

ANNOTATIONS FROM THE LITERATURE

ECOLOGY

Naeem S, Thompson LJ, Lawler SP, Lawton JH, Woodfin RM. 1994. Declining biodiversity can alter the performance of ecosystems. *Nature* 368:734-737.

Summary: The relationship of biomass to species diversity was investigated in this study. Three types of artificial communities were maintained under controlled conditions for at least 200 days. The number of trophic levels was the same in each community, but the total number of species varied. The less-diverse communities were subsets of the more diverse communities. Productivity was determined from measurements of community respiration, carbon fixation by photosynthesis, and plant size. The higher diversity community had, on average, greater productivity.

Comment: This result may have implications for the pre-flood biomass problem. It appears from the fossil record that the pre-flood world had much greater diversity than the present world. If productivity increases with diversity, as suggested by this experiment, the pre-flood world may have had much greater productivity than the present world.

GENETICS

Zhu N, Liggitt D, Liu Y, Debs R. 1994. Systemic gene expression after intravenous DNA delivery into adult mice. *Science* 261:209-211.

Summary: Under the right conditions, genes can be transferred into mice by intravenous injection. The injection includes an expression plasmid and a cationic liposome in a preferred ratio. Depending on the DNA dosage, the gene may be expressed in a few or many tissues, and over a period of time ranging from a few days to at least several months. This technique could facilitate gene therapy and other forms of genetic engineering.

Comment: Gene transfer has frequently been proposed as an agent of morphological change. Transfer of genes is generally thought to be

rare. If gene transfer is not so difficult as thought, its significance in morphological change is likely to be enhanced.

GENOME SEQUENCING STUDIES

Adams MD, Kerlavage AR, Fleischmann RD, Fuldner RA, Bult CJ, Lee NH, Kirkness EF, Weinstock KG, Gocayne JD, White O, + 74 other authors + Venter JC. 1995. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. *Nature* 377S:3-174 (p 3-17 = text; p 18-174 = Tables 2,6,9,10).

Summary: The structure and function of the human genome is of great interest to biologists, and much effort has recently been expended in an effort to sequence human DNA. This is a report of the results of sequencing some 83 million nucleotides, over 52 million of which are reported on here for the first time. Nearly 88,000 putative gene sequences were identified. Of these, 10,214 were previously known genes; the remainder had not been identified previously.

Comment: The total size of the human genome is about 3 billion base pairs, so the amount sequenced is still a rather small proportion of the total. Previous estimates of the number of human genes were on the order of 100,000 or 150,000 genes. The discovery of 88,000 likely gene sequences in such a small proportion of the genome suggests there may be many surprises remaining to be discovered.

Fleischmann RD, Adams MD, White O, Clayton RA, Kirkness EF, Kerlavage AR, Bult CJ, Tomb J-F, Dougherty BA, Merrick JM + 29 other authors + Venter JC. 1995. Whole-genome random sequencing of *Haemophilus influenzae* Rd. *Science* 269:496-512.

Summary: Is it possible for humans to understand how life operates? A critical step in doing so would be to have the complete DNA sequence for an organism. Now this has been accomplished. In this report, the entire DNA sequence is reported for the parasitic bacterium, *Haemophilus influenzae*. Since this species is parasitic, it probably does not represent the simplest possible living cell, but its genes might shed some light on the question of the simplest possible life form. The genome of *Haemophilus* has about 1.83 million base pairs, fairly typical for bacteria. A total of 1,743 coding genes were identified. A function could be assigned for 1007 of these genes. Another 347 genes matched

previously known DNA sequences for which the protein products are not known. The remaining 389 genes are newly discovered.

Comment: The ability to sequence DNA holds the promise that scientists will be able to identify the molecular mechanisms that maintain the living condition. Whether scientists will someday understand life remains to be seen, but it now appears, for the first time, that such knowledge may potentially be within our grasp. However, the large number of previously unknown genes show that our knowledge of even the simplest organisms is meager.

Fraser CM, Gocayne JD, White O, Adams MD, Clayton RA, Fleischmann RD, Bult CJ, Kerlavage AR, Sutton G, Kelley JM + 18 other authors + Venter JC. 1995. The minimal gene complement of *Mycoplasma genitalium*. *Science* 270:397-403.

Summary: This is the second organism to have its entire genome sequenced, *Mycoplasma genitalium* is thought to have the smallest genome for a self-replicating organism. Its genome is about 580,000 base pairs, and contains 470 predicted genes. Of the 470 genes identified, 318 represented known proteins and another 56 had been discovered in other organisms. The remaining 96 were previously unknown, and may represent genes unique to mycoplasmas. This species is missing several genes, but can survive because it is parasitic.

Comment: The genome sequence of this species may help in estimates of the minimum genome size needed for independent life. It seems likely that independent life is not possible with fewer than perhaps 250 or 300 genes. This estimate constrains explanations of the origin of life, making a naturalistic origin seem highly implausible. Another feature that may contribute to a better understanding of life is the possibility of identifying the number of gene families present, and comparing this with the numbers of gene families present in other types of organisms. New gene families require an explanation as to their origin, and it seems likely that a better understanding of the magnitude of this problem will show naturalistic processes to be implausible.

MOLECULAR PALEONTOLOGY

Cano RJ, Poinar HN, Pleniasek NJ, Acra A, Poinar GO. 1993. Amplification and sequencing of DNA from a 120-135-million-year-old weevil. *Nature* 363:536-538.

Summary: Recovery and sequencing of the gene for ribosomal RNA (rRNA) from a Cretaceous fossil weevil is reported here. The weevil was recovered from Lebanese amber thought to be Lower Cretaceous (Neocomian). The amber has been identified as coming from araucarian trees. The DNA sequence of the gene for the small ribosomal subunit (18S rRNA) was compared with sequences for several other insects, including an extant species from the same family (Nemonychidae). The two weevils differed by eight nucleotide positions (2.5%) in a 315 base-pair portion of the 5' region, and 34 positions plus 3 gaps (16.4%) in a 226 base-pair sequence from the internal transcribed spacer of the gene. The fossil weevil differs by 2.5% from the mealworm (*Tenebrio*), whereas the living weevil differs from the mealworm by 4.8%. The total difference for human and frog 18S rRNA genes is reported to be about 5%. These results are inconsistent with expectations of clock-like behavior of mutation rate in ribosomal RNA. They also provide another example of the discordance between molecular and morphological measures of similarity.

MOLECULAR PHYLOGENY

Litman GW, Rast JP, Shamblott MJ, Haire RN, Hulst M, Roess W, Litman RT, Hinds-frey KR, Zilch A, Amemiya CT. 1993. Phylogenetic diversification of immunoglobulin genes and the antibody repertoire. *Molecular Biology and Evolution* 10:60-72.

Summary: Typical vertebrate antibodies are made of two heavy chains and two light chains, containing V (variable), D (diversity), J (joining) and C (constant) regions. Each region is coded for by different DNA units (exons). Gene rearrangement in somatic cells is involved in producing the antibodies. Three patterns of arrangement are known for the heavy-chain gene. The most common gene arrangement is the "tetrapod-type," in which all the genes are arranged in a single sequence. The sequence consists of several hundred different V elements, 20-30 D elements, fewer than 10 J elements, and apparently a single C region with six exons. In somatic gene rearrangement, single V, D and

J regions are recombined with the C region to form a gene cluster for a specific antibody. Teleost fish apparently have a similar arrangement, although the numbers of elements vary.

Sharks have a different gene arrangement, with hundreds of separate gene clusters, each consisting of a V, two Ds, a J and a six-exon C region. Another unique feature of shark immunoglobulin genes is that about half the genes are joined in the germ line instead of somatically. A third unique feature is the absence of the regulatory octamer which is found associated with the B cell-specific immunoglobulin promoter in teleosts and tetrapods. The coelacanth has a pattern somewhat intermediate between the “tetrapod” and shark patterns. In the coelacanth, C and J regions are lacking, and V regions may be tandemly linked and may or may not be associated with a single D region.

Birds have a third pattern of gene arrangement. Here, “a single functional gene is the target for extensive gene conversion by flanking pseudogenes.” Cyclostomes appear to lack immunoglobulin genes, having “humoral immunity” instead.

Comment: The diversity of immunoglobulin gene arrangements suggests separate design in their creation.

PALEONTOLOGY

Conway Morris S. 1993. Ediacaran-like fossils in Cambrian Burgess Shale-type faunas of North America. *Palaeontology* 36:593-635.

Summary: Frond-like fossils, possibly similar to sea-pens, have been discovered in the Burgess Shale of British Columbia and in Vermont. These fossils resemble Precambrian Ediacaran fossils, which have usually been found separated from Cambrian fossils. This unusual combination is interpreted as indicating that the Ediacaran fauna is not phylogenetically isolated from the Cambrian fossils.

Gingerich PD, Raza SM, Arif M, Anwar M, Zhou X. 1994. New whale from the Eocene of Pakistan and the origin of cetacean swimming. *Nature* 368:844-847.

Summary: Living whales are of two types: toothed whales and baleen whales. A third type, the archaeocetes, are found only as fossils. Two families of archaeocetes are known. A new genus of fossil archaeocete, named *Rodhocetus*, is described from Pakistan. The new fossil has characteristics suggesting it was fully able to swim as whales

do, while having some features resembling those of terrestrial mammals. Thus it is interpreted as being intermediate between land mammals and aquatic whales.

Comment: Archaeocetes are significantly different from living whales, and their relationship to living whales is somewhat uncertain. The stratigraphically lowest archaeocetes include both families and as many as eight genera, found in India, Pakistan, Egypt and Nigeria. The large taxonomic diversity and wide geographic range at first appearance seem inconsistent with the hypothesis of gradual origin by evolution. Attempts have been made to arrange archaeocete fossils in a morphological sequence from semiterrestrial to fully aquatic. The result is interesting, but the known genera are thought not to be a series of actual ancestors and descendants.

Thewissen JGM, Hussain ST, Arif M. 1994. Fossil evidence for the origin of aquatic locomotion in archaeocete whales. *Science* 263:210-212.

Summary: A new kind of fossil mammal has been discovered with a unique combination of features found in whales and in terrestrial mammals. The fossil was found in Eocene sediments in Pakistan. The authors propose that it should be classified as an archeocete whale, an extinct group of whale-like aquatic mammals. The fossil is named *Ambulocetus*, which means “walking whale.” *Ambulocetus* had four limbs with large feet, and is thought to have had a long tail, features typical of terrestrial mammals. The proportionally large skull, the shape of the lumbar vertebrae, and the teeth are similar to other archaeocete whales. The authors infer an animal vaguely similar to a sea lion, which could walk awkwardly on land but was more at home in the water.

Comment: Conventional evolutionary theory proposes that living whales were derived from archaeocete whales, which were derived from a group of terrestrial mammals known as mesonychids. Mesonychids are found in Paleocene to Oligocene sediments; archaeocetes are apparently confined to Eocene sediments, and modern-type whales first appear in Eocene sediments. Living families first appear in Oligocene sediments.

The relationships of archaeocetes to living whales are not well understood. The near-simultaneous appearance in the geologic column of both archaeocete whales and toothed whales may indicate they have separate ancestries. The stratigraphically lowest archaeocete is *Pakicetus*, which is found below *Ambulocetus*. The “walking whale”

has been hailed as an evolutionary transition, but there are several important issues to be resolved before its status can be properly evaluated.