

Diversity of Life Forms

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9.A Principles and methods of taxonomy

9.A.1 Concepts of species and hierarchical taxa

➤ Biological species concept

The biological species concept defines a species as members of the population that actually or potentially interbreed in nature, not according to similarity of appearance. Although their appearance is helpful in identifying species, but it does not define species. The biological species concept is the most widely accepted species concept. It defines species in terms of interbreeding. Ernst Mayr defined a species, as "*groups of interbreeding natural populations that are reproductively isolated from other such groups*". The biological species concept explains why the members of a species resemble one another, i.e., form **phenetic** clusters, and differ from other species. When two organisms breed within their species, their genes pass into their combined offspring. As this process is repeated, the genes of different organisms are constantly shuffled around the species gene pool. The shared gene pool gives the species its identity. By contrast, genes are not (by definition) transferred to other species, and different species therefore take on a different appearance. This explanation should be compared with the one given by the ecological species concept. Interbreeding between species is prevented by the isolating mechanisms.

➤ Subspecies

In biological classification, subspecies is either a taxonomic rank subordinate to species, or a taxonomic unit in that rank. A subspecies cannot be recognized in isolation: a species will either be recognized as having no subspecies at all or two or more (including any that are extinct), never just one. Organisms that belong to different subspecies of the same species are capable of interbreeding and producing fertile offspring, but they often do not interbreed in nature due to geographic isolation or other factors. The differences between subspecies are usually less distinct than the differences between species. The characteristics attributed to subspecies generally have evolved as a result of geographical distribution or isolation.

➤ Hierarchical taxa

- **Taxonomy** is the branch of biology that deals with the three different aspects of the organisms, i.e. identification, nomenclature and classification of organisms.
- **Systematics** deals with the relationships between taxa, especially at the higher levels and is known as the process of organizing taxonomic information about organisms into a logical classification that provides the framework for all the comparative studies. It is the scientific study of biological diversity and its evolutionary history.
- **Systematic biology** Systematic and taxonomy are collectively referred to as the systematic biology.

9.A.2 Biological Nomenclature

Taxonomy (sometimes called "**systematics**") is the science of classifying organisms. The Linnean system of classification, used for both plants and animals, was developed more than two centuries ago by the great Swedish botanist Carolus Linnaeus (born Carl von Linné). It is a hierarchical system that is; each organism belongs to a series of ranked taxonomic categories, such as a subspecies, species, genus, family, etc. At any rank (level) in the hierarchy any organism can belong to only one taxon, or taxonomic group. For instance, the Yellow-rumped Warbler can be a member of only one genus and one class. Each taxon is given a formal, latinized name that is recognized by scientists around the world. Nomenclature is a formal system of names used to label taxonomic groups.

Birds compose the class Aves, which is in the phylum Chordata (Chordata also includes mammals, reptiles, fishes, and tunicates everything with an internal skeletal rod called a "**notochord**," which in vertebrates is enclosed in cartilage or within a backbone). The living (non-fossil) members of the class Aves are placed into more than two dozen orders, such as the Passeriformes (perching birds), Piciformes (woodpeckers, etc.), Columbiformes (pigeons and doves), Procellariiformes (albatrosses, petrels, etc.), Apodiformes (swifts and hummingbirds), and so on. The orders are divided into about 160 families an average 6-7 families per order. Family names can be recognized because they all end in "idae". For example, in the order

Passeriformes are such families as the Tyrannidae (the tyrant flycatchers), the Laniidae (the shrikes) and the Emberizidae, a large family that includes, among others, the wood warblers, sparrows, blackbirds, and orioles.

Families, in turn, are divided into subfamilies, with names ending in "inae." The wood warblers make up the subfamily Parulinae and the black-birds and orioles are the Icterinae. Within subfamilies, tribes (name ending "ini") are often recognized: blackbirds are the Agelaiini and orioles the Icterini within the Icterinae. The next commonly used category is the genus: the Yellow-rumped Warbler is in the genus *Dendroica*, along with more than two-dozen very similar species. Its latinized specific name is *Dendroica coronata*, made up of the name of the genus combined with a trivial name to distinguish it from congeners (other members of the same genus).

Because the Linnean system features a two-part specific name, it is often referred to as a system of "binomial nomenclature." Often, as in this book, the name of the author who first described and named the species in the scientific literature is added to the specific name thus, *Dendroica coronata* (Linnaeus). Traditionally, generic and specific names are set in italic type and in some works the name of the author is put in parentheses if he or she originally placed the species in a different genus. Thus if you find the Yellow-rumped Warbler listed as *Dendroica coronata* (Linnaeus), it is because Linnaeus originally placed it in the genus *Motacilla*, not *Dendroica*. We have not followed this procedure, since most bird species have long since been moved from their original genera as the taxonomic system has been refined.

Finally, subspecies may be recognized with trinomial nomenclature by adding a third name to the specific name. Thus the eastern Yellow-rumped Warbler (formerly the Myrtle Warbler) is *Dendroica coronata* (Linnaeus), and the western Yellow-rumped Warbler (formerly Audubon's Warbler) is *Dendroica coronata auduboni* Townsend.

The taxonomic-nomenclatural system is a device for communicating about the complexly interrelated products of evolution. Generally it works well, even though many aspects of it are arbitrary. For example, whether *Dendroica* is distinct enough to be recognized as a full genus, or should be merged with *Vermivora* and *Parula* is not self-evident, and ornithological taxonomists disagree on it. Some taxonomists are "lumpers" and would like to combine the three; others are "splitters" and wish to keep them separate. Furthermore, as new studies of the relationships of various higher categories are published, scientists must modify the taxonomic system, and as a result names of taxonomic groups may change, as may the organisms included in them. For example, recent DNA-DNA hybridization studies have led some scientists to conclude that the Emberizidae should be considered a subfamily (Emberizinae) of the family Fringillidae, the wood warblers a tribe (Parulini) of that subfamily, and both the orioles and blackbirds combined in yet another emberizine tribe, Icterini, with the tribal name Agelaiini disappearing.

Changes in latinized specific names are inevitable as knowledge about birds increases, and most should simply be accepted as the price of progress. Common names, at least within North America, show more stability and facilitate regional communication. But for worldwide communication, the level on which professional ornithologists often operate, the latinized names are essential. One need only note that the "robin" in North America is *Turdus migratorius*, while in England it is *Erithacus rubicula* (which, in turn, is "roodborst" in Holland, "rotkehlchen" in Germany, "rödihake" in Switzerland, and "rougegorge" in France). An American birdwatcher told by a traveling friend returning from Europe that she had added the "Ring Ousel" and "Blackbird" to her life list might be left pretty much in the dark. But if the American knew that those birds were *Turdus torquatus* and *Turdus merula*, he or she would at least know that both were sizable thrushes.

➤ Classification

Taxonomy is the science of classification of organisms. Biologists classify organisms based on their evolutionary relationships, using a hierarchical system of grouping by shared features.

The fundamental unit of life on Earth is what biologists refer to as the species. Although the concept of a natural unit for classification is critical to many fields within the biological sciences, biologists are far from agreeing on its exact definition, and the meaning of a species may vary somewhat depending on the type of biologist you question. For our purposes, the widely accepted "biological species concept" is quite appropriate. The biological species concept states that a species is a population or series of populations whose members are able to interbreed freely under natural conditions and who do not breed with other species. Although there are exceptions to and difficulties with this definition, it works for

most organisms. A simpler way to define species, which is not complete but will work for young audiences, is that a species is a unit of classification that refers to a population (group) or series of populations (group) of closely related and similar organisms.

Closely related species are combined into a genus, while closely related genera form a family, and so on up the classification hierarchy.

TAXONOMIC CATEGORY	HUMAN BEING	HIBISCUS PLANT
Kingdom	Animalia (Metazoa)	Plantae (Metaphyta)
Sub Kingdom	Eumetazoa	Tracheophyta
Phylum/Division	Chordata	Angiospermae
Sub Phylum/Sub Division	Vertebrata	—
Class	Mammalia	Dicotyledonae
Sub Class	Eutheria	—
Order	Primates	Malvales
Family	Hominidae	Malvaceae
Genus	Homo	Hibiscus
Species	Sapiens	Rosa sinensis

This classification hierarchy, listed from the largest or most inclusive category, is shown below. Taxa for the white-footed mouse are listed in the right-hand column as an example. Note that the genus and species names are always either italicized or underlined, with the genus name capitalized and the species name given in lower case.

- **Phenetics** is the study of relationships among a group of organisms on the basis of the degree of similarity between them, i.e., molecular, phenotypic, or anatomical. A tree-like network expressing phenetic relationships is called a *phenogram*. In biology, phenetics, also known as *taximetrics*, is an attempt to classify organisms based on overall similarity, usually in morphology or other observable traits, regardless of their phylogeny or evolutionary relation. It is closely related to numerical taxonomy, which is concerned with the use of numerical methods for taxonomic classification. Phenetics has largely been superseded by cladistics for research into evolutionary relationships among species. However, certain phenetic methods, such as neighbor joining, have found their way into cladistics, as a reasonable approximation of phylogeny when more advanced methods (such as Bayesian inference) are too computationally expensive. Phenetic techniques include various forms of clustering and ordination. These are sophisticated ways of reducing the variation displayed by organisms to a manageable level. In practice this means measuring dozens of variables, and then presenting them as two or three-dimensional graphs. Much of the technical challenge in phenetics revolves around balancing the loss of information in such a reduction against the ease of interpreting the resulting graphs.
- **Cladistic** can be defined as the study of the pathways of evolution or it is a branch of biology that determines the evolutionary relationships between organisms based on derived similarities. It is the most prominent of several forms of phylogenetic systematics, which study the evolutionary relationships between organisms. Cladistics is a method of rigorous analysis, using "shared derived traits" (synapomorphies) of the organisms being studied. Cladistic analysis forms the basis for most modern systems of biological classification, which seek to group organisms by evolutionary relationships. In contrast, phenetics groups organisms based on their overall similarity, while approaches that are more traditional tend to rely on key characters (morphology). A tree-like network that expresses such ancestor-descendant relationships is called a *cladogram*. Thus, a cladogram refers to the topology of a rooted phylogenetic tree.
 - **Cladistic methods** a cladistic analysis is applied to a certain set of information. To organize this information a distinction is made between characters, and character states. Consider the color of feathers; this may be blue in one species but red in another. Thus, "red feathers" and "blue feathers" are two character states of the character "feather-color." The researcher decides which character states were present before the last common ancestor of the species group (plesiomorphies) and which were present in the last common ancestor (synapomorphies) by considering one or more outgroups. An out-group is an organism that is considered not to be part of the group in question, but is closely related to the group. This makes the choice of an out-group an important task, since this choice can profoundly change the topology of a tree. Note that only synapomorphies are of use in characterizing clades. Next, different possible cladograms are drawn up and evaluated. Clades ideally have many "agreeing" synapomorphies. Ideally there is a sufficient number of true synapomorphies to overwhelm homoplasies caused by convergent evolution (i.e. characters that resemble each other because of environmental conditions or function, not because of common ancestry). A well-

known example of homoplasy due to convergent evolution is the character wings. Though the wings of birds and insects may superficially resemble one another and serve the same function, each evolved independently. If a bird and an insect are both accidentally scored "POSITIVE" for the character "presence of wings", a homoplasy would be introduced into the dataset, and this gives a false picture of evolution.

Many cladograms are possible for any given set of taxa, but one is chosen based on the principle of parsimony: the most compact arrangement, that is, with the fewest character state changes (synapomorphies), is the hypothesis of relationship we tentatively accept. Though at one time this analysis was done by hand, computers are now used to evaluate much larger data sets. Sophisticated software packages such as PAUP allow the statistical evaluation of the confidence we have in the veracity of the nodes of a cladogram. As DNA sequencing has become cheaper and easier, molecular systematics has become a more and more popular way to reconstruct phylogenies. Using a parsimony criterion is only one of several methods to infer a phylogeny from molecular data; maximum likelihood and Bayesian inference, which incorporate explicit models of sequence evolution, are non-Hennigian ways to evaluate sequence data. Another powerful method of reconstructing phylogenies is the use of genomic retrotransposon markers, which are thought to be less prone to the reversion and convergence that plagues sequence data.

Ideally, morphological, molecular and possibly other (behavioral etc.) phylogenies should be combined: none of the methods is "superior", but all have different intrinsic sources of error. For example, character convergence (homoplasy) is much more common in morphological data than in molecular sequence data, but character reversions are more common in the latter. Cladistics does not assume any particular theory of evolution, only the background knowledge of descent with modification. Thus, cladistic methods can be, and recently have been, usefully applied to non-biological systems, including determining language families in historical linguistics and the filiation of manuscripts in textual criticism.

- **Cladistic classification**

Three ways to define a clade for use in a cladistic taxonomy

- i. **Node-based** The most recent common ancestor of A and B and all its descendants.
- ii. **Stem-based** All descendants of the oldest common ancestor of A and B that is not also an ancestor of Z.
- iii. **Apomorphy-based** The most recent common ancestor of A and B possessing a certain apomorphy (derived character) and all its descendants.

A recent trend in biology since the 1960s, called *cladism or cladistic taxonomy*, requires taxa to be clades. In other words, cladists argue that the classification system should be reformed to eliminate all non-clades. In contrast, other taxonomists insist that groups reflect phylogenies and often make use of cladistic techniques, but allow both monophyletic and paraphyletic groups as taxa. A monophyletic group is a clade, comprising an ancestral form and all of its descendants and so forming one (and only one) evolutionary group. A paraphyletic group is similar, but excludes some of the descendants that have undergone significant changes. For instance, the traditional class Reptilia excludes birds even though they evolved from the ancestral reptile. Similarly, the traditional Invertebrates are paraphyletic because Vertebrates are excluded, although the latter evolved from an Invertebrate. A group with members from separate evolutionary lines is called *polyphyletic*. For instance, the once-recognized Pachydermata was found to be polyphyletic because elephants and rhinoceroses arose from non-pachyderms separately. Evolutionary taxonomists consider polyphyletic groups to be errors in classification, often occurring because convergence or other homoplasy was misinterpreted as homology.

Following Hennig, cladists argue that paraphyly is as harmful as polyphyly. The idea is that monophyletic groups can be defined objectively, in terms of common ancestors or the presence of synapomorphies. In contrast, paraphyletic and polyphyletic groups are both defined based on key characters and the decision of which characters are of taxonomic import is inherently subjective. Many argue that they lead to "gradistic" thinking, where groups advance from "lowly" grades to "advanced" grades, which can in turn lead to teleology. In evolutionary studies, teleology is usually avoided because it implies a plan that cannot be empirically demonstrated. Going further, some cladists argue that ranks for groups above species are too subjective to present any meaningful information, and so argue that they should be abandoned. Thus they have moved away from Linnaean taxonomy towards a simple hierarchy of clades. The validity of this argument hinges crucially on how often in evolution gradualist near-equilibria are punctuated. A quasi-stable