
Origins

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OM1.1 WHAT DNA CAN REVEAL ABOUT PHYLOGENY AND EVOLUTION

DNA sequences from living organisms can be used to determine the order of speciation events – the formation and divergence of new species – among groups of related species. Changes, or mutations, in chromosomal DNA occur from time to time, and these heritable mutations are passed down through lineages. So, by comparing the DNA molecules of different species, a tree of relatedness, called a **cladogram**, can be constructed. A cladogram is a statistical representation of the hypothetical relationships within a group of organisms and can be interpreted as representative of their phylogeny, or historical origins. The relative positions of species on the branches of the phylogenetic tree provide evidence for the order in which species arose. These hypotheses can then be tested as further data become available.

DNA sequences can also be used to give estimates of how long ago the branches of a phylogenetic tree formed. If the mutation rate is constant, it can be used like the ticking of a clock – a **molecular clock**. According to the molecular clock hypothesis, if the rate of mutation is constant in a group of organisms, the difference in DNA sequences among the organisms can be used to determine the time when species arose. However, the molecular clock runs at different rates in different lineages, so this variability must be taken into account across a phylogenetic tree. Various analytical methods have been developed to counteract the effects of this variability. In setting a baseline for the rate at which the clock ticks, at least one piece of fossil evidence is usually required. Additional fossil evidence can then be used to test the ages derived from the “gene tree” or to add further constraints on the ages of particular branches. Estimates based on fossil age and molecular clocks often differ because neither technique is perfect. Because the fossil record is incomplete, fossil evidence consistently underestimates the ages of clades. The first appearance of a fossil can only ever provide a *minimum* age constraint for a particular group. The clock has been used to date the times of divergences (**speciation** events) of lineages that lack a good fossil record. For example, the fossil record indicates that land plants were present on the continents around 470 million years ago, but it does not tell us when the first land plants evolved from their green algal ancestors. Based on the molecular clock, it has been suggested that these lineages diverged much earlier – perhaps in the Cambrian. It is important to remember that cladograms of relationships and their derivatives, such as calibrated phylogenies, are working hypotheses that can be tested and modified as new data become available.