

What is systematics and why is it important?

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Systematics is the study of the units of biodiversity. Systematics differs from ecology in that the latter is concerned with the interactions of individuals (and therefore species) in a particular time, while the former is concerned with the diversification of lineages through time. Systematics includes the discovery of the basic units of biodiversity (species), reconstructing the patterns of relationships of species at successively higher levels, building classifications based on these patterns and naming appropriate taxa (taxonomy), and the application of this pattern knowledge to studying changes in organismal features through time. It also includes the building and maintenance of biodiversity collections, upon which all the products of systematic studies are based. These are museum collections of preserved specimens of all kinds.

Systematics has undergone a revolution in its basic paradigm over the last 50 years. This revolution is just the latest step in a progression that has paralleled advances in other academic disciplines through the history of man. Some concept of relationship -- the idea, for example, that a bluebird is more like an ostrich than it is like an antelope -- has existed since the early sentience of man. During the 1700's, very basic, utility-driven systems of classification (such as those used by the herbalists through the Middle Ages, and, notably, by Linnaeus) began to be replaced by "natural" systems that were based on a comparison of large numbers of features, or characters, of the organisms under study. During the next century, the concept of evolution gave causal explanation for the patterns that were being observed -- for how a group of jawbones in reptiles could be transformed into the ear bones of mammals, as an example. A new classification criterion was then possible -- that taxa be grouped according to evolutionary relationship. An intrinsic part of this idea is that groups of organisms change over time. Yet it took until the middle of the 20th century for biologists to realize that it is the changed form of a character in time, the "advanced state", that gives us the best clue to phylogenetic relationships and that can be used to group organisms together because it signifies that they share a common history. This realization is the key component to the methodology known as cladistics, which is our current systematic paradigm. The method uses these advanced characters, or synapomorphies, to produce explicit, testable patterns of phylogenetic relationship among organisms. In recent years, researchers have continued to refine the methodology, seeking the best ways by which to analyze character data to produce these patterns, as well as devising methods for evaluating the strength of these hypotheses, developing new sources of character information, and realizing the power of the resulting patterns when applied to any questions that deal with the evolution of organisms or their characters.

The study of evolution is often considered to be closely related to systematics. In fact, the two are essentially cause and effect. Although systematics can be done without regard to any process, since in its starkest form it is only a study of patterns without regard to how they came about, most researchers see evolution as the causal agent for these patterns. Hence, studies of evolution examine the processes, at the individual and population level, that lead to the patterns that we study in systematics.

What are the roles and products of systematics in modern biology?

As the sub-discipline of biology that investigates relationships of taxa, systematics is the foundation for comparative biology. Comparative biology is that type of study that attempts

to relate features of one organism, or type of organism, to features in another type of organism. This always is a question of homology, or sameness due to common evolutionary origin. In systematic studies we hypothesize homology of features among taxa and then gather data to test these hypotheses. This is important because appearance alone is often not a good indicator that features in different taxa are homologous -- many times similar structures will evolve independently in different lineages. If they are homologous, we expect that they will share many things because of their common ancestry, while if they are not, it is impossible to predict just how similar they will be. Hence, any study that asks why or how about a feature in more than one taxon, and draws comparative conclusions about them, rests on a systematic foundation.

We can identify specific roles for systematic studies and the patterns they produce, as follows:

1. *Systematists identify and document Earth's biodiversity, and organize this information in a form that can be utilized by others.*

A long-standing role for systematists is that of going into the field and collecting samples of organisms, then comparing them with known specimens in order to determine whether something significantly different has been found -- a new species. Such work depends upon the expertise of specialists who are intimately familiar with the natural variation in a particular group. This expertise can only be gained by first-hand experience with the organisms, both in the field and in biodiversity collections. Once species have been defined, names are given to them according to rules of nomenclature for the group. Higher level taxa (genera, families, etc.), which are successively larger assemblages of species, can then be named based on the phylogenetic relationships of the species. The resulting classifications provide a basis for communication about taxa for the scientific community and for the world at large. Because biodiversity collections are intended to be permanent, and are assembled over time, they provide a way of documenting change in the world's flora and fauna, and can therefore provide supporting evidence for phenomena such as human-caused climate change.

2. *Systematic patterns are hypotheses of the history of life and form the basis for modern classifications.*

Once we know what organisms exist, we can then ask questions about how they came to be as they are today. Phylogenetic analysis allows us to combine data from extant organisms with data from fossils to provide hypotheses of relationship -- to actually reconstruct the history of life. It allows us to determine, for example, which living taxa are most closely related to the dinosaurs, which characters may have been key to the success of the flowering plants, and how many times HIV may have shifted hosts (e.g., between simians and man). This is because our phylogenetic hypotheses are both hypotheses of relationships of taxa and of character transformation. These patterns are framed as hypotheses because they are always subject to testing by additional characters. We build classifications from well-supported phylogenetic patterns.

3. *Phylogenetic patterns that result from systematic studies, and classifications derived from them, have predictive value.*

Common ancestry means that organisms will share more or fewer character states depending upon how closely related they are. This principle can be put to immediate use when one seeks additional taxa that may possess a feature of interest found in a specific

taxon. For example, the anti-cancer compound *taxol* was isolated from a particular species of conifer, the Pacific Yew (*Taxus brevifolia*). Where else would we look to find other sources of this compound? The logical place to look would be in taxa that are most closely related to *T. brevifolia*. Armed with information about relationships in the genus, researchers found *taxol* in a closely related species, the European Yew (*T. baccata*). This alternate source is less costly and will alleviate pressure on the rarer *T. brevifolia*. There is no guarantee in cases such as this that we will find what we are looking for, since the substance may have arisen only within one species, but rather than searching blindly, we increase our chances of success by looking in related species. Having the systematic guide for where to look is especially important in large groups (a genus of say, 500 species) to maximize use of time and resources. The list of biodiversity attributes of interest to man that such information can be applied to is endless, including all types of substances from, and characteristics of, organisms.

4. *Systematics provides a basis for biodiversity conservation priorities.*

With increasing pressures from a growing world population and resulting pressure on biotic resources, we now and in the future have to make difficult decisions about what parts of the Earth will be maintained in a “natural” state in order to conserve the biodiversity present there. How do we decide, given limited resources, which to protect? If we decide that we want to maximize biodiversity, then the phylogenetic patterns produced by systematists give us a way to prioritize areas based upon the diversity they contain. In order to maximize diversity, it makes sense to try to preserve groups from throughout the tree of life, rather than large numbers from one branch. In this way we will tend to preserve a wider array of features that have potential use for humans, though their uses may presently be unknown, but it does mean that we have to know something about the relationships of the organisms involved.

5. *Systematics provides independent evidence for patterns of geological change.*

The continents have not always held the positions on the Earth that they do today, nor have they been the same size and shape. Geologists use data from the Earth itself to reconstruct past arrangements of land masses. However, there is an independent source of data for such reconstructions, which lies in the current distribution of taxa when viewed in the light of their relationships. When land masses fragment or experience other fundamental change, the taxa that live on them record this change. By constructing organismal phylogenies and mapping on current distributions of taxa, and doing this for many groups, general patterns emerge that may best be explained by historical geological events. This is the objective of historical biogeography.

6. *Systematists and systematic collections provide identification services and documentation of identity.*

Another crucial role for systematists is that of identification specialists. They are in a unique position to provide this service, with experience and the necessary tools. The importance of correct identification cannot be overstated -- when a life, for instance, hangs in the balance depending on whether the plant or mushroom that has been ingested is poisonous or not, this service is critical. Other types of biological research are essentially valueless if their subjects are misidentified, since closely related taxa can have very different properties and generalizations must be made carefully. Hence, documentation is important so that subsequent investigators can confirm identifications. The only lasting way to document identity is to deposit a voucher specimen in an appropriate collection. Studies that do not

utilize this service will have less value in the long term because of the impossibility of verifying identification.

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The Importance of Systematic Biology in Defining Units of Conservation

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Abstract

Conservation biology is linked inextricably with systematic biology. The principles of systematic biology, however, have not been integrated completely into the practice and principles of conservation biology. Systematists have recognized for some time that a number of evolutionary processes lead to the diversification of lineages. Yet some present units of conservation, such as the evolutionarily significant unit (Waples 1991), primarily emphasize only one of these processes, adaptation. Allopatric speciation produces biodiversity without requiring any adaptive shift (and consequent adaptive differences between daughter species), so definitions of conservation units that emphasize adaptation may underestimate biodiversity. We estimated the frequency of different modes of speciation for three groups of vertebrates. The frequency of allopatric speciation varies among these groups, but is an important type of speciation in two of the three groups studied. Our results, and the results of other published studies of the frequency of modes of speciation, demonstrate that any unit of conservation defined solely in terms of adaptation is likely to underestimate biological diversity.

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The importance of systematics in parasitological research.

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[Abstract](#)

The discipline of systematics plays a central role in all branches of biology. In today's technology-orientated research world, it is important to realise the continuing value of systematics, the basic tenet of which is to combine diverse types of data to produce classifications that reflect the natural history of living organisms. Accurate classification systems are crucial in the field of parasitology, not only because they provide the means to identify species and strains of parasites, but also because they provide a framework around which a parasite's biology can be studied. The construction of such a classification system is

often hampered by the parasite's biology, which may preclude the application of traditional techniques or concepts (such as morphological differentiation or the biological species concept) to delineate species. It is often the case that these difficulties can be overcome by the use of molecular systematic techniques. In this paper, it is proposed that a detailed understanding of the phylogeny of a group of organisms can be used as a basis to examine other aspects of their systematics. This is illustrated using the protozoan parasite *Giardia intestinalis*. Data gathered using the complementary techniques of allozyme electrophoresis and nucleotide sequencing have been used to infer the phylogenetic relationships of *G. intestinalis* isolated from various host species. The results, supported by biological data, suggest that *G. intestinalis* is a species-complex. As we move towards the year 2000, molecular systematics will play an increasingly important role in elucidating host-parasite relationships. However, its use as a taxonomic tool will require a general acceptance by parasitologists and the adoption of formal procedures to allow the description of new species by these methods. The aim of this approach is not to dismiss traditional methods, but to use them in combination with contemporary methods in the true spirit of the discipline of systematics.

Systematics, taxonomy, classification

Systematics is the study of biological diversity and its evolution. Taxonomy, a subdivision of systematics, is the science of biological classification.

Classification systems help to clarify relationships among organisms; they help us remember organisms and their traits; they enable us to communicate clearly the identity of organisms being studied; they improve our predictive powers; and they provide stable names.

Taxonomic systems used by biologists are hierarchical, that is, each higher group contains all the groups below it.

A major goal of biological classification systems is to reflect evolutionary relationships among organisms. Many different traits are used to classify organisms because no one type of information is always the most appropriate. Knowing phylogenetic relationships is essential for interpreting the evolution of traits of organisms.

Life has evolved into the almost overwhelming richness of species found today. People have long been interested in the richness of the living world and have attempted to understand its origin and maintenance. At first, the study of biological diversity was motivated by purely practical reasons - to determine which plants and animals might be useful sources of food, medicine, and other products. During the seventeenth and eighteenth centuries, the study of nature was strongly stimulated in Western culture by the desire to reveal the hidden order and harmony as thought to have been provided by God. Because God was assumed to have had a plan in mind, scientists of that period believed that the diversity of living organisms must obey some general laws, and that these laws could be revealed, in part, by the way organisms were classified. These early attempts at classification led to the complex systems we use today.

THE IMPORTANCE OF BIOLOGICAL CLASSIFICATION

Dealing with a complex world requires an ability to recognize similarities and differences among objects. Classification systems serve four very important roles.

First, they are an aid to memory. It is impossible to remember the characteristics of a large number of different things unless we can group them into categories, whose members share many characteristics.

Second, classification systems greatly improve our predictive powers. If, for example, we know that females of all known mammalian species have mammary glands with which they produce milk for their offspring, we can be quite certain that a newly discovered animal with other typical mammalian traits, such as hair and a constant, high body temperature, will also have this method of provisioning its offspring, even if the first individuals we happen to find are males, and hence lack functional mammary glands.

Third, classification systems improve our ability to explain relationships among things. For biologists, this is especially important when we attempt to reconstruct the evolutionary pathways that have produced the diversity of organisms living today.

Fourth, taxonomic systems provide relatively stable, unique, and unequivocal names for organisms. If those names are changed, the systems provide means of tracing the changes. Common names, even if they exist (most organisms do not have common names at all), are unreliable and often confusing. For, example, there are plants called "bluebells" in England, Scotland, the eastern United States, and the Rocky Mountains - but none of the bluebells in any of those places is closely related to the bluebells in any of the other places [\[Click here for FIGURE\]](#). Fish called pickerel are prized for eating in central Ontario, Canada, whereas to the south, in the Great Lakes region, pickerels are regarded as undesirable for the table. The inconsistency is due to the fact that around the Great Lakes the name "pickerel" is applied to a fish species that is called the "grass pike" in central Ontario. In neither location is that species regarded as good eating. A different species is called "pickerel" in central Ontario. These cases illustrate the need for formal, unique names for organisms.

TAXONOMIC HIERARCHIES

Recognizing and interpreting similarities and differences among organisms is easier if the organisms are assigned to groups that are ordered and ranked that is, if the organisms are classified. Any group of organisms treated as a unit in a classification system is called a taxon (plural, taxa). Taxonomy is the theory and practice of classifying organisms. Systematics is the scientific study of the diversity of organisms. Its goal is to assess evolutionary relationships among organisms and to express these relationships as taxonomic systems.

The biological classification system used today is based on the work of the great Swedish biologist Carolus Linnaeus (1707-1778). In the Linnaean system, each species is assigned two names, one identifying the species itself and the other the genus to which the species belongs. A genus is a group of closely related species (the plural of genus is genera, and its adjectival form is generic). In many cases the name of the taxonomist who first proposed the species name is added at the end. Thus, *Homo sapiens* Linnaeus is the name of the modern human species. *Homo* is the genus to which the species belongs, *sapiens* identifies the species, and Linnaeus proposed the species name *sapiens*. You can think of the generic name *Homo* as being equivalent to your surname and the specific name *sapiens* as being equivalent to your first name. This two-name system, referred to as binomial nomenclature, is universally employed throughout biology. The generic name is always capitalized; the species name is

not. As I have done in this paragraph, both the generic and specific names are always italicized, whereas common names are not. A reference to more than one species in a genus is expressed with the abbreviation spp. after the generic name (for example, *Drosophila* spp.); the abbreviation sp. is used after a genus name when the identity of the species is uncertain. Rather than repeating a genus name when it is used several times in the same paragraph, it is spelled out once and abbreviated to the initial letter thereafter.

Most classification systems group smaller units into successively larger ones. The number of features shared by members of the larger units are fewer than the number shared by members of smaller units. For instance, ostriches, owls, hummingbirds, and sparrows are quite different animals, but they share more features with one another than they do with whales, cats, mice, or deer. By calling the former birds and the latter mammals, and placing them in separate but equivalent categories, we direct attention to certain significant features that serve to unite the members of each taxon and distinguish them from members of other taxa.

In the Linnaean system, the species are grouped into higher taxonomic categories. The number and limits of these categories are somewhat arbitrary, but there are some guiding rules. One is purely practical: If every species were put into its own genus, or conversely, all species were lumped into one genus, the genus would not carry any information not already present in the designation of the species. A second consideration is the relative amount of similarity or dissimilarity among the organisms. A higher taxonomic category may have a single species in it if that species is very different from all other species. Some genera, on the other hand, contain hundreds of species. In a taxonomic system designed to reflect evolutionary relationships, genera and higher taxonomic categories are based on the length of time since the taxa last shared a common ancestor. For example, genera might be separated by, say, 15 million years of independent evolution; higher taxonomic categories by still longer times. [\[click here for Figure\]](#)

The category above the genus in the Linnaean system is the family. The names of animal families end in -idae. Thus, Formicidae is the family that contains all ant species, whereas Hominidae contains humans and a few of our fossil relatives. Family names are based on the name of a member genus. Formicidae is based on Formica (remove the -a and add -idae); Hominidae is based on Homo. Plant classification follows the same procedure except that the ending -aceae is used instead of -idae. Thus Rosaceae is the family that includes the genus of roses (*Rosa*) and its immediate relatives. Unlike the generic and species names, family names are not italicized, but they are capitalized.

Families are, in turn, grouped into orders, and orders into classes. Classes of animals and protists are grouped into phyla (singular, phylum), and the equivalent category in plants, bacteria, and fungi is division. Phyla are grouped into kingdoms. See these figures for the hierarchical units into which the [blackburnian warbler](#) (*Dendroica fusca*) and the [moss rose](#) (*Rosa gallica*). [\[click here for another example\]](#) [\[click here for yet another example\]](#)

THE GOALS OF CLASSIFICATION SYSTEMS

The different biological classification systems all are designed to express relationships among organisms, but they differ with respect to the kinds of relationships they attempt to express. Classifications are based on features selected according to the goals of the system. If, for instance, we were interested in a system that would help us decide what plants and animals were desirable as food, we might erect a classification system based on palatability, ease of capture, and the edible parts each organism possessed. Early Hindu classifications of plants

were designed according to such criteria. Hindu classifications of animals were made from several points of view, such as method of reproduction, habitat, mode of life, usefulness to people, and number of senses. One ancient system divided animals into (1) those with placentas, (2) those formed from eggs, (3) those that generated spontaneously, and (4) those born of vegetable matter. Another system divided animals into (1) those born of moisture and heat, (2) those that bear live young, (3) those that lay eggs, and (4) those that burst forth from the ground.

We do not use such systems today, but they served the needs of the people who developed them. It is inappropriate to ask whether those classifications, or any others, including contemporary ones, are right or wrong. Classification systems can be judged only in terms of their utility and consistency with their stated goals. To evaluate any classification system we must first ask: What is it trying to accomplish? Then we can ask: How well does it accomplish those objectives?

The major goal of the biological classification systems in regular use today is to reflect evolutionary relationships. Evolutionary history has two important components. One is phylogeny, the pattern of genetic linkages between ancestors and their descendants. The other is the rate of evolution of traits among groups of organisms. Because the rates of change in the structures of organisms differ among lineages, some organisms that are very similar to one another have been evolving independently within their lineages much longer than organisms in other lineages that are structurally much more different from one another. Classification systems that combined both phylogeny and rate of morphological change preceded in time those that emphasize only one of these factors.

Orthodox Systematics

The Linnaean classification system was developed before biologists were aware of the length of evolutionary time and when only a few methods for comparing organisms were available. Consequently, organisms were grouped primarily on the basis of their gross morphological similarities and differences. Later, when biologists accepted the fact of evolution, existing classifications were modified to reflect evolutionary relationships. Therefore, most currently used classifications reflect both evolutionary relationships and the amount of morphological difference among organisms. As evolutionary relationships have become better known, taxonomies have been modified to more closely reflect phylogenies.

In general, current classifications deviate from phylogeny when a descendant is so different from its ancestor that it is more similar to organisms in other lineages than it is to other descendants of the same ancestor. For example, we know that birds and crocodiles share a more recent common ancestor than crocodiles do with snakes and lizards. However, the commonly used classification places crocodiles with snakes, lizards, and turtles, and separates birds into their own group. This classification emphasizes the similarity of crocodiles to snakes, lizards, and turtles, and the great differences between birds and those animals, but is not in accord with evolutionary relationships [[click here for Figure](#)]. In recent classification systems designed to show only evolutionary relationships, birds are grouped with crocodiles and their ancestors into a single taxon separate from snakes, lizards, and turtles [[click here for Figure](#)]. Many taxa that reflect both evolutionary relationships and morphological similarity are in use today. They persist because they are so familiar to workers in the field and also because they emphasize some important morphological and physiological differences.

Phenetic Systematics

Phenetic systematics, a school of systematics that arose in the 1950s and 1960s, attempts to erect classification systems strictly on the basis of overall similarity among organisms. Systematists of this school measure as many traits as possible and use the measurements to estimate overall similarity. They argue that because no information on evolutionary history is available for most organisms, it is a mistake to attempt to reflect that history in classifications.

It might seem to be a straightforward task to measure a large number of traits of organisms and then assess the degree of similarity among them. In practice, however, this is not so simple, because decisions must be made about whether some traits are more important than others, and about whether a group of traits that are all direct responses to a single selective pressure should be given the same weight as traits influenced by different selective pressures. For example, most salamanders metamorphose from an aquatic larval form to a terrestrial adult before becoming reproductively mature. However, some salamanders reproduce while they are still in an aquatic larval form, a pattern known as neotony. Many traits are associated with this reproductive pattern. If they were all treated as separate traits, then all neotenic salamanders would be grouped together in a phenetic classification system. However, if neoteny was considered to be one general trait, which is reproduction during the larval stage, then the neotenic species would be separated from one another and grouped with a number of different terrestrial species. Another difficulty is that, because morphological traits often vary in response to environmental conditions, environmentally induced variation may be confused with genetically based differences.

Cladistic Systematics

Some recent classifications attempt to show only evolutionary relationships among organisms, ignoring their degree of morphological similarity or difference. The objective of cladistic systematics is to determine the evolutionary histories of organisms and then to express those relationships in phylogenetic trees. A clade is the entire portion of a phylogeny that is descended from a single ancestral species. The closeness of organisms on a cladogram indicates the presumed time since they diverged from their most recent common ancestor. Because the goal is to show phylogenies, taxa in a cladistic classification are clades and are monophyletic; that is each taxon is a single lineage that includes all-and only-the descendants of a single ancestor.

Traits shared due to descent from a common ancestor are called ancestral traits. But how can ancestral traits be recognized? One important way is to study the traces of organisms that lived in the past. A fossil is any recognizable structure from an organism, or any impression from such a structure, that has been preserved. Every living organism is a potential fossil, but few actually become fossils. After they die, most organisms are destroyed quickly by biological degradation (decay), mechanical breakage, or chemical dissolution. Despite these difficulties, we do have an extensive supply of fossils available to us. A good fossil record helps reveal ancestral traits. For example, the excellent fossil record of horses shows that modern horses, which have one toe on each foot, evolved from ancestors that had multiple toes. A trait, such as the modern horse's single toe, that differs from the ancestral trait in the lineage is called a derived trait.

Even in the absence of a fossil record, however, reasonable inferences about ancestral traits can sometimes be made. For example, among butterflies, species in two families, the brush-footed butterflies (Nymphalidae) and the monarchs (Danainidae) have four functional and two very small legs, whereas the swallowtails (Papilionidae) and the sulfurs (Pieridae) have six functional legs. Given that moths and all other orders of insects have six functional legs,

having six legs is probably ancestral. By inference, then, the four-legged trait in monarchs and brush-footed butterflies is probably a derived trait of butterflies descended from six-legged ancestors.

Deciphering ancestry is often difficult because over evolutionary time, a character may be lost from a lineage and later regained. Also, the same trait may appear independently in several lineages. To erect classification systems that accurately reflect phylogenies, it is necessary to be able to distinguish ancestral from derived traits. Therefore, cladists devote much effort to gathering and interpreting evidence to determine which traits are really ancestral and which are derived in different groups of organisms.

HOMOLOGY. Any two structures derived from a common ancestral structure are said to be homologous. Although homologous structures have a common ancestor, they may not have similar appearances or functions because, over time, such structures can diverge until they are very different. Nevertheless, homologous structures usually retain certain basic features that betray their common ancestry. Consider, for example, the leaves of plants. Several lines of evidence, especially details of their structure, indicate that all leaves are homologous, but they have been modified in many ways to become not only light trapping devices but also protective spines, tendrils, and brightly colored lures that attract pollinators. Because all these structures are modified leaves, they are all homologues of one another. You will understand more about this later when I discuss modern ways in unravelling the genetic basis of plant development.

HOMOPLASY. Not all resemblances are products of a common ancestry. If a structure evolves in different lineages, so that it is possessed by several species although it was not found in their most recent common ancestor, it exhibits homoplasy. Homoplasy can result from convergent evolution, reverse evolution, or parallel evolution. Under convergent evolution, structures that were formerly very different come to resemble one another because they have undergone selection to perform similar functions. For example, the structures that aid plants in climbing over other plants have evolved from stipules, leaflets, leaves, and inflorescences.

Under parallel evolution, the same character evolves in different lineages, often from a common basis. This is clearly seen among butterflies and moths where similar patterns of banding in the wings have evolved a number of times as a result of similar modifications of a common basic banding pattern shared by most species. Homoplasy is strongly suspected when organisms that are known to have been separated evolutionarily for a long time share some derived trait that appears to have evolved independently in each lineage after the two lineages separated.

Comparison of Taxonomic Methods

For all classification systems, the more information that is available, the better. Therefore, new knowledge from all areas of biological inquiry is rapidly incorporated into modern taxonomies. However, as we have just seen, that information is used very differently by orthodox, phenetic, and cladistic taxonomists. The similarities and differences among these schools are summarized in the Table.

CONSTRUCTING PHYLOGENIES

Biologists are interested in the phylogenetic relationships among organisms for many reasons. To understand the evolution of structures they need to know which traits are ancestral and which are derived. To determine how fast various traits have evolved in different lineages they need a good phylogeny. Phylogenetic information is essential for the study of nearly all aspects of adaptation. Indeed, it is difficult to think of a problem in biology that is not made easier to solve by the availability of a good phylogeny of the organisms being studied.

For several reasons, many different types of data are used in developing phylogenetic classifications. Traits that evolve slowly are useful for determining evolutionary relationships at the level of phyla or classes in the taxonomic hierarchy. Traits that evolve rapidly are useful at the level of families and genera. The traits that can be measured in flowering plants, for example, differ from those that can be measured in mammals. Some traits are readily preserved in fossils, whereas others, such as behavior and molecular structure, rarely survive fossilization processes. Therefore taxonomists use many different traits and use them differently when constructing phylogenies.

Structure and Behavior

An important source of taxonomic information is gross morphology, that is, sizes and shapes of body parts. Living organisms have been measured for centuries, so we have a wealth of morphological data. This is also the kind of information that is most readily available from fossils. Sophisticated methods are now available for measuring morphology and for estimating the amount of morphological variability among individuals, populations, and species.

The early developmental stages of many organisms reveal similarities with other organisms that are lost by the time adulthood is reached. For example, the larvae of some marine creatures called sea squirts have a dorsal supporting rod in their backs that disappears as they develop into adults. Many other animals—all the animals called "vertebrates"—also have such a structure. Because larval sea squirts share this and other structures with vertebrates, they are known to be more closely related to vertebrates than would be suspected by examining adult sea squirts. Larval morphology does not, however, always reflect evolutionary ancestry. Many larvae have been highly modified by evolution for their particular existence. Butterflies are not closely related to animals that resemble their caterpillars. Therefore, care must be taken when using different stages of organisms to infer their phylogenies.

Living organisms often reveal their close affinities by similarities in their behavior. This information is most useful for detecting relationships among rather closely related organisms. For example, the German ethologist Konrad Lorenz showed that similarities in courtship behavior patterns support other evidence that several species of ducks with quite different plumages are nonetheless very closely related. Many of these ducks, despite these substantial differences in plumage, can mate and produce fertile hybrid offspring, showing that they are genetically similar.

Biochemical Traits

The molecules of organisms constitute their micromorphology just as shapes of body parts constitute their gross morphology. Among the most important biochemical traits of organisms are their nucleic acids—DNA and RNA—and the proteins whose synthesis the nucleic acids direct. Because they are so important for determining phylogenies, especially for groups with poor fossil records, we will discuss these biochemical traits in some detail.

PROTEIN STRUCTURE.

It is possible to estimate similarities and differences among proteins without knowing the details of their structures by measuring the immunological distance between them. If a small amount of blood serum from an animal is injected into a test animal, such as a rat, the foreign blood acts as an antigen, causing the rat to produce antibodies that combine with the antigen and destroy it. If the immunized rat is then reinjected with blood from the same species, large antigen-antibody aggregates form and will precipitate from solution. Antigen-antibody reactions are highly specific; an antibody that precipitates the blood of one species does not react, as strongly with the blood of other species. Nonetheless, there are interspecific reactions that decrease as the proteins become less similar. The strength of such immunological reactions can be used to estimate the similarity of proteins from different species. For example, a rat can be immunized with the blood of a salamander. Serum from the rat can then be divided among several test tubes, to which serum from other species of salamanders is added. The amount of precipitate formed is proportional to the similarities in amino acid sequences in the serum proteins of the different species [\[click here for Figure\]](#).

This procedure has been used to study lineages among the plethodontines, a group of three genera of terrestrial North American salamanders- *Plethodon*, *Ensatina*, and *Aneides*. Based on studies of morphology, the distributions of living species, and fossils, investigators many years ago concluded that *Plethodon* resembles the ancestor of the group; that *Ensatina* is derived from that ancient stock; and that *Aneides* diverged from *Plethodon* by specializing for arboreal life. Immunological data confirm these conclusions and suggest that *Aneides* separated from *Plethodon* about 50 million years ago. The immunological data indicate that there was a burst of change among the species of *Aneides*, all of which apparently evolved at about the same time. *Plethodon*, on the other hand, has changed very little over the past 50 million years. In a purely cladistic system, the *Aneides* species would be included in the *Plethodon* genus even though the *Aneides* species are very different from their ancestors. Maintaining *Aneides* as a separate genus emphasizes the substantial differences between those species and the living species of *Plethodon*. To do so, however, requires that *Plethodon* violate the cladistic criterion that taxa should include all the species within their lineages. However, whatever system is chosen, the true phylogeny of this group has been established. It was correctly deduced from morphological data, and it has been confirmed by immunological data.

Electrophoresis, a method for separating molecules, can be used on both whole proteins and protein fragments. Because proteins of similar sizes move through an electrophoretic gel at similar rates, an estimate of the difference between proteins can be made from the difference in their mobility. Some proteins, such as collagens of bone and skin, keratins, and seed proteins, are often well preserved over geological time, allowing the method to be applied to fossil as well as living materials.

More precise information about phylogenies can be obtained by comparing the microstructure of proteins. The amino acid sequences of proteins can be determined easily by a process that sequentially removes amino acids from the amino terminus of polypeptides. The cleaved amino acids are then identified by gas-liquid or thin-layer chromatography, or by mass spectroscopy. A direct measure of genetic differences between two taxa is given by obtaining homologous proteins from the two taxa and determining the number of amino acids that have changed since the lineages of the taxa diverged from a common ancestor. This information can reveal a great deal about how natural selection has influenced evolution of a protein. It can also be used to estimate the approximate times that the lineages of organisms separated.

NUCLEIC ACID STRUCTURE. The structure of the genes themselves - their base sequences - provides the most direct evidence of evolutionary relationships among organisms. DNAs can be compared, even-if the precise sequences of their bases are not known, by a process called nucleic acid hybridization. The two strands of the DNA double helix can be separated by heating them, but they will re-anneal when cooled. If DNAs from two species are mixed and heated, they form interspecific double helices when cooled. However, because of differences in the base sequences of the two DNAs, they do not match up well. Less heat is required to separate these hybrid helices than helices composed of DNA from a single species. The degree of mismatching of the DNA is related to its thermal stability in a very consistent way. About 1 percent base-pair mismatching lowers by 1 percent the temperature at which 50 percent of the helices dissociate. DNA sequences differing by more than about 20 percent of their base pairs do not form stable duplexes, so this method can be used to compare only relatively similar species.

Nucleic acid hybridization has already yielded some surprising results. For instance, the DNAs of humans and chimpanzees are much more similar than would be expected given the considerable morphological differences between the two species (Table). This indicates that humans and chimps diverged from a common ancestor more recently than previously thought. A long-standing debate among biologists over whether the giant panda of China was related to bears or to racoons was resolved by DNA hybridization data, which clearly indicate that the giant panda is a bear. The unusual features of the giant panda are recent adaptations to its specialized diet-bamboo.

Attempts to resolve avian phylogenies using only morphological data never produced a consensus; different morphological traits gave different phylogenies. As a result of DNA hybridization studies, avian phylogenies are being extensively revised. For example, New World vultures were revealed to be closely related to storks, whereas the Old World vultures are closely related to hawks and eagles. Convergent evolution for life as a scavenger -rather than descent from a common ancestor produced the obvious similarities between Old and New World vultures.

Base sequences are determined in several ways, among which is the cleavage of DNA and RNA into short sections by the use of enzymes that recognize specific base sequences. These cleaved pieces can then be separated electrophoretically and their sequences are determined.

Electrophoretic analysis has been carried out on three regions of the chicken's nuclear genome: those containing structural genes for lysosome c, those for three different "alpha-like" globins, and those for four "beta-like" globins. Each of these regions is located on a different chromosome. These parts of the genome have also been measured in other members of the group called phasianoid birds: jungle fowl (the ancestor of modern chickens), chukar, turkeys, pheasants, peafowl, and guinea fowl. The genealogy suggested by these data differs significantly from the one based on traditional morphological criteria [\[click here for Figure\]](#). Taxonomists were misled by considerable convergent evolution among phasianoid birds, just as they were by convergent evolution between New World and Old World vultures.

The Future of Systematics

Biochemical methods will certainly continue to increase in importance. Nonetheless, information from many sources will always be valuable for determining lineages of organisms. The fossil record, which reveals when lineages diverges and began their independent evolutionary histories, is necessary to provide absolute timing for evolutionary

events. Also, no one method is suitable for all time frames and for all kinds of organisms. Therefore, the range of data used in classification is likely to increase rather than decrease in the future. For this reason, systematics integrates activities from many different biological disciplines. A systematist needs to have a command of both molecular techniques and natural history.

Many kinds of information are needed because molecular data do not always resolve taxonomic problems. Mammals are among the best known groups of animals. Their fossil record is extensive, and nearly all extant species have been named and described. The fossil record reveals that there was an explosive radiation of mammals about 60 million years ago. At that time all recent orders of mammals, as well as a number of groups not very similar to any of the surviving lineages, evolved. However, the mammalian groups radiated over such a short period that the phylogenies could not be reconstructed from the fossil discoveries. Molecular data, including data on myoglobin, hemoglobin, lens proteins, fibrinopeptides, cytochrome c, and ribonuclease, have been gathered for mammals for more than 20 years. By using this information, researchers have erected cladograms for the mammalian lineages. These attempts have been only partly successful owing to gaps in the data and to the fact that different molecules do not suggest the same phylogenies. Also, the computer programs used to generate phylogenies from the molecular and morphological data assume that there has been very little parallel evolution or reverse evolution, both of which probably occurred rather frequently. In addition, extensive work with fossils had already resolved those aspects of the phylogenies that were most readily dealt with by molecular techniques. Thus, despite two decades of extensive work, mammalian phylogenies are almost as uncertain as they were when molecular techniques were first employed. More research, using an even wider variety of data, will be necessary to resolve mammalian phylogenies.

TAXONOMIC KEYS

Taxonomic systems are used not only to indicate relationships among organisms, but also to help identify organisms, whether we wish to do so purely for pleasure or for research purposes. Taxonomists publish written descriptions of species being characterized and named for the first time. In addition, a description of a group of organisms is usually accompanied by a taxonomic key, which taxonomists design to help identify specimens belonging to the group in question. One of the most useful forms of key is dichotomous: At each step, species are divided into two groups on the basis of the presence, absence, or degree of development of some characters. As an example, consider the key in the Figure for the identification of insects belonging to the order Odonata. This simple key allows identification only to the family level. Other keys must be used to identify species. Note that the characters chosen for use in the key are simple and easy to see. They are not necessarily the characters that reveal the most about evolutionary relationships among dragonflies and damselflies.

It is not necessary to know anything about evolutionary relationships within a group to make a useful taxonomic key. All you need are characters that clearly separate the organisms and that can be used on most specimens. For example, it is often important to be able to identify plants that are not in flower. To do so requires the use of keys based on leaf and stem features. However, evolutionary relationships among plants are revealed much more clearly by their reproductive structures (flowers) because those structures evolve more slowly than leaves and stems do.

SUMMARY

Classification is a basic and vital activity. By means of it we order our environment to make it easier to respond appropriately to complex inputs. All biological classification systems are designed to serve particular purposes and must be judged with reference to their specific goals. Such systems can reflect similarities in the measurable traits of organisms (phenetic classifications), their phylogenetic relationships (cladistic classifications), or some combination of the two (orthodox classifications). Mixed systems are common because often people wish to accommodate more than one goal within a system.

In biology we give organisms two names, a generic name and a specific name. We group species into higher taxonomic categories such as genera, families, orders, classes, phyla, and kingdoms. The size and number of these higher categories is somewhat arbitrary.

Classification systems are erected from a wide variety of data—mostly from gross morphology, embryology, behavior, sequences of amino acids in proteins, and base sequences in DNA. Molecular techniques are increasingly being used. In some cases they are causing major changes in previously hypothesized phylogenies. In other cases, molecular data confirm earlier classifications. In still other cases, all available data in combination do not resolve the uncertainties.

Taxonomic keys serve in identifying specimens. They may be based either on characters that reflect actual evolutionary relationships or on characters that are simply convenient. Knowing evolutionary relationships among organisms is important for almost all types of biological investigations.

Importance of Plant Systematics

Plant systematics has great importance for the study of botany:

1. It is used to describe different species. The description of each new species is preserved. It is used for comparison.
2. Plant systematics is used to name different plants. It sets rules for nomenclature. This nomenclature has eliminated the confusion among different botanists. Now knowledge of plants can be shared between botanists of different countries without the problem of language and culture.
3. Plant systematics develops evolutionary relationships among the different groups of plants. It gives evolutionary trends among the plants.
4. Plant systematics provides a basis for the comparison of morphological, anatomical and cytological structures among different structures.
5. Plant systematics also provides a basis for genetics. Genetic analyses are performed on the basis of systematics.
6. Plant systematics has great importance in agriculture and herbal medicines. It provides us with the economic importance of different plants.

Importance of Taxonomy in Biology| an Overview

Every student of biology comes across taxonomy during his course of study as one of the important topics. Most of the students dislike it and feel bored not knowing why they have to study and mug up the taxonomy. But yet taxonomy is mentioned in almost every chapter during classification of any plant or animal.

Taxonomy definition: *“Taxonomy is a branch of science which tries to scientifically classify all the existing living organisms based on certain set of characters for easy of identification and study.”*



AKARAKINGDOMS

Taxonomy was described by Linnaeus and hence he is called as Father of taxonomy. You notice many plant specie' s scientific names ending with Linn. Taxonomy is the scientific way of classification of all the living creatures on the earth. Even human is called as homosapeian as per taxonomy.

Establishing taxonomy for entire biological species is a very task but these scientists completed it very successfully during their time. Any new plants or animals discovered latter were given name as per the rules of taxonomy established by Linnaeus.

This taxonomy is divided as plant taxonomy, animal or zoological taxonomy, microbial taxonomy etc.

Importance of Taxonomy in Biology:

1. Taxonomy aims to classify living creature: There are millions of organisms on the Earth of different physical, physiological, regional differences. Taxonomy helps to classify these millions of organisms scientifically into some categories like family, genus, species etc. for ease of study and understanding.

2. Taxonomy helps to ascertain the number of living species on the earth. We have discovered till now some thousands of plants and animal species and are recorded as per taxonomy.

3. Taxonomy helps in getting an idea of what type of characters are present in the plant or animal possess even before seeing or studying them in detail.

Ex: a) *In plants*: When one hears a plant to be of leguminous family, the characters we can ascertain are that they have nitrogen synthesising bacteria in their root nodules. They have a seed which can be broken into exact two half etc..

b) *In animals*: If a living creature is mentioned under mollusc's, it means the animals has some sort of hard shell as a protective factor (like snail). If an animal is called a mammal, it means the creature gives birth to well formed babies and also rears them with milk during growth.

4. Taxonomy gives an ideas level of physical development: Taxonomy gives an idea of how far an animal has physical and mental development and its position in the evolution tree of organisms.

Ex: When you hear the word bacteria, you get an idea of single celled organism and fungi as a multi-celled organism yet both or microbes. Physically & evolutionary wise, [fungi](#) are advanced than [bacteria](#).

5. Gives an idea of local fauna: Not all plants and animal species are found in all regions of the earth. Example kangaroo is limited to Australia like wise kiwi to New-Zealand etc. Even plants like Neem named as Azadirachta Indica (Indica= India) due its prominent presence in India. Hence taxonomy helps to identify or ascertain the types of plants and animals that can be found in particular region. This helps new scientists to go to the place of existence of the species to collect them in case they need to experiment on them.

How is taxonomy done: Taxonomy is done based on large view to smaller view like

- a. Domain: 1. Archea (no nucleus, no organelles in cell), 2. Bacteria No well formed nucleus but has organelles 3. Eukarya: which means well formed nucleus and cell organelles.
- b. Kingdom: gives ideas as 1. Animal 2. plant. 3. Fungi 4. protista.
- c. Phylum: For zoology it gives idea if it is a insect type or worm type etc.
- d. Class: Specifies the organism as mammal, bird, reptile etc.
- e. Order: If you consider mammal it say whether it is a herbivore or carnivore etc.
- f. Family: In botany plants are categorized or leguminous, solanaceae, euphorbeacea etc.families where in the plants in one family have few set of common physical characters.
- g. Genus: This keeps the animals more specific ex: Frog as “Rana”
- h. Species: This gives even specificity and in the above example of frog it sayplace of existence or physical character like

Rana tigrina : Indian bull frog, Rana Italica, Italian frog, Rana japonica-Japanese frog.

See for more [Rana genus](#).

So taxonomy for Frog is as

Kingdom: **Animalia**- Means it is "animal type" and not a plant.

Phylum: **Chordata**- Means has "Spinal cord"

Subphylum: **Vertebrata**- Has vertebral column dorsally.

Class: **Amphibia**- **Can live both in water and on land** (Amphi- two; Bia- living).

Order: **Anura** – No tail (An= No; Ura = Tail)

Suborder: **Neobatrachia**- New type of frogs (Neo= new)

Family: **Ranidae**

Genus: **Rana**

he Role of Taxonomy

The primary way basic information about animals and plants is organized and stored is by taxonomic categories (typically species) [another way is by subject, such as vision or food and feeding]. It is important to understand (1) why good taxonomic databases are essential for studying biodiversity, (2) what taxonomy entails, (3) why a hierarchical classification is useful, and (4) why classifications and names change, thereby making it more difficult to accumulate and keep track of information for many purposes from conservation management to inventories, to species entering commerce, etc.

Taxonomists have two important tasks...

Taxonomists have two important tasks: to name organisms and to classify them. The system of hierarchical classification and a two-word system for naming species began with Linnaeus in 1758. The system was codified in 1842 (Strickland et al. 1843), and it became the system used by all zoologists worldwide from 1843 to the present, with changes and improvements along the way. (The present **Code** which all zoologists follow is discussed in Appendix A of the *Catalog*). The two-word name for species consists of a generic name and a specific name. A genus may contain more than one species, and species are placed together in a genus based on perceived genetic affinity (as determined mostly by morphological differences and similarities, although biochemical techniques are providing new, additional information). (Subspecies are sometimes used to define smaller categories within a species). Taxonomists discover or describe species (1) by assembling specimens through fieldwork and/or by borrowing from museum collections, (2) by studying variation, (3) by

grouping the specimens into species categories, (4) by comparing these with previously described species, (5) then naming the new species following specific rules (ITZN 1985, 1999) and (6) by publishing the information in scientific journals and books. Monographs contain thorough treatments of all the species in a larger group, such as a genus or family, and monographs represent the latest summary of information for that group.

Classifications contain information about relationships

Classifications are useful because they contain information about relationships. For example, when a chemical suitable for a pharmaceutical product is found in one species, biochemists can quickly learn from classifications of the close relatives (e.g., other species in the same genus or the sister-species) that might contain similar or even better chemicals. All species in the same genus should share many behavioral, biochemical, ecological and biological properties because they are closely related evolutionarily. The effect of pollution on a species at one location should be similar to the effect on a close relative living in a different area. Those in the same family (next primary category up) similarly share many but fewer features. Classifications thereby have predictive value. Since the late 1960s, most taxonomists have used cladistic methods of forming classifications (i.e., Hennig's method, see Box 3), basing them on shared advanced (new) features. This approach results in cladograms or trees that reflect ancestry as well as relatedness of individual taxa.

Names keep changing

The changing nature of classifications and scientific names (because of changing ideas of relationships and because of technical [nomenclatural] rules changes) makes it almost impossible to know under which species, genus, or even family names one will find pertinent information in the prior literature or in specimen collections. For example, in 1989 both the genus name and specific name of the rainbow trout were changed (see Smith and Stearley 1989). Thousands of publications cite *Salmo gairdneri* as the name of the rainbow trout; now we call it *Oncorhynchus mykiss*. The genus name was changed from *Salmo* to *Oncorhynchus* partly based on fossil evidence because the Pacific trouts were thought to be more closely related to the Pacific salmon than to the Atlantic salmon [the name carrier or type of *Salmo*]. Pacific trout and salmon are now classified as *Oncorhynchus*. The species name *gairdneri* was changed to *mykiss* when it was thought that *mykiss* from Kamchatka, Russia, was the same as *gairdneri*; since *mykiss* was described first, that name had priority for use over *gairdneri*.

Another major activity of taxonomists is to make synonymies that summarize prior accumulated knowledge about species. Unfortunately, scientific names

change for several reasons, which makes inventory especially difficult since information about a single species may be found under several scientific names. Names change because:

1. One species may have been described more than once (such as from different geographical areas, from different sexes, from atypical specimens, or from a lack of knowledge of earlier descriptions). As these ♦duplicates♦ are discovered, the first described name is selected as the valid name, often resulting in a name change, such as for the rainbow trout.
2. Scientists may differ on what species to include in a particular genus, or species are moved to different genera based on perceived relatedness. This results in the first half (generic) of the name changing; sometimes the ending of a scientific name also changes since, if it is an adjective, it must agree (decline) in gender with the genus.
3. Sometimes names are changed for technical reasons.

Scientific names are frequently misspelled

Another problem is that scientific names are frequently misspelled in scientific publications, in collection records for museum holdings, and by abstracting services. Often a name is misspelled because the spelling as originally presented was not verified by subsequent workers. Although there are current arguments about how to incorporate fossils into classifications, and especially how to treat them in higher taxa, the present system probably will continue for many years. Numbering taxa has not worked either. Often common names are more stable than scientific names, and they can be useful in some groups.

Number taxa has not worked

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