

# Phylogenetic systematics

The classification of organisms, which is based on evolutionary history, is called phylogenetic systematics. *When constructing phylogenetic trees, knowledge from fossil finds is of course used, as well as a comparison of the relationships between living species and their anatomy or a comparison of DNA of two species, which connects their hereditary relationships at the molecular level. But the main principle, how these data are put together, is based on **cladistic analysis - cladistics**. We can consider the German entomologist **Willi Henig** as the first one who started using this analysis.*

## Monophyletic groups

- The key element on which cladistic analysis is based is **monophyletic groups**. **A phylogenetic diagram based on cladistics is called a cladogram**. It is actually a tree that is made up of a series of dichotomies, i.e. two-way branches. Each branching point represents the divergence of two species from a common ancestor. Each branch of a cladogram is called a clade. Clades, as well as taxonomic levels, can be incorporated into larger clades. Not all groups of organisms can be classified as clades. A clade consists of an ancestor species and all its descendants. Such a group of species, for example a genus, family or some other higher taxon, is called monophyletic, which actually means that it contains a single stock.
- Another possibility, however, which cannot be classified as a true taxon derived from cladograms, is for example a paraphyletic taxon *that consists of an ancestor and some, but not all, of its descendants*.
- Another possibility is a **polyphyletic taxon**, which, however, lacks a common ancestor that could unify the species as a monophyletic group.

## Compilation of cladograms

- When constructing cladograms, it is important to *'distinguish between homology and analogy*.
- Similarity between organisms that can be attributed to a common origin is called *'homology*. For example, the hind limbs of mammals are homologous. But not all similarities can be classified as homologies.
- Species from different evolutionary branches can be similar even if they have similar ecological roles and natural selection has created **analogous adaptations**. **This similarity is therefore an analogy, and the process by which these analogies arise is called convergent evolution**. For example, we can consider the wings of bats and birds as an analogy. The general rule is that the greater the number of homologous parts between two species, the more related these two species are to each other.



Cladogram of mammals

## Shared derived properties

- In addition to distinguishing homologous and analogical similarities, systematists must sort homologies to identify so-called derived properties. A characteristic here is considered to be any character possessed by a certain taxon. A property that arose on the basis of the same phylogeny is homology. For example, fur is a feature shared by all mammals, but so is a spine. The presence of a spine does not help us distinguish mammals from other vertebrates, because other vertebrates also have a backbone. In other words, backbone is a homology that predates the branching of the mammalian clade from the vertebrate tree, that is, it is a **shared primitive feature** (a homology common to a higher taxon than the one we attempted to define).
- In contrast, fur is a homology found only among vertebrates that are also mammals, so mammalian fur is, compared to other vertebrates, a **shared derived trait**, meaning that it is an evolutionary novelty unique to a particular clade.
- The branching order of the cladogram thus represents the order in which evolutionary novelties, i.e. shared derived properties, developed.

## Links

- ws: [Fylogenetická systematika](#)

## Related Articles

- Building phylogenetic trees
- Evolution

## References

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