

# ANNOTATIONS FROM THE LITERATURE

## DEVELOPMENT: ECHINODERMS SIMILAR TO BILATERIANS

Martinez P, Rast JP, Arenas-Mena C, Davidson EH. 1999. Organization of an echinoderm *Hox* gene cluster. Proceedings of the National Academy of Sciences (USA) 96:1469-1474.

**Summary.** Echinoderms have 5-fold symmetry, whereas most other multicellular animals have bilateral symmetry. *Hox* genes are thought to be major determinants of body plan through their influence on development. Thus, one might expect to find some notable differences in the *hox* gene arrangement of echinoderms compared with bilaterians. This hypothesis was tested by comparing the *hox* complex of the sea urchin *Strongylocentrotus purpuratus* with the *hox* complex in chordates. Although there were some differences, the two *hox* complexes were remarkably similar, despite their radical differences in body plans.

**Comment.** This result adds to evidence that development is far more complex than indicated by comparisons of *Hox* gene complexes. *Hox* genes may function as gene regulatory elements that turn on and off other genes, with developmental differences being due to differences in the genes being regulated.

## DEVELOPMENT: HOX FOR ADULTS?

Arenas-Mena C, Martinez P, Cameron RA, Davidson EH. 1998. Expression of the *hox* gene complex in the indirect development of a sea urchin. Proceedings of the National Academy of Sciences (USA) 95:13062-13067.

**Summary.** Sea urchins have a *hox* gene complex of 10 genes that play an important role in development. Sea urchin development includes two major phases — first a bilateral larval stage, then a 5-fold symmetric adult. Only two of the ten sea urchin *hox* genes are expressed throughout development, while all of them are expressed during formation of the adult body plan. There was no obvious relationship between sequence of genes in the cluster and location of gene activity during development. It appears that larval development may not depend on the *hox* genes,

while development of the adult does. This suggests that the *Hox* cluster may not be required for development of all bilaterians, although it may be necessary for development of the adult body plan in complex metazoans.

**Comment.** In conventional evolutionary theory, organisms are more similar in their earlier developmental stages, but diverge in later stages. Similarities in *hox* gene sequences are interpreted as indicating common ancestry. However, if the earlier stages of development are the most similar, and the *hox* genes affect primarily the adult stages, the *hox* genes do not really seem to be good evidence for common ancestry.

### **DINOSAURS: A BIRD IN THE HANDS?**

Wagner GP, Gauthier JA. 1999. 1,2,3 = 2,3,4: a solution to the problem of the homology of the digits in the avian hand. *Proceedings of the National Academy of Sciences (USA)* 96:5111-5116.

**Summary.** Differences in “fingers” of dinosaurs and birds have been used to argue against the dinosaurian ancestry of birds. Theropod digits are identified as numbers 1, 2, and 3, whereas embryological evidence indicates that birds have digits 2, 3, and 4. This paper argues that the digits may not be strictly homologous in the classical sense, but that their development is affected by the presence of nearby morphological structures. Alligators in which mitosis is inhibited during development produce a single finger with mixtures of first and second finger traits. Kiwis have only two fingers (2 and 3), but when finger 2 is absent or reduced, finger 3 may assume some of its traits. Thus, there may have been a shift in development so that avian digits 2,3 and 4 have assumed the morphological traits of theropod digits 1,2 and 3.

Feduccia A. 1999. 1,2,3 = 2,3,4: accommodating the cladogram. *Proceedings of the National Academy of Sciences* 96:4740-4742.

**Summary.** The hypothesis that birds descended from dinosaurs faces insuperable problems. There is no evidence to support the proposal that avian and dinosaurian fingers should be considered homologous because of a frameshift in development. No theropod fossils indicate a frameshift occurring. The hand of *Archaeopteryx* is not as similar to theropod hands as some drawings seem to indicate. Avian forelimb and hindlimb development show the same developmental pattern, and

it seems implausible that this could be due to a frameshift in the forelimb but not in the hindlimb.

The dinosaurian ancestry of birds is linked to the notion that avian flight began from the ground up, in “hot-blooded” dinosaurs. The ground-up theory of the origin of flight is considered a near biophysical impossibility. *Archaeopteryx* appears in the fossil record 30 to 80 million years before its putative dinosaurian ancestors, which become more and more superficially birdlike toward the end of the Cretaceous. The hypothesis that dinosaurs were warm-blooded has been refuted. *Archaeopteryx* has been shown to be distinctly birdlike, with wings similar to woodland birds, asymmetric flight feathers, a scapula/coracoid arrangement for flight, and a reversed hallux found only in perching birds.

Claims of feathered dinosaurs have been refuted. Preserved theropod skin is clearly reptilian, with no trace of feathers. *Sinosauropteryx* does not have feathers, but a row of collagen fibers that supported a frill along the back. *Caudipteryx* has features indicating it is a secondarily flightless bird, including a propterygostyle, an avian occipit, and a probable herbivorous diet. *Protoarchaeopteryx* teeth appear to lack theropod-like serrations. *Confuciusornis* is clearly an arboreal bird, not a terrestrial predator.

Further problems with the dinosaur-bird hypothesis include the conversion of a piston-like breathing system to the avian flow-through lung, change in body balance, and re-elongation of previously shortened forelimbs. The 1,2,3 = 2,3,4 hypothesis is an example of allowing the cladogram to determine the data rather than the reverse.

**Comment.** Although there are some similarities among dinosaurs and birds, there are some severe problems with the hypothesis of an evolutionary link between them. Separate ancestries for the two groups is still a reasonable position to take.

## DINOSAURS: NON-AVIAN LUNGS

Ruben JA, Dal Sasso C, Geist NR, Hillenius WJ, Jones TD, Signore M. 1999. Pulmonary function and metabolic physiology of theropod dinosaurs. *Science* 283:514-516.

**Summary.** Birds are widely claimed to be descended from theropod dinosaurs. However, theropod osteology resembles that of crocodiles

more than of birds, and suggests that theropods may have lungs resembling those of crocodiles instead of the unique system found in birds. Well-preserved remains of certain dinosaurs appear to indicate a non-avian respiratory system. For example, the theropod *Sinosauropteryx* (Compsognathidae) appears to have a vertical separation between the thoracic and abdominal cavities, as in crocodilians. *Scipionyx samniticus* is a new maniraptoran dinosaur from Italy, with excellent preservation. Portions of the internal organs are preserved, and indicate the posterior colon is located in the crocodilian position rather than the avian position. Remnants of what appear to be the diaphragm are also preserved, along with evidence the thoracic and abdominal cavities were separated by the liver. All these features point to a theropod metabolism more similar to crocodiles than to birds.

**Comment.** Dinosaurs and birds share several similarities which have been used to argue for their evolutionary linkage. However, significant differences are also known, which may be used to argue against their evolutionary linkage. Although the supposed evolutionary relationship of dinosaurs and birds is strongly promoted by some, many find the scientific obstacles too great to accept this hypothesis.

## **EVOLUTION: PARALLEL MORPHOLOGICAL CHANGES IN DARWIN'S FINCHES?**

Freeland JR, Boag PT. 1999. The mitochondrial and nuclear genetic homogeneity of the phenotypically diverse Darwin's ground finches. *Evolution* 53:1553-1563.

**Summary.** Darwin's finches are among the most famous birds in the world, but surprisingly little is known about their evolutionary history. The group includes four genera, including six species of ground finches in the genus *Geospiza*. Mitochondrial DNA sequences were compared for several species.

Groupings of species of *Geospiza* based on DNA sequence similarities were different from those based on morphology. Birds from a given "species" were in some cases more similar to birds from another "species" on the same or a different island. None of the studied "species" was monophyletic. For example, one grouping consisted of some *G. scandens* and some *G. fortis* from Santa Cruz Island and *G. conirostris* and *G. magnirostris* from Genovesa Island. Other

*G. scandens* from Santa Cruz were closest to *G. difficilis* from Genovesa, while other *G. fortis* from Santa Rosa Island were closest to *G. scandens* from Marchena and *G. fuliginosa* from Santa Cruz. The lack of genetic separation of morphological species might reflect ancestral polymorphism, but the strongest factor is likely to be hybridization, which is known to occur. Failure to identify genetic markers for the *Geospiza* morphological species calls into question the validity of considering them as different biological species.

**Comment.** This example illustrates the degree of variability present in these birds, and the potential for splitting one species into several. The possibility of parallel evolution in these birds, producing similar morphologies from different ancestral stocks, would make an interesting study.

## EVOLUTION: DARWIN'S FINCHES — HOW MANY SPECIES?

Sato A, O'hUigin C, Figueroa F, Grant PR, Grant BR, Tichy H, Klein J. 1999. Phylogeny of Darwin's finches as revealed by mtDNA sequences. *Proceedings of the National Academy of Sciences (USA)* 96:5101-5106.

**Summary.** Mitochondrial DNA sequences were compared for the 14 recognized species of Darwin's finches. The group includes six species of ground finches, six species of tree finches, and two species of warbler finches. All are confined to the Galapagos Islands except for one species of warbler finch, which lives only on Cocos Island. Molecular data provided different results from the morphological data. The ground finches grouped together, but no separate species could be distinguished. Four of the five tree finches (one species was not available for study) grouped together with the Cocos island warbler finch. The four tree finch "species" were not reliably distinguished by molecular data. The other tree finch, *Platyspiza crassirostris*, did not group with any other species. The Galapagos warbler finch also was separate. Failure to distinguish morphologically based species of ground and tree finches was explained as due to retention of ancestral polymorphisms and hybridization.

**Comment.** Populations that hybridize sufficiently so that they cannot be reliably distinguished on molecular grounds could legitimately be considered the same species. The Galapagos finches studied could be considered to be four species rather than 13. Constructing a

satisfactory definition of species is difficult in situations like this where morphological patterns are inconsistent with molecular patterns.

## **EVOLUTION AND THE PUBLIC: SCIENTISTS RETAIN THEIR FAITH**

Larson EJ, Witham L. 1999. Scientists and religion in America. *Scientific American* (September):88-93.

**Summary.** James H. Leuba conducted a survey of religious faith among scientists in 1914 and again in 1933. The survey asked whether the scientist believed in a God who answers prayer and an afterlife. Leuba noted that there was less belief in God among the scientific elite (as noted in *American Men of Science*), and predicted that belief among all scientists would decline. This survey was repeated in 1996 and 1998, and the results reported here. Leuba's prediction was refuted. The number of believing scientists remains at the same level as in 1914 — about 40%. The number of disbelieving “elite” scientists has increased from 80% to 90%. (The more recent survey defined “elite” scientists as members of the National Academy of Sciences.) According to Ernst Mayr, scientists have difficulty believing in the supernatural, and in a god who would tolerate all the evil in the world. Some scientists have found a “religious” experience in evolutionary belief. The authors attribute the current conflict between science and religion as due to the desire of religious people to use the authority of science to support their views.

**Comment.** It is interesting that the proportion of believing scientists has remained the same, despite what appears to be an increasing secularization of culture.

## **GENETICS: NO END TO VARIABILITY**

Papadopoulos D, Schneider D, Meier-Eiss J, Arber W, Lenski RE, Blot M. 1999. Genomic evolution during a 10,000 generation experiment with bacteria. *Proceedings of the National Academy of Sciences (USA)* 96:3807-3812.

**Summary.** Twelve populations of the bacterium *E. coli* were established from a single common ancestor. For two populations, samples were chosen at intervals and analyzed for mutations using restriction enzymes. The other 10 populations were not analyzed until generation 10,000. Numerous mutant strains were detected. Some

strains increased in number, then disappeared as new strains appeared. The phylogeny has the shape of a single trunk, with all branches attenuated. Most detected mutations were probably due to transpositions and chromosomal rearrangements rather than to point mutations. At the end of 10,000 generations, nearly every sample had a unique genotype. These results show that the bacterial genome undergoes significant changes over relatively short time spans.

**Comment.** Many creationists believe that biodiversity has increased significantly in a relatively short time, which suggests that genomic changes may occur rapidly. This experiment supports that idea, although it is uncertain whether conclusions drawn from bacterial genomes can be applied to genomes of multicellular animals.

## **GENETICS: MAINTAINING GENETIC DIVERSITY**

Finkel SE, Kolter R. 1999. Evolution of microbial diversity during prolonged starvation. *Proceedings of the National Academy of Sciences (USA)* 96:4023-4027.

**Summary.** Cultures of *Escherichia coli* were incubated for more than a year without adding nutrients or removing bacteria, leading to starvation conditions. Comparison of bacterial samples showed that different mutants arose in different cultures, despite identical culture conditions. Rapid changes in DNA sequence were detected even after several months of incubation. As no single mutant strain took over a culture completely, genetic diversity was always present.

**Comment.** Apparently, genetic variability is not lost during starvation conditions. Other experiments indicate that stress conditions may stimulate mechanisms that produce genetic variation. Maintenance of high levels of genetic variability may make it possible for species to change rapidly.

## **GENETICS: IS HUMAN EXTINCTION IMMINENT?**

Eyre-Walker A, Keightley PD. 1999. High genomic deleterious mutation rates in hominids. *Nature* 397:344-347. Commentary: Crow JF. 1999. The odds of losing at genetic roulette. *Nature* 397:293-294.

**Summary.** Harmful mutations may accumulate in a population unless they are eliminated by natural selection. The rate at which harmful mutations occur and are eliminated can be estimated by comparing

DNA sequences for necessary genes such as proteins, with non-useful sequences such as introns and pseudogenes. Comparisons are made between similar sequences in humans and chimpanzees, assuming a common ancestry some six million years ago. Since natural selection does not eliminate mutations in non-useful sequences, mutants accumulate at a rate equal to the rate of mutation (neutral theory).

This report is the first estimate of the rate of harmful mutations in humans. The resulting calculation of 1.6 harmful mutations per person per generation is based on conservative estimates of 60,000 human genes and a generation time of 25 years. It may be more realistic to estimate that humans have 80,000 genes and a generation time of 30 years. These estimates change the calculation to three harmful mutations per person per generation.

If some mutations are beneficial, the harmful mutation rate would be calculated to be higher still. These results indicate that, for every person who survives to reproduce, three persons must die due to genetic inferiority. Why are we not extinct? A more immediate concern is that these calculations suggest that human health may be in decline. Reduction in effects of natural selection through improvements in health care could accelerate the decline.

**Comment.** Creationists operate under different assumptions than those on which this study is based, so we may question some of the conclusions. For example, mutation rates could be measured directly from human populations, such as by comparing sequences in family members from different generations, rather than calibrating rates against the geological time scale and assumed common ancestry. In addition, recent studies indicate the human genome may have no more than 40,000 genes.

However, the overall point seems plausible, that harmful mutations are probably accumulating in human populations, and that improvements in health care will probably increase the rate of accumulation. The reason humans have not yet become extinct may be because harmful mutations have not been accumulating for six million years, but for a much shorter period of time.



## HUMAN ORIGINS

Clark GA. 1999. Highly visible, curiously intangible. *Science* 283:2029-2032.

**Summary.** After more than a century of research, the origins of modern humans remains controversial. Though more data would be helpful, it would not bring consensus. Many issues are due to differences in biases and assumptions on the part of those studying the question. The study of European archaeological artifacts illustrates the problem. Variations in details of stone tools have often been interpreted as evidence of different people groups, but this results in implications of social groups with unreasonably large geographic extent and persistence in time. These variations have been shown to be explainable on the basis of the size and shape of the starting piece of stone. A greater recognition of the biases in interpretation would lead to doubts about some of the widely accepted generalizations of European prehistory.

**Comment.** The critical role of preconceived opinions in interpretation of data is seldom recognized by scientists as explicitly as here. Non-experts tend to assume they have little choice but to trust the conclusions of the experts, but, in the historical sciences especially, this entails the risk of being led astray by the power and biases of the prevailing paradigm.

## HUMAN FOSSILS: NEANDERTAL MAN ... OR NOT?

Krings M, Geisert H, Schmitz RW, Krainitzki H, Paabo S. 1999. DNA sequence of the mitochondrial hypervariable region II from the Neandertal type specimen. *Proceedings of the National Academy of Sciences (USA)* 96:5581-5585.

**Summary.** A previously published comparison of Neandertal and modern human mitochondrial DNA was based on a sequence of only 333 base pairs. This paper reports the comparison of an additional 340 base pairs. The number of differences between modern humans and the Neandertal sequence averages about 35 positions, with a range from 29 to 43. Modern humans differ among themselves at an average of about 11 positions, ranging up to 35. Humans differ from chimps at about 93 positions. Chimp subspecies differ at about 17 to 42 positions. Europeans were not more similar than non-Europeans to

the Neandertal sequence. Based on molecular clock assumptions, the estimated time of divergence of Neandertals and modern humans is about 465,000 years. Neandertals are probably not ancestors of modern humans.

**Comment.** Neandertals have been proposed to be ancestral to modern Europeans. Although this study suggests otherwise, a few caveats are in order. Molecular clock estimates of rates of DNA sequence divergence are not determined experimentally, but are calibrated from estimated dates of common ancestry based on the geologic time scale. Further, it is conceivable that separately derived lineages may resemble each other more than any of them resemble their ancestor (see Schluter and Nagel 1995. *American Naturalist* 146:292-301). Surely we have not heard the end of the Neandertal story.

## MOLECULAR EVOLUTION: NEW GENE FROM OLD

Nurminsky DI, Nurminskaya MV, De Agular D, Hartl DL. 1999. Selective sweep of a newly evolved sperm-specific gene in *Drosophila*. *Nature* 396:572-576.

**Summary.** The fruit fly, *Drosophila melanogaster*, belongs to a group of very similar flies, but it has a unique DNA sequence located between the genes for the cell-adhesion protein annexin and the cytoplasmic dynein intermediate chain protein. In the other species, these two genes are adjacent, but in *D. melanogaster* they are separated by ten copies of a hybrid gene. The hybrid gene consists of a portion of the annexin gene combined with a portion of the dynein gene. The hybrid gene has a function — it produces a protein used in dynein in the sperm axoneme. A portion of the hybrid gene acts as a promoter, permitting regulation of the gene's activity. It is not known whether the new gene is essential, or how it functions.

The appearance of the new gene can be explained by a series of duplications and deletions. Some intronic sequences were included in the functional portion of the hybrid gene. This explanation contrasts with widely held views of how genes evolve. First, the promoter region did not “evolve,” it appeared fortuitously in a single step. Second, regulatory and coding sequences were not conserved, but a new regulatory sequence formed from a previous coding sequence, while

a new coding region formed from a previous intronic sequence. Third, similarities among the promoter sequences of the genes involved are not due to common ancestry, but are of independent origin.

**Comment.** Assuming this interpretation is correct, this is a remarkable discovery. Evidence that a complex series of mutations may be preserved and produce new functional sequences may help creationists explain how species could change rapidly in a much shorter time span than commonly thought. Although it is stretching the point to call the hybrid gene a new gene, the production of newly functional sequences through apparently random mutations does seem to fly in the face of some probability arguments used by creationists to reject evolutionary claims. The bottom line may be that the genome contains many surprises for everyone.

## **ORIGIN OF LIFE: A NEW EXPLANATION FOR CHIRALITY?**

Service RF. 1999. Does life's handedness come from within? *Science* 286:1282-1283.

**Summary.** Amino acids and sugars are produced chemically in mixtures of equal numbers of left-handed and right-handed mirror-image forms, but life depends on only left-handed amino acids and right-handed sugars. Science has been unable to explain how the two forms could be separated in the origin of life. New studies suggest the weak nuclear force might play a role in selecting one "handed" form over the other. Electrons produced during radioactive decay always have a left-handed spin. The researchers aimed a stream of left-spinning electrons at a solution of sodium chlorate, which can form either left- or right-handed crystals. The left-handed electrons produced an excess of right-handed sodium chlorate crystals. When the solution was bombarded with right-spinning positrons, an excess of left-handed chlorate crystals was produced. It is not known whether these results have any bearing on the handedness of biomolecules.

**Comment.** It is too early to tell how this theory will fare, but it is not obvious that crystal behavior is a good analog for formation of biological molecules.

## **PALEOBIOGEOGRAPHY: MADAGASCAR AND SOUTH AMERICA?**

Krause DW, Rogers RR, Forster CA, Hartman JH, Buckley GA, Sampson SD. 1999. The Late Cretaceous vertebrate fauna of Madagascar: implications for Gondwana paleobiogeography. *GSA [Geological Society of America] Today* 9(8):1-7.

**Summary.** Present plate tectonics models show Madagascar separating from Africa during the Lower Cretaceous, and remaining isolated to the present. This isolation is difficult to reconcile with the widespread distributions of several fossil vertebrate taxa found in the uppermost Cretaceous Maevarano Formation of northwestern Madagascar. The fossil taxa include titanosaurid dinosaurs, sudamericid mammals, and possibly peirosaurid crocodiles. Each of these groups is known also from South America. This suggests Madagascar might not have been isolated during the Cretaceous. An alternative plate reconstruction shows Madagascar linked to Antarctica through the Kerguelen Plateau throughout the Lower Cretaceous. This interpretation is more consistent with the widespread distributions of Upper Cretaceous vertebrates. Curiously, none of the fossil vertebrates seems linked to any of the living Madagascan fauna.

**Comment.** Conflicts between plate tectonics reconstructions and fossil distributions raise serious doubts about the accuracy of plate-tectonics models. Perhaps the models can be adjusted to provide satisfactory explanations, but the history of biogeography is replete with ad hoc land bridges, disappearing continents, and unsubstantiated plate movements. Perhaps it would be useful to consider whether catastrophic models might help explain fossil distribution patterns.

## **PALEONTOLOGY: COMPLETENESS OF THE FOSSIL RECORD**

Foote M, Sepkoski JJ. 1999. Absolute measures of the completeness of the fossil record. *Nature* 398:415-417.

**Summary.** Completeness of the fossil record can be estimated in different ways, such as stratigraphic completeness for a taxon, or overall taxonomic completeness. These two approaches are compared here. The probability of genus preservation per stratigraphic interval (i.e., stratigraphic completeness) is compared with the proportion of living families represented in the fossil record (i.e., taxonomic

completeness). Results show that the two measures are highly correlated, which suggests that one might be useful in estimating the other. Correlation occurred despite the fact that the stratigraphic completeness estimates are based largely on Paleozoic and Mesozoic fossils, while the Cenozoic record is quite important in estimates of taxonomic completeness. Cephalopods were an exception, in that they had a relatively complete genus-level stratigraphic record, but a poor fossil record of living families. Chondrichthyes showed the opposite tendencies, a relatively complete record for living families, but a poor record measured by stratigraphic completeness. Trilobites, graptolites and conodonts have relatively complete fossil records, contributing to their utility as stratigraphic markers.

**Comment.** The completeness of the fossil record is a contentious issue. If the record is highly complete, one would expect to find evolutionary links for most transitions. If the record is highly incomplete, one would expect not to be able to use fossils to correlate strata. This paper suggests that the fossil record is rather complete for certain important groups. Study of extent and rates of morphological change among such groups should be instructive in evaluating proposed evolutionary sequences.

## **PHYLOGENY: DISCORDANCE IN MICROBE PHYLOGENY**

Lake JA, Jain R, Rivera MC. 1999. Mix and match in the tree of life. *Science* 283:2027-2028.

**Summary.** The basic evolutionary tree of life has been constructed from rRNA sequence comparisons. As evolutionary trees have been constructed from other gene sequences, discordance has become apparent. With whole-genome sequence comparisons now possible, it is evident that genes do not form the nested sets that would be predicted. The discordance may be explained by lateral gene transfer, where any one microorganism may contain genes from many different species. Operational genes (e.g., metabolic enzymes) seem especially subject to lateral transfer, whereas informational genes (e.g., genes in transcription, translation) do not. Genes may have been transferred from one species to another through the activity of lysogenic coliphage viruses, which are known to insert preferentially in genes for transfer RNA. Further genome sequencing is likely to reveal additional discordancies in the proposed evolutionary trees.

**Comment.** Lateral transfer appears to be an important cause of discordance in gene phylogenies. However, the results seem consistent also with polyphyly.

## **PHYLOGENY: MOLECULES VS MORPHOLOGY IN WHALES**

Gatesy J, Milinkovitch M, Waddell V, Stanhope M. 2000. Stability of cladistic relationships between Cetacea and higher-level artiodactyl taxa. *Systematic Biology* 48:16-20.

**Summary.** Artiodactyls include the even-toed hoofed mammals such as antelopes, deer, camels, pigs and hippos. Morphological evidence indicates the monophyly of this group, but molecular evidence indicates that whales should be included. Seventeen phylogenies were compared, 16 of which are based on molecular data, with one based on skeletal and dental data. As expected, the skeletal phylogeny excluded whales from the artiodactyls. All 16 of the molecular phylogenies included the whales among the artiodactyls. The artiodactyl groups most closely linked with whales were the Hippopotamidae (six phylogenies) and the ruminants (4 phylogenies). The other six phylogenies gave more ambiguous results. When all data were considered together in a single analysis, whales grouped with hippos. Stable groups include Cetacea + Hippopotamidae, Cetacea + Hippopotamidae + Ruminantia, and Cetacea + Hippopotamidae + Ruminantia + Suina.

**Comment.** Conflict between molecular and morphological phylogenies is a common observation, and whales provide a good example. Molecular biologists may have the ascendancy for the moment, but one suspects the paleontologists may have the last word. The specializations of modern whales suggest to creationists that both types of phylogenies might be wrong, and that whales may not share a common ancestry with any other group.

O'Leary MA, Geisler JH. 1999. The position of Cetacea within mammalia: phylogenetic analysis of morphological data from extinct and extant taxa. *Systematic Biology* 48:455-490.

**Summary.** Analysis of morphological data permits inclusion of fossils in phylogenetic hypotheses. Phylogenetic trees that include fossils often have different topologies from trees based solely on extant

taxa. This analysis is based on 123 morphological characters from 10 extant and 30 extinct taxa. When fossils are included, Artiodactyla is monophyletic, and the closest group to Cetacea. When fossils are excluded, Artiodactyla is paraphyletic, with Cetacea nested within it as the sister taxon to either Ruminantia or Hippopotamidae.

**Comment.** If, as these authors suggest, whales are not nested within artiodactyls, the molecular similarities of whales and artiodactyls must be due to some factor other than heredity. Perhaps lateral transfer, which seems common in bacteria, occurs also in multicellular organisms. If so, similar molecular sequences could be the result of either common ancestry or common “infection.”