

# ANNOTATIONS FROM THE LITERATURE

## COMPARATIVE GENOMICS

Blattner FR, Plunkett G, Bloch CA, + 14 others. 1997. The complete genome sequence of *Escherichia coli*. *Science* 277:1453-1462.

**Summary:** *Escherichia coli*, common in animal digestive tracts, has what is probably the most intensively studied genetic system of any species. Complete sequencing of its genome not only contributes to a greater understanding of how *E. coli* operates, but will also provide an excellent check on conclusions drawn from many years of research. The genome contains 4288 protein-coding genes, of which 1632 (38%) were previously unknown. This number may be reduced, since 383 known *E. coli* proteins have not yet been matched with any gene sequence, but this would still leave 29% of the genes classified as previously unknown. As expected, *E. coli* is similar to *Haemophilus influenzae* — the two species share 1130 genes, nearly two-thirds of the entire genic complement of *H. influenzae*. The archaeon *Methanococcus jannaschii* shares only about 231 (13%) of its genes with *E. coli*, and the eukaryote *Saccharomyces cerevisiae* shares about 254 (less than 5%) of its genes with *E. coli*.

**Comment:** From the limited sample available, it appears that species considered to be closely related on other grounds also have similar sets of genes, while species considered to be only distantly related share a relatively small number of genes. This is not surprising, but it does confirm that bacteria are an extremely heterogeneous group.

Bult CJ, White O, Olsen GJ, + 36 others + Venter JC. 1996. Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* 273:1058-1073.

**Summary:** The genome sequencing era continues with the first member of the group of bacteria known as Archaea. Archaea include a variety of autotrophic bacteria that live in such inhospitable places as hydrothermal vents, hot springs and deep underground. Their relationships, if any, to other organisms are controversial, and distant

at best. This is the first report of the genome sequence of an archaean species. The genome consists of three circular elements, containing 1682, 44 and 12 apparent genes. Most of the genes were new to science. The function of only 38% of the genes could be identified with confidence, while another 6% matched apparent genes in other organisms for which the protein function is unknown. Comparisons with two other species of bacteria showed an overlap of only 11% (*Haemophilus influenzae*) and 17% (*Mycoplasma genitalium*) of their genes. Genes involved in cell division, energy production, and metabolism were more similar to those of Eubacteria, while genes involved in gene processing (transcription, translation, replication) were more similar to those of eukaryotes. In general, *Methanococcus* has greater similarities to eukaryotes than to ordinary bacteria.

**Comment:** The differences between this archaean bacteria and the known ordinary bacteria are startling, although suggested by previous studies. We are reminded again of the great complexity and diversity of living organisms, and the great amount of study that must be done if we are to understand how life operates at even the simplest level.

Fraser CM, Casjens S, Huang WM, + 35 others. 1997. Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*. Nature 390:580-586.

**Summary:** Bacteria include a group of spiral-shaped forms known as spirochaetes. Many spirochaetes are pathogenic, including *Borrelia burgdorferi*. Lyme disease was apparently present in Europe since the beginning of the 1900s, but was first identified in the United States in the mid 1970s. It is now known to occur widely in the Northern Hemisphere. The causative agent, *B. burgdorferi*, was finally isolated in the early 1980s. The genome consists of a linear chromosome with 853 coding sequences, of which 249 (29%) have not been identified in any other organism. Another 430 coding sequences are present in a total of 11 plasmids. More than half (250, 58%) of these have not previously been seen.

**Comment:** Nearly every newly sequenced bacterial species seems to have a large complement of genes never observed previously. The great diversity of gene complements in different

types of bacteria complicates the search for a possible suite of genes that represents the minimal genetic requirements for a living cell. *Mycoplasma genitalium* has the smallest genome of any cell capable of independent living (even *M. genitalium* is a parasite). The genome of *M. genitalium* is believed to approximate the minimal genetic requirements for a living cell, yet it contains 310 genes not identified in *Escherichia coli*. The remaining 158 of its 468 proteins are probably not enough for survival, so the minimal genetic complement must be greater than 158, but less than 468.

Klenk H-P, Clayton RA, Tomb J-F, + 48 others. 1997. The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon *Archaeoglobus fulgidus*. *Nature* 390:364-370.

**Summary:** This sulphur-metabolizing organism has a genome of 2436 coding regions, of which 639 (26%) have no match with previously known genes. The only other archaeon to be sequenced so far is *Methanococcus jannaschii*. Comparison of the two genomes shows a match of 916 genes, about 53% of the *M. jannaschii* genome. Genes for processing information are similar in the two archaeon species, while genes for intermediary metabolism show notable differences.

**Comment:** This result shows that even among bacteria in the same group, Archaea, there is great diversity in the gene complement.

Kunst F, Ogasawara N, Moszer I, +148 others. 1997. The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. *Nature* 390:249-256.

**Summary:** *Bacillus subtilis* is probably the best-known Gram-positive bacterium. It is common in soil, water and plants, and is non-pathogenic. The genome contains about 4100 protein-coding genes, of which 58% have known functions and 30% do not match any genes previously discovered. The remaining 12% match sequences previously discovered, but for which the function remains unknown. Sequences were identified indicating infection with at least ten different prophages (viruses), which could have transmitted genes to *B. subtilis* from other species. *Mycoplasma genitalium* is thought to be derived from bacteria similar to *B. subtilis*. Comparison of their two genomes identified 300 genes in common,

and reduced the number of unique genes in *M. genitalium* from 96 genes to 90 genes. The intestinal bacterium, *Escherichia coli*, is a Gram-negative bacterium, believed to be only distantly related to *B. subtilis*. The two species share about 1000 clearly identifiable genes.

**Comment:** About 20% of the genes of *M. genitalium* are not identifiable in its putative relative, *B. subtilis*. Perhaps further study will reveal whether these genes have been lost in *B. subtilis* or gained in *M. genitalium*. If they have been gained in *M. genitalium*, it will be of interest to determine whether the best explanation is cross-species gene transfer, or within-species mutations.

Mewes HW, Albermann K, Bahr M, + 9 others. 1997. Overview of the yeast genome. *Nature* 387:7-65. Reaction: Clayton RA, White O, Ketchum KA, Venter JC. 1997. The first genome from the third domain of life. *Nature* 387:459-462.

**Summary:** The common baker's yeast, *Saccharomyces cerevisiae*, is a single-celled eukaryote. It is the first species with an organized nucleus to have its genome completely sequenced. The genome contains perhaps 5800 genes, which is almost half again as many as either *Escherichia coli* or *Bacillus subtilis*. Functions could be identified for 3167 genes. Some 2000 "orphan" genes remain without known function or matches in other organisms.

**Comment:** With fewer than 20 species sequenced so far, the number of genes shared by all species is surprisingly low, and each species appears unique. The uniqueness of each bacterial species makes it dubious to use any one of them as representative of a large group of species. It seems likely that uniqueness is pervasive among eukaryotes, and that yeast should not be taken as representative of eukaryotes.

Tomb J-F, White O, Kerlavage AR, + 39 others. 1997. The complete genome sequence of the gastric pathogen *Helicobacter pylori*. *Nature* 388:539-547.

**Summary:** Nearly half the population of the world is believed infected with *Helicobacter pylori*, which causes peptic ulcers and is associated with some kinds of cancer. Of the 1590 recognizable coding sequences in *H. pylori*, a member of the Gram-negative Eubacteria, nearly one-third (499) do not match previously known

sequences. Many proteins of *H. pylori* are similar to those of *Escherichia coli* and *Haemophilus influenzae*, which are thought to be closely related. However, many other proteins involving production of amino acids, production of proteins, and other cellular processes are more similar to bacteria thought to be only distantly related. This could be due to horizontal gene transfer, or to retention of original forms of proteins.

**Comment:** The situation where some genes suggest one set of relationships while other genes suggest different relationships provides an interesting problem for understanding the origins of biodiversity.

## DESIGN

Dembski WA. 1997. Intelligent design as a theory of information. *Perspectives on Science and Christian Faith* 49:180-190.

**Summary** Intelligent design can be regarded as a theory dealing with the origin and flow of information. Information itself is difficult to define, but is related to probability. The lower the probability of an event, the greater the information that can be derived from the event. For example, the probability of being dealt a royal flush in a hand of playing cards is about  $2 \times 10^{-6}$ . Knowledge that such a hand was dealt carries more information than knowledge that a person was not dealt a royal flush (which carries a probability of about 0.999998). Information can be defined as the negative base 2 logarithm of the probability of an event.

Information can be “specified” or “unspecified.” It is specified if the event can be independently identified by a pattern; otherwise it is unspecified. For example, suppose an archer shoots an arrow at the wall. The probability is very low that any specific spot will be struck. However, this low probability is not enough to infer intelligent design, because the event is unspecified. If a target is first painted on the wall, and the arrow strikes the “bull’s-eye”, one can readily identify a specification of the event. Specification of information is easily understood when the pattern is identified before the event occurs, but it may also occur in some cases when the pattern is identified after the event. In the latter case, the key is that the pattern produced by the event is sufficient to identify the occurrence of the event, independently of knowledge of the occurrence of the event. Information that is both specified and complex is indicative of

intelligent design. Another way of expressing this is to say that intelligent design is characterized by choice, and choice is identified by the actualization of a specified event, to the exclusion of other possibilities.

According to Dembski, information cannot originate from natural causes. This is because natural causes are based on chance and necessity. Information is based on contingency, which means that it cannot be derived from necessity. Chance may produce information that is complex, or that is specified, but it is inadequate to produce information that is both complex and specified. Combining chance and necessity merely means arranging their effects in some sequence, which does not solve the problem. Because complex specified information (CSI) cannot be generated by natural causes, certain conclusions can be drawn relative to intelligent design: the CSI in a closed system of natural causes remains constant or decreases, and the CSI in any closed system of natural causes must have been put there before the system became closed. Since life requires CSI, it must be the product of intelligent design.

*Comment:* The necessity for “intelligent design” is being promoted by a number of scholars, including William Dembski. Critics of intelligent design have pointed to the lack of a suitable definition of design. This paper is a useful and thoughtful response to these criticisms.

## **GENETIC ENGINEERING**

Wilmut I, Schnieke AE, McWhir J, Kind AJ, Campbell KHS. 1997. Viable offspring derived from fetal and adult mammalian cells. *Nature* 385:810-813.

*Summary:* Cloning of animals generally requires material from very early in development, as it appears that cells become committed to a specific function (differentiated) early in development. Thus they lose their ability to produce an entire individual, because many genes have been permanently turned on or off, in accordance with the specific function of the cell. This paper is the first report of production of an individual from a body cell of an adult mammal. The procedure involved transfer of a cell nucleus into an unfertilized sheep egg from which the nucleus had been removed. Three types of donor cells were used, including adult mammary gland cells.

All three cell types successfully produced viable young, although the fetal mortality rate was high. In each case, the characteristics exhibited by the lamb were those of the donor of the nucleus, rather than of the egg.

**Comment:** This result opens up many new possibilities in biological research, and many new questions in bioethics. It also serves as a lesson that many of the things we know may be wrong.

## GEOLOGY

Evans DA, Beukes NJ, Kirschvink JL. 1997. Low-latitude glaciation in the Palaeoproterozoic era. *Nature* 386:262-266.

**Summary:** Ancient glaciations have been inferred on the basis of deposits of unsorted clasts of mixed sizes, striated rocks, and polished rocks. Yet such deposits are sometimes found closely associated with evidence of tropical conditions, such as carbonate rocks and evaporites. In such cases, estimates of paleolatitude might indicate whether the area of the supposed glaciation was located near the poles. The Precambrian Makganyene diamictite of South Africa is one such deposit. It is overlain by volcanic rocks, the Ongeluk Lava, for which it is possible to take paleomagnetic measurements. Results are interpreted to indicate a paleolatitude of about 11 degrees. This result merely deepens the enigma of the supposed tropical ice ages.

**Comment:** Although the authors do not propose it, an alternative explanation for the geological evidence that does not include glaciation seems in order.

Renne PR, Sharp WD, Deino AL, Orsi G, Civetta L. 1997.  $^{40}\text{Ar}/^{39}\text{Ar}$  dating into the historical realm: calibration against Pliny the Younger. *Science* 277:1279-1280.

**Summary:** Volcanic material from the 79 A.D. eruption of Mt. Vesuvius in Italy was dated by the argon/argon method at 1925 +/- 94 years ago. This is in good agreement with the historical date of 1918 years ago for the eruption. This result shows that argon/argon dating can be used for events within historical times. During the procedure, significant amounts of "excess argon" were noted, yielding ages up to 521,000 years. By gradual, stepwise heating of

the sample, it was possible to obtain ages that agreed with the known historical age of the sample.

*Comment:* It is remarkable that such precision was achieved. However, without knowledge of the true age of the sample, it might be difficult to know whether to accept the 521,000-year age instead.

## HUMAN FOSSILS

Krings M, Stone A, Schmitz RW, + 3 others. 1997. Neandertal DNA sequences and the origin of modern humans. *Cell* 90:19-30.

*Summary:* The original specimen of “Neandertal Man” was used as a source of DNA, which was sequenced and compared with DNA from living humans. Results indicate that the Neandertal specimen differed from the reference sequence, taken from a living human, at 27 positions out of 360. Living humans differ from each other at an average of 8 positions. This is interpreted to mean that Neandertals were a separate species, and were not directly ancestral to living humans. Modern humans differ from chimps at an average of 55 positions. Unfortunately, no comparable figure was reported for a Neandertal/chimp comparison. Although numerous problems are involved in sequencing DNA from fossils, the results of this study were obtained in two independent trials, supporting its reliability.

*Comment:* It seems premature to conclude that Neandertals were a separate species from modern humans on the basis of this study. Although replication of the results lends credibility to the report, it should not be overlooked that scientists have failed in attempts to extract DNA from fossils associated with Neandertal skeletons. It would be helpful if DNA could be recovered from another Neandertal skeleton and compared with the results reported here. Another point of interest is that modern humans vary at 225 positions in the sequence, although the full range of variation is not seen in any single comparison. Of the 27 differences reported here in the Neandertal sequence, 25 have been previously reported in modern humans. Thus only two positions in the Neandertal sequence are not known to be shared with some humans. Another point to consider is that mitochondrial DNA may be much more changeable than has been generally thought, as illustrated by recent studies.



## LIFE ON MARS?

McKay DS, Gibson EK, Thomas-Keprta KL, + 6 others. 1996. Search for past life on Mars: possible relic biogenic activity in Martian meteorite ALH84001. *Science* 273:924-930.

*Summary:* A meteorite discovered in the Antarctic in 1984 contains carbonate globules and polycyclic aromatic hydrocarbons, which could have been produced by bacteria. The mineralogy of the meteorite suggests an origin on Mars, and it is thought that it was blasted to Earth by an asteroidal or cometary impact. If the carbonate globules and hydrocarbons are due to biological activity, it could indicate that life is present on Mars. Magnetite and iron sulfides are also present. Each of these features could be produced by either biological or inorganic processes, but when considered collectively, they point to a biogenic origin for the carbonates in the meteorite.

*Comment:* This sensational proposal has stimulated a great deal of discussion, both in the scientific literature and in the public press. The announcement was made at a NASA press conference, the timing of which seemed remarkably close to Congressional consideration of funding for NASA's budget. Some of the scientific responses are described below.

Shearer CK, Papike JJ. 1996. Evaluating the evidence for past life on Mars. *Science* 274:2121.

*Summary:* Living organisms produce fractionation of sulfur isotopes, but study of sulfur isotope ratios in pyrite grains of the "Martian meteorite" do not support the inference of bacterial activity. Sulfur isotope ratios in the "Martian meteorite" are consistent with impact processes or low temperature weathering processes.

Bradley JP, Harvey RP, McSween HY. 1997. No 'nanofossils' in Martian meteorite. *Nature* 390:454.

*Summary:* Many of the elongated forms found on surfaces within the Martian meteorite are actually the emergent edges of microstructural elements of minerals in the meteorite. Others appear to be "magnetite whiskers." The majority of these structures appear to be inorganic, although a biogenic origin cannot be ruled out in every case.

McSween HY. 1997. Evidence of life in a Martian meteorite? Geological Society of America Today 7(7):1-7.

**Summary:** Terrestrial contamination by Antarctic meltwater may explain the presence of organic matter in cracks in the Martian meteorite. The polycyclic aromatic hydrocarbons found in the meteorite resemble those found in Antarctic ice. Some reports of carbon isotopic fractionation may be due to laboratory contamination. The supposed microorganisms match in size and shape the magnetite whiskers reported by Bradley et al., and it is unlikely they represent fossilized bacteria. A critical but unresolved issue is the temperature at which the carbonate globules formed. Kirschvink et al. (1997: Science 274:1629-1633) claim a low temperature origin, while Scott et al. (1997: Nature 387:377-379) argued for a high-temperature history of the meteorite.

Scott ERD, Yamaguchi A, Krot AN. 1997. Petrological evidence for shock melting of carbonates in the Martian meteorite ALH84001. Nature 387:377-379.

**Summary:** Petrological studies of the Martian meteorite show that carbonate, plagioclase and silica in the meteorite were melted by a shock event which also locally crushed the pyroxene. This shock event would have raised the temperature of the carbonate sufficiently to melt it, destroying any evidence of life if it were present. Therefore, the carbonate globules cannot represent the effects of bacterial action, but are inorganic in origin.

Yockey HP. 1997. Life on Mars? Did it come from Earth? Origins and Design 18:10-15.

**Summary:** Arguing against the notion that an Antarctic meteorite has evidence of life on Mars, Yockey points out that Mars is an unlikely place to find life. The Martian atmosphere is only 0.6% as dense as that on Earth, and is 95.3% carbon dioxide, with tiny amounts of water vapor, oxygen, and other gases. There is no ozone shield to protect organisms from ultraviolet light. There is no appreciable magnetic field to protect life against ionizing radiation from solar flares. With respect to the meteorite, it is igneous rather than sedimentary. No amino acids have been found in the meteorite, and the organic compounds detected do not appear to be biogenic.

*Comment:* Eventually, scientists concluded that the meteorite ALH84001 does not provide evidence for life on Mars. However, this conclusion did not receive the extensive publicity given to the original claim.

## MOLECULAR EVOLUTION

Cunningham CW, Jeng K, Husti J, + 4 others. 1997. Parallel molecular evolution of deletions and nonsense mutations in bacteriophage T7. *Molecular Biology and Evolution* 14:113-116.

*Summary:* Six lines of Bacteriophage T7 were grown in a medium containing a mutagen, with periodic sampling to determine changes in DNA within a sequence of five genes. Each line was divided into two, so that a total of six pairs of lineages were studied. Each pair of lineages began as a single individual, and each lineage was bottlenecked to a single individual three additional times. Mutants were compared with each other and with previously identified mutants. Every lineage experienced a similar deletion, involving the loss of genes 2,3, and 4, and the loss of function of gene 5. The deletion had no observable effect on the bacteriophages. Nine independent breakpoints were identified; seven of these were identical to a previously described “H1” deletion. All lineages also developed nonsense (“stop”) mutations in the remaining portion of the last gene of the sequence. A total of 14 independent nonsense mutations were detected; these were confined to only 7 nucleotide positions, although 14 mutational sites were available for single-step nonsense mutations. Nonsense mutations occurred more frequently than expected by chance in lineages without a previous nonsense mutation, but not in lineages already possessing one. In each case, the H1 deletion occurred before the nonsense mutation.

*Comment:* The independent occurrence of the same change in DNA sequence is known as parallel evolution, a widely recognized difficulty in studies of phylogeny. The results of this experiment indicate that specific deletions and nonsense mutations may arise independently, and may not always be reliable indicators of common ancestry.

Kidwell MG, Lisch D. 1997. Transposable elements as sources of variation in animals and plants. *Proceedings of the National Academy of Sciences (USA)* 94:7704-7711.

**Summary:** Transposable elements (TEs) are discrete DNA sequences that can move and replicate within the genome. They have been found in all living species that have been examined. They may comprise a major fraction of the genome — more than 50% in maize, 10-15% in *Drosophila*. Two major classes exist. Class I TEs transpose by reverse transcription of an RNA intermediate. Class II TEs transpose directly from DNA to DNA. Some recently discovered TEs (MITEs) have an unknown transposition mechanism. Some TEs (autonomous) code for their own transposition, while others (nonautonomous) lack this ability.

TEs are an important cause of mutations, from changing a single nucleotide to inserting or deleting long stretches of DNA, or even causing massive chromosome breakage. Their effects vary from none to lethal. They may insert in an exon, an intron, a regulatory region, or heterochromatin. They may also affect the rate of recombination, perhaps by providing additional recombinational sites. Movement of TEs, and accompanying increases in mutation rates, seems to be stimulated by stress.

Insertion of TEs may be nonrandom. *P* elements in *Drosophila* show a preference for insertion into regulatory regions of genes, rather than exons. The yeast *Tyl* TE seems to insert preferentially into or near tRNA genes, or in preexisting long terminal repeats, rather than within ordinary genes. Some TEs are tissue specific; for example, the *Drosophila P* element infects only the germ line. Several TEs have been implicated in affecting gene regulation, for example, certain *Alu*-containing sequences in humans. A beneficial function of TEs is the repair of chromosomal ends (telomeres) by certain retroelements in *Drosophila*.

**Comment:** It appears that TEs have the potential for causing significant changes in species physiology and metabolism. It may be conjectured that they also have the potential for causing significant morphological change, but the extent to which this may have occurred is not known.

## MOLECULAR PALEONTOLOGY

Austin JJ, Ross AJ, Smith AB, Fortey RA, Thomas RH. 1997. Problems of reproducibility — does geologically ancient DNA survive in amber-preserved insects? *Proceedings of the Royal Society of London B* 264:467-474.

**Summary:** Several reports have been made of recovery of DNA from insects preserved in amber thought to be Oligocene. But amber is permeable to some liquids, and has had long exposure to seawater. Attempts to recover DNA from stingless bees and scuttle flies in Dominican amber proved unsuccessful. This raises doubts about previous reports of DNA preserved in ancient amber.

**Comment:** Previous reports of DNA from ancient amber were greeted positively by creationists, including herein (*Origins* 19:77, 1992; *Origins* 22:77, 1995). It now appears that these reports may have been based on contamination or misinterpretation.

Schweitzer MH, Marshall M, Carron K, + 6 others. 1997. Heme compounds in dinosaur trabecular bone. *Proceedings of the National Academy of Sciences (USA)* 94:6291-6296.

**Summary:** Chemical breakdown products of hemoglobin have been identified within bony tissue of the hind leg of a fossil *Tyrannosaurus rex* from Montana. The result was confirmed by six different techniques. Further analysis of this and possibly other biomolecules from fossils might permit sequence comparisons with various groups.

**Comment:** Recovery and comparison of biomolecules and their decomposition products could provide data bearing on the history of the fossil, as well as possible relationships among species.

## ORIGIN OF LIFE

Bradley D. 1994. A new twist in the tale of nature's asymmetry. *Science* 264:908.

**Summary:** In a magnetic field, virtually pure chiral enantiomers (composed of only one of two "mirror image" forms of a biomolecule)

may be produced. (This was reported by E. Breitmaier et al. in *Angewandte Chemie*.) A field of 1.2 to 2.1 teslas applied to the reaction solution produced 98% of a single enantiomer. By adding a “seed” of the preferred chiral form, they could select which enantiomer was produced. The team was working with aldehyde alkylations and ketone reductions. This discovery has been hailed by Tony Barrett of London “as the single most important finding since chemists discovered the chiral carbon atom itself.”

**Comment:** This discovery opens up new possibilities for the experimental purification of chiral molecules. However, it does not appear to be a satisfactory method for producing the chiral molecules needed in origin-of-life scenarios. The strength of Earth’s magnetic field is about 0.00005 teslas. This is about five orders of magnitude weaker than the experimental conditions, leaving the problem of chirality still unexplained.

Lee DH, Granja JR, Martinez JA, Severin K, Ghadiri MR. 1996. A self-replicating peptide. *Nature* 382:525-528.

**Summary:** A 32-unit alpha-helical peptide can accelerate the condensation of 15-unit and 17-unit fragments to produce more copies of itself. The 32-unit peptide is based on the leucine zipper domain of the yeast transcription factor GCN4. Templates with a conservative substitution, alanine for leucine at position 26, lose the self-replication ability. The possibility should be considered that self-replicating proteins were important in the origin of life.

**Comment:** This result does not help explain the origin of life. No prebiotic source for the peptides was identified, and no cell or cell component was formed. The sensitivity of the protein to amino-acid substitution illustrates the improbability of producing a functional protein molecule by random processes.

Melendez-Hevia E, Waddell TG, Cascante M. 1996. The puzzle of the Krebs Citric Acid Cycle: assembling the pieces of chemically feasible reactions, and opportunism in the design of metabolic pathways during evolution. *Journal of Molecular Evolution* 43:293-303.

**Summary:** Life depends on biochemical pathways in which specific enzymes control the flow of energy and materials so that the products of one reaction are the reactants of the next

reaction in the pathway. The resulting chemical activity must be useful to the cell, interacting with other biochemical processes to form the cellular metabolism. But how could such a system originate in small evolutionary steps? And are current metabolic pathways optimal, or could they be improved through evolution? Mathematical principles have previously been applied theoretically to evaluate the degree of optimization of the pentose phosphate and Calvin cycles. Here they are applied to a hypothetical scenario for the evolution of the citric acid cycle (CAC).

The authors propose three stages in the evolution of the CAC. The proposed first stage in the evolution of the CAC involved the minimal metabolism of glucose, the pentose cycle, and the pathways for synthesis of amino acids, nitrogen bases, some coenzymes, and fatty acids. In the second proposed stage, the respiratory chain was organized, while the proposed third stage involved organization of the CAC. Addition of the CAC would require only one additional enzyme (succinyl-CoA synthetase) beyond those already present but used for very different purposes. The result was the best chemically possible design for the CAC.

The authors conclude that the CAC is organized around the best possible chemical design. It has the least possible number of steps and the greatest possible yield of ATP. A chemical engineer could not have done better.

**Comment:** Creationists cannot assume *a priori* that all cellular processes are optimal, since these processes may have degenerated since their origin. However, it is interesting to find that the citric acid cycle does appear to be optimally designed. The haphazard nature of evolutionary processes and the existence of other potential biochemical pathways makes such optimality seem highly improbable. Such systems can readily be considered evidence of an intelligent Creator.

## PALEONTOLOGY

Agosti D, Grimaldi D, Carpenter JM. 1997. Oldest known ant fossils discovered. *Nature* 391:447.

**Summary:** Seven fossil ants were discovered in amber from New Jersey. The amber is from the Turonian portion of the Upper

Cretaceous, and contains the stratigraphically lowest known fossil ants. Four different genera are represented. One of these is *Sphecomyrma*, a previously known genus interpreted as primitive. Another specimen, as yet unnamed, has traits linking it with the Ponerinae, a living subfamily. The Ponerinae were previously unknown from deposits lower than the Eocene.

**Comment:** The presence of diversity at first fossil appearance, and the mixture of taxa interpreted as primitive and derived, provide interesting subjects for further study.

Bengston S, Zhao Y. 1997. Fossilized metazoan embryos from the earliest Cambrian. *Science* 277:1645-1648.

**Summary:** A reexamination of tiny spherical fossils in Lower Cambrian deposits has resulted in interpretation of them as fossilized developing eggs, containing embryos of marine animals. Two distinct types of eggs have been discovered. Identification of the specific kinds of animals is uncertain, but one type may be a jellyfish-like animal, while the other may resemble an annelid or arthropod. The fossils are phosphatized, which permits detailed preservation. Precambrian and other sediments should be more carefully examined to see whether similar tiny fossil invertebrate eggs may be present.

**Comment:** This exciting discovery, if verified, raises the possibility that the fossil record may contain much more information than hitherto suspected.

Burke AC, Feduccia A. 1997. Developmental patterns and the identification of homologies in the avian hand. *Science* 278:666-668.

**Summary:** Many evolutionary paleontologists believe that birds evolved from dinosaurs. Another group of paleontologists dissents from that view, claiming the required physiological and anatomical changes are biologically implausible. A strong case is made here for rejecting the dinosaurian ancestry of birds. The argument is based on identification of the digits in the “hand” of birds and dinosaurs. The basic vertebral “hand” has five digits. *Herrerasaurus*, one of the first dinosaurs in the fossil record, shows dramatic reduction in digits 4 and 5, with digits 1, 2 and 3 fully developed. Similar digital arrangements have been found in some other dinosaurs.



The inference is that three-toed descendants of these dinosaurs should have digits 1, 2 and 3. Developmental evidence reported here shows instead that the three digits in the hands of birds are actually 2, 3 and 4.

**Comment:** Dinosaurs and birds share some character traits, and we cannot *a priori* determine which traits were or were not shared. However, reports such as this show that there is good scientific reason to doubt the proposed dinosaurian ancestry of birds, despite its present popularity.

Ruben JA, Jones TD, Geist NR, Hillenius WJ. 1997. Lung structure and ventilation in theropod dinosaurs and early birds. *Science* 278:1267-1270.

**Summary:** Dinosaurs are widely promoted as the ancestors of birds, but this hypothesis is difficult to reconcile with differences in lung structure. Birds and reptiles both have lungs with a structure like an open sac with partitions (septa). The reptilian lung functions like a bellows, with air flowing in and out through the same pathway, powered by muscles attached to the diaphragm. Crocodiles have such a system.

Bird lungs, on the other hand, have a more complex structure. Portions of the lung are expanded into air sacs, returning the air through a pathway different from the incurrent pathway. This permits unidirectional air flow and a higher rate of metabolic activity. Avian lung air flow is powered by movements of the ribs, tail and pelvic girdle, and there is no diaphragm. Differences in respiratory movements are reflected in differences in pelvic structure between crocodiles and theropods on one hand, and ordinary birds on the other. Enantiornithine birds, including *Archaeopteryx*, apparently lacked typical avian flow-through lungs, and were probably ectothermic (“cold-blooded”). The authors conclude that theropods were probably ectothermic, that *Archaeopteryx* and the enantiornithine birds were tree-dwellers, that flight originated in trees rather than on the ground, and that theropods do not make suitable ancestors for birds.

**Comment:** Differences between avian and reptilian lungs seem more readily explained by design and separate origins, than by a genealogical link between theropods and birds.

## RELIGIOUS SCIENTISTS?

Larson EJ, Witham L. 1997. Scientists are still keeping the faith. *Nature* 386:435-436.

**Summary:** James Leuba conducted a survey of 1,000 scientists in 1916, and found that only 40% believed in a God. Leuba predicted that such belief would decline as the population became increasingly educated. This prediction was tested in a 1996 survey. Surprisingly, the percentage of believers in God has changed very little, remaining at almost 40%. Nearly as many believe in human immortality, although this does reflect a decline since 1916, when an additional 10% reported belief in God but not in immortality.

**Comment:** Although few scientists accept the Bible as a reliable history of origins, a strong number still believe in a God who has interacted in nature in some way. We can hope that it will become more acceptable for a scientist to acknowledge that nature cannot be understood completely without reference to the supernatural.

A later study (*Nature* 394:313) noted that members of the prestigious National Academy of Sciences were much less likely to believe in a personal God.

## SPECIATION

Reznick DN, Shaw RH, Rodd FH, Shaw RG. 1997. Evaluation of the rate of evolution in natural populations of guppies (*Poecilia reticulata*). *Science* 275:1934-1937.

**Summary:** Guppies on Trinidad may live in communities where waterfalls divide the streams into regions where predators are common (below the falls) or rare (above the falls). Guppies from below the falls were transplanted to regions above the falls to determine what changes might occur when predators were few. Populations from the two types of habitats were compared after eleven years. Results showed that the guppies from low-predator habitats matured at a later age, were larger in size, and produced fewer offspring. Phenotypic changes occurred at a rate from 10,000 to 10,000,000 times faster than those inferred from the geological time scale.

*Comment:* The authors ask, “If evolution can be so fast, why does it appear to be so slow in the fossil record?” A variety of answers has been proposed to this question, but one answer worthy of consideration is that the fossil record is not a record of long ages of history, but of a short, catastrophic interval.