

# ANNOTATIONS FROM THE LITERATURE

## GENETICS

Wilson R, et al. (55 authors). 1994. 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*. Nature 368:32-38.

**Summary.** The small, free-living roundworm, *Caenorhabditis elegans*, has a genome of about 100 million base pairs. An attempt is underway to sequence the entire genome of this worm. The DNA sequence reported, about 2% of the genome, is one of the largest contiguous DNA sequences known. Perhaps unsurprisingly, the data has revealed some surprises.

First, genes are more numerous than expected. On average, one gene was found for about every 5000 base pairs. Assuming this is characteristic of the entire genome, the total number of genes in the genome is estimated at nearly 18,000. Second, a much higher than expected proportion of the genome is involved in coding. Putative coding sequences account for 29% of the sequenced genome. When introns are included, the total rises to 48%. This is perhaps ten times the proportion previously estimated as typical. Third, the number of genes not shared with other phyla appears to be larger than previously thought. The authors estimate that at least 60% of the genes are unique to roundworms. Fourth, inverted repeats are the most common type of repeat, and are located in introns twice as frequently as in other parts of the genome. Most of the inverted repeats have characteristics that suggest they may be remnants of mobile elements. By contrast, most tandem repeats were located between genes. Fifth, some sequences with 98% similarity are found widely separated on the chromosome. These might be duplicated genes, but how they became so widely separated is not clear.

**Comment.** This report, together with advances in other genome studies, demonstrates that we still have a great deal to learn about how the genome operates.

## GEOLOGY

Acton GD, Gordon RG. 1994. Paleomagnetic tests of Pacific Plate reconstructions and implications for motion between hotspots. *Science* 263:1246-1254.

*Summary.* The chain of islands and seamounts terminating with the Hawaiian Islands is thought to have been produced by an upwelling of magma from the mantle, known as a “hotspot.” The hotspot is thought to be stationary, producing a chain of islands as the Pacific Plate moves over it. It is thought that Earth’s plates are driven by slow motion of the mantle. One might wonder how the mantle can move enough to cause plate motion while allowing the hotspots in the mantle to remain fixed in position. It now appears that hotspots may not have been entirely stationary, but have also been moving.

*Comment.* Estimates of the past locations of Earth’s poles and tectonic plates have generally relied on the assumption of fixed-position hotspots. This means that plate reconstructions for the lower Tertiary may need adjustment, by an amount estimated to be approximately 500 to 1000 km.

Lowe DR. 1994. Abiological origin of described stromatolites older than 3.2 Ga. *Geology* 22:387-390.

*Summary.* Stromatolites are laminated sedimentological features produced by surface concentrations of bacteria or algae. Three examples of stromatolites with supposed ages of more than 3.2 billion years have been reported and widely accepted. However, fossil bacteria have not been found associated with any of them. This paper reports that none of these “stromatolites” are biological in origin. Of the two occurrences in Western Australia, one is interpreted as produced by evaporitic precipitation and the other as soft-sediment deformation. The third example, from South Africa, is interpreted as produced by inorganic precipitation.

## MOLECULAR EVOLUTION

McKenzie JA, Batterham P. 1994. The genetic, molecular and phenotypic consequences of selection for insecticide resistance. *Trends in Evolution and Ecology* 9:166-169.

**Summary.** Development of pesticide resistance in insects is an interesting example of rapid genetic change. The discovery that DDT resistance in *Drosophila* had a polygenic basis led to the inference that resistance in most insect populations had a polygenic basis. However, pesticide resistance in most natural populations involves only one or two genes. This makes the study of pesticide resistance easier than first thought.

Several different mechanisms may operate to produce pesticide resistance. Among these are increased cuticular thickness (which reduces penetration of the pesticide), chemical detoxification, target-site modification, increased excretion, and behavioral avoidance. Combinations of these mechanisms may provide the polygenic basis of resistance. Similar responses to the same pesticide are frequently observed in different populations or species.

In one studied example of resistance of *Culex* (mosquito) to an organophosphate, gene amplification of an esterase was the mechanism by which resistance was achieved. Amplification was at least 250-fold. Migration of the resulting resistant strain was deemed more significant than the rate of mutation. In another studied example of resistance of *Drosophila* to dieldrin, a single amino acid substitution was discovered in a chloride channel pore, reducing the binding of dieldrin. Amino acid substitution at the same site is believed to explain resistance in three different insect orders, although the exact substitution is not identical in all cases. Certain carboxylesterases mediate resistance to diazinon and malathion. The ordinary function of these enzymes is not yet well understood. Insect resistance appears to be based on undirected mutations, rather than to be environmentally induced. It appears that these mutations often may be small changes in amino acid sequence or gene regulation.

**Comment.** The rapid development of insect resistance to pesticides illustrates the point that genetic change may be rapid. This point may help to explain how such a large number of species could be produced in a relatively short time. Another point illustrated is that much genetic change is decoupled from morphological change.

## PALEONTOLOGY

Bowring SA, Grotzinger JP, Isachsen CE, Knoll AH, Pelechaty SM, Kolosov P. 1993. Calibrating rates of Early Cambrian evolution. *Science* 261:1293-1298.

*Summary.* Cambrian rocks contain the first abundant record of shelly fossils. The sudden appearance of a large diversity of fossils within a relatively small portion of the geologic column has been referred to as the “Cambrian explosion.” Most extant phyla and classes of animals appear in Cambrian sediments. The standard interpretation of the Cambrian system has supposed that it extended from 570-510 million years ago, with most of the “explosion” having occurred between 570 and 554 million years ago. The appearance of so many new body types in only 16 million years has been much discussed in the literature. New radiometric dates are now interpreted as indicating the period of time was even shorter. Zircon crystals taken from rocks at the base of the Cambrian in Siberia gave uranium-lead dates of 544 million years. Revised dates suggest the “Cambrian explosion” occurred within a supposed period of 5-10 million years.

*Comment.* The sudden appearance of a diversity of higher taxa, each represented by a small number of species, seems to be a common feature of the fossil record. If diversity were produced by evolutionary change, one would expect to see first a higher diversity of species within a small number of higher taxa, followed by stepwise addition of additional higher taxa. The observed pattern of diversity seems more consistent with the pattern expected from a catastrophic mass mortality event than from a record of gradual evolutionary change.