

Evolutionary history

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The study of the evolutionary history of groups of organisms is called **phylogeny**. Two useful approaches in phylogeny are study of the fossil record and comparison of molecular structure.

DATING FOSSILS

To place fossils into a sequence, it is necessary to know their dates. Fossils, or the rocks containing fossils can be dated using radioisotopes – radioactive isotopes of chemical elements. When an atom of a radioisotope decays, it changes into another isotope and gives off radiation. The rate of decay varies between different radioisotopes and is expressed as the **half-life**. *The half-life is the time taken for the radioactivity to fall to half of its original level.* The figure (right) shows a decay curve for radioisotopes.

The two radioisotopes that are most commonly used are ^{14}C and ^{40}K . In radiocarbon dating the percentage of surviving ^{14}C atoms in the sample is measured. In potassium-argon dating, the proportions of parent ^{40}K atoms and daughter ^{40}Ar atoms are measured. In both methods the age in half-lives can then be deduced from the decay curve. The half-life of ^{14}C is 5730 years, so it is useful for dating samples that are between 1000 and 100 000 years old. The half-life of ^{40}K is 1250 million years so it is useful for dating samples older than 100 000 years.

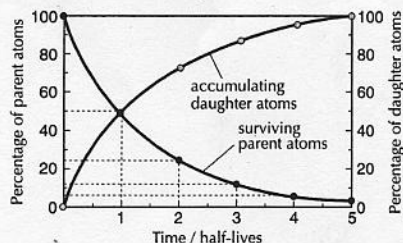
METHODS OF PRESERVATION

The remains of past living organisms can be trapped and preserved in various ways.

- In resins, which turn to amber.
- Frozen, in ice or snow.
- In acid peat, which prevents decay.
- In sediments that turn to rock.

The last method is the most important. Sediments accumulate in layers in parts of the sea and sometimes on land. The weight of sediments compresses those beneath until they become rock. If hard parts of animals such as shells or bones form part of the sediment, they will be preserved in the rock. Sometimes, the shape of an organism is preserved as a cast. Minerals sometimes seep into the soft parts of an organism as it decays and harden to form a petrified replica of the organism.

Decay curves for radioisotopes



COMPARING MOLECULAR STRUCTURE

The phylogeny of many groups of organisms has been studied by comparing the structure of a protein or other biochemical that they contain. For example, the amino acid sequence of the polypeptide of hemoglobin has been compared in many vertebrates. The figure (below) shows the numbers of differences in the amino acid sequence in ten vertebrates. Differences in amino acid sequence accumulate gradually over long periods of time. There is evidence that differences accumulate at a roughly constant rate. They can therefore be used as an evolutionary clock. The number of differences in amino acid sequence can be used to deduce how long ago species split from a common ancestor. Using this information and the details of what the amino acid differences are, the probable phylogeny of groups of organisms can be deduced. The figure (bottom) shows the probable phylogeny of the ten organisms.

The phylogeny of many groups has been studied in this way. Usually, the results fit in with earlier studies of fossils, or anatomical studies, but sometimes there are surprises. For example, figure (bottom) shows larger than expected differences between the various types of fish.

Numbers of differences in the amino acid sequence of hemoglobin in ten vertebrates

	Elephant	Platypus	Ostrich	Starling	Crocodile	Lungfish	Coelacanth	Goldfish	Shark
Human	→ 26	40	43	41	47	83	70	68	71
Elephant	→ 45	→ 45	45	48	50	84	72	63	74
Platypus	→ 54	→ 54	→ 54	52	51	89	74	70	76
Ostrich	→ 26	→ 45	→ 54	→ 26	36	91	75	68	73
Starling	→ 41	→ 48	→ 52	→ 47	→ 47	91	77	67	70
Crocodile	→ 47	→ 50	→ 51	→ 50	→ 85	→ 85	78	70	77
Lungfish	→ 83	→ 84	→ 89	→ 91	→ 91	→ 90	→ 90	94	86
Coelacanth	→ 70	→ 72	→ 74	→ 75	→ 78	→ 83	→ 83	→ 83	78
Goldfish	→ 68	→ 63	→ 70	→ 68	→ 70	→ 94	→ 78	→ 88	→ 88

Phylogenetic tree diagram for ten vertebrates

