

TOPIC: MOLECULAR EVIDENCE

Key Knowledge:

- Evidence of relatedness between species: molecular homology – DNA and amino acid sequences
- The use and interpretation of phylogenetic trees as evidence for the relatedness between species

MOLECULAR HOMOLOGY

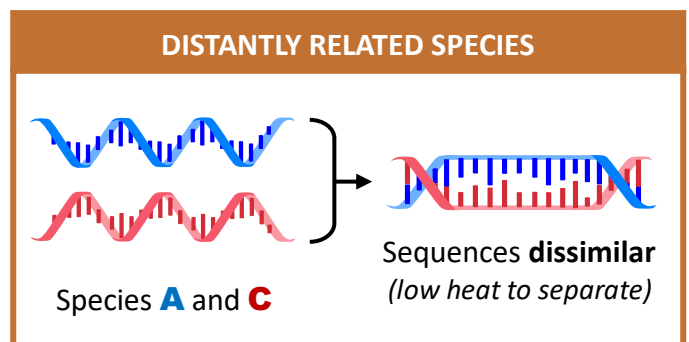
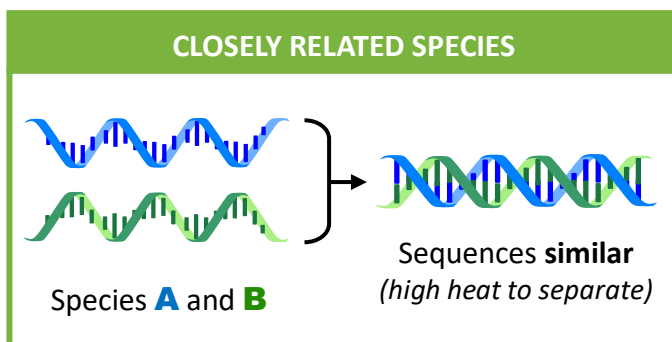
All organisms use DNA or RNA as genetic material to produce proteins (amino acid chains). Mutations will cause differences to accumulate within gene or protein sequences, which may be inherited by offspring. Hence, the number of differences in a conserved sequence between two organisms represents the amount of time that has passed since evolutionary divergence occurred (which reflects the degree of relatedness).

Amino acid sequences are typically used to compare distantly related species, as these sequences mutate at the slowest rate (due to codon degeneracy). **DNA sequences** are used to compare more closely related species, as these sequences mutate at a faster rate (non-coding DNA mutates faster than gene sequences as changes do not affect protein structure). Comparisons require sequences to be shared by both species.

DNA HYBRIDISATION

The degree of conservation between two DNA sequences can be determined using a technique known as DNA hybridisation. In this process, **heat** is used to separate double-stranded DNA sequences (by breaking the hydrogen bonds between complementary base pairs). The comparable sequences from two species are then annealed together (**hybridisation**). The amount of heat required to separate this hybrid molecules indicates how similar the two sequences are (and hence the degree of relatedness between both species).

- More heat indicates more complementary base pairings between strands (high degree of relatedness)
- Less heat indicates fewer complementary base pairings between strands (low degree of relatedness)

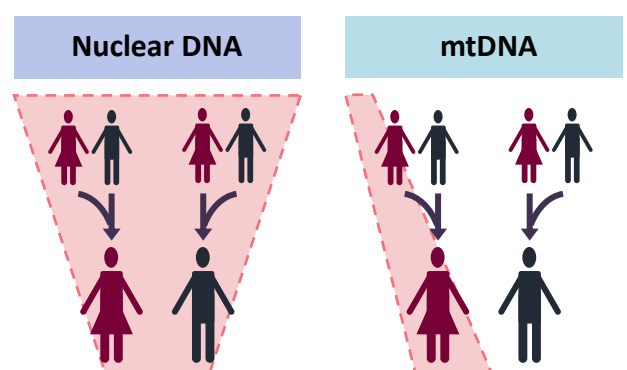


MITOCHONDRIAL DNA

Mitochondria possess their own DNA, which differs from nuclear DNA in a number of important ways:

- It is inherited maternally (from mother to child)
- It does not undergo meiotic recombination
- It has a higher mutation rate than nuclear DNA
- There are multiple copies (many mitochondria)

This makes mtDNA ideal for comparing species that have recently diverged (or haplogroups within species).



MOLECULAR CLOCKS

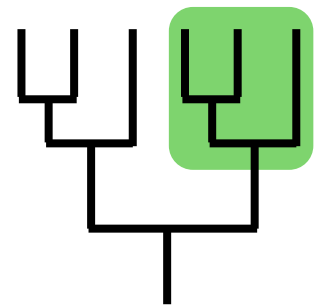
Some genes or protein sequences may accumulate mutations at a relatively constant rate (e.g. one change per million years). If this rate of change is reliable, scientists can calculate the time of divergence based on the number of sequence differences. This concept is called the **molecular clock**. While useful for mapping evolutionary relationships, the molecular clock concept is limited by a number of key factors:

- Different genes may change at different rates (there is not a universal rate of mutation)
- The rate of change for a particular gene may vary between different species (preventing comparisons)
- Earlier sequence changes may be reversed by later changes (confounding the accuracy of predictions)

Molecular clocks are commonly applied to **mitochondrial DNA** and **ribosomal RNA** sequences, as these sequences tend to be highly conserved and found across nearly all organisms.

PHYLOGENETICS

The term phylogeny describes the evolutionary history of species, which can be represented by branching diagrams called phylogeny trees (**cladograms**). These diagrams are organised into clades, consisting of an ancestral species and all of its evolutionary descendants. Members of a clade possess common characteristics as a result of their shared evolutionary lineage. Each branch point (node) in a cladogram represents a speciation event, by which distinct species are formed via divergent evolution. The fewer the number of nodes between any two species, the more closely related they are expected to be.



Cladogram (+ **clade**)

PHYLOGENY TREES

While cladograms can be based on structural evidence, most are constructed using molecular evidence – as convergent evolution can cause distantly related species to exhibit similar characteristics (i.e. analogous structures). If a molecular clock is used to determine the chronology of speciation events, then a phylogeny tree can show the time since evolutionary divergence has occurred (the length of lines will represent the length of time since a speciation event). Closely related species will have more recent common ancestors.

