ANNOTATIONS FROM THE LITERATURE

BIOGEOGRAPHY: DISPERSAL OF SOUTHERN FISHES?

McDowall RM. 2002. Accumulating evidence for a dispersal biogeography of southern cool temperate freshwater fishes. Journal of Biogeography 29:207-219.

Summary. Certain taxa are found on two or more of the southern continents, but are absent from the northern continents. This is usually explained as due to the movement of continental plates. According to vicariance theory, such groups were once widely distributed on Gondwana, and were separated by division of Gondwana into the present southern continents. Freshwater fish are often thought to be especially good indicators of past continental connections, because of their supposed inability to tolerate salt water for extensive periods of time. Two families of lampreys and two families of bony fish (Galaxiidae and Retropinnidae) are restricted to the southern continents, and have been used as evidence for previous continental connections. However, these families all have some members that enter the sea, and some of the distribution patterns suggest dispersal. There is no compelling evidence to rule out dispersal as the best explanation for the distribution of these fishes.

Comment. Numerous groups of organisms are restricted to the southern continents, isolated from each other by wide expanses of ocean. Two types of explanations have been offered for such distribution patterns: dispersalist and vicariance. According to dispersalists, isolated populations represent immigration and colonization of new regions by dispersal across barriers. Vicariance theory proposes that dispersal is too rare and untestable to be a useful explanation. Instead, isolated populations represent a historical fracturing and separation of an ancestral range as continents broke apart and drifted away from each other. Vicariance explanations have dominated biogeography for the past couple of decades, but dispersalist explanations are coming to be increasingly recognized. Even multiple congruent phylogenetic patterns in different groups can be the result of multiple dispersals, especially where consistent patterns of wind or ocean currents occur.

One should be cautious in accepting claims that present distribution patterns can be traced back to the breakup of Gondwana.

EVO-DEVO: TEETH IN CHICKS

Mitsiadis TA, Chéraud Y, Sharpe P, Fontaine-Pérus J. 2003. Development of teeth in chick embryos after mouse neural crest transplantations. Proceedings of the National Academy of Sciences (USA) 100(11):6541-6545.

Summary. In vertebrates, teeth develop via inductive interactions between neural crest-derived mesenchyme and overlying oral ectoderm. Mitsiadis et al. created mouse/chick chimeras by grafting mouse anterior neural tube into chick embryos from which the anterior neural tube had been removed. In these chimeras, migration of mouse neural crest cells to the oral region and induction of tooth germ-like structures was demonstrated. These results were interpreted to support the hypothesis that ancestors of modern birds lost the ability to produce teeth when avian mesenchymal cell's ability to be induced by ectoderm during tooth development disappeared.

Comment. Other papers have demonstrated the ability of avian ectoderm to induce dentin production in mammal cells. In possibly the most spectacular of these papers,[1] at least one fully formed tooth was produced with "enamel matrix proteins" apparently derived from the avian ectoderm. Both creationist and Darwinist authors have commented on these papers.[2] In Mitsiadis et al., tooth germs that were produced lack many of the structures characteristic of more developed teeth. This may be attributed to termination of the experiment prior to full tooth development.

The important question from an evolutionary standpoint is, does this experiment, and others like it, demonstrate that bird's ancestors once had teeth? The answer is, not necessarily. What has been demonstrated is induction of tooth production by avian ectoderm in mouse cells that are thought to have last shared a common ancestor with birds 300 million years ago.[3] In addition, Mitsiadis et al. appear to show that the induction is via pathways similar to those used in normal mouse tooth development. That signaling mechanisms of this complexity would be maintained over the time period suggested seems incredible, especially considering other profound changes that have occurred in these two animal classes.

An alternative explanation may be that a Designer used similar tools to signal the location of oral ectoderm in a wide range of organisms. While these signals are necessary for normal facial development in birds and mammals, differences between the two groups result from the interaction of these signals with other cells. Use of off-the-shelf components like those demonstrated to be expressed in both mouse and bird facial development by Mitsiadis et al. suggests a single Designer more than they suggest common ancestry. This is especially true given the time periods and mechanism suggested for evolution of birds and mammals. (T.S.)

NOTES

1. Kollar EJ, Fisher C. 1980. Tooth induction in chick epithelium: expression of quiescent genes for enamel synthesis. Science 207: 993-995.
2. See Leonard Brand's comments on Endnote 1, in: Brand L. 1997. Faith, reason and Earth history: a paradigm of earth and biological origins by intelligent design. Berrien Springs, MI: Andrews University Press, p 130; and Stephen J. Gould's comments on the same paper in Gould SJ. 1993. Hen's teeth and horses toes: further reflections on natural history. NY: WW Norton, p 177-186.
3. The mammal reptile split is thought to have occurred before the reptile bird split. The mammal reptile split is put at 300 million years ago by Vaughan TA. 1986. Mammalogy, 3rd Edition. Philadelphia, PA: Saunders College Publishing, p 26.

EVO-DEVO: WINGS ON AND OFF

Whiting MF, Bradler S, Maxwell T. 2003. Loss and recovery of wings in stick insects. Nature 421:264–267.

Summary. Molecular phylogenies of the stick insects (Phasmatodea) require that wings and flight evolved independently at least four times. Of the three families, 500 genera and approximately 3,000 described Phasmid species, only 40 % are fully winged. The wings when present show a high degree of homology with other insect wings. Instead of following the traditional dogma that once wings are lost, they cannot re-evolve, Whiting et al. suggest that selective pressure exists to maintain genetic information necessary for wings. In this particular group of insects, they suggest that genes for production of wings were present in a common ancestor and were maintained over the course of evolutionary time in wingless species, being activated when selective pressure made wings adaptive.

Comment. Evolution of the original genetic information used for production of wings is not discussed in this paper. In addition, evidence other than that inferred from molecular phylogenies is not presented to make a convincing case for the absence then presence of wings. For example, no fossil sequences that trace absence and appearance of wings in stick insects are presented. However, the model suggested is consistent with the design argument that information cannot be generated for free. Whiting et al. argue that the information for wings was present ever since the Phasmid order arose. The problem is that evolution of these various taxa within the Phasmatodea is thought to have occurred over millions of years. The explanation given, that some information necessary for wings is needed for production of other structures like legs, begs the question of how the information unique to wing formation could have survived in absence of direct selective pressure over such long time spans. It also suggest an interesting pathway for investigation, genetic analysis of information necessary for wing formation and a study of whether this information is in fact present in living wingless stick insects. (T.S.)

EVOLUTION AND RELIGION

Ruse M. 2003. Is evolution a secular religion? Science 299:1523-1524.

Summary. Creationists sometimes assert that evolution functions as a secular religion rather than a scientific theory. Is there any merit to this claim, or is it merely another “creationist trick?” The answer can be found in the history of evolution. This history can be divided into three phases: pre-Darwinian; Darwinian; and neo-Darwinian.

In the pre-Darwinian stage, evolution was a pseudoscience, much as mesmerism or phrenology. Darwin brought evolution into the scientific arena, but it never really caught on very well. Evolutionary theory had no practical application, and other areas of science received prominence. Thomas Huxley saw the Anglican Church as a competitor for the evolutionary theory of origins, and attempted to establish his own church, based on evolution. Huxley helped establish “new cathedrals of evolution” otherwise known as natural history museums.

In the neo-Darwinian stage, evolutionary theory became quantitative and gained prominence in the universities as a fully scientific field of study. However, even the secular neo-Darwinians felt the need to comment on morals, values, and cultural needs. This trend has continued to the present. We have two kinds of evolution. One is the professional, scientific evolutionism, which is not a secular religion any more than industrial chemistry. The other type of evolution is a popularized form where evolution is used to develop claims about the nature of reality, the meaning of life, and rules for behavior. This latter form of evolution can be fairly described as a kind of secular religion, and should not be a part of science classroom teaching.

Comment. Ruse has made an important point — that much of what passes for scientific thinking in the popular culture actually functions as a form of secular religion. However, one wonders if this can be avoided by those who adopt and promote a theory of origins. Even the "scientific" type of evolution has implications for morality, the nature of reality, and other issues of a generally religious nature. Few among us can think about these issues for very long without facing the question of how they apply to our own lives. Perhaps there is no way to make the study of origins a neutral subject within a science classroom.

EVOLUTION AND SCIENCE

Sober E, Steel M. 2002. Testing the hypothesis of common ancestry. Journal of Theoretical Biology 218:395-408.

Summary. The idea that all living organisms descended from a single common ancestor is widely accepted but with little attention to testing this assumption. As the authors state "the typical question is *which* tree is the best one, not *whether* there is a tree in the first place" (italics in original). At least three arguments for common ancestry have been proposed. Crick proposed that the genetic code is a "frozen accident." If the code arose by chance, independent lineages might be expected to have different genetic codes. The same argument could apply to left-handed amino acids and other biochemical universals.

A second argument for common ancestry was proposed by Oparin and others: that living organisms altered their environment so that conditions were no longer favorable for life to originate a second time. This argument can be supplemented by the observation of the tendency for one lineage to eventually eliminate the others. Given enough time, all the survivors are probably from the same lineage.

A third argument developed by Penny and others states that species of a single lineage are more likely to exhibit congruence in character state patterns that species of multiple lineages. When species show similar patterns of relationship based on different data sets, they are probably truly related. None of these tests is quantitative, nor conclusive. Sober and Steel present a model based on information theory, and recommend its use in testing common ancestry. Evidence for some genealogical relationships may be irretrievably lost with the passage of time.

Comment. We salute Sober and Steel for addressing this issue in an open manner. We suspect that it may be impossible to distinguish evidence for independently created lineages from loss of information with time.

Penny D, Hendy MD, Poole AM. 2003. Testing fundamental evolutionary hypotheses. Journal of Theoretical Biology 223:377-385.

Summary. This is a response to the paper by Sober and Steel, who argued that common ancestry might be untestable because long ages of time might have erased the pertinent evidence. In contrast, the authors of this paper claim that some alternatives to the theory of common ancestry can be formulated and tested. Two types of arguments are presented. First, Penny et al. respond to Sober and Steel's argument that methods of tree construction based on parsimony assume common ancestry. Their response is that methods other than parsimony can be used, and should be favored if they give more consistent results when analyzing and comparing different data sets. The second argument by Penny et al. is that alternative hypotheses of ancestry can be tested and rejected. They give two examples: the theory of influenza viruses from outer space, and the theory that every species was created separately (which they call "intelligent design"). They conclude by noting the difficulty of testing common ancestry, but propose that further analysis will produce tests of competing hypotheses.

Comment. This paper illustrates the difficulty all of us have in responding to criticisms made by persons with presuppositions that clash with our own. I will discuss three problems with the arguments presented.

First, Penny et al. argue that the best method for tree construction is the method that gives the most congruent results from different data sets. However, this is true only if the species actually do share a common ancestor. If they have separate origins, the best method might be the one that shows the greatest conflict in the different trees. Conflict among evolutionary trees based on different data sets is so widespread and common that one may prefer the conclusion that common ancestry has been falsified.

Second, there is an inconsistency in one of their arguments. In discussing how to test for common ancestry, Penny et al. make the statement that "a minimal-length Steiner tree can be calculated for any data…". This statement is followed later in the same paragraph by a defense of their ability to test the theory of descent for mammals because it "allows a comparison against a null alternative (that there was no treelike information in the data)." A null hypothesis (there is no treelike information in the data) that must be rejected in every case (because a tree can be constructed for every data set) can hardly serve as a test of a hypothesis.

Third, the alternative hypotheses for which tests are proposed seem more like straw men than real competing hypotheses. One alternative hypothesis is that influenza viruses have repeatedly come from outer space, rather than descending from a common ancestor. The other alternative hypothesis was that every species was created individually, optimally designed for its present environment. Neither of these hypotheses is taken seriously by those who are skeptical of common ancestry. What would be more interesting would be a test of a hypothesis that there exist multiple independent lineages, each of which has diversified into numerous species. A hypothesis of this type seems to fit the data better than any competitor, notably including the hypothesis of a single common ancestor.

GEOLOGY AND THE BLACK SEA FLOOD

Aksu EE, Hiscott RN, Mudie PJ, Rochon A, Kaminski MA, Abrajano T, Yasar D. 2002. Persistent Holocene outflow from the Black Sea to the Eastern Mediterranean contradicts Noah's Flood hypothesis. GSA Today (May):4-9.

Summary. In 1998 Ryan and Pitman proposed that the Black Sea had experienced a catastrophic inflow of water about 7500 years ago, and that this might have been the basis for the biblical flood story. The catastrophic inflow occurred when a sediment dam across the Bosphorus Strait was eroded by encroaching waters from the Mediterranean. This supposedly released a huge amount of seawater that poured into the brackish Black Sea, which had a low water level. Evidence reported in this paper indicates that brackish water has flowed continuously from the Black Sea to the Mediterranean for the past 10,000 years. This implies that there was no catastrophic flood in the Black Sea 7500 years ago.

Ryan WBF, Çagatay N, Major CO, Lericolais G. 2003. Evidence for a Black Sea flooding event. Geological Society of America Abstracts with Program 35(6):460 (189-1).

Summary: Seafloor topography of the Black Sea shows an old exposed landscape with shorelines, lagoons, and river channels. Molluscs have strontium ratios indicative of freshwater habitats. Two lowstands are recorded, the second ending at 8,400 radiocarbon years ago, and punctuated by an abrupt shift to marine conditions, based on faunal composition of benthic foraminifera, molluscs, and dinoflagellates. The best explanation for the sudden change from freshwater to marine conditions is a saltwater flood that occurred as the ocean rose and spilled over the Bosphorus barrier. Aksu’s criticisms of the Black Sea flood hypothesis were based on misinterpretation of the data.

Tchepalyga A. 2003. Late glacial great flood in the Black Sea and Caspian Sea. Geological Society of America Abstracts with Program 35(6):460 (189-2).

Summary: Runoff from melting glaciers drained into a Great Eurasian Basin System, as evidenced by endemic Caspian molluscs distributed from the Caspian Sea to the Dardanelles. This created a flood that overflowed the Caspian depression into the ancient Black Sea depression, and then into the Sea of Marmara. This freshwater flood may have been the source of the story of Noah’s flood.

Preisinger A, Aslanian S. 2003. The Black Sea during the last 20,000 years: sea level salinity and climate. Geological Society of America Abstracts with Program 35(6):461 (189-9) .

Summary: Both the level of the Black Sea and its salinity have risen continuously since the last glacial maximum. At the time that water from the Mediterranean began to overflow the Bosphorus, the level of the Black Sea was about 34 m below present level. The level has increased since that time to the present.

Comment. The hypothesis that the Biblical Flood was based on a catastrophic flood in the Black Sea attracted a great deal of interest and comment, but was not consistent with the Biblical record. Different data sets and observations are used to support conflicting interpretations. The idea that saline Mediterranean waters once flowed into a previously freshwater Black Sea seems widely accepted. More controversial are questions over exactly when this happened and how rapidly it occurred. Regardless of whatever consensus develops on these questions, the Black Sea does not provide a plausible setting for the biblical flood.

MOLECULAR BIOLOGY AND EVOLUTION: GENE DUPLICATION

Force A, Lynch M, Pickett FB, Amores A, Yan Y-L, Postlethwait J. 1999. Preservation of duplicate genes by complementary degenerative mutations. Genetics 151:1531-1545.

Summary. The origin of new genes is a problem for evolutionary theory. The favored view is that genes are occasionally accidentally duplicated, with one gene copy remaining functional while the other copy is free to mutate. The extra gene copy may degenerate into a nonfunctional pseudogene, or it may happen to become a gene for a new function. Degeneration is the most likely result. However, sequence studies indicate that genes thought to be duplicated are preserved more often than theory predicts; hence, some explanation is needed. The explanation proposed here is that genes often have multiple functions, and the different functions may be regulated by different regulatory elements. Thus, one gene copy may lose part of its function, but the other gene copy may compensate for this loss by retaining the function. Losses of different functions in each gene copy would result in preservation of both gene copies. This hypothesis needs further testing.

Comment. The gene duplication theory seems inadequate to explain the gain of function required by evolutionary theory. The hypothesis proposed here may explain how certain genes lose some of their function yet remain useful, but it is not clear how partial loss of function could free a gene to mutate to a new function. It would seem more likely that both gene copies would be subjected to increased stabilizing selection to prevent further loss of function. Although a few putative examples of gain of function have been proposed, skepticism of such hypotheses seems fully justified on theoretical grounds.

PALEOCLIMATE AND CARBON DIOXIDE

Royer DL, Osborne CP, Beerling DJ. 2002. High CO^2 increases the freezing sensitivity of plants: implications for paleoclimatic reconstructions from fossil floras. Geology 30:963-966.

Summary. Paleoclimatic reconstructions are often based on climatic tolerances of living plants thought to be related to fossils found in an area. Experimental study has revealed that carbon dioxide levels affect the sensitivity of plants to freezing, thus altering estimates of paleoclimate. Increasing the carbon dioxide concentration increases the freezing sensitivity of living plants. If the past concentration of carbon dioxide were double the present value, estimates of paleotemperature minima based on fossil leaves would need to be raised by at least 1.5 to 3^{o}C.

Comment. This discovery could significantly alter interpretations of past climates.

PALEONTOLOGY: PERMIAN BACTERIA IN SALT OR MODERN CONTAMINATION?

Nickle DC, Learn GH, Rain MW, Mullins JL, Mittler JE. 2002. Curiously modern DNA for a “250-Million-Year-Old” bacterium. Journal of Molecular Evolution 54:134-137.

Summary. Vreeland et al recently claimed to have extracted and cultured bacteria from a salt crystal supposedly 250 million years old. However, the DNA sequence of 16S ribosomal DNA has only three clear differences from the sequence of the modern bacterium, *Salicbacillus marismortui*, which is found in salt deposits. This is far less than the amount of DNA differences one would expect to find in such ancient bacteria, and indicates that the bacteria in question were much younger than 250 million years.

Comment. It is difficult to believe that a bacterium could survive for 250 million years. Yet the original researchers used meticulous methods that seem likely to prevent contamination. Might the explanation be that the bacteria were actually present in the salt crystals and were not contaminants, but that the time since emplacement is much less than the conventional geological age of the material?

PALEONTOLOGY: TRIASSIC BIRD TRACKS?

Melchor RN, de Valais S, Genise JF. 2002. Bird-like fossil footprints from the Late Triassic. Nature 417:936-939.

Summary. Bird-like footprints have been found in the Santo Domingo Formation, an Upper Triassic redbed in Argentina. The tracks are well-preserved and abundant, and exhibit nearly all the features of modern bird tracks. No suitable track-makers are known from Triassic sediments, and it is presumed that the tracks must have been produced by an unknown group of somewhat bird-like theropods.

Comment. The most natural explanation for these tracks is that they were produced by birds. The tracks are significantly separated stratigraphically from any known bird fossils. This stratigraphic separation is somewhat unusual, but not unprecedented. The interpretation that tracks were produced by an unknown theropod, rather than by birds, is drawn by evolutionary assumption instead of the data. If the tracks were made by birds, the hypothesized theropod ancestry of birds would be difficult to defend.

SCIENCE: TESTING THE PAST

Miller K. 2002. The similarity of theory testing in the historical and “hard” sciences. Perspectives on Science and Christian Faith 54:119-122.

Summary. Science proceeds by gathering information, proposing an explanation (hypothesis), and then testing the explanation. This methodology is the same for all branches of science, whether experimental or historical. Strictly speaking, no event is repeatable, so repeatability should not be a strict criterion of hypothesis testing. Both historical and experimental sciences are predictive, testable, and generate new questions for research. Thus, historical sciences such as evolutionary biology, geology and paleontology should not be compared unfavorably with the “hard” experimental sciences such as physics and chemistry.

Comment: Knowledge of initial conditions is a fundamental difference between historical science and experimental sciences. The two types of investigation may require similar amounts of effort and ingenuity, but there is a difference in the degree of confidence that one should place in the results.

SCIENCE: HISTORY AND THE SCIENTIFIC METHOD

Cleland CE. 2001. Historical science, experimental science, and the scientific method. Geology 29:987-990. See Geology 30:951-954 for some reactions.

Summary. Historical science and experimental science have different methodologies, but neither should be considered more objective, more rational or more securely established by evidential support. Neither inductivism nor falsificationism is actually practiced by real scientists. Experimental scientists make predictions and then try to use experimental tests to rule out false positives and false negatives. Historical scientists construct multiple competing hypotheses and then try to find a “smoking gun” that will favor one hypothesis. Differences between the two methodologies “reflect an objective difference in the evidential relations at the disposal of historical and experimental researchers for evaluating their hypotheses.” There is no basis to claim that one of these kinds of hypotheses is “more securely established by evidence.”

Comment. The term “science” has become such a culturally powerful word that many find it irresistible to fight to attach this symbol to one’s own activities. It is widely agreed that there are clear differences in methodology between “historical scientists” and “experimental scientists.” Cleland admits that there are differences in the nature of the evidence available to the different systems of investigation. In view of this, it is quite reasonable to suppose that one methodology actually does reproduce results that are more reliable and “more securely established by evidence” than the other.

SPECIATION IN PARALLEL

Rundle HD, Nagel L, Boughman JW, Schluter D. 2000. Natural selection and parallel speciation in sympatric sticklebacks. Science 287:306-309.

Summary. Several lakes in coastal British Columbia are believed to have been covered by ice until after the Ice Age, so any fish living in them must be relatively recent colonists. Several of these lakes are inhabited by two different forms of three-spined stickleback fish, which are apparently derived from a nearby marine species. The two forms differ in shape and habits. One form — the Benthic — is larger bodied and feeds on invertebrates in shallow water. The other, Limnetic form, is more slender and feeds largely on plankton in the open water. In each lake, the two forms are reproductively isolated, and it appears at first glance that the two forms represent two species that originally colonized each of the lakes. This idea is supported by experiments that show that the similar forms from different lakes will interbreed with each other, but not with the contrasting form from their own lake. However, molecular studies indicate that the Benthic and Limnetic forms from each lake are more closely related to each other than to the similar forms in other lakes. This implies that parallel speciation has occurred. In other words, the ancestral species invaded each of the lakes, and developed into two forms that are reproductively isolated from each other, but not from similar forms in other lakes. This appears to be an excellent example of natural selection in the wild.

Comment. The explanation from natural selection seems reasonable, and is consistent with creationist theory. This study has rather negative implications for attempts to reconstruct phylogeny solely on the basis of morphology, which is essentially the only basis available for studies of fossils.