

Taxonomy and Phylogenetic Systematics

Taxonomy

In the mid 18th century a Swedish botanist Carolus Linnaeus published *Systema Naturae* and the modern science of **taxonomy** (the identification and classification of species) was born

It was a **binomial system of nomenclature**:

1. the first word of the name is the **genus** to which the species belongs
2. the second word is the **specific epithet** of the species

What is a genus?

A group of very similar organisms

What is a species?

A specific kind of organism in a genus

Linnaeus was also responsible for developing a filing system for grouping species into a hierarchy of increasing general categories

For example, the complete classification of the common box turtle is as follows:

Kingdom: Animalia
Phylum: Chordata
Class: Reptilia
Order: Chelonia (turtles and tortoises)
Family: Emydidae (freshwater and marsh turtles)
Genus: *Terrapene* (box turtles)
Species: *carolina* (common box turtle)

The named taxonomic unit at any level is called the **taxon (pl., taxa)**

During the time of Linnaeus 2 kingdoms were recognized:

1. Organisms were animals: they move, eat (ingest plants or animals) - **K. Animalia**
2. Organisms were plants: did not move; did not eat (made their own food) - **K. Plantae**

Schemes with additional kingdoms have been proposed, but none became popular with a majority of biologists until Robert Whittaker argued effectively for a 5-kingdom system. The kingdoms are as follows: **Monera, Protista, Plantae, Fungi, and Animalia**

K. Monera are prokaryotes

The remaining kingdoms are unicellular or multicellular **eukaryotes**

The **K. Protista** (also known as **Protoctista**) generally includes mostly unicellular organisms; however, some members of this group are simple multicellular forms that are structurally very similar to the single celled protists (protozoans and algae)

The **K. Plantae, Fungi, and Animalia** are all multicellular eukaryotes
Generally speaking, members of these kingdoms are distinguished based on their **mode of nutrition**

Plants are **autotrophic**

Fungi are **heterotrophic** with an absorptive mode of nutrition.

Animals are also heterotrophs but they ingest food and then digest it in specialized cavities.

And at least 3 alternative classification systems have been proposed:

1. *A six-kingdom system* - This alternative divides the prokaryotes into 2 kingdoms
This modification is based on molecular evidence for an early evolutionary divergence between **eubacteria** (most bacteria) and **archaeobacteria** (an ancient lineage of prokaryotes with many unique characteristics)

2. *A three-domain system* - This scheme assigns even more significance to the ancient evolutionary split between eubacteria and archaeobacteria by using a superkingdom taxon called the **domain**

The first 2 domains are **bacteria** and **archaea**; the third domain is the **eukarya**
The eukarya consists of 4 kingdoms of eukaryotic organisms

3. *An eight-kingdom system* - In addition to 2 separate prokaryotic kingdoms, this system also splits the protists into 3 kingdoms

Of all the taxa, *only the species actually exists in nature as a biologically cohesive unit that is bonded by interbreeding and separated from other species via reproductive isolation*

Only the species is a real entity

Combining species into higher taxonomic categories is somewhat subjective involving judgment by the taxonomists

Systematics: Tracing Phylogeny

Systematics is the study of biological diversity from an evolutionary perspective
 The precise goal of systematics is to reconstruct the evolutionary history (**=phylogeny**) of a species or group of related species
 These genealogies are traditionally diagrammed as phylogenetic trees that trace putative evolutionary relationships

Taxonomic Characters and Phylogeny Reconstruction

The phylogeny (phylogenetic tree) of organisms is constructed by studying organismal features (**=characters**) that vary among species
 The whole notion is that if two organisms possess similar characters, it is likely that they inherited these features from a common ancestor

The likeness of organisms due to shared ancestry is called **homology**
 However, it is important to realize that not all likeness is inherited from a common ancestor
 The acquisition of similar characteristics in species from different evolutionary branches due to sharing similar ecological roles with NS shaping analogous adaptations is called **convergent evolution**
 Similarity due to convergent evolution is termed nonhomologous similarity or **homoplasy**

There is an important clue to identifying homology and sorting it from homoplasy: *The more complex two similar structures are, the less likely it is they have evolved independently*

Terminology and Basic Methods of Phylogenetic Systematics

Groups of Organisms in Phylogenetic Systematics

A **taxon** is a group of organisms that is given a name

A **natural taxon** is a group of organisms that exists as a result of evolutionary process:

A **species** is a lineage, a collection of organisms that share a unique evolutionary history and are held together by the cohesive forces of reproduction

A **monophyletic group**, or **clade** is a group of taxa encompassing an ancestral species and all its descendents

An **artificial taxon** represents an incomplete or invalid evolutionary unit

A **paraphyletic group** is a taxon that includes an ancestor but not all of the descendents of that ancestor

Polyphyletic groups are also artificial because its members are derived from 2 or more ancestral forms not common to all members

Approaches to Systematics (Putting together Evolutionary Hypotheses)

All phylogenetic trees have 2 significant structural features

1. One feature is the location of branch points along the tree, symbolizing the time of origin of different taxa
2. The second is the extent of divergence between branches, representing how different two taxa have become since branching from a common ancestor

Q. If classification is based on evolutionary history, which property of phylogenetic trees should be given the greatest weight when grouping species into taxa?

The question has divided systematics into three schools: evolutionary systematics, phenetics, and phylogenetic systematics (cladistics)

1. Evolutionary Systematics (Taxonomy)

It recognizes and ranks taxa based on:

Common descent, which is assumed by the degree of similarity and difference among organisms

The amount of adaptive evolution change

It attempts to use both the criteria of extent of divergence and branching sequence in tracing the history of life

In cases where this leads to conflict, a subjective judgment is made about which type of information should be given higher priority

The branching diagrams prepared by evolutionary systematists are called **phylogenetic trees**

2. Phenetics

Phenetics is a quantitative approach to systematics - mathematical models and computer-aided techniques are used to group organisms on the basis of their overall similarity. Specifically, pheneticists use a method called **numerical taxonomy**, which measures and records similarities for large numbers of characters.

A single composite quantity - *the distance measure* - is derived.

Species are then grouped and compared using the distance measure.

Pheneticists do not seek to make the distinction between homologous and analogous similarities.

A **phenogram** (=branching diagram) of species is then constructed using these distance measures.

3. Phylogenetic Systematics (Cladistics)

Cladistics is a phylogenetic hypothesis that attempts to reconstruct the course of evolution by grouping organisms relative to a common ancestor.

Assumptions:

- a. There is a single phylogeny of life as a result of evolutionary descent.
- b. Characteristics are passed on from generation to generation.

Cladists erect branching diagrams called **cladograms** - these are hypotheses about the relationship among taxa based on certain shared characteristics.

Each branch point is defined by novel homologies unique to the species on the branch.

Important in the formation of the cladogram is the distinction between:

Homologous characters that already exist in a common ancestor - **primitive characters** or **plesiomorphic character**.

Also, characters shared by *all* members of the group, including the ancestor, are referred to as **symplesiomorphies**.

Homologous characters that have evolved more recently and, therefore, only occur among certain species in the cladogram - **derived characters** or **apomorphic characters**.

The term **synapomorphies** is used to define characters that have arisen within the group since it diverged from a common ancestor.

Organisms or species that share derived character states form subsets called **clades**.

The Process of reconstructing the Phylogeny of a Group using Character Variation

Choose an **ingroup**, any group of theoretically related organisms of interest to an investigator

Select an **outgroup** is any group used for comparative purposes in a phylogenetic analysis

Outgroups are used to assess the evolutionary sequence of appearance of homologous characters independently

Because genealogy is so important in evolution, it is not surprising that the most important outgroup in any study is the **sister group** - the taxon that is most closely related genealogically to the ingroup to the taxa being investigated

To determine whether a character is derived (apomorphic) or ancestral (plesiomorphic) is accomplished via a method called **outgroup comparison**

By examining the outgroup one can infer that any character state found both within the study group and the outgroup is ancestral for the study group as primitive

All character states found in the study group that are absent in the outgroup are considered derived

Phylogenetic Assumptions - Parsimony

There are many approaches to reconstructing phylogenies, most of which have different advantages and purposes.

Parsimony argues that a reasonable estimate of evolutionary history is one that requires us to make the fewest additional assumptions about our data.

We use the parsimony approach to seek the tree with the fewest number of evolutionary steps; that is, the tree with the fewest number of character state changes.

If we can measure the “size” of a phylogenetic tree by the number of steps, then the most reasonable tree is the shortest tree.