

Classification and cladistics **HL only**

Why is classification needed?

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Traditional hierarchy of taxa

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Why is the traditional hierarchy a problem?

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Advantage of classification by evolutionary relationships

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Clade

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Most objective evidence for placing organisms in a clade

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Molecular clock

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Why does a molecular clock give only estimates?

Kingdom, phylum, class, order, family, genus, species.

Because of the immense diversity of species; once classified, a broad range of further study is facilitated.

All members share a common ancestor, so characteristics can be predicted because they are shared within a clade.

Fixed ranks are arbitrary and do not always correspond to the patterns of divergence generated by evolution.

Base sequences of genes or amino acid sequences of proteins.

A group of organisms with common ancestry and shared characteristics: an ancestor and all its descendants.

Mutation rates are affected by generation time, population size, intensity of selective pressure and other factors.

Estimating when clades diverged from a common ancestor using the number of accumulated sequence differences.

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Parsimony analysis

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Root, node and terminal branch

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How do you find the closest relative of a species on a cladogram?

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What did cladistics show about the figwort family (Scrophulariaceae)?

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The three domains

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Why is rRNA useful for comparing all organisms?

Root: common ancestor of all. Node: branching point, a hypothetical common ancestor. Terminal branch: ends at a species compared.

Selecting the most probable cladogram: the one that accounts for observed sequence variation with the fewest sequence changes.

It was not a single clade; similar morphology was due to convergent evolution, so many species were moved to other families.

Find the species sharing the most recent node (common ancestor) with it, not simply the neighbour at the tips.

It is present in all cells and its base sequence changes slowly, so distantly related organisms can be compared.

Bacteria, Archaea and Eukarya, proposed in 1977 from rRNA base sequences as a level above kingdoms.