters in law lived in the recent past. This is not what this paper is saying. However, Rhode et al. do show the feasibility of recent common ancestry of all humans and suggests a tighter genealogical link between all people than previously supposed. (TS)

MOLECULAR EVOLUTION: FALSE PSEUDOGENE

Hirotsune S, Yoshida N, Chen A, Garrett L, Suglyama F, Takahashi S, Yagami K-I, Wynshaw-Boris A, Yoshiki A. 2003. An expressed pseudogene regulates the messenger-RNA stability of its homologous coding gene. *Nature* 423:91-96. Comment, *Nature* 423:26-27.

Summary. Studies of abnormalities associated with a gene transplant led to the discovery that a pseudogene functions in regulating its functional counterpart. The gene Makarin1 is found on mouse chromosome 6, and is thought to encode an RNA binding protein. It has a pseudogene, named Makorin1-p1, on chromosome 5. A “sex-lethal” *Drosophila* gene was randomly inserted into the mouse DNA, in one case inserting into the pseudogene, resulting in developmental abnormalities. Detailed study revealed that only the paternal pseudogene is expressed as RNA, and that it functions to stabilize the Makarin1 protein. Thus, disruption of the pseudogene reduced expression of the functional gene, resulting in the abnormalities. Thus, both the functional gene and the pseudogene are necessary for normal development, and neither gene can function without the other. This is the first time a pseudogene function has been identified. The number of human pseudogenes (about 20,000) is quite large compared to the number of functional genes (about 30,000 to 50,000). This research suggests the possibility that a role in gene regulation may be a common feature of pseudogenes.

Comment. It would be ironic if pseudogenes, which have been claimed as evidence against design, should turn out to suggest further evidence in favor of design by providing another layer of complexity in gene regulation. However, there are different classes of pseudogenes, and it should not be assumed that this research implies all pseudogenes have a function. Degeneration is implicit in creation theory, and it should not be surprising if genes have degenerated.

This research should remind us to be cautious in accepting scientific claims, especially when tempted to extrapolate beyond the data.

MOLECULAR EVOLUTION: MUTATION RATES AND STRESS

Bjedov I, Tenaillon O, Gerard B, Souza V, Denamur E, Radman M, Taddei F, Matic I. 2003. Stress-induced mutagenesis in bacteria. *Science* 300:1404-1409. *Note Science* 300:1382-1383.

Summary. Different strains of bacteria differ in their mutation rates. When nutrient supply is limited in culture, natural selection favors those strains with elevated mutation rates. Bacterial colonies allowed to reach starvation showed a mutation rate increased ten to 100 times over the typical rate. The explanation seems to be a decrease in activity of the mismatch repair system, allowing an increase in the number of mutations. Stress-induced mutations may provide greater genetic variation, increasing the probability that a favorable mutation will occur and increase the survival chances of the population.

Comment. Increased mutation rate would provide more genetic variation for natural selection, and might increase the possibility of useful mutation. However, if the mutation rate goes too high, an error catastrophe could ensue, causing the population to crash. This could favor bacteria that have the capacity to increase their mutation rates during stress, but normally keep their mutation rates low. Increases in mutation rates due to stress have been reported from other organisms as well, suggesting that genetic variability might be higher than average during stressful conditions such as might follow a catastrophe. This effect might help explain the rapid rate of variation and speciation that seems to have occurred after the Genesis flood.

MOLECULAR EVOLUTION: NATURAL SELECTION TOWARD EXTINCTION?

Buckling A, Wills MA, Colegrave N. 2003. Adaptation limits diversification of experimental bacterial populations. *Science* 302:2107-2109. *Note, Science* 302:2074-2075.

Summary. Bacteria grown in culture bottles diversified into three types in a nutrient-rich medium. The three types were spatially separated and considered to be specialized with respect to the

generalized ancestral type. A total of six sequential cultures were prepared, selecting one of the specialist types in each case, and the ending culture was tested for its response to the nutrient-rich culture bottle as in the beginning. The final cultures were able to out-compete the ancestral type, showing they had increased in fitness. However, the number of different genotypes decreased as the experiment progressed, showing a genetic loss of ability to diversify. It seems that specialization came at the expense of variability.

Comment. This seems to support the suggestion of some creationists that natural selection may improve fitness for specific environments, but does so at the loss of genetic flexibility. This may be due to loss of certain alleles that have lowered value in the specified environment, resulting in a purifying selection. It does not require, or even suggest, that new genetic information has been produced.

PALEONTOLOGY: CHINESE FLYING DRAGON

Xu X, Zhou Z, Wang X, Kuang X, Zhang F, Du X. 2003. Four-winged dinosaurs from China. *Nature* 421:335-340.

Summary. A fossil dinosaur with four wings was discovered in Liaoning Province, China. The fossil, named *Microraptor*, is classified in the family Dromaeosauridae, and was found in the lower Cretaceous Jiufotang Formation. The skull is in poor condition, but the organism may have been a predator. It appears to have had feathers not only on the forelimbs, but also along the hindlimbs and tail, giving the appearance of a four-winged, gliding dinosaur. This is interpreted as a possible evolutionary stage in the development of flight in birds.

Comment. This remarkable fossil gives evidence of a rich biodiversity that has no modern survivors. *Confuciusornis*, a true bird with modern feathers, a pair of wings, and overall avian characteristics, is found in the same geological formation. The four-winged fossils, as noted in a commentary in *Science* 299:491, are not ancestral to modern birds.

PALEONTOLOGY: DIVERSITY TRENDS

Lockwood R. 2003. Abundance not linked to survival across the end-Cretaceous mass extinction: Patterns in North American bivalves. *Proceedings of the National Academy of Sciences (USA)* 100:2478-2482.

Summary. Experience with living species indicates that rare species are more likely to suffer extinction than are abundant species. Not much attention has been given to the question of whether this relationship holds in the fossil record. This paper reports on a study of more than 100 subgenera of end-Cretaceous (Maastrichtian) bivalves, with the conclusion that abundant subgenera were just as likely to go extinct as rare subgenera. Neither body size nor feeding mode could be shown to affect survival probability. Survival through a mass extinction must be controlled by factors other than the factors controlling survival in more ordinary times.

Comment. The lack of relationship between abundance and survival seems counter-intuitive, and adds to the enigma of mass extinctions. Whatever physical process that resulted in fossilization and extinction of these taxa must have been global and catastrophic.

PALEONTOLOGY: DIVERSITY TRENDS AND PULL OF THE RECENT

Jablonski D, Roy K, Valentine JW, Price RM, Anderson PS. 2003. The impact of the Pull of the Recent on the history of marine diversity. *Science* 300:1133-1135.

Summary. The number of fossil genera generally trends upward through the geologic column, dramatically so through the Cenozoic. One explanation for the increase in numbers of genera is that counts of fossil genera from the upper part of the record are inflated by knowledge of living species that are missing from the incomplete fossil record. This explanation is known as the "Pull of the Recent." However, a study of Pliocene and Pleistocene fossil bivalves revealed that 95% of living genera and subgenera have a fossil record in the Pliocene or Pleistocene. Thus the Pull of the Recent can account for no more than 5% of the trend toward increasing diversity through the Cenozoic. The increase in diversity appears to be real.

Comment. Bivalves are well studied, both in the fossil record and in modern environments. Thus, this study serves as a good

indicator of the reliability of the fossil record for durably skeletonized taxa. It also is a reminder that biodiversity patterns in the fossil record can be no more accurate than the taxonomy on which they are based.

PALEONTOLOGY: FEATHERED THEROPODS

Kundrát M. 2004. When did theropods become feathered? — evidence from pre-Archaeopteryx feathery appendages. *Journal of Experimental Zoology (Mol Dev Evol)* 302B:355-364.

Summary. In 1865 Hitchcock¹ described fossil footprints with associated impressions from the Lower Jurassic Turners Falls Formation of Massachusetts. In this paper Martin Kundrát reexamines these trace fossils (ichnia) and concludes that the impressions associated with the footprints were made by feathers on the abdomen of a theropod dinosaur. These “feathers” were filamentous structures distributed along pterylae (feather tracts) in the same way that feathers are distributed on the bodies of many modern birds. Much of Kundrát’s argument relies on extrapolation from the appearance of feathers on modern emus and ostriches just prior to hatching.

Comment. Given recent evidence of an “explosion” of birds in the Upper Jurassic and Lower Cretaceous,² any evidence of earlier bird-like features, and especially feathers, is of interest. Unfortunately, Kundrát’s argument follows a torturous path. To demonstrate that the organism that made the impression was a theropod requires him to “partly correct” at least one of his previous observations about this fossil. Further complicating the argument, he contradicts another author’s published observation³ and invokes wet feathers in the absence of rain. In addition, the organism seems to have adopted a hard to imagine position in which most of its weight rested on one side, the torso was raised off the ground and so was the tail. He also relies so strongly on evidence from the pre-hatched chicks of ostriches and emus that he runs dangerously close to invoking the “ontogeny recapitulates phylogeny” fallacy.

Kundrát appeals to Prum’s evolutionary scenario for feathers⁴ in which the second stage produces a simple tuft. These tufts then would be the “feathers” that produced the impressions visible on this fossil. If Kundrát’s interpretation is correct, it does seem remarkable that modern looking pterylae would be present along with “proto” feathers.

Given the convoluted nature of the argument made in this paper, these fossils do not appear to be particularly strong evidence in support of either Prum's scenario or of the early evolution of feathers. If Kundrát's interpretation is correct, it presents a problem in the timing of feather evolution; the earlier feathers of any type appear, the greater the difficulty in explaining their origin given the reduced time available for their evolution. On the other hand, evolving feathers earlier does allow time for the specialization of feathers found on fossil birds in the Upper Jurassic and Lower Cretaceous. (TS)

ENDNOTES

1. Hitchcock E. 1865 (1963 reprint). Supplement to the ichnology of New England. A report to the Government of Massachusetts. Boston: Wright and Potter, State Printers.
2. Standish TG. 2004. Fossil birds. Geoscience Reports 37:1-5.
3. Gierlinski G. 1997. What type of feathers could nonavian dinosaurs have, according to an Early Jurassic ichnological evidence from Massachusetts? *Przegląd Geologiczny* 45:419-422.
4. Prum R. 1999. Development and evolutionary origin of feathers. *Journal of Experimental Zoology* 285:291-306.

PALEONTOLOGY: SPECIALIZED INTERMEDIATES

Clack JA, Ahlbert PE, Finney SM, Dominguez Alonso P, Robinson J, Ketcham RA. 2003. A uniquely specialized ear in a very early tetrapod. *Nature* 425:65-69.

Summary. *Ichthyostega* is an amphibian-like vertebrate with some features intermediate between fish and terrestrial vertebrates. The morphology of its ear region has been very difficult to interpret. Computer-assisted tomography (CAT scan) of new fossil material has revealed a highly specialized ear unlike that of either the fish or the tetrapods which it was thought to link evolutionarily. Gill bars indicate that *Ichthyostega* was primarily aquatic rather than terrestrial.

Comment. Distinct specializations that are not transitional between purported evolutionary ancestors and descendants disqualify *Ichthyostega* as a evolutionary link. Proposed evolutionary links are frequently either derived with respect to their supposed descendants, or simply divergent rather than ancestral.

PHYLOGENETICS: EVOLUTIONARY TREE REPLACED BY NET?

Wolf YI, Rogozin G, Grishin NV, Koonin EV. 2003. Genome trees and the tree of life. *Trends in Genetics* 18:472-479.

Summary. Phylogenetic (evolutionary) trees are typically based on sequence comparisons of nucleotides or amino acids. Ribosomal RNA (rRNA) has probably been the most popular molecule for estimating phylogenetic trees, in part because it is relatively easy to sequence. However, trees based on different genes or proteins often produce conflicting trees. The advent of comparative genomics has added a new layer of complexity to the effort to produce phylogenetic trees, and has raised new questions about the reliability of phylogenies based on rRNA. Comparative genomics has indicated extensive lateral gene transfer and selective gene loss, particularly among prokaryotes. An extensive study of 28 protein families concluded that there was no reliable phylogenetic signal present after probable horizontal transfers were removed from the data set. Comparative genomics seems to produce consistent results when comparing closely related species, and consistently separates the major kingdoms of organisms, but seems difficult to interpret when comparing species with intermediate differences. The simple notion of a single Tree of Life that accurately portrays the evolutionary relationships of all species is probably “gone forever.”

Comment. Construction of a single tree of life is the holy grail of evolutionary biology. Many types of data have been applied in efforts to construct such a tree, along with increasingly sophisticated methodology. Amino acid sequences, chromosomal banding patterns, DNA sequences, and now complete genome sequences have all been utilized, but the results remain contradictory and frustrating. It is interesting to note that consistent results are obtained with closely related species, but not at higher taxonomic categories. Perhaps this reflects reality — there is not a single tree, but a forest of trees representing multiple independent lineages, each of which has diversified within limits. The latter pattern would fit a model that includes an initial creation, with subsequent diversification.

PHYLOGENETICS: MANY GENES BETTER THAN ONE

Rokas A, Williams BL, King N, Carroll SB. 2003. Genome-scale approaches to resolving incongruence in molecular phylogenies. *Nature* 425:798-804.

Summary. Gene sequences are often used to estimate the phylogeny of a group of species. Such studies are commonly plagued by conflicting phylogenies based on different genes. This problem was addressed by selecting 106 genes to develop a phylogeny for seven species of yeasts in the genus *Saccharomyces*. Results showed that phylogenies based on single genes were often in conflict, and there was no way to predict which genes would give more acceptable results. When all 106 genes were concatenated and analyzed, a single phylogenetic tree was recovered, which was the same using three different analytical methods. Further analysis revealed that consistent results could be obtained from concatenation of only twenty genes. This result should be tested in other groups of organisms.

Comment. Phylogenetic incongruence is well-known. This study involved a group of species in a single genus, and a common ancestry seems highly probable. However, it is difficult to be certain whether the phylogenetic tree recovered is the true tree. This might be expected if the group diversified rapidly from a single ancestral species, rather than sequentially and gradually. It would be interesting to test the hypothesis that species with independent ancestries might exhibit such a high level of incongruence among different gene phylogenies that no clear result could be obtained by concatenating the sequences.

POPULATION GENETICS OF MICE

Pergams ORW, Barnes WM, Nyberg D. 2003. Rapid change in mouse mitochondrial DNA. *Nature* 423:397.

Summary. The title of this article is misleading in that mitochondrial DNA in the mice studied, *Peromyscus leucopus*, has not been documented to change. What has been documented is a change in frequency of three mitochondrial DNA haplotypes in populations of mice in the Chicago area. These three haplotypes — M, Mw and A — represent slightly different ways of coding for the same protein, cytochrome oxidase II. The protein products of the gene remain identical because different, but synonymous, codons are used.

Comment. While data presented in this paper demonstrate that mitochondrial haplotypes may alter in frequency over the course of a century, why this might happen is left to speculation. The authors suggest that the M haplotype may provide an advantage in an environment that has experienced rapid human population growth. This may or may not be reasonable, but no mechanism by which this might happen is proposed. If changes in this particular mitochondrial DNA gene produced polymorphic proteins, selection would appear to be a reasonable explanation. But for selection to work in this case, differences in mitochondrial DNA sequences would be required to have a direct impact on fitness.

Rapid changes in mitochondrial haplotype frequencies reported in this paper do not document an evolutionary change in *Peromyscus* mitochondria in the sense that the DNA itself changed producing an increase in fitness. All haplotypes were present in specimens collected in both older and more recent groups, although the Mw haplotype occurred at low frequency in both groups. Thus, no new genetic information was generated, but variation already present in *Peromyscus* populations appears to have changed in frequency. Selection may be a reasonable explanation if a mechanism can be proposed for DNA sequences to directly impact fitness. Absent this mechanism, other explanations, including bottleneck effects, founder effects, emigration and immigration may appear equally valid. One tempting alternative explanation may be chance association of the more successful M haplotype with a particularly fit female. Because mitochondria in mammals appear to be inherited maternally¹, the M haplotype may have ridden along with a particularly advantageous set of nuclear alleles. (TS)

ENDNOTE

1. See the annotation under Human Ancestry for evidence against this assumption.