

Syn-same, shared
Pleis-ancestral
Simpleis-shared ancestral
Mono-1
Para-on the side
Poly-many

Pleisomorphic: primitive, ancestral, more general
Apomorphic: derived, more recent character
Synapomorphic: shared& derived
Autapomorphic: unique characters. Derived but not shared, not particularly useful for determining relationships
Homologous: Inherited from a common ancestor, same basic plan but potentially different functions
Analogous: similar functions arise from different structures(potentially misleading in phylogenetics)

*For phylogenetic inference, we want homologous, synapomorphic characters.

Convergent evolution

-independent development of similar structures in unrelated organisms, often living in similar environments. By convergent evolution, these organisms come to resemble one another superficially. Structures that have a similar function as a result of convergence are called analogous.

DNA Sequences

With the development of techniques for sequencing amino acids in proteins and nucleotides in DNA. We can now compare organisms at the molecular level. Furthermore, molecules allow us to compare organisms that have no apparent morphological homologies

- nucleotides at each position are homologous characters
- DNA is particularly useful when homologous morphological characters are absent

Outgroup helps to resolve relationships

	Base position		
	1156	2311	3257
Mouse, <i>Mus</i>	T	A	G
Cockatoo, <i>Cacatua</i>	C	G	G
Frog, <i>Xenopus</i>	T	G	A
Insect, <i>Drosophila</i>	T	G	A



Including an outgroup helps to determine ancestral versus derived character states (*pleisomorphic* v *apomorphic*).

If we include the sequence for the insect *Drosophila*, which we assume is an earlier branch on the phylogenetic tree below the vertebrates, we can determine which base positions are phylogenetically informative within the vertebrates. In this case, the insect functions as an **outgroup**, a related organism that is outside the group whose phylogeny is being investigated (the ingroup). We assume that a base that is in both the *Drosophila* sequence and any of the vertebrate sequences (e.g. A at position 3257) must have been inherited from a more remote common ancestor. A different base (G)

at the same position in the vertebrate sequences must have evolved within that group. In this case, G is a derived character (G substituted for A). G at position 3257 for mouse and cockatoo, therefore, tells us that tree 3 best fits the data (Fig. 31.7). G at position 3257 is an informative character. The bases at the other two positions are not informative of a vertebrate relationship because only the cockatoo has the derived character (C) at 1156, and only the mouse (A) at 2311.

DNA phylogenetics

The previous example uses only three base positions, but in reality a biologist would compare hundred or thousands of positions to be more confident of finding the correct phylogenetic tree.

- Mitochondrial DNA(mtDNA)
transitions(AT,CG) occur faster than transversions; only good for divergences <20 million years ago. But a few regions(ribosomal RNA genes) do evolve more slowly
- Chloroplast DNA(cpDNA)
Ex.rbcL gene useful for major plant groups
- Nuclear DNA
Many genes. Ribosomal genes coding for rRNA are particularly common and some regions are highly conserved-useful for beginning of life 3.7 billion years ago

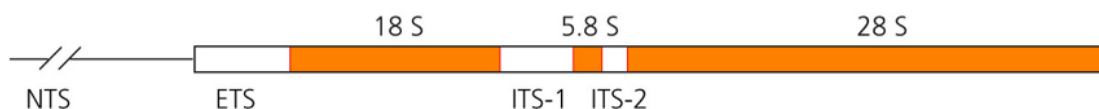


Figure 1. The ribosomal DNA repeat unit of vertebrates. The unit consists of three genes(18s, 5.8s and 28s) separated by internal transcribed spacer regions(ITS) and external transcribed spaces(ETS). Each unit is separated by a non-transcribed spacer(NTS)

Molecular clocks: nucleotide changes(mutations) that adversely affect the function of a critical gene are eliminated by natural selection; on the other hand, changes that are neutral(ones that do not affect function) accumulate. If neutral mutations accumulate at a more or less constant rate, they can be used to measure evolutionary time, and act as molecular clock. E.g: two organisms that have 30 nucleotide differences in a particular sequence of DNA could be interpreted as having a common ancestor that is three times older than two organisms with only 10 nucleotide differences.

Taxonomy

Taxon(Taxa)-general name for any rank

Taxonomy-methods and rules used to name organisms

Binomial nomenclature-genus species(E.g. *Apis mellifera*)

Purposes of classification: Information storage, retrieval and prediction