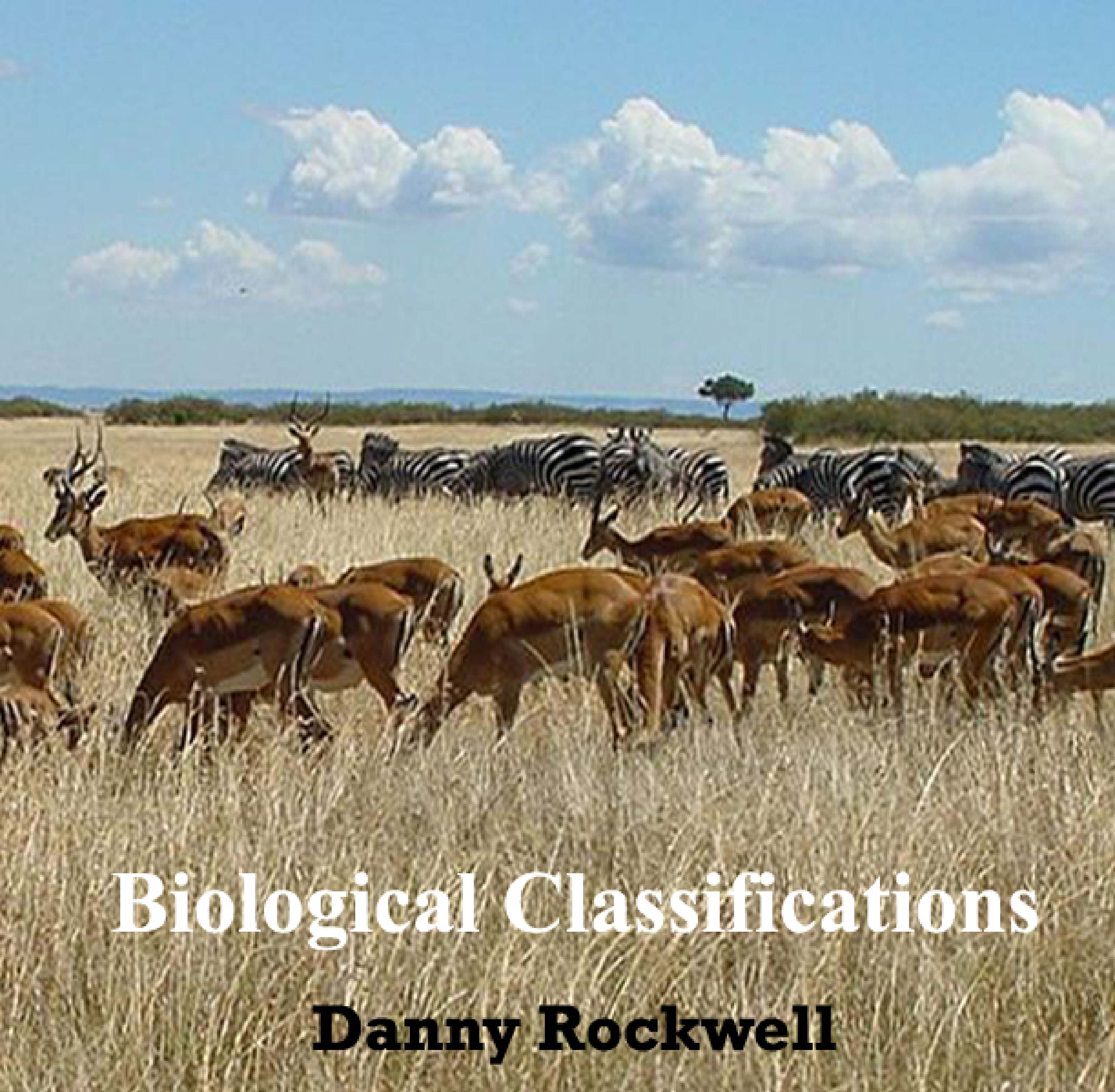

Biological Classifications

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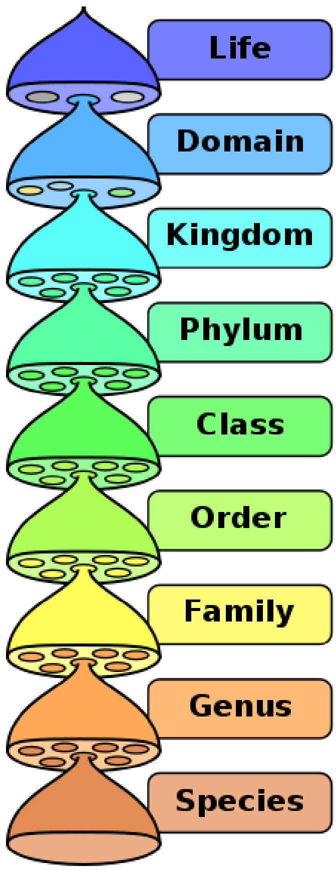
Biological Classification



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. Intermediate minor rankings are not shown.

Biological classification, or *scientific classification in biology*, is a method by which biologists group and categorize organisms by biological type, such as genus or species. Biological classification is a form of scientific taxonomy.

Modern biological classification has its root in the work of Carolus Linnaeus, who grouped species according to shared physical characteristics. These groupings have since been revised to improve consistency with the Darwinian principle of common descent. Molecular phylogenetics, which uses DNA sequences as data, has driven many recent revisions and is likely to continue to do so. Biological classification belongs to the science of biological systematics.

Definition

Classification has been defined by Mayr as "The arrangement of entities in a hierarchical series of nested classes, in which similar or related classes at one hierarchical level are combined comprehensively into more inclusive classes at the next higher level." A class is defined as "a collection of similar entities", where the similarity consists of the entities having attributes or traits in common.

What makes biological classification different from other classification systems (e.g. classifying books in a library) is evolution: the similarity between organisms placed in the same taxon is not arbitrary, but is instead a result of shared descent from their nearest common ancestor. Accordingly the important attributes or traits for biological classification are those which are 'homologous', i.e. inherited from common ancestors. Thus birds and bats both have the power of flight, but this similarity is not used to classify them into a taxon, because it is not inherited from a common ancestor. In spite of all the other differences between them, the fact that bats and whales both feed their young on milk is one of the features used to classify both as mammals, since it was inherited from a common ancestor.

Determining whether similarities are homologous or not can be difficult. Thus until recently, golden moles, found in South Africa, were placed in the same taxon (insectivores) as Northern Hemisphere moles, on the basis of morphological and behavioural similarities. However, molecular analysis has shown that they are not closely related, so that their similarities must be due to convergent evolution and not to shared descent, and so should not be used to place them in the same taxon.

Taxonomic ranks

A classification, as defined above, is necessarily hierarchical. In a biological classification, **rank** is the level (the relative position) in a hierarchy. (Rarely, the term "taxonomic category" is used instead of "rank".) There are seven main ranks defined by the international nomenclature codes: kingdom, phylum/division, class, order, family, genus, species. "Domain", a level above kingdom, has become popular in recent years, but has not been accepted into the codes.

The most basic rank is that of species, the next higher is genus, and then family. Ranks are somewhat arbitrary, but hope to encapsulate the diversity contained within a group — a rough measure of the number of diversifications that the group has been through.

The *International Code of Zoological Nomenclature* defines rank, in the nomenclatural sense, as:

The level, for nomenclatural purposes, of a taxon in a taxonomic hierarchy (e.g. all families are for nomenclatural purposes at the same rank, which lies between superfamily and subfamily). The ranks of the family group, the genus group, and the species group at which nominal taxa may be established are stated in Articles 10.3, 10.4, 35.1, 42.1 and 45.1.

There are slightly different ranks for zoology and for botany, including subdivisions such as tribe.

Early systems

Ancient through medieval times

Current systems of classifying forms of life descend from the thought presented by the Greek philosopher Aristotle, who published in his metaphysical works the first known classification of everything whatsoever, or "being". This is the scheme that gave such words as 'substance', 'species' and 'genus' and was retained in modified and less general form by Linnaeus.

Aristotle also studied animals and classified them according to method of reproduction, as did Linnaeus later with plants. Aristotle's animal classification was eventually made obsolete by additional knowledge and forgotten.

The philosophical classification is in brief as follows: Primary substance is the individual being; for example, Peter, Paul, etc. Secondary substance is a predicate that can properly or characteristically be said of a class of primary substances; for example, man of Peter, Paul, etc. The characteristic must not be merely in the individual; for example, being skilled in grammar. Grammatical skill leaves most of Peter out and therefore is not characteristic of him. Similarly man (all of mankind) is not in Peter; rather, he is in man.

Species is the secondary substance that is most proper to its individuals. The most characteristic thing that can be said of Peter is that Peter is a man. An identity is being postulated: "man" is equal to all its individuals and only those individuals. Members of a species differ only in number but are totally the same type.

Genus is a secondary substance less characteristic of and more general than the species; for example, man is an animal, but not all animals are men. It is clear that a genus contains species. There is no limit to the number of Aristotelian genera that might be found to contain the species. Aristotle does not structure the genera into phylum, class, etc., as the Linnaean classification does.

The secondary substance that distinguishes one species from another within a genus is the specific difference. Man can thus be comprehended as the sum of specific differences (the "differentiae" of biology) in less and less general categories. This sum is the definition; for example, man is an animate, sensate, rational substance. The most characteristic definition contains the species and the next most general genus: man is a rational animal. Definition is thus based on the unity problem: the species is but one yet has many differentiae.

The very top genera are the categories. There are ten: one of substance and nine of "accidents", universals that must be "in" a substance. Substances exist by themselves; accidents are only in them: quantity, quality, etc. There is no higher category, "being", because of the following problem, which was only solved in the Middle Ages by Thomas Aquinas: a specific difference is not characteristic of its genus. If man is a rational animal, then rationality is not a property of animals. Substance therefore cannot be a *kind* of being because it can have no specific difference, which would have to be *non*-being.

The problem of being occupied the attention of scholastics during the time of the Middle Ages. The solution of St. Thomas, termed the analogy of being, established the field of ontology, which received the better part of the publicity and also drew the line between philosophy and experimental science. The latter rose in the Renaissance from practical technique. Linnaeus, a classical scholar, combined the two on the threshold of the neo-classicist revival now called the Age of Enlightenment.

Renaissance through Age of Reason

An important advance was made by the Swiss professor, Conrad von Gesner (1516–1565). Gesner's work was a critical compilation of life known at the time.

The exploration of parts of the New World by Europeans produced large numbers of new plants and animals that needed descriptions and classification. The old systems made it difficult to study and locate all these new specimens within a collection and often the same plants or animals were given different names simply because there were too many species to keep track of. A system was needed that could group these specimens together so they could be found; the binomial system was developed based on morphology with groups having similar appearances. In the latter part of the 16th century and the beginning of the 17th, careful study of animals commenced, which, directed first to familiar kinds, was gradually extended until it formed a sufficient body of knowledge to serve as an anatomical basis for classification. Advances in using this knowledge to classify living beings bear a debt to the research of medical anatomists, such as Fabricius (1537–1619), Petrus Severinus (1580–1656), William Harvey (1578–1657), and Edward Tyson (1649–1708). Advances in classification due to the work of entomologists and the first microscopists is due to the research of people like Marcello Malpighi (1628–1694), Jan Swammerdam (1637–1680), and Robert Hooke (1635–1702). Lord Monboddo (1714–1799) was one of the early abstract thinkers whose works illustrate knowledge of species relationships and who foreshadowed the theory of evolution.

Early methodists

Since late in the 15th century, a number of authors had become concerned with what they called *methodus,* (method). By method authors mean an arrangement of minerals, plants, and animals according to the principles of logical division. The term *Methodists* was coined by Carolus Linnaeus in his *Bibliotheca Botanica* to denote the authors who care about the principles of classification (in contrast to the mere *collectors* who are concerned primarily with the description of plants paying little or no attention to their arrangement into genera, etc.). Important early Methodists were Italian philosopher, physician, and botanist Andrea Caesalpino, English naturalist John Ray, German physician and botanist Augustus Quirinus Rivinus, and French physician, botanist, and traveller Joseph Pitton de Tournefort.

Andrea Caesalpino (1519–1603) in his *De plantis libri XVI* (1583) proposed the first methodical arrangement of plants. On the basis of the structure of trunk and fructification he divided plants into fifteen "higher genera".

John Ray (1627–1705) was an English naturalist who published important works on plants, animals, and natural theology. The approach he took to the classification of plants in his Historia Plantarum was an important step towards modern taxonomy. Ray rejected the system of dichotomous division by which species were classified according to a pre-conceived, either/or type system, and instead classified plants according to similarities and differences that emerged from observation.

Both Caesalpino and Ray used traditional plant names and thus, the name of a plant did not reflect its taxonomic position (e.g. even though the apple and the peach belonged to different "higher genera" of John Ray's *methodus*, both retained their traditional names *Malus* and *Malus Persica* respectively). A further step was taken by Rivinus and Pitton de Tournefort who made genus a distinct rank within taxonomic hierarchy and introduced the practice of naming the plants according to their genera.

Augustus Quirinus Rivinus (1652–1723), in his classification of plants based on the characters of the flower, introduced the category of order (corresponding to the "higher" genera of John Ray and Andrea Caesalpino). He was the first to abolish the ancient division of plants into herbs and trees and insisted that the true method of division should be based on the parts of the fructification alone. Rivinus extensively used dichotomous keys to define both orders and genera. His method of naming plant species resembled that of Joseph Pitton de Tournefort. The names of all plants belonging to the same genus should begin with the same word (generic name). In the genera containing more than one species the first species was named with generic name only, while the second, etc. were named with a combination of the generic name and a modifier (*differentia specifica*).

Joseph Pitton de Tournefort (1656–1708) introduced an even more sophisticated hierarchy of class, section, genus, and species. He was the first to use consistently the uniformly composed species names that consisted of a generic name and a many-worded diagnostic phrase *differentia specifica.* Unlike Rivinus, he used *differentiae* with all species of polytypic genera.

Linnaean taxonomy

Carolus Linnaeus' great work, the *Systema Naturæ* (1st ed. 1735), ran through twelve editions during his lifetime. In this work, nature was divided into three kingdoms: mineral, vegetable and animal. Linnaeus used five ranks: class, order, genus, species, and variety.

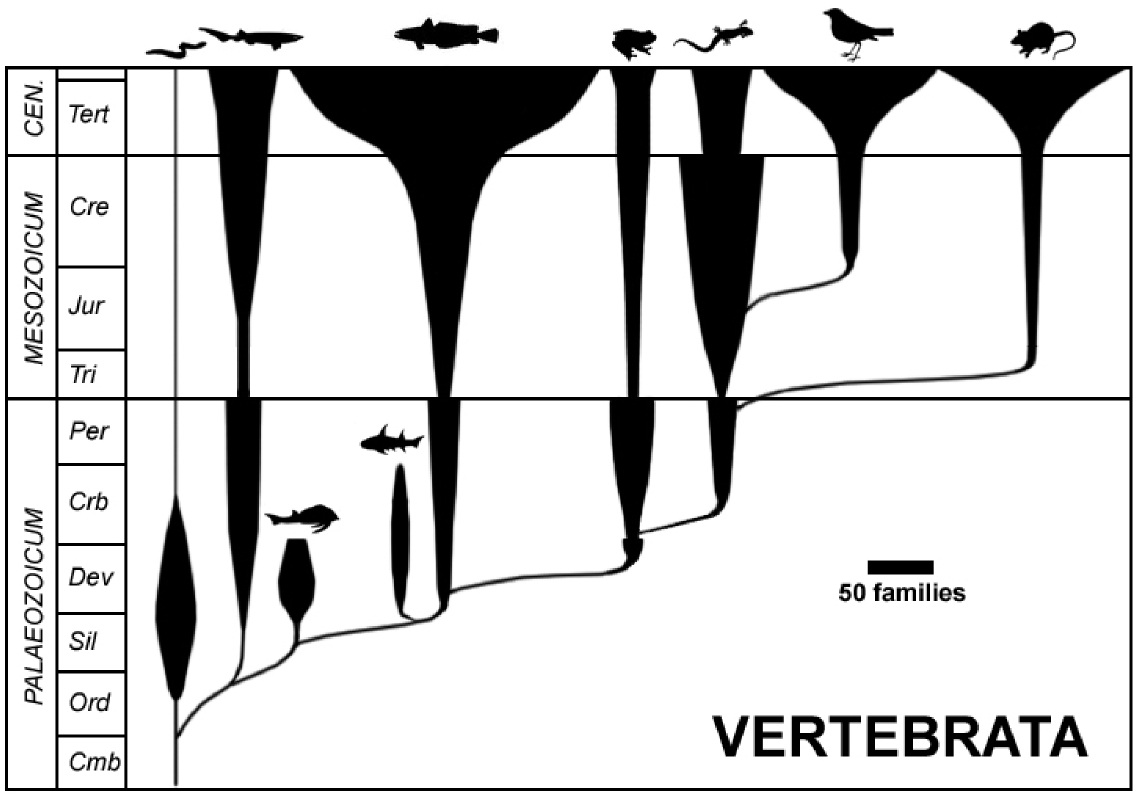
He abandoned long descriptive names of classes and orders and two-word generic names (e. g. *Trifolium repens*) still used by his immediate predecessors (Rivinus and Pitton de Tournefort) and replaced them with single-word names, provided genera with detailed diagnoses (*characteres naturales*), and reduced numerous varieties to their species, thus saving botany from the chaos of new forms produced by horticulturalists.

Linnaeus is best known for his introduction of the method still used to formulate the scientific name of every species. Before Linnaeus, long many-worded names (composed of a generic name and a *differentia specifica*) had been used, but as these names gave a description of the species, they were not fixed. In his *Philosophia Botanica* (1751) Linnaeus took every effort to improve the composition and reduce the length of the many-worded names by abolishing unnecessary rhetorics, introducing new descriptive terms and defining their meaning with an unprecedented precision. In the late 1740s Linnaeus began to use a parallel system of naming species with *nomina trivialia. Nomen triviale*, a trivial name, was a single- or two-word epithet placed on the margin of the page next to the many-worded "scientific" name. The only rules Linnaeus applied to them was that the trivial names should be short, unique within a given genus, and that they should not be changed. Linnaeus consistently applied *nomina trivialia* to the species of plants in *Species Plantarum* (1st edn. 1753) and to the species of animals in the 10th edition of *Systema Naturæ* (1758).

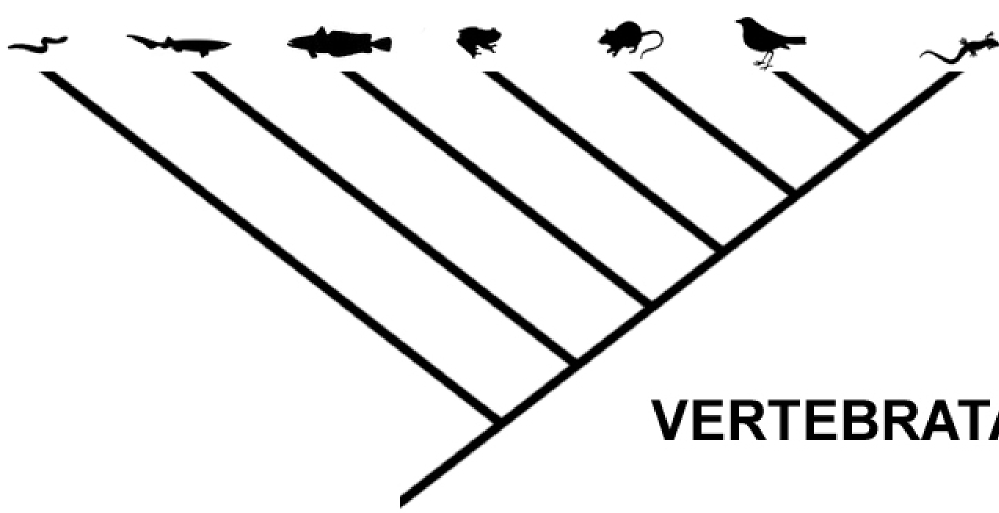
By consistently using these specific epithets, Linnaeus separated nomenclature from taxonomy. Even though the parallel use of *nomina trivialia* and many-worded descriptive names continued until late in the eighteenth century, it was gradually replaced by the practice of using shorter proper names consisting of the generic name and the trivial name of the species. In the nineteenth century, this new practice was codified in the first Rules and Laws of Nomenclature, and the 1st edn. of *Species Plantarum* and the 10th edn. of *Systema Naturae* were chosen as starting points for the Botanical and Zoological Nomenclature respectively. This convention for naming species is referred to as binomial nomenclature.

Today, nomenclature is regulated by Nomenclature Codes, which allows names divided into taxonomic ranks.

Modern system



Evolution of the vertebrates at class level, width of spindles indicating number of families. Spindle diagrams are typical for Evolutionary taxonomy



The same relationship, expressed as a cladogram typical for cladistics

Whereas Linnaeus classified for ease of identification, the idea of the Linnaean taxonomy as translating into a sort of dendrogram of the Animal- and Plant Kingdoms was formulated toward the end of the 18th century, well before the *On the Origin of Species* was published. Among early works exploring the idea of a transmutation of species was Erasmus Darwin's 1796 Zoönomia and Jean-Baptiste Lamarck's Philosophie Zoologique of 1809. The idea was popularised in the Anglophone world by the speculative, but widely read Vestiges of the Natural History of Creation, published anonymously by Robert Chambers in 1844.

With Darwin's theory, a general acceptance that classification should reflect the Darwinian principle of common descent quickly appeared. Tree of Life representations became popular in scientific works, with known fossil groups incorporated. One of the first fossil groups to be tied to an existing group was dinosaurs, formally named by Richard Owen in 1842. Using the then newly discovered fossils of *Archaeopteryx* and *Hesperornis*, Thomas Henry Huxley pronounce the birds descendants of the dinosaurs. The resulting description, that of dinosaurs "giving rise to" or being "the ancestors of" birds, is the essential hallmark of evolutionary taxonomic thinking. As more and more fossil groups were found and recognized in the late 19th and early 20th century, palaeontologists worked to understand the history of animals through the ages by linking together known groups With the modern evolutionary synthesis of the early 1940s, an essentially modern understanding of evolution of the major groups was in place. The evolutionary taxonomy being based on Linnaean taxonomic ranks, the two terms are largely interchangeable in modern use.

Since the 1960s a trend called cladistic taxonomy (or cladistics or cladism) has emerged, arranging taxa in a hierarchical evolutionary tree, ignoring ranks. If a taxon includes all the descendants of some ancestral form, it is called monophyletic. Groups that have descendant groups removed from them (e.g. dinosaurs, with birds as offspring group) are termed paraphyletic, while groups representing more than one branch from the tree of life (science) are called polyphyletic. A formal code of nomenclature, the *International Code of Phylogenetic Nomenclature*, or *PhyloCode* for short, is currently under development, intended to deal with names of clades. Linnaean ranks will be optional under the *PhyloCode*, which is intended to coexist with the current, rank-based codes.

Kingdoms and domains

From well before Linnaeus, plants and animals were considered separate Kingdoms. Linnaeus used this as the top rank, dividing the physical world into the plant, animal and mineral kingdoms. As advances in microscopy made classification of microorganisms possible, the number of kingdoms increased, five and six-kingdom systems being the most common.

Domains are a relatively new grouping. The three-domain system was first invented in 1990, but not generally accepted until later. One main characteristic of the three-domain method is the separation of Archaea and Bacteria, previously grouped into the single kingdom Bacteria (a kingdom also sometimes called Monera). Consequently, the three domains of life are conceptualized as Archaea, Bacteria, and Eukaryota (comprising the nuclei-bearing eukaryotes). A small minority of scientists add Archaea as a sixth kingdom, but do not accept the domain method.

Thomas Cavalier-Smith, who has published extensively on the classification of protists, has recently proposed that the Neomura, the clade that groups together the Archaea and Eukarya, would have evolved from Bacteria, more precisely from Actinobacteria. His classification of 2004 treats the archaebacteria as part of a subkingdom of the Kingdom Bacteria, i.e. he rejects the three-domain system entirely.

Linnaeus 1735 2 kingdoms	**Haeckel 1866 3 kingdoms**	**Chatton 1925 2 empires**	**Copeland 1938 4 kingdoms**	**Whittaker 1969 5 kingdoms**	**Woese et al. 1977 6 kingdoms**	**Woese et al. 1990 3 domains**	**Cavalier-Smith 2004 6 kingdoms**
(not treated)	Protista	Prokaryota	Mychota	Monera	Eubacteria	Bacteria	Bacteria
					Archaebacteria	Archaea	
		Eukaryota	Protoctista	Protista	Protista	Eukarya	Protozoa
							Chromista
Vegetabilia	Plantae		Plantae	Plantae	Plantae		Plantae
			Protoctista	Fungi	Fungi		Fungi
Animalia	Animalia		Animalia	Animalia	Animalia		Animalia

Authorities (author citation)

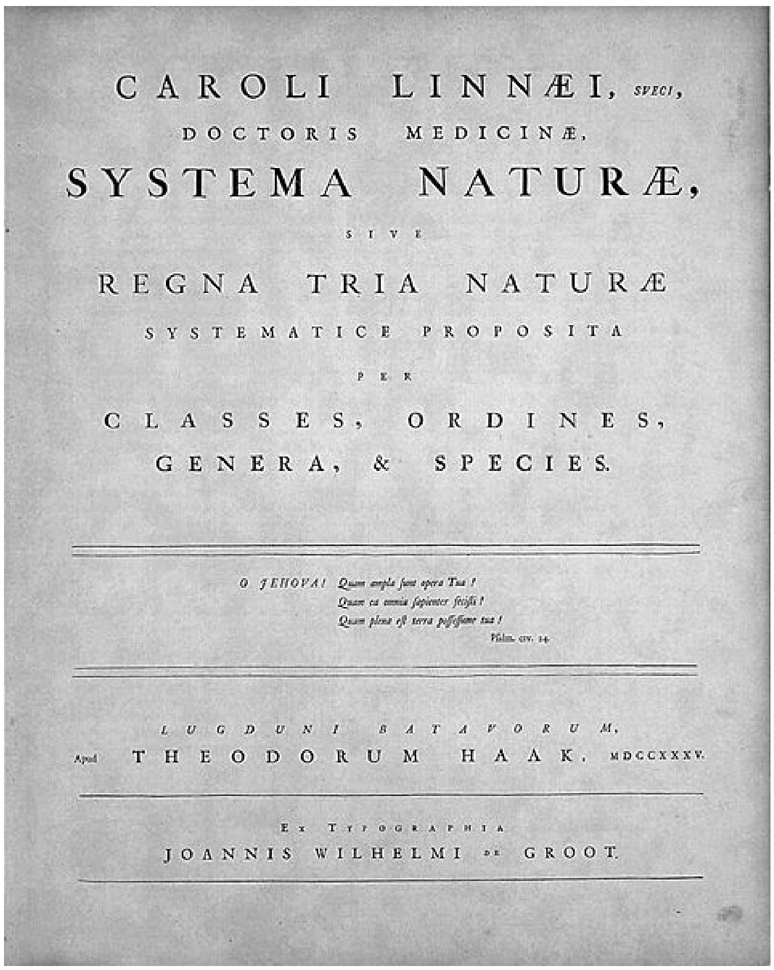
The name of any taxon may be followed by the "authority" for the name, that is, the name of the author who first published a valid description of it. These names are frequently abbreviated: the abbreviation "L." is universally accepted for Linnaeus, and in botany there is a regulated list of standard abbreviations. The system for assigning authorities is slightly different in different branches of biology. However, it is standard that if a name or placement has been changed since the original description, the first authority's name is placed in parentheses and the authority for the new name or placement may be placed after it (usually only in botany and zoology).

Globally Unique Identifiers for names

There is a movement within the biodiversity informatics community to provide Globally Unique Identifiers in the form of Life Science Identifiers (LSID) for all biological names. This would allow authors to cite names unambiguously in electronic media and reduce the significance of errors in the spelling of names or the abbreviation of authority names. Three large nomenclatural databases (referred to as nomenclators) have already begun this process, these are Index Fungorum, International Plant Names Index and ZooBank. Other databases, that publish taxonomic rather than nomenclatural data, have also started using LSIDs to identify **taxa**. The key example of this is Catalogue of Life. The next step in integration will be when these taxonomic databases include references to the nomenclatural databases using LSIDs.

Chapter 2

Linnaean Taxonomy


CAROLI LINNÆI, SVECI,
DOCTORIS MEDICINÆ,
SYSTEMA NATURÆ,
SIVE
REGNA TRIA NATURÆ
SYSTEMATICE PROPOSITA
PER
CLASSES, ORDINES,
GENERA, & SPECIES.

O JEHOVA! Quam ampla sunt opera Tua!
Quam ea omnia sapienter fecisti!
Quam plena est terra possessione tua!
Psalm. civ. 24.

LUGDUNI BATAVORUM,
Apud THEODORUM HAAK, MDCCXXXV.

Ex Typographia
JOANNIS WILHELMI DE GROOT.

Title page of *Systema Naturae*, Leiden, 1735

Linnaean taxonomy

1. the particular form of biological classification (taxonomy) of Carl Linnaeus, as set forth in his *Systema Naturæ* (1735) and subsequent works. In the taxonomy of

Linnaeus there are three kingdoms, divided into *classes*, and they, in turn, into *orders*, *genera* (singular: *genus*), and *species* (singular: *species*), with an additional rank lower than species.

2. a term for rank-based classification of organisms, in general. That is, taxonomy in the traditional sense of the word: rank-based scientific classification. This term is especially used as opposed to cladistic systematics, which groups organisms into clades. It is attributed to Linnaeus, although he neither invented the concept of ranked classification (it goes back to Aristotle) nor gave it its present form. In fact, it does not have an exact present form, as "Linnaean taxonomy" as such does not really exist: it is a collective (abstracting) term for what actually are several separate fields, which use similar approaches.

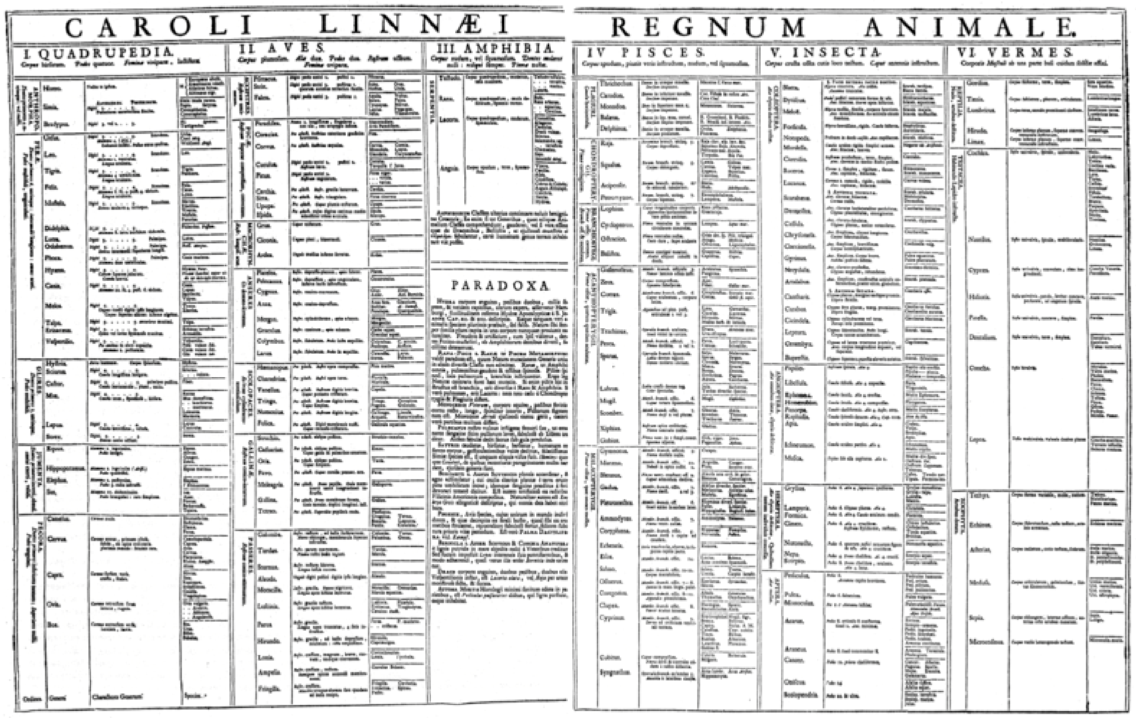
The same applies to "Linnaean name": depending on the context this may either be a formal name given by Linnaeus (personally), such as *Giraffa camelopardalis* Linnaeus, 1758, or a formal name in the accepted nomenclature (as opposed to a modernistic clade name).

The taxonomy of Linnaeus

In his *Imperium Naturae*, Linnaeus established three kingdoms, namely *Regnum Animale*, *Regnum Vegetabile* and *Regnum Lapideum*. This approach, the Animal, Vegetable and Mineral Kingdoms, survives today in the popular mind, notably in the form of the parlour game question: "Is it animal, vegetable or mineral?".

The work of Linnaeus had a huge impact on science; it was indispensable as a foundation for biological nomenclature, now regulated by the Nomenclature Codes. Two of his works, the first edition of the *Species Plantarum* (1753) for plants and the tenth edition of the *Systema Naturae* (1758), are accepted as among the starting points of nomenclature; his binomials (names for species) and his generic names take priority over those of others. However, the impact he had on science was not because of the value of his taxonomy.

For animals



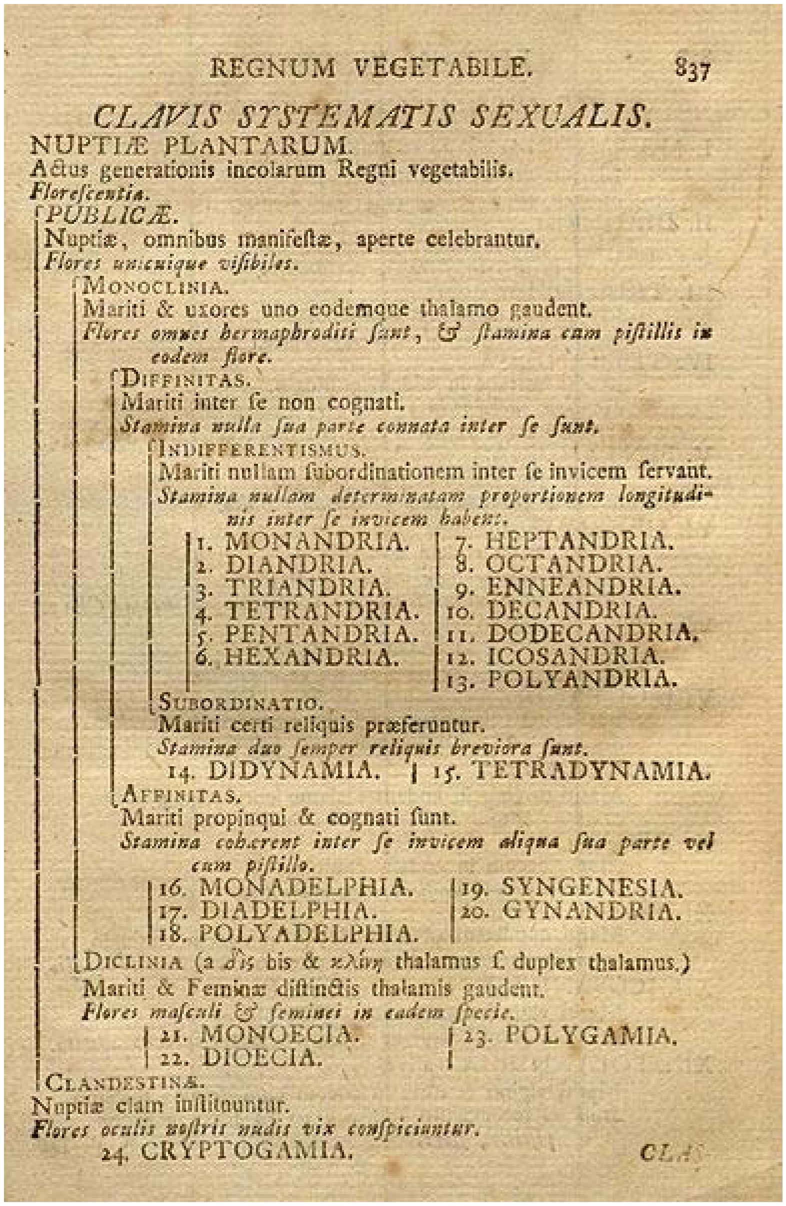
The 1735 classification of animals

Only in the Animal Kingdom is the higher taxonomy of Linnaeus still more or less recognizable and some of these names are still in use, but usually not quite for the same groups as used by Linnaeus. He divided the Animal Kingdom into six classes, in the tenth edition, of 1758, these were:

- Classis 1. Mammalia
- Classis 2. Aves
- Classis 3. Amphibia
- Classis 4. Pisces
- Classis 5. Insecta
- Classis 6. Vermes

For plants

His orders and classes of plants, according to his *Systema Sexuale*, were never intended to represent natural groups (as opposed to his *ordines naturales* in his *Philosophia Botanica*) but only for use in identification. They were used in that sense well into the nineteenth century.



REGNUM VEGETABILE. 837

CLAVIS SYSTEMATIS SEXUALIS.

NUPTIÆ PLANTARUM.
Actus generationis incolarum Regni vegetabilis.
Floreſcentia.

PUBLICÆ.
Nuptiæ, omnibus manifeſtæ, aperte celebrantur.
Flores unicuique viſibiles.

MONOCLINIA.
Mariti & uxores uno eodemque thalamo gaudent.
Flores omnes hermaphroditi ſunt, & ſtamina cum piſtillis in eodem flore.

DIFFINITAS.
Mariti inter ſe non cognati.
Stamina nulla ſua parte connata inter ſe ſunt.

INDIFFERENTISMUS.
Mariti nullam ſubordinationem inter ſe invicem ſervant.
Stamina nullam determinatam proportionem longitudinis inter ſe invicem habent.

1. MONANDRIA.
2. DIANDRIA.
3. TRIANDRIA.
4. TETRANDRIA.
5. PENTANDRIA.
6. HEXANDRIA.
7. HEPTANDRIA.
8. OCTANDRIA.
9. ENNEANDRIA.
10. DECANDRIA.
11. DODECANDRIA.
12. ICOSANDRIA.
13. POLYANDRIA.

SUBORDINATIO.
Mariti certi reliquis præferuntur.
Stamina duo ſemper reliquis breviora ſunt.

14. DIDYNAMIA.
15. TETRADYNAMIA.

AFFINITAS.
Mariti propinqui & cognati ſunt.
Stamina cohærent inter ſe invicem aliqua ſua parte vel cum piſtillo.

16. MONADELPHIA.
17. DIADELPHIA.
18. POLYADELPHIA.
19. SYNGENESIA.
20. GYNANDRIA.

DICLINIA (a δὶς bis & κλίνη thalamus ſ. duplex thalamus.)
Mariti & Feminæ diſtinctis thalamis gaudent.
Flores maſculi & feminei in eadem ſpecie.

21. MONOECIA.
22. DIOECIA.
23. POLYGAMIA.

CLANDESTINÆ.
Nuptiæ clam inſtituuntur.
Flores oculis noſtris nudis vix conſpiciuntur.

24. CRYPTOGAMIA.

CLAS-

Key to the Sexual System (from the 10th, 1758, edition of the *Systema Naturae*)

The Linnaean classes for plants, in the Sexual System, were:

- Classis 1. Monandria
- Classis 2. Diandria
- Classis 3. Triandria
- Classis 4. Tetrandria
- Classis 5. Pentandria
- Classis 6. Hexandria
- Classis 7. Heptandria
- Classis 8. Octandria
- Classis 9. Enneandria

- Classis 10. Decandria
- Classis 11. Dodecandria
- Classis 12. Icosandria
- Classis 13. Polyandria
- Classis 14. Didynamia
- Classis 15. Tetradynamia
- Classis 16. Monadelphia
- Classis 17. Diadelphia
- Classis 18. Polyadelphia
- Classis 19. Syngenesia
- Classis 20. Gynandria
- Classis 21. Monoecia
- Classis 22. Dioecia
- Classis 23. Polygamia
- Classis 24. Cryptogamia

For minerals

His taxonomy of minerals has dropped long since from use. In the tenth edition, 1758, of the *Systema Naturæ*, the Linnaean classes were:

- Classis 1. Petræ
- Classis 2. Mineræ
- Classis 3. Fossilia
- Classis 4. Vitamentra

Rank-based scientific classification

This rank-based method of classifying living organisms was originally popularized by (and much later named for) Linnaeus, although it has changed considerably since his time. The greatest innovation of Linnaeus, and still the most important aspect of this system, is the general use of binomial nomenclature, the combination of a genus name and a second term, which together uniquely identify each species of organism. For example, the human species is uniquely identified by the name *Homo sapiens*. No other species of organism can have this same binomen (the technical term for a binomial in the case of animals). Prior to Linnaean taxonomy, animals were classified according to their mode of movement.

A strength of Linnaean taxonomy is that it can be used to organize the different kinds of living organisms, simply and practically. Every species can be given a unique (and, one hopes, stable) name, as compared with common names that are often neither unique nor consistent from place to place and language to language. This uniqueness and stability are, of course, a result of the acceptance by working systematists (biologists specializing in taxonomy), not merely of the binomial names themselves, but of the rules governing the use of these names, which are laid down in formal Nomenclature Codes.

Species can be placed in a ranked hierarchy, starting with either *domains* or *kingdoms*. Domains are divided into kingdoms. Kingdoms are divided into *phyla* (singular: *phylum*) — for animals; the term *division*, used for plants and fungi, is equivalent to the rank of phylum (and the current International Code of Botanical Nomenclature allows the use of either term). Phyla (or divisions) are divided into *classes*, and they, in turn, into *orders*, *families*, *genera* (singular: *genus*), and *species* (singular: *species*). There are ranks below species: in zoology, *subspecies*; in botany, *variety* (varietas) and *form* (forma), etc.

Groups of organisms at any of these ranks are called *taxa* (singular: *taxon*) or *taxonomic groups*.

The Linnaean system has proven robust and it remains the only extant working classification system at present that enjoys universal scientific acceptance. However, although the number of ranks is unlimited, in practice any classification becomes more cumbersome the more ranks are added. Among the later subdivisions that have arisen are such entities as phyla, families, and tribes, as well as any number of ranks with prefixes (superfamilies, subfamilies, etc.). The use of newer taxonomic tools such as cladistics and phylogenetic nomenclature has led to a different way of looking at evolution (expressed in many nested clades) and this sometimes leads to a desire for more ranks.

The alternative

Over time, the understanding of the relationships between living things has changed. Linnaeus could only base his scheme on the structural similarities of the different organisms. The greatest change was the widespread acceptance of evolution as the mechanism of biological diversity and species formation, following the 1859 publication of Charles Darwin's *On the Origin of Species*. It then became generally understood that classifications ought to reflect the phylogeny of organisms, their descent by evolution. This led to evolutionary taxonomy, where the various extant and extinct are linked together to construct a phylogeny. This is largely what is meant by the term 'Linnaean taxonomy' when used in a modern context.

In cladistics, originating in the work of Willi Hennig, 1950 onwards, each taxon is grouped so as to include the common ancestor of the group's members (and thus to avoid polyphyly). Such taxa may be either monophyletic (including all descendants) such as genus *Homo*, or paraphyletic (excluding some descendants), such as genus *Australopithecus*.

Originally, Linnaeus established three kingdoms in his scheme, namely for Plants, Animals and an additional group for minerals, which has long since been abandoned. Since then, various life forms have been moved into three new kingdoms: Monera, for prokaryotes (i.e., bacteria); Protista, for protozoans and most algae; and Fungi. This five kingdom scheme is still far from the phylogenetic ideal and has largely been supplanted in modern taxonomic work by a division into three domains: Bacteria and Archaea, which contain the prokaryotes, and Eukaryota, comprising the remaining forms. These arrangements should not be seen as definitive. They are based on the genomes of the organisms; as knowledge on this increases, so will classifications change.

Representing presumptive evolutionary relationships, especially given the wide acceptance of cladistic methodology and numerous molecular phylogenies that have challenged long-accepted classifications, within the framework of Linnaean taxonomy, is sometimes seen as problematic. Therefore, some systematists have proposed a PhyloCode to replace it.

Chapter 3

Taxonomic Rank

In biological classification, **rank** is the level (the relative position) in a taxonomic hierarchy. Examples of taxonomic ranks are species, genus, family, and class. Each rank subsumes under it a number of less general categories. The rank of *species*, and specification of the *genus* to which the species belongs is *basic*, which means that it may not be necessary to specify ranks other than these. The *International Code of Zoological Nomenclature* defines rank as:

The level, for nomenclatural purposes, of a taxon in a taxonomic hierarchy (e.g. all families are for nomenclatural purposes at the same rank, which lies between superfamily and subfamily)

Significance

Ranks are assigned based on subjective dissimilarity, and do not fully reflect the gradational nature of variation within nature. In most cases, higher taxonomic groupings arise further back in time: not because the rate of diversification was higher in the past, but because each subsequent diversification event results in an increase of diversity and thus increases the taxonomic rank assigned by present-day taxonomists.

Main ranks

"2.1. Every individual plant is treated as belonging to an indefinite number of taxa of consecutively subordinate rank, among which the rank of species (species) is basic."

In his landmark publications, such as the *Systema Naturae*, Carl Linnaeus used a ranking scale limited to: kingdom, class, order, genus, species, and one rank below species. Today, nomenclature is regulated by the nomenclature codes, which allow names divided into an indefinite number of ranks. There are seven main taxonomic ranks: kingdom, phylum or division, class, order, family, genus, species. In addition, the *domain* (proposed by Carl Woese) is now widely used as one of the fundamental ranks, although it is not mentioned in any of the nomenclature codes.

Main taxonomic ranks	
Latin	English
regio	domain
regnum	kingdom
phylum *divisio*	phylum (in zoology) division (in botany)
classis	class
ordo	order
familia	family
genus	genus
species	species

A taxon is usually assigned a rank when it is given its formal name. The basic rank is that of species. The next most important rank is that of genus: when an organism is given a species name it is assigned to a genus, and the genus name is part of the species name. The third-most important rank, although it was not used by Linnaeus, is that of family.

The species name is sometimes called a binomial, that is, a two-term name. For example, the zoological name for the human species is *Homo sapiens*: this is usually italicized in print (and underlined when italics are not available). In this case, *Homo* is the generic name and refers to the genus; it is capitalized; *sapiens* indicates the species: it is not capitalized.

Ranks in zoology

There are definitions of the following taxonomic ranks in the International Code of Zoological Nomenclature: superfamily, family, subfamily, tribe, subtribe, genus, subgenus, species, subspecies.

The International Code of Zoological Nomenclature divides names into "family-group names", "genus-group names" and "species-group names". The Code explicitly mentions:

Superfamily

Family

Subfamily
Tribe
Subtribe

Genus

Subgenus

Species

Subspecies

The rules in the Code apply to the ranks of superfamily to subspecies, and only to some extent to those above the rank of superfamily. In the "genus group" and "species group" no further ranks are allowed. Among zoologists, additional terms such as *species group*, *species subgroup*, *species complex* and *superspecies* are sometimes used for convenience as extra, but unofficial, ranks between the subgenus and species levels in taxa with many species (e.g., the genus *Drosophila*).

At higher ranks (family and above) a lower level may be denoted by adding the prefix "*infra*", meaning *lower*, to the rank. For example *infra*order (below suborder) or *infra*family (below subfamily).

Names of zoological taxa

- A taxon above the rank of species gets a scientific name in one part (a uninominal name).
- A species gets a name composed of two parts (a binomial name or binomen): generic name + specific name; for example *Canis lupus*.
- A subspecies gets a name composed of three parts (a trinomial name or trinomen): generic name + specific name + subspecific name; for example *Canis lupus familiaris*. As there is only one rank below that of species, no connecting term to indicate rank is used.

Ranks in botany

There are definitions of the following taxonomic ranks in the International Code of Botanical Nomenclature (ICBN): kingdom (regnum), subregnum, division or phylum (divisio, phylum), subdivisio or subphylum, class (classis), subclassis, order (ordo), subordo, family (familia), subfamilia, tribe (tribus), subtribus, genus (genus), subgenus, section (sectio), subsectio, series (series), subseries, species (species), subspecies, variety (varietas), subvarietas, form (forma), subforma.

There are definitions of following taxonomic ranks in International Code of Nomenclature for Cultivated Plants: cultivar group, cultivar.

According to Art 3.1 of the ICBN the most important ranks of taxa are: kingdom, division or phylum, class, order, family, genus, and species. According to Art 4.1 the secondary ranks of taxa are tribe, section, series, variety and form. There is an indeterminate number of ranks. The ICBN explicitly mentions:

primary ranks

secondary ranks
further ranks

kingdom (*regnum*)

subregnum

division or **phylum** (*divisio*, *phylum*)

subdivisio or *subphylum*

class (*classis*)

subclassis

order (*ordo*)

subordo

family (*familia*)

subfamilia
tribe (*tribus*)
subtribus

genus (*genus*)

subgenus
section (*sectio*)
subsectio
series (*series*)
subseries

species (*species*)

subspecies
variety (*varietas*)
subvarietas
form (*forma*)
subforma

The rules in the ICBN apply primarily to the ranks of family and below, and only to some extent to those above the rank of family.

Names of botanical taxa

Of the botanical names used by Linnaeus only names of genera, species and varieties are still used.

Taxa at the rank of genus and above get a botanical name in one part (unitary name); those at the rank of species and above (but below genus) get a botanical name in two parts (binary name); all taxa below the rank of species get a botanical name in three parts (ternary name).

For hybrids getting a hybrid name, the same ranks apply, preceded by "notho", with nothogenus as the highest permitted rank. (The hybrid's nothotaxon is an alias for a list of all of the taxa which are ancestral to the hybrid.)

Out-dated names for botanical ranks

If a different term for the rank was used in an in old publication, but the intention is clear, botanical nomenclature specifies certain substitutions:

- If names were "intended as names of orders, but published with their rank denoted by a term such as": "cohors" [Latin for "cohort"], "nixus", "alliance", or "Reihe" instead of "order" (Article 17.2), they are treated as names of orders.
- "Family" is substituted for "order" (ordo) or "natural order" (ordo naturalis) under certain conditions where the modern meaning of "order" was not intended. (Article 18.2)
- "Subfamily is substituted for "suborder" (subordo) under certain conditions where the modern meaning of "suborder" was not intended. (Article 19.2)
- In a publication prior to 1 January 1890, if only one infraspecific rank is used, it is considered to be that of variety. (Article 35.4) This commonly applies to publications that labelled infraspecific taxa with Greek letters, α, β, γ, ...

Examples

Classifications of five species follow: the fruit fly so familiar in genetics laboratories (*Drosophila melanogaster*), humans (*Homo sapiens*), the peas used by Gregor Mendel in his discovery of genetics (*Pisum sativum*), the "fly agaric" mushroom *Amanita muscaria*, and the bacterium *Escherichia coli*. The eight major ranks are given in bold; a selection of minor ranks are given as well.

Rank	**Fruit fly**	**Human**	**Pea**	**Fly Agaric**	***E. coli***
Domain	Eukarya	Eukarya	Eukarya	Eukarya	Bacteria
Kingdom	Animalia	Animalia	Plantae	Fungi	Bacteria
Phylum or **Division**	Arthropoda	Chordata	Magnoliophyta	Basidiomycota	Proteobacteria
Subphylum or subdivision	Hexapoda	Vertebrata	Magnoliophytina	Agaricomycotina	
Class	Insecta	Mammalia	Magnoliopsida	Agaricomycetes	Gammaproteobacteria
Subclass	Pterygota	Theria	Rosidae	Agaricomycetidae	
Order	Diptera	Primates	Fabales	Agaricales	Enterobacteriales
Suborder	Brachycera	Haplorrhini	Fabineae	Agaricineae	
Family	Drosophilidae	Hominidae	Fabaceae	Amanitaceae	Enterobacteriaceae
Subfamily	Drosophilinae	Homininae	Faboideae	Amanitoideae	
Genus	*Drosophila*	*Homo*	*Pisum*	*Amanita*	*Escherichia*
Species	*D. melanogaster*	*H. sapiens*	*P. sativum*	*A. muscaria*	*E. coli*

Notes:

- The ranks of higher taxa, especially intermediate ranks, are prone to revision as new information about relationships is discovered. For example, the traditional classification of primates (class Mammalia — subclass Theria — infraclass Eutheria — order Primates) has been modified by new classifications such as McKenna and Bell (class Mammalia — subclass Theriformes — infraclass Holotheria) with Theria and Eutheria assigned lower ranks between infraclass and the order Primates. These differences arise because there are only a small number of ranks available and a large number of branching points in the fossil record.
- Within species further units may be recognised. Animals may be classified into subspecies (for example, *Homo sapiens sapiens*, modern humans) or morphs (for example *Corvus corax varius* morpha *leucophaeus*, the Pied Raven). Plants may be classified into subspecies (for example, *Pisum sativum* subsp. *sativum*, the garden pea) or varieties (for example, *Pisum sativum* var. *macrocarpon*, snow pea), with cultivated plants getting a cultivar name (for example, *Pisum sativum* var. *macrocarpon* 'Snowbird'). Bacteria may be classified by strains (for example *Escherichia coli* O157:H7, a strain that can cause food poisoning).

All ranks

There is an indeterminate number of ranks, as a taxonomist may invent a new rank at will, at any time, if they feel this is necessary. In doing so, there are some restrictions, which will vary with the nomenclature code which applies.

The following is an artificial synthesis, solely for purposes of demonstration of relative rank, from most general to most specific:

- **Domain** *or* **Empire**
  - **Kingdom**
    - Subkingdom
      - Branch
        - Infrakingdom
- Superphylum (*or* Superdivision *in botany*)
  - **Phylum** (*or* **Division** *in botany*)
    - Subphylum (*or* Subdivision *in botany*)
      - Infraphylum (*or* Infradivision *in botany*)
        - Microphylum
- Supercohort (*botany*)
  - Cohort (*botany*)
    - Subcohort (*botany*)

            - Infracohort (*botany*)

- Superclass

  - **Class**
    - Subclass
      - Infraclass
        - Parvclass

- Superdivision (*zoology*)

  - Division (*zoology*)
    - Subdivision (*zoology*)
      - Infradivision (*zoology*)

- Superlegion (*zoology*)

  - Legion (*zoology*)
    - Sublegion (*zoology*)
      - Infralegion (*zoology*)

- Supercohort (*zoology*)

  - Cohort (*zoology*)
    - Subcohort (*zoology*)
      - Infracohort (*zoology*)

- Gigaorder (*zoology*)

  - Magnorder *or* Megaorder (*zoology*)

Grandorder *or* Capaxorder (*zoology*)

  - Mirorder *or* Hyperorder (*zoology*)
    - Superorder
      - Series (*for fishes*)
        - **Order**

Parvorder (*position in some zoological classifications*)

  - Nanorder (*zoology*)
    - Hypoorder (*zoology*)
      - Minorder (*zoology*)
        - Suborder

  - Infraorder

- Parvorder (*usual position*) *or* Microorder (*zoology*)

- Section (*zoology*)
  - Subsection (*zoology*)
- Gigafamily (*zoology*)
  - Megafamily (*zoology*)
    - Grandfamily (*zoology*)
      - Hyperfamily (*zoology*)
        - Superfamily

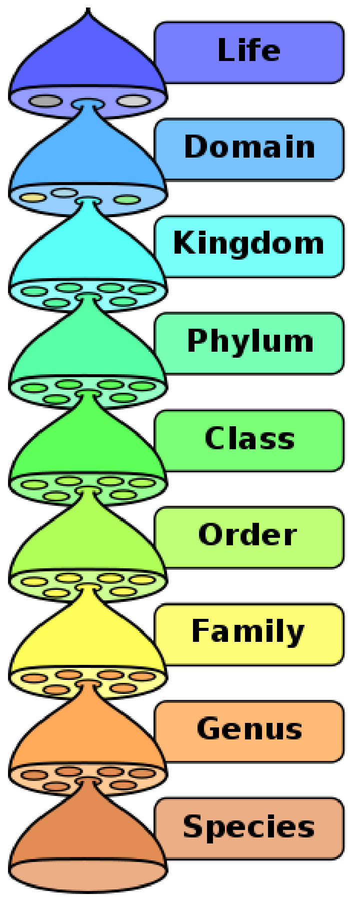
Epifamily (*zoology*)

- Series (*for Lepidoptera*)
  - Group (*for Lepidoptera*)
    - **Family**
      - Subfamily
        - Infrafamily
- Supertribe
  - Tribe
    - Subtribe
      - Infratribe
- **Genus**
  - Subgenus
    - Section (*botany*)
      - Subsection (*botany*)
        - Series (*botany*)
          - Subseries (*botany*)
- Superspecies *or* Species-group
  - **Species**
    - Subspecies (*or* Forma Specialis *for fungi, or* Variety *for bacteria*)
      - Variety (*botany*) or Form/Morph (*zoology*)
        - Subvariety (*botany*)
          - Form (*botany*)
            - Subform (*botany*)

Of these many ranks, the most basic is species. However, this is not to say that a taxon at any other rank may not be sharply defined, or that any species is guaranteed to be sharply defined. It varies from case to case. Ideally, nowadays, a taxon is intended to represent the phylogeny of the organisms under discussion, but in itself this is not a requirement.

Chapter 4

Species



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. A genus contains one or more species. Intermediate minor rankings are not shown.

In biology, a **species** is one of the basic units of biological classification and a taxonomic rank. A species is often defined as a group of organisms capable of interbreeding and producing fertile offspring. While in many cases this definition is adequate, more precise or differing measures are often used, such as similarity of DNA, morphology or ecological niche. Presence of specific locally adapted traits may further subdivide species into subspecies.

The commonly used names for plant and animal taxa sometimes correspond to species: for example, "lion," "walrus," and "Camphor tree" – each refers to a species. In other cases common names do not: for example, "deer" refers to a family of 34 species, including Eld's Deer, Red Deer and Elk (Wapiti). The last two species were once considered a single species, illustrating how species boundaries may change with increased scientific knowledge.

Species that are believed to have the same ancestors are grouped together, and this group is called a genus. A species can only belong to one genus that it was grouped into. The belief is best checked by a similarity of their DNA, but for practical reasons, other similar properties are used. For plants similarities of flowers are used. All species are given a two part name (called a "binomial name" - "bi" for two, "nomial" for name). The first part of a binomial name is the generic name, the genus of the species. The second part is the specific name (or specific epithet). For example, *Boa constrictor*, which is commonly called by its bionomial name, and is one of five species of the *Boa* genus. The first part of the name is capitalized, and the second part has a lower case. The two part name is written in italics.

A usable definition of the word "species" and reliable methods of identifying particular species are essential for stating and testing biological theories and for measuring biodiversity. Traditionally, multiple examples of a proposed species must be studied for unifying characters before it can be regarded as a species. Extinct species known only from fossils are generally difficult to assign precise taxonomic rankings.

Because of the difficulties with both defining and tallying the total numbers of different species in the world, it is estimated that there are anywhere between 2 and 100 million different species.

Biologists' working definition

A usable definition of the word "species" and reliable methods of identifying particular species is essential for stating and testing biological theories and for measuring biodiversity. Traditionally, multiple examples of a proposed species must be studied for unifying characters before it can be regarded as a species. It is generally difficult to give precise taxonomic rankings to extinct species known only from fossils.

Some biologists may view species as statistical phenomena, as opposed to the traditional idea, with a species seen as a class of organisms. In that case, a species is defined as a separately evolving lineage that forms a single gene pool. Although properties such as DNA-sequences and morphology are used to help separate closely related lineages, this definition has fuzzy boundaries. However, the exact definition of the term "species" is still controversial, particularly in prokaryotes, and this is called the species problem.

Biologists have proposed a range of more precise definitions, but the definition used is a pragmatic choice that depends on the particularities of the species of concern.

Common names and species

The commonly used names for plant and animal taxa sometimes correspond to species: for example, "lion", "walrus", and "Camphor tree" – each refers to a species. In other cases common names do not: for example, "deer" refers to a family of 34 species, including Eld's Deer, Red Deer and Elk (Wapiti). The last two species were once considered a single species, illustrating how species boundaries may change with increased scientific knowledge.

Because of the difficulties with both defining and tallying the total numbers of different species in the world, it is estimated that there are anywhere between 2 and 100 million different species.

Placement within genera

Ideally, a species is given a formal, scientific name, although in practice there are very many unnamed species (which have only been described, not named). When a species is named, it is placed within a genus. From a scientific point of view this can be regarded as a hypothesis that the species is more closely related to other species within its genus (if any) than to species of other genera. Species and genus are usually defined as part of a larger taxonomic hierarchy. The best-known taxonomic ranks are, in order: life, domain, kingdom, phylum, class, order, family, genus, and species. This assignment to a genus is not immutable; later a different (or the same) taxonomist may assign it to a different genus, in which case the name will also change.

In biological nomenclature, the name for a species is a two-part name (a binomial name), treated as Latin, although roots from any language can be used as well as names of locales or individuals. The generic name is listed first (with its leading letter capitalized), followed by a second term, the specific name (or specific epithet). For example, the species commonly known as the Longleaf Pine is *Pinus palustris*; gray wolves belong to the species *Canis lupus*, coyotes to *Canis latrans*, golden jackals to *Canis aureus*, etc., and all of those belong to the genus *Canis* (which also contains many other species). The name of the species is the whole binomial, not just the second term (which may be called the specific name for animals).

This binomial naming convention, later formalized in the biological codes of nomenclature, was first used by Leonhart Fuchs and introduced as the standard by Carolus Linnaeus in his 1753, *Species Plantarum* (followed by his, 1758 *Systema Naturae*, 10th edition). At that time, the chief biological theory was that species represented independent acts of creation by God and were therefore considered objectively real and immutable, so the hypothesis of common descent did not apply.

Abbreviated names

Books and articles sometimes intentionally do not identify species fully and use the abbreviation "**sp.**" in the singular or "**spp.**" in the plural in place of the specific epithet: for example, ***Canis*** **sp.** This commonly occurs in the following types of situations:

- The authors are confident that some individuals belong to a particular genus but are not sure to which exact species they belong. This is particularly common in paleontology.
- The authors use "spp." as a short way of saying that something applies to many species within a genus, but do not wish to say that it applies to all species within that genus. If scientists mean that something applies to all species within a genus, they use the genus name without the specific epithet.

In books and articles, genus and species names are usually printed in italics. If using "sp." and "spp.", these should not be italicized.

Difficulty of defining "species" and identifying particular species

The Greenish Warbler demonstrates the concept of a ring species.

It is surprisingly difficult to define the word "species" in a way that applies to all naturally occurring organisms, and the debate among biologists about how to define "species" and how to identify actual species is called the species problem. Over two dozen distinct definitions of "species" are in use amongst biologists.

Most textbooks follow Ernst Mayr's definition of a species as "groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups".

Various parts of this definition serve to exclude some unusual or artificial matings:

- Those that occur only in captivity (when the animal's normal mating partners may not be available) or as a result of deliberate human action

- Animals that may be physically and physiologically capable of mating but, for various reasons, do not normally do so in the wild

The typical textbook definition above works well for most multi-celled organisms, but there are several types of situations in which it breaks down:

- By definition it applies only to organisms that reproduce sexually. So it does not work for asexually reproducing single-celled organisms and for the relatively few parthenogenetic multi-celled organisms. The term "phylotype" is often applied to such organisms.
- Biologists frequently do not know whether two morphologically similar groups of organisms are "potentially" capable of interbreeding.
- There is considerable variation in the degree to which hybridization may succeed under natural conditions, or even in the degree to which some organisms use sexual reproduction between individuals to breed.
- In ring species, members of adjacent populations interbreed successfully but members of some non-adjacent populations do not.
- In a few cases it may be physically impossible for animals that are members of the same species to mate. However, these are cases in which human intervention has caused gross morphological changes, and are therefore excluded by the biological species concept.

Horizontal gene transfer makes it even more difficult to define the word "species". There is strong evidence of horizontal gene transfer between very dissimilar groups of prokaryotes, and at least occasionally between dissimilar groups of eukaryotes; and Williamson argues that there is evidence for it in some crustaceans and echinoderms. All definitions of the word "species" assume that an organism gets all its genes from one or two parents that are very like that organism, but horizontal gene transfer makes that assumption false.

Definitions of species

The question of how best to define "species" is one that has occupied biologists for centuries, and the debate itself has become known as the species problem. Darwin wrote in chapter II of *On the Origin of Species*:

No one definition has satisfied all naturalists; yet every naturalist knows vaguely what he means when he speaks of a species. Generally the term includes the unknown element of a distinct act of creation.

But later, in *The Descent of Man*, when addressing "The question whether mankind consists of one or several species", Darwin revised his opinion to say:

it is a hopeless endeavour to decide this point on sound grounds, until some definition of the term "species" is generally accepted; and the definition must not include an element that cannot possibly be ascertained, such as an act of creation.

The modern theory of evolution depends on a fundamental redefinition of "species". Prior to Darwin, naturalists viewed species as ideal or general types, which could be exemplified by an ideal specimen bearing all the traits general to the species. Darwin's theories shifted attention from uniformity to variation and from the general to the particular. According to intellectual historian Louis Menand,

Once our attention is redirected to the individual, we need another way of making generalizations. We are no longer interested in the conformity of an individual to an ideal type; we are now interested in the relation of an individual to the other individuals with which it interacts. To generalize about groups of interacting individuals, we need to drop the language of types and essences, which is prescriptive (telling us what finches should be), and adopt the language of statistics and probability, which is predictive (telling us what the average finch, under specified conditions, is likely to do). Relations will be more important than categories; functions, which are variable, will be more important than purposes; transitions will be more important than boundaries; sequences will be more important than hierarchies.

This shift results in a new approach to "species"; Darwin

concluded that species are what they appear to be: ideas, which are provisionally useful for naming groups of interacting individuals. "I look at the term species", he wrote, "as one arbitrarily given for the sake of convenience to a set of individuals closely resembling each other ... It does not essentially differ from the word variety, which is given to less distinct and more fluctuating forms. The term variety, again, in comparison with mere individual differences, is also applied arbitrarily, and for convenience sake."

Practically, biologists define species as *populations of organisms that have a high level of genetic similarity*. This may reflect an adaptation to the same niche, and the transfer of genetic material from one individual to others, through a variety of possible means. The exact level of similarity used in such a definition is arbitrary, but this is the most common definition used for organisms that reproduce asexually (asexual reproduction), such as some plants and microorganisms.

This lack of any clear species concept in microbiology has led to some authors arguing that the term "species" is not useful when studying bacterial evolution. Instead they see genes as moving freely between even distantly related bacteria, with the entire bacterial domain being a single gene pool. Nevertheless, a kind of rule of thumb has been established, saying that species of *Bacteria* or *Archaea* with 16S rRNA gene sequences more similar than 97% to each other need to be checked by DNA-DNA Hybridization if they belong to the same species or not. This concept has been updated recently, saying that the border of 97% was too low and can be raised to 98.7%.

In the study of sexually reproducing organisms, where genetic material is shared through the process of reproduction, the ability of two organisms to interbreed and produce fertile offspring of both sexes is generally accepted as a simple indicator that the organisms share enough genes to be considered members of the same species. Thus a "species" is a group of interbreeding organisms.

This definition can be extended to say that a species is a group of organisms that could potentially interbreed – fish could still be classed as the same species even if they live in different lakes, as long as they could still interbreed were they ever to come into contact with each other. On the other hand, there are many examples of series of three or more distinct populations, where individuals of the population in the middle can interbreed with the populations to either side, but individuals of the populations on either side cannot interbreed. Thus, one could argue that these populations constitute a single species, or two distinct species. This is not a paradox; it is evidence that species are defined by gene frequencies, and thus have fuzzy boundaries.

Consequently, any single, universal definition of "species" is necessarily arbitrary. Instead, biologists have proposed a range of definitions; which definition a biologists uses is a pragmatic choice, depending on the particularities of that biologist's research.

Typological species

A group of organisms in which individuals are members of the species if they sufficiently conform to certain fixed properties or "rights of passage". The clusters of variations or phenotypes within specimens (i.e. longer or shorter tails) would differentiate the species. This method was used as a "classical" method of determining species, such as with Linnaeus early in evolutionary theory. However, we now know that different phenotypes do not always constitute different species (e.g.: a 4-winged Drosophila born to a 2-winged mother is not a different species). Species named in this manner are called *morphospecies*.

Morphological species

A population or group of populations that differs morphologically from other populations. For example, we can distinguish between a chicken and a duck because they have different shaped bills and the duck has webbed feet. Species have been defined in this way since well before the beginning of recorded history. This species concept is highly criticized because more recent genetic data reveal that genetically distinct populations may look very similar and, contrarily, large morphological differences sometimes exist between very closely related populations. Nonetheless, most species known have been described solely from morphology.

Biological / Isolation species

A set of actually or potentially interbreeding populations. This is generally a useful formulation for scientists working with living examples of the higher taxa like mammals, fish, and birds, but more problematic for organisms that do not reproduce sexually. The results of breeding experiments done in artificial conditions may or may not reflect what would happen if the same organisms encountered each other in the wild, making it difficult to gauge whether or not the results of such experiments are meaningful in reference to natural populations.

Biological / reproductive species

Two organisms that are able to reproduce naturally to produce fertile offspring of both sexes. Organisms that can reproduce but almost always make infertile hybrids of at least one sex, such as a mule, hinny or F1 male cattalo are not considered to be the same species.

Recognition species

Based on shared reproductive systems, including mating behavior. The Recognition concept of species has been introduced by Hugh E. H. Paterson, after earlier work by Wilhelm Petersen.

Mate-recognition species

A group of organisms that are known to recognize one another as potential mates. Like the isolation species concept above, it applies only to organisms that reproduce sexually. Unlike the isolation species concept, it focuses specifically on pre-mating reproductive isolation.

Evolutionary / Darwinian species

A group of organisms that shares an ancestor; a lineage that maintains its integrity with respect to other lineages through both time and space. At some point in the progress of such a group, some members may diverge from the main population and evolve into a subspecies, a process that eventually will lead to the formation of a new full species if isolation (geographical or ecological) is maintained.

Phylogenetic (Cladistic)

A group of organisms that shares an ancestor; a lineage that maintains its integrity with respect to other lineages through both time and space. At some point in the progress of such a group, members may diverge from one another: when such a divergence becomes sufficiently clear, the two populations are regarded as separate species. This differs from evolutionary species in that the parent species goes extinct taxonomically when a new species evolve, the mother and daughter populations now forming two new species. Subspecies as such are not recognized under this approach; either a population is a phylogenetic species or it is not taxonomically distinguishable.

Ecological species

A set of organisms adapted to a particular set of resources, called a niche, in the environment. According to this concept, populations form the discrete phonetic clusters that we recognize as species because the ecological and evolutionary processes controlling how resources are divided up tend to produce those clusters.

Genetic species

Based on similarity of DNA of individuals or populations. Techniques to compare similarity of DNA include DNA-DNA hybridization, and genetic fingerprinting (or DNA barcoding).

Phenetic species

Based on phenotypes.

Microspecies

Species that reproduce without meiosis or fertilization so that each generation is genetically identical to the previous generation.

Cohesion species

Most inclusive population of individuals having the potential for phenotypic cohesion through intrinsic cohesion mechanisms. This is an expansion of the mate-recognition species concept to allow for post-mating isolation mechanisms; no matter whether populations can hybridize successfully, they are still distinct cohesion species if the amount of hybridization is insufficient to completely mix their respective gene pools.

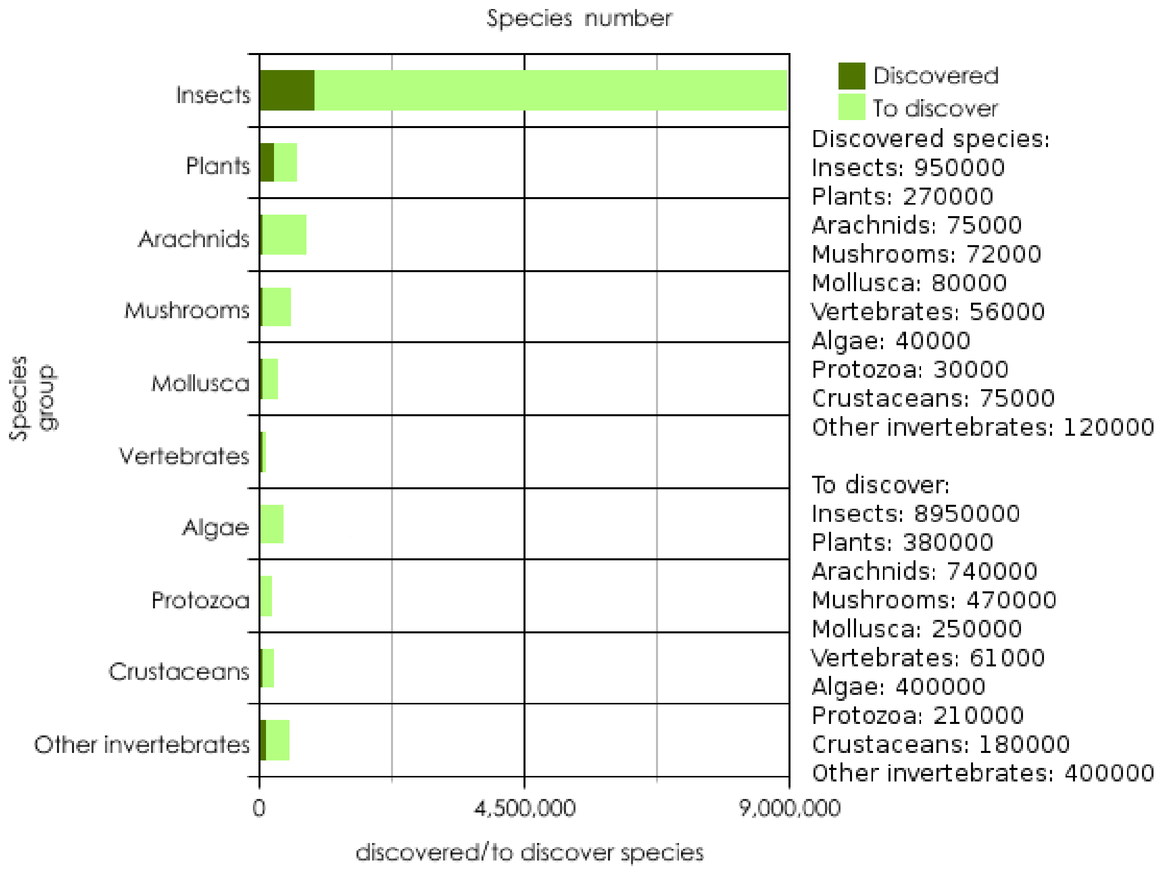
Evolutionarily Significant Unit (ESU)

An evolutionarily significant unit is a population of organisms that is considered distinct for purposes of conservation. Often referred to as a species or a *wildlife species*, an ESU also has several possible definitions, which coincide with definitions of species.

In practice, these definitions often coincide, and the differences between them are more a matter of emphasis than of outright contradiction. Nevertheless, no species concept yet proposed is entirely objective, or can be applied in all cases without resorting to judgment. Given the complexity of life, some have argued that such an objective definition is in all likelihood impossible, and biologists should settle for the most practical definition.

For most vertebrates, this is the biological species concept (BSC), and to a lesser extent (or for different purposes) the phylogenetic species concept (PSC). Many BSC subspecies are considered species under the PSC; the difference between the BSC and the PSC can be summed up insofar as that the BSC defines a species as a consequence of manifest evolutionary *history*, while the PSC defines a species as a consequence of manifest evolutionary *potential*. Thus, a PSC species is "made" as soon as an evolutionary lineage has started to separate, while a BSC species starts to exist only when the lineage separation is complete. Accordingly, there can be considerable conflict between alternative classifications based upon the PSC versus BSC, as they differ completely in their treatment of taxa that would be considered subspecies under the latter model (e.g., the numerous subspecies of honey bees).

Numbers of species



Undiscovered and discovered species

Bearing in mind the aforementioned problems with categorising species, the following numbers are only a soft guide. In 2007, they broke down as follows:

Total number of species (estimated): 7–100 millions (identified and unidentified), including:

- 5–10 million bacteria;
- 74,000–120,000 fungi;

Of the *identified* eukaryote species we have:

- 1.6 million, including:
  - 297,326 plants, including:
    - 15,000 mosses,
    - 13,025 Ferns and horsetails,
    - 980 gymnosperms,
    - 258,650 angiosperms,
      - 199,350 dicotyledons,

        - 59,300 monocotyledons,
    - 9,671 Red and green algae,
- 28,849 fungi & other non-animals, including:
    - 10,000 lichens,
    - 16,000 mushrooms,
    - 2,849 brown algae,
- 1,250,000 animals, including:
    - 1,203,375 invertebrates:
        - 950,000 insects,
        - 81,000 mollusks,
        - 40,000 crustaceans,
        - 2,175 corals,
        - 130,200 others;
    - 59,811 vertebrates:
        - 29,300 fish,
        - 6,199 amphibians,
        - 8,240 reptiles,
        - 9,956 birds,
        - 5,416 mammals

At present, organisations such as the Global Taxonomy Initiative, the European Distributed Institute of Taxonomy and the Census of Marine Life (the latter only for marine organisms) are trying to improve taxonomy and implement previously undiscovered species to the taxonomy system. Because we know but a portion of the organisms in the biosphere, we do not have a complete understanding of the workings of our environment. To make matters worse, despite the discovery of new species, according to professor James Mallet, we are wiping out these species at an unprecedented rate. This means that even before a new species has had the chance of being studied and classified, it may already be extinct.

Importance in biological classification

The idea of *species* has a long history. It is one of the most important levels of classification, for several reasons:

- It often corresponds to what lay people treat as the different basic kinds of organism – dogs are one species, cats another.
- It is the standard binomial nomenclature (or trinomial nomenclature) by which scientists typically refer to organisms.
- It is the highest taxonomic level that cannot be made more or less inclusionary.

After years of use, the concept remains central to biology and a host of related fields, and yet also remains at times ill-defined.

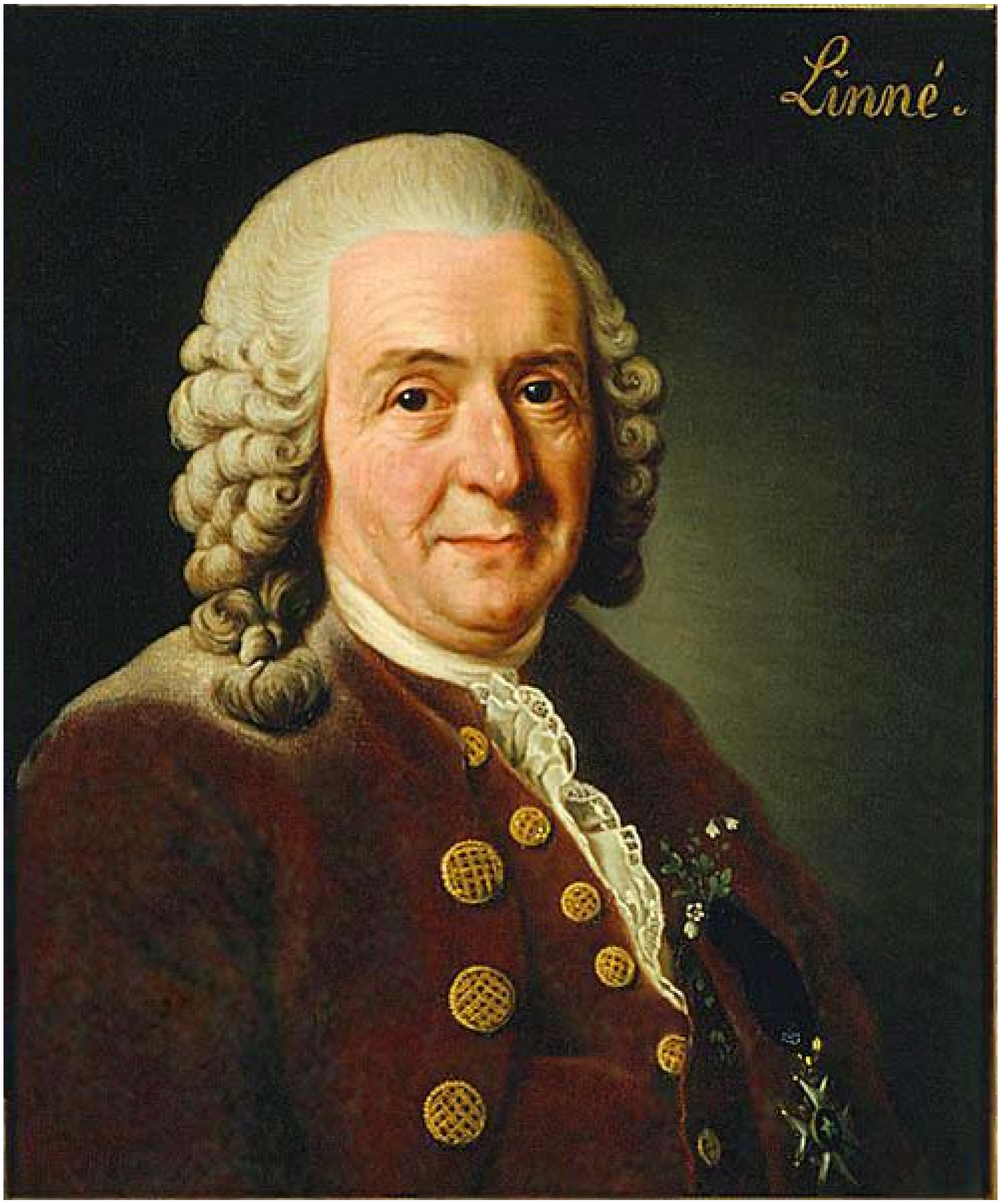
Implications of assignment of species status

The naming of a particular species may be regarded as a *hypothesis* about the evolutionary relationships and distinguishability of that group of organisms. As further information comes to hand, the hypothesis may be confirmed or refuted. Sometimes, especially in the past when communication was more difficult, taxonomists working in isolation have given two distinct names to individual organisms later identified as the same species. When two named species are discovered to be of the same species, the older species name is usually retained, and the newer species name dropped, a process called *synonymization*, or colloquially, as **lumping**. Dividing a taxon into multiple, often new, taxons is called **splitting**. Taxonomists are often referred to as "lumpers" or "splitters" by their colleagues, depending on their personal approach to recognizing differences or commonalities between organisms.

Traditionally, researchers relied on observations of anatomical differences, and on observations of whether different populations were able to interbreed successfully, to distinguish species; both anatomy and breeding behavior are still important to assigning species status. As a result of the revolutionary (and still ongoing) advance in microbiological research techniques, including DNA analysis, in the last few decades, a great deal of additional knowledge about the differences and similarities between species has become available. Many populations formerly regarded as separate species are now considered a single taxon, and many formerly grouped populations have been split. Any taxonomic level (species, genus, family, etc.) can be synonymized or split, and at higher taxonomic levels, these revisions have been still more profound.

From a taxonomical point of view, groups within a species can be defined as being of a taxon hierarchically lower than a species. In zoology only the subspecies is used, while in botany the variety, subvariety, and form are used as well. In conservation biology, the concept of evolutionary significant units (ESU) is used, which may be define either species or smaller distinct population segments. Identifying and naming species is the providence of alpha taxonomy.

Historical development of the species concept



Linnaeus believed in the fixity of species.

In the earliest works of science, a species was simply an individual organism that represented a group of similar or nearly identical organisms. No other relationships beyond that group were implied. Aristotle used the words *genus* and *species* to mean generic and specific categories. Aristotle and other pre-Darwinian scientists took the species to be distinct and unchanging, with an "essence", like the chemical elements. When early observers began to develop systems of organization for living things, they began to place formerly isolated species into a context. Many of these early delineation schemes would now be considered whimsical and these included consanguinity based on color (all plants with yellow flowers) or behavior (snakes, scorpions and certain biting ants).

In the 18th century Swedish scientist Carolus Linnaeus classified organisms according to differences in the form of reproductive apparatus. Although his system of classification sorts organisms according to degrees of similarity, it made no claims about the relationship between similar species. At that time, it was still widely believed that there was no organic connection between species, no matter how similar they appeared. This approach also suggested a type of idealism: the notion that each species existed as an "ideal form". Although there are always differences (although sometimes minute) between individual organisms, Linnaeus considered such variation problematic. He strove to identify individual organisms that were exemplary of the species, and considered other non-exemplary organisms to be deviant and imperfect.

By the 19th century most naturalists understood that species could change form over time, and that the history of the planet provided enough time for major changes. Jean-Baptiste Lamarck, in his 1809 *Zoological Philosophy*, offered one of the first logical arguments against creationism. The new emphasis was on determining *how* a species could change over time. Lamarck suggested that an organism could pass on an acquired trait to its offspring, i.e., the giraffe's long neck was attributed to generations of giraffes stretching to reach the leaves of higher treetops (this well-known and simplistic example, however, does not do justice to the breadth and subtlety of Lamarck's ideas). With the acceptance of the natural selection idea of Charles Darwin in the 1860s, however, Lamarck's view of goal-oriented evolution, also known as a teleological process, was eclipsed. Recent interest in inheritance of acquired characteristics centers around epigenetic processes, e.g. methylation, that do not affect DNA sequences, but instead alter expression in an inheritable manner. Thus, neo-lamarckism, as it is sometimes termed, is not a challenge to the theory of evolution by natural selection.

Charles Darwin and Alfred Wallace provided what scientists now consider as the most powerful and compelling theory of evolution. Darwin argued that it was populations that evolved, not individuals. His argument relied on a radical shift in perspective from that of Linnaeus: rather than defining species in ideal terms (and searching for an ideal representative and rejecting deviations), Darwin considered variation among individuals to be natural. He further argued that variation, far from being problematic, actually provides the *explanation* for the existence of distinct species.

Darwin's work drew on Thomas Malthus' insight that the rate of growth of a biological population will always outpace the rate of growth of the resources in the environment, such as the food supply. As a result, Darwin argued, not all the members of a population will be able to survive and reproduce. Those that did will, on average, be the ones possessing variations—however slight—that make them slightly better adapted to the environment. If these variable traits are heritable, then the offspring of the survivors will also possess them. Thus, over many generations, adaptive variations will accumulate in the population, while counter-adaptive traits will tend to be eliminated.

Whether a variation is adaptive or non-adaptive depends on the environment: different environments favor different traits. Since the environment effectively selects which organisms live to reproduce, it is the environment (the "fight for existence") that selects the traits to be passed on. This is the theory of evolution by natural selection. In this model, the length of a giraffe's neck would be explained by positing that proto-giraffes with longer necks would have had a significant reproductive advantage to those with shorter necks. Over many generations, the entire population would be a species of long-necked animals.

In 1859, when Darwin published his theory of natural selection, the mechanism behind the inheritance of individual traits was unknown. Although Darwin made some speculations on how traits are inherited (pangenesis), his theory relies only on the fact that inheritable traits *exist*, and are variable (which makes his accomplishment even more remarkable.) Although Gregor Mendel's paper on genetics was published in 1866, its significance was not recognized. It was not until 1900 that his work was rediscovered by Hugo de Vries, Carl Correns and Erich von Tschermak, who realised that the "inheritable traits" in Darwin's theory are genes.

The theory of the evolution of species through natural selection has two important implications for discussions of species—consequences that fundamentally challenge the assumptions behind Linnaeus' taxonomy. First, it suggests that species are not just similar, they may actually be related. Some students of Darwin argue that *all* species are descended from a common ancestor. Second, it supposes that "species" are not homogeneous, fixed, permanent things; members of a species are all different, and over time species change. This suggests that species do not have any clear boundaries but are rather momentary statistical effects of constantly changing gene-frequencies. One may still use Linnaeus' taxonomy to identify individual plants and animals, but one can no longer think of species as independent and immutable.

The rise of a new species from a parental line is called speciation. There is no clear line demarcating the ancestral species from the descendant species.

Although the current scientific understanding of species suggests that there is no rigorous and comprehensive way to distinguish between different species in *all* cases, biologists continue to seek concrete ways to operationalize the idea. One of the most popular biological definitions of species is in terms of reproductive isolation; if two creatures cannot reproduce to produce fertile offspring of both sexes, then they are in different species. This definition captures a number of intuitive species boundaries, but it remains imperfect. It has nothing to say about species that reproduce asexually, for example, and it is very difficult to apply to extinct species. Moreover, boundaries between species are often fuzzy: there are examples where members of one population can produce fertile offspring of both sexes with a second population, and members of the second population can produce fertile offspring of both sexes with members of a third population, but members of the first and third population cannot produce fertile offspring, or can only produce fertile offspring of the homozygous sex. Consequently, some people reject this definition of a species.

Richard Dawkins defines two organisms as conspecific if and only if they have the same number of chromosomes and, for each chromosome, both organisms have the same number of nucleotides (*The Blind Watchmaker*, p. 118). However, most if not all taxonomists would strongly disagree. For example, in many amphibians, most notably in New Zealand's *Leiopelma* frogs, the genome consists of "core" chromosomes that are mostly invariable and accessory chromosomes, of which exist a number of possible combinations. Even though the chromosome numbers are highly variable between populations, these can interbreed successfully and form a single evolutionary unit. In plants, polyploidy is extremely commonplace with few restrictions on interbreeding; as individuals with an odd number of chromosome sets are usually sterile, depending on the actual number of chromosome sets present, this results in the odd situation where some individuals of the same evolutionary unit can interbreed with certain others and some cannot, with all populations being eventually linked as to form a common gene pool.

The classification of species has been profoundly affected by technological advances that have allowed researchers to determine relatedness based on molecular markers, starting with the comparatively crude blood plasma precipitation assays in the mid-20th century to Charles Sibley's ground-breaking DNA-DNA hybridization studies in the 1970s leading to DNA sequencing techniques. The results of these techniques caused revolutionary changes in the higher taxonomic categories (such as phyla and classes), resulting in the reordering of many branches of the phylogenetic tree. For taxonomic categories below genera, the results have been mixed so far; the pace of evolutionary change on the molecular level is rather slow, yielding clear differences only after considerable periods of reproductive separation. DNA-DNA hybridization results have led to misleading conclusions, the Pomarine Skua – Great Skua phenomenon being a famous example. Turtles have been determined to evolve with just one-eighth of the speed of other reptiles on the molecular level, and the rate of molecular evolution in albatrosses is half of what is found in the rather closely related storm-petrels. The hybridization technique is now obsolete and is replaced by more reliable computational approaches for sequence comparison. Molecular taxonomy is not directly based on the evolutionary processes, but rather on the overall change brought upon by these processes. The processes that lead to the generation and maintenance of variation such as mutation, crossover and selection are not uniform. DNA is only extremely rarely a direct target of natural selection rather than changes in the DNA sequence enduring over generations being a result of the latter; for example, silent transition-transversion combinations would alter the melting point of the DNA sequence, but not the sequence of the encoded proteins and thus are a possible example where, for example in microorganisms, a mutation confers a change in fitness all by itself.

Species as taxa

The scientific name of a species (often of Latin or Greek origin) in the binominal nomenclature introduced by Carl Linnaeus in 1753 is composed of two parts, which are written in italic font and for which there are different expressions in botany and zoology. The first part of that name is spelled upper case and is in both disciplines known as the genus name (also called the *generic name*). The second part is always spelled lower case and in botany it is called the *specific epithet*.

- Example: in the European beech (*Fagus sylvatica*) the component *Fagus* refers to the genus, *sylvatica* is the specific epithet.

In zoology, the second part is called the *specific name*.

- Example: in the lion (*Panthera leo*) the component *Panthera* refers to the genus, *leo* is the specific name.

The scientific name is completed when authors, years and parentheses are added.

In botany the name of the author is usually abbreviated, for example "L." stands for "Linnaeus".

- Example: shiitake *Lentinula edodes* (Berk.) Pegler
  M. J. Berkeley was the first to describe the species, D. Pegler has placed it into the currently used system.

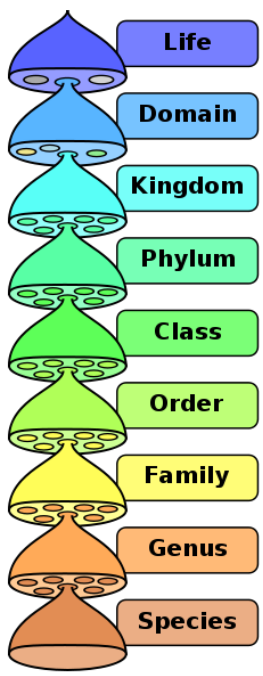
In zoology, the addition of author and year are optional, *Panthera leo* is thus an entirely correct name. The International Code of Zoological Nomenclature prescribes how to add author(s) (if possible not abbreviated) and year (or author alone without year). If the species is cited in different genus than the one in which it was originally described, author(s) and year are given in parentheses. Between author and year often a comma is set (but not required).

- Example: lion *Panthera leo* (Linnaeus, 1758)
  Carl Nilsson Linnæus described the lion first and as *Felis leo*. The person who first placed the lion in the genus *Panthera* Oken, 1816 is not relevant in zoology. Instead of Linnæus, usually Linnaeus is spelled.

Chapter 5

Genus

In biology, a **genus** (plural: **genera**) is a low-level taxonomic rank used in the classification of living and fossil organisms, which is an example of definition by genus and differentia. The term comes from Latin genus "descent, family, type, gender", cognate with Greek: *γένος – genos*, "race, stock, kin".



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. A family contains one or more genera. Intermediate minor rankings are not shown.

The composition of a genus is determined by a taxonomist. The standards for genus classification are not strictly codified, and hence different authorities often produce different classifications for genera. In the hierarchy of the binomial classification system, genus comes above species and below family.

Generic name

The scientific name of a genus may be called the **generic name** or **generic epithet**: it is always capitalized. It plays a pivotal role in binomial nomenclature, the system of biological nomenclature.

Binomial nomenclature

The rules for scientific names are laid down in the Nomenclature Codes; depending on the kind of organism and the Kingdom it belongs to, a different Code may apply, with different rules, laid down in a different terminology. The advantages of scientific over common names are that they are accepted by speakers of all languages, and that each species has only one name. This reduces the confusion that may arise from the use of a common name to designate different things in different places (example elk), or from the existence of several common names for a single species.

It is possible for a genus to be assigned to a kingdom governed by one particular Nomenclature Code by one taxonomist, while other taxonomists assign it to a kingdom governed by a different Code, but this is the exception, not the rule.

Pivotal in binomial nomenclature

The generic name often is a component of the names of taxa of lower rank. For example, *Canis lupus* is the scientific name of the Gray wolf, a species, with *Canis* the generic name for the dog and its close relatives, and with *lupus* particular (specific) for the wolf (*lupus* is written in lower case). Similarly, *Canis lupus familiaris* is the scientific name for the domestic dog.

Taxonomic units in higher ranks often have a name that is based on a generic name, such as the family name Canidae, which is based on *Canis*. However, not all names in higher ranks are necessarily based on the name of a genus: for example, Carnivora is the name for the order to which the dog belongs.

The problem of identical names used for different genera

A genus in one kingdom is allowed to bear a scientific name that is in use as a generic name (or the name of a taxon in another rank) in a kingdom that is governed by a different Nomenclature Code. Although this is discouraged by both the International Code of Zoological Nomenclature and the International Code of Botanical Nomenclature, there are some five thousand such names that are in use in more than one kingdom. For instance, *Anura* is the name of the order of frogs but also is the name of a genus of plants (although not current: it is a synonym); *Aotus* is the genus of golden peas and night monkeys; *Oenanthe* is the genus of wheatears and water dropworts, *Prunella* is the genus of accentors and self-heal, and *Proboscidea* is the order of elephants and the genus of devil's claws.

Within the same kingdom one generic name can apply to only one genus. This explains why the platypus genus is named *Ornithorhynchus*—George Shaw named it *Platypus* in 1799, but the name *Platypus* had already been given to a group of ambrosia beetles by Johann Friedrich Wilhelm Herbst in 1793. Names with the same form but applying to different taxa are called homonyms. Since beetles and platypuses are both members of the kingdom Animalia, the name *Platypus* could not be used for both. Johann Friedrich Blumenbach published the replacement name *Ornithorhynchus* in 1800.

Types and genera

Because of the rules of scientific naming, or "binomial nomenclature", each genus should have a designated type, although in practice there is a backlog of older names that may not yet have a type. In zoology this is the type species; the generic name is permanently associated with the type specimen of its type species. Should this specimen turn out to be assignable to another genus, the generic name linked to it becomes a junior synonym, and the remaining taxa in the former genus need to be reassessed.

Guidelines

There are no hard and fast rules that a taxonomist has to follow in deciding what does and what does not belong in a particular genus. This does not mean that there is no common ground among taxonomists in what constitutes a "good" genus. For instance, some rules-of-thumb for delimiting a genus are outlined in Gill. According to these, a genus should fulfill three criteria to be descriptively useful:

1. monophyly – all descendants of an ancestral taxon are grouped together;
2. reasonable compactness – a genus should not be expanded needlessly; and
3. distinctness – in regards of evolutionarily relevant criteria, i.e. ecology, morphology, or biogeography; note that DNA sequences are a *consequence* rather than a *condition* of diverging evolutionary lineages except in cases where they directly inhibit gene flow (e.g. postzygotic barriers).

Nomenclature

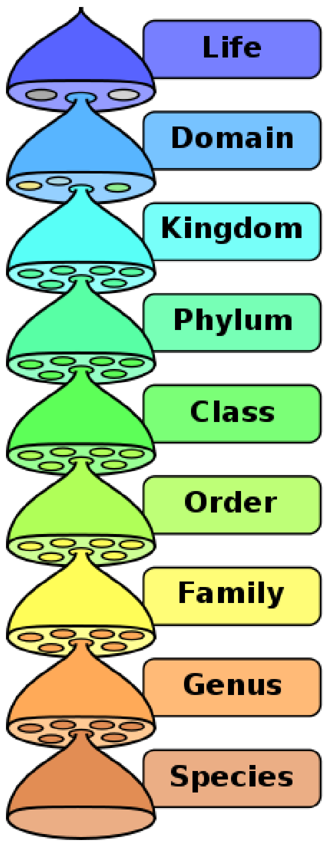
> ...difficulties occurring in generic nomenclature: similar cases abound, and become complicated by the different views taken of the matter by the various taxonomists.
>
> Prof. C. S. Rafinesque. 1836

None of the Nomenclature Codes require such criteria for defining a genus, because these are concerned with the nomenclature rules, not with taxonomy. These regulate formal nomenclature, aiming for universal and stable scientific names.

Chapter 6

Family (Biology) and Order (Biology)

Family (biology)



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. An order contains one or more families. Intermediate minor rankings are not shown.

In biological classification, **family** (Latin: *familia*) is

- a taxonomic rank. Other well-known ranks are life, domain, kingdom, phylum, class, order, genus, and species, with family fitting between order and genus. As for the other well-known ranks, there is the option of an immediately lower rank, indicated by the prefix *sub-*: subfamily (Latin: *subfamilia*).

- a taxonomic unit, a taxon, in that rank. In that case the plural is families (Latin *familiae*)

  Example: Walnuts and hickories belong to the Juglandaceae, or walnut family.

What does and does not belong to each family is determined by a taxonomist. Similarly for the question if a particular family should be recognized at all. Often there is no exact agreement, with different taxonomists each taking a different position. There are no hard rules that a taxonomist needs to follow in describing or recognizing a family. Some taxa are accepted almost universally, while others are recognised only rarely.

History of the concept

The taxonomic term *familia* was first used by French botanist Pierre Magnol in his *Prodromus historiae generalis plantarum, in quo familiae plantarum per tabulas disponuntur* (1689) where he called the seventy-six groups of plants he recognised in his tables families (*familiae*). The concept of rank at that time was not yet settled, and in the preface to the *Prodromus* Magnol spoke of uniting his families into larger *genera*, which is far from how the term is used today.

Carolus Linnaeus used the word *familia* in his *Philosophia botanica* (1751) to denote major groups of plants: trees, herbs, ferns, palms, and so on. He used this term only in the morphological section of the book, discussing the vegetative and generative organs of plants. Subsequently, in French botanical publications, from Michel Adanson's *Familles naturelles des plantes* (1763) and until the end of the 19th century, the word *famille* was used as a French equivalent of the Latin *ordo* (or *ordo naturalis*). In nineteenth century works such as the *Prodromus* of Augustin Pyramus de Candolle and the *Genera Plantarum* of George Bentham and Joseph Dalton Hooker this word *ordo* was used for what now is given the rank of family.

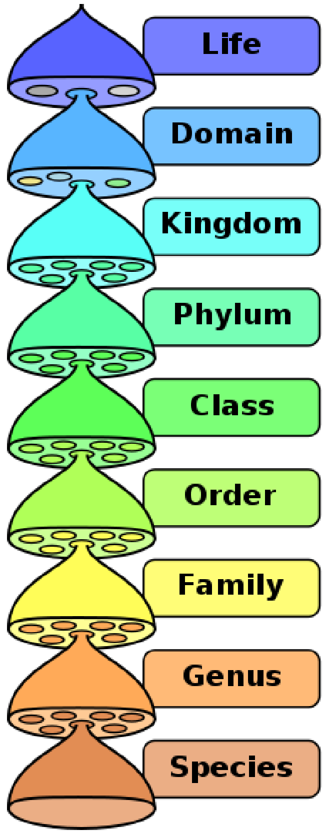
In zoology, the family as a rank intermediate between order and genus was introduced by Pierre André Latreille in his *Précis des caractères génériques des insectes, disposés dans un ordre naturel* (1796). He used families (some of them not named) in some but not in all his orders of "insects" (which then included all arthropods).

Since the beginning of the 20th century, however, the term has been consistently used in its modern sense. Its usage and characteristic ending of the names belonging to this category are governed by the various nomenclature codes. These are "-idae" in the zoological code, and "-aceae" in the botanical and bacteriological codes.

Uses

Families may be used for evolutionary, palaeontological and generic studies because they are more stable than lower taxonomic levels such as genera and species.

Order (biology)



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. A class contains one or more orders. Intermediate minor rankings are not shown.

In scientific classification used in biology, the **order** (Latin: *ordo*) is

1. a taxonomic rank used in the classification of organisms. Other well-known ranks are life, domain, kingdom, phylum, class, family, genus, and species, with order fitting in between class and family. An immediately higher rank, **superorder**, may be added directly above order, while **suborder** would be a lower rank.
2. a taxonomic unit, a taxon, in that rank. In that case the plural is orders (Latin *ordines*).

   Example: Walnuts and hickories belong to the family Juglandaceae (or walnut family), which is placed in the order Fagales.

What does and does not belong to each order is determined by a taxonomist. Similarly for the question if a particular order should be recognized at all. Often there is no exact agreement, with different taxonomists each taking a different position. There are no hard rules that a taxonomist needs to follow in describing or recognizing an order. Some taxa are accepted almost universally, while others are recognised only rarely.

For some groups of organisms, consistent suffixes are used to denote that the rank is an order. The Latin suffix *-(i)formes* meaning "having the form of" is used for the scientific name of orders of birds and fishes, but not for those of mammals and invertebrates. The suffix *-ales* is for the name of orders of vascular plants.

Hierarchy of ranks

For some clades, a number of additional classifications are used.

Name	Meaning of prefix	Example
Magnorder	magnus: large, great, important	Epitheria
Superorder	super: above	Euarchontoglires
Order		Primates
Suborder	sub: under	Haplorrhini
Infraorder	infra: below	Simiiformes
Parvorder	parvus: small, unimportant	Catarrhini

In their 1997 classification of mammals, McKenna and Bell used two extra levels between Superorder and Order: "Grandorder" and "Mirorder".

History of the concept

The order as a distinct rank of biological classification having its own distinctive name (and not just called a *higher genus (genus summum))* was first introduced by a German botanist Augustus Quirinus Rivinus in his classification of plants (appeared in a series of treatises in the 1690s). Carolus Linnaeus was the first to apply it consistently to the division of all three kingdoms of Nature (minerals, plants, and animals) in his *Systema Naturae* (1735, 1st. Ed.).

Botany

For plants the Linnaean orders, in the *Systema Naturae* and the *Species Plantarum*, were strictly artificial, introduced to subdivide the artificial classes into more comprehensible smaller groups. When the word *ordo* was first consistently used for natural units of plants, in nineteenth century works such as the *Prodromus* of de Candolle and the *Genera Plantarum* of Bentham & Hooker, it indicated taxa that are now given the rank of family.

In French botanical publications, from Michel Adanson's *Familles naturelles des plantes* (1763) and until the end of the 19th century, the word *famille* (plural: *familles*) was used as a French equivalent for this Latin *ordo*. This equivalence was explicitly stated in the

Alphonse De Candolle's *Lois de la nomenclature botanique* (1868), the precursor of the currently used *International Code of Botanical Nomenclature*.

In the first international *Rules* of botanical nomenclature of 1906 the word family (*familia*) was assigned to the rank indicated by the French "famille", while order (*ordo*) was reserved for a higher rank, for what in the nineteenth century had often been named a *cohors* (plural *cohortes*).

Some of the plant families still retain the names of Linnaean "natural orders" or even the names of pre-Linnaean natural groups recognised by Linnaeus as orders in his natural classification (e.g. *Palmae* or *Labiatae*). Such names are known as descriptive family names.

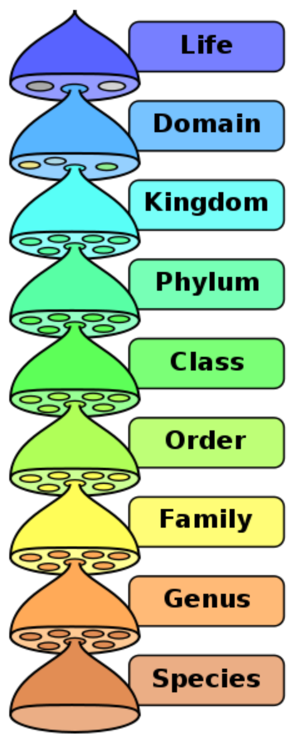
Zoology

In zoology, the Linnaean orders were used more consistently. That is, the orders in the zoology part of the *Systema Naturae* refer to natural groups. Some of his ordinal names are still in use (e.g. Lepidoptera for the order of moths and butterflies, or Diptera for the order of flies, mosquitoes, midges, and gnats).

Chapter 7

Class (Biology) and Kingdom (Biology)

Class (biology)



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. Intermediate minor rankings are not shown.

In biological classification, **class** (Latin: *classis*) is

- a taxonomic rank. Other well-known ranks are life, domain, kingdom, phylum, order, family, genus, and species, with class fitting between phylum and order. As for the other well-known ranks, there is the option of an immediately lower rank, indicated by the prefix *sub-*: subclass (Latin: *subclassis*).

- a taxonomic unit, a taxon, in that rank. In that case the plural is classes (Latin *classes*)

The composition of each class is determined by a taxonomist. Often there is no exact agreement, with different taxonomists taking different positions. There are no hard rules that a taxonomist needs to follow in describing a class, but for well-known animals there is likely to be consensus. For example, dogs are usually assigned to the phylum Chordata (animals with notochords); in the class Mammalia; in the order Carnivora (mammals that eat meat).

Hierarchy of ranks

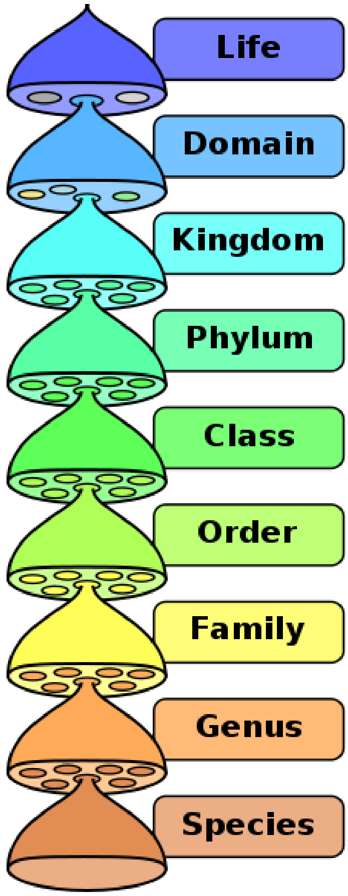
For some clades, a number of additional classifications are used. The different classes are used relatively rarely.

Name	Meaning of prefix	Example 1	Example 2	Example 3
Superclass	super: above	Tetrapoda		
Class		Mammalia	Maxillopoda	Sauropsida
Subclass	sub: under		Thecostraca	Avialae
Infraclass	infra: below		Cirripedia	Aves
Parvclass	parvus: small, unimportant			Neornithes

History of the concept

The class as a distinct rank of biological classification having its own distinctive name (and not just called a *top-level genus (genus summum)* was first introduced by a French botanist Joseph Pitton de Tournefort in his classification of plants (appeared in his 1694 *Eléments de botanique*). Carolus Linnaeus was the first to use it consistently, in dividing of all three of his kingdoms of Nature (minerals, plants, and animals) in his *Systema Naturae* (1735, 1st ed.). Since then class had been considered the highest level of the taxonomic hierarchy until the *embranchements*, now called phyla, and divisions were introduced in the nineteenth century.

Kingdom (biology)



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. A domain contains one or more kingdoms. Intermediate minor rankings are not shown.

In biology, **kingdom** (Latin: **regnum**, pl. **regna**) is a taxonomic rank, which is either the highest rank or in the more recent three-domain system, the rank below domain. Kingdoms are divided into smaller groups called phyla (in zoology) or divisions in botany. The complete sequence of ranks is life, domain, kingdom, phylum, class, order, family, genus, and species.

Currently, textbooks from the United States use a system of six kingdoms (Animalia, Plantae, Fungi, Protista, Archaea, Bacteria) while British, Australian and Latin American textbooks may describe five kingdoms (Animalia, Plantae, Fungi, Protista, and Prokaryota or Monera).

Historically, the number of kingdoms in widely accepted classifications has grown from two to six. However, phylogenetic research from about 2000 onwards does not support any of the traditional systems.

Two kingdoms

The classification of living things into animals and plants is an ancient one. Aristotle (384 BC–322 BC) classified animal species in his work the History of Animals, and his pupil Theophrastus (c. 371–c. 287 BC) wrote a parallel work on plants (the History of Plants).

Carolus Linnaeus (1707–1778) laid the foundations for modern biological nomenclature, now regulated by the Nomenclature Codes. He distinguished two kingdoms of living things: *Regnum Animale* ('animal kingdom') for animals and *Regnum Vegetabile* ('vegetable kingdom') for plants. (Linnaeus also included minerals, placing them in a third kingdom, *Regnum Lapideum*.) Linnaeus divided each kingdom into classes, later grouped into phyla for animals and divisions for plants.

Three kingdoms

In 1674, Antonie van Leeuwenhoek, often called the "father of microscopy", sent the Royal Society of London a copy of his first observations of microscopic single-celled organisms. Until then the existence of such microscopic organisms was entirely unknown. At first these organisms were divided into animals and plants and placed in the appropriate Kingdom. However, by the mid-19th century it had become clear that "the existing dichotomy of the plant and animal kingdoms [had become] rapidly blurred at its boundaries and outmoded". In 1866, following earlier proposals by Richard Owen and John Hogg, Ernst Haeckel proposed a third kingdom of life. Haeckel revised the content of this kingdom a number of times before settling on a division based on whether organisms were unicellular (Protista) or multicellular (animals and plants).

Four kingdoms

The development of microscopy, and the electron microscope in particular, revealed an important distinction between those unicellular organisms whose cells do not have a distinct nucleus, prokaryotes, and those unicellular and multicellular organisms whose cells do have a distinct nucleus, eukaryotes. In 1938, Herbert F. Copeland proposed a four-kingdom classification, moving the two prokaryotic groups, bacteria and "blue-green algae", into a separate Kingdom Monera.

It gradually became apparent how important the prokaryote/eukaryote distinction is, and Stanier and van Niel popularized Édouard Chatton's proposal in the 1960s to recognize this division in a formal classification. This required the creation, for the first time, of a rank above kingdom, a *superkingdom* or *empire*, also called a *domain*.

Five kingdoms

The differences between fungi and other organisms regarded as plants had long been recognized. For example, at one point Haeckel moved the fungi out of Plantae into Protista, before changing his mind. Robert Whittaker recognized an additional kingdom for the Fungi. The resulting five-kingdom system, proposed in 1969 by Whittaker, has become a popular standard and with some refinement is still used in many works and forms the basis for new multi-kingdom systems. It is based mainly on differences in nutrition; his Plantae were mostly multicellular autotrophs, his Animalia multicellular heterotrophs, and his Fungi multicellular saprotrophs. The remaining two kingdoms, Protista and Monera, included unicellular and simple cellular colonies.

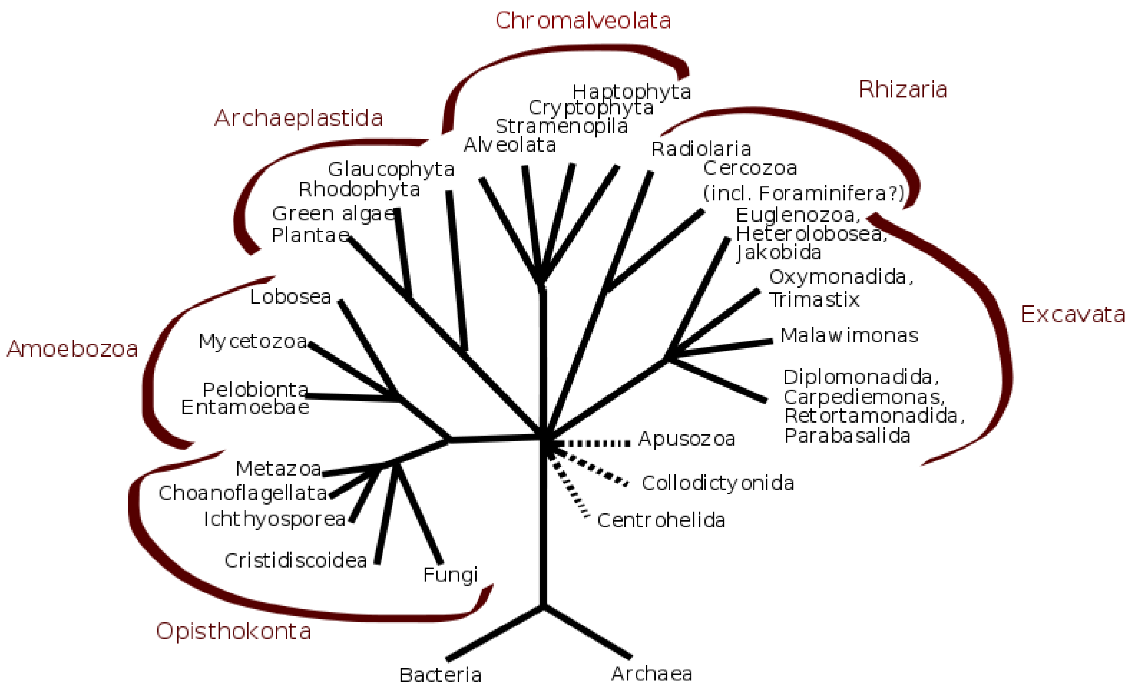
Six kingdoms

From around the mid-1970s onwards, there was an increasing emphasis on molecular level comparisons of genes (initially ribosomal RNA genes) as the primary factor in classification; genetic similarity was stressed over outward appearances and behavior. Taxonomic ranks, including kingdoms, were to be groups of organisms with a common ancestor, whether monophyletic (*all* descendants of a common ancestor) or paraphyletic (only some descendants of a common ancestor). Based on such RNA studies, Carl Woese divided the prokaryotes (Kingdom Monera) into two groups, called Eubacteria and Archaebacteria, stressing that there was as much genetic difference between these two groups as between either of them and all eukaryotes. Eukaryote groups, such as plants, fungi and animals may look different, but are more similar to each other in their genetic makeup at the molecular level than they are to either the Eubacteria or Archaebacteria. (It was also found that the eukaryotes are more closely related, genetically, to the Archaebacteria than they are to the Eubacteria.) Although the primacy of the eubacteria-archaebacteria divide has been questioned, it has also been upheld by subsequent research.

Cavalier-Smith's six kingdoms

Thomas Cavalier-Smith has published extensively on the evolution and classification of life, particularly protists. His views have been influential but controversial, and not always widely accepted. In 1998, he published a six-kingdom model, which has been revised in subsequent papers. The version published in 2009 is shown below. (Compared to the version he published in 2004, the alveolates and the rhizarians have been moved from Kingdom Protozoa to Kingdom Chromista.) Cavalier-Smith does not accept the importance of the fundamental eubacteria–archaebacteria divide put forward by Woese and others and supported by recent research. His Kingdom Bacteria includes the Archaebacteria as part of a subkingdom along with a group of eubacteria (Posibacteria). Nor does he accept the requirement for groups to be monophyletic. His Kingdom Protozoa includes the ancestors of Animalia and Fungi .

International Society of Protistologists Classification 2005



One hypothesis of eukaryotic relationships, modified from Simpson and Roger (2004).

The "classic" six-kingdom system is still recognizably a modification of the original two-kingdom system: Animalia remains; the original category of plants has been split into Plantae and Fungi; and single-celled organisms have been introduced and split into Bacteria, Archaea and Protista.

Research published in the 21st century has produced a rather different picture. In 2004, a review article by Simpson and Roger noted that the Protista were "a grab-bag for all eukaryotes that are not animals, plants or fungi". They argued that only monophyletic groups–an ancestor and *all* of its descendents — should be accepted as formal ranks in a classification. On this basis, the diagram opposite (redrawn from their article) showed the real "kingdoms" (their quotation marks) of the eukaryotes. A classification produced in 2005 for the International Society of Protistologists, which reflected the consensus of the time, followed this approach, dividing the eukaryotes into the same six "supergroups". Although the published classification deliberately did not use formal taxonomic ranks, other sources have treated each of the six as a separate Kingdom.

In this system, the traditional kingdoms have vanished. For example, research shows that the multicellular animals (Metazoa) are descended from the same ancestor as the unicellular choanoflagellates and the fungi. A classification system which places these three groups into different kingdoms (with multicellular animals forming Animalia, choanoflagellates part of Protista and Fungi a separate kingdom) is not monophyletic. The monophyletic group is the Opisthokonta, made up of all those organisms believed to have descended from a common ancestor, some of which are unicellular (choanoflagellates), some of which are multicellular but not closely related to animals (some fungi), and others of which are traditional multicellular animals.

However, in the same year as the International Society of Protistologists' classification was published (2005), doubts were being expressed as to whether some of these supergroups were monophyletic, particularly the Chromalveolata, and a review in 2006 noted the lack of evidence for several of the supposed six supergroups.

As of 2010, there is widespread agreement that the Rhizaria belong with the Stramenopiles and the Alveolata, in a clade dubbed the SAR supergroup, so that Rhizara is not one of the main eukaryote groups. Beyond this, there does not appear to be a consensus. Rogozin *et al.* in 2009 noted that "The deep phylogeny of eukaryotes is an extremely difficult and controversial problem." As of December 2010, there appears to be a consensus that the 2005 six supergroup model does not reflect the true phylogeny of the eukaryotes and hence how they should be classified, although there is no agreement as to the model which should replace it.

Summary

The sequence from the two-kingdom system up to Cavalier-Smith's six-kingdom system can be summarized in the table below.

Linnaeus 1735 2 kingdoms	**Haeckel 1866 3 kingdoms**	**Chatton 1925 2 empires**	**Copeland 1938 4 kingdoms**	**Whittaker 1969 5 kingdoms**	**Woese et al. 1977 6 kingdoms**	**Woese et al. 1990 3 domains**	**Cavalier-Smith 2004 6 kingdoms**
(not treated)	Protista	Prokaryota	Mychota	Monera	Eubacteria	Bacteria	Bacteria
					Archaebacteria	Archaea	
		Eukaryota	Protoctista	Protista	Protista	Eukarya	Protozoa
							Chromista
Vegetabilia	Plantae		Plantae	Plantae	Plantae		Plantae
			Protoctista	Fungi	Fungi		Fungi
Animalia	Animalia		Animalia	Animalia	Animalia		Animalia

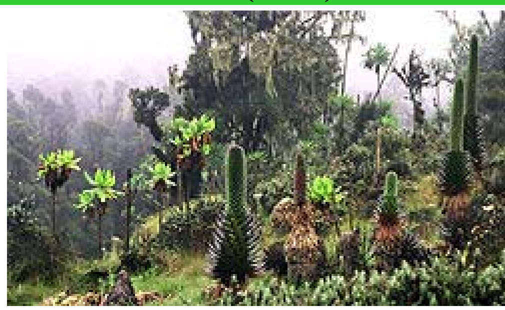
Note that the equivalences in this table are not perfect. For example, Haeckel placed the red algae (his Florideae, modern Florideophyceae) and blue-green algae (his Archephyta, modern Cyanobacteria) in his Plantae.

One or other of the kingdom-level classifications of life is still widely employed as a useful way of grouping organisms, notwithstanding the problems with this approach:

- Kingdoms such as Bacteria represent grades rather than clades, and so are rejected by phylogenetic classification systems.
- Research in the 21st century does not support the classification of the eukaryotes into *any* of the standard systems. As of April 2010, the situation appears to be that there is no set of kingdoms sufficiently supported by current research to gain widespread acceptance; as Roger & Simpson say: "with the current pace of change in our understanding of the eukaryote tree of life, we should proceed with caution."

Chapter 8

Life

Life (*Biota*)

Scientific classification [e]
Domains and Kingdoms

Life on Earth:

- Non-cellular life (viruses)
- Cellular life
  - Bacteria
  - Archaea
  - Eukarya
    - Protista
    - Fungi
    - Plantae
    - Animalia

Life (cf. biota) is a characteristic that distinguishes objects that have signaling and self-sustaining processes (i. e., living organisms) from those that do not, either because such functions have ceased (death), or else because they lack such functions and are classified as inanimate. Biology is the science concerned with the study of life.

Living organisms undergo metabolism, maintain homeostasis, possess a capacity to grow, respond to stimuli, reproduce and, through natural selection, adapt to their environment in successive generations. More complex living organisms can communicate through various means. A diverse array of living organisms (life forms) can be found in the biosphere on Earth, and the properties common to these organisms—plants, animals, fungi, protists, archaea, and bacteria—are a carbon- and water-based cellular form with complex organization and heritable genetic information.

In philosophy and religion, the conception of life and its nature varies. Both offer interpretations as to how life relates to existence and consciousness, and both touch on many related issues, including life stance, purpose, conception of a god or gods, a soul or an afterlife.

Early theories about life

Materialism

Plant life

Herds of zebra and impala gathering on the Maasai Mara plain

An aerial photo of microbial mats around the Grand Prismatic Spring of Yellowstone National Park.

Some of the earliest theories of life were materialist, holding that all that exists is matter, and that all life is merely a complex form or arrangement of matter. Empedocles (430 BC) argued that every thing in the universe is made up of a combination of four eternal "elements" or "roots of all": earth, water, air, and fire. All change is explained by the arrangement and rearrangement of these four elements. The various forms of life are caused by an appropriate mixture of elements. For example, growth in plants is explained by the natural downward movement of earth and the natural upward movement of fire.

Democritus (460 BC), the disciple of Leucippus, thought that the essential characteristic of life is having a soul (*psyche*). In common with other ancient writers, he used the term to mean the principle of living things that causes them to function as a living thing. He thought the soul was composed of fire atoms, because of the apparent connection between life and heat, and because fire moves. He also suggested that humans originally lived like animals, gradually developing communities to help one another, originating language, and developing crafts and agriculture.

In the scientific revolution of the 17th century, mechanistic ideas were revived by philosophers like Descartes.

Hylomorphism

Hylomorphism is the theory (originating with Aristotle (322 BC)) that all things are a combination of matter and form. Aristotle was one of the first ancient writers to approach the subject of life in a scientific way. Biology was one of his main interests, and there is extensive biological material in his extant writings. According to him, all things in the material universe have both matter and form. The form of a living thing is its soul (Greek *psyche*, Latin *anima*). There are three kinds of souls: the "vegetative soul" of plants, which causes them to grow and decay and nourish themselves, but does not cause motion and sensation; the "animal soul" which causes animals to move and feel; and the rational soul which is the source of consciousness and reasoning which (Aristotle believed) is found only in man. Each higher soul has all the attributes of the lower one. Aristotle believed that while matter can exist without form, form cannot exist without matter, and therefore the soul cannot exist without the body.

Consistent with this account is a teleological explanation of life. A teleological explanation accounts for phenomena in terms of their purpose or goal-directedness. Thus, the whiteness of the polar bear's coat is explained by its *purpose* of camouflage. The direction of causality is the other way round from materialistic science, which explains the consequence in terms of a prior cause. Modern biologists now reject this functional view in terms of a material and causal one: biological features are to be explained not by looking *forward* to future optimal results, but by looking *backwards* to the past evolutionary history of a species, which led to the natural selection of the features in question.

Vitalism

Vitalism is the belief that the life-principle is essentially immaterial. This originated with Stahl (17th century), and held sway until the middle of the 19th century. It appealed to philosophers such as Henri Bergson, Nietzsche, Wilhelm Dilthey, anatomists like Bichat, and chemists like Liebig.

Vitalism underpinned the idea of a fundamental separation of organic and inorganic material, and the belief that organic material can only be derived from living things. This was disproved in 1828 when Friedrich Wöhler prepared urea from inorganic materials. This so-called Wöhler synthesis is considered the starting point of modern organic chemistry. It is of great historical significance because for the first time an organic compound was produced from inorganic reactants.

Later, Helmholtz, anticipated by Mayer, demonstrated that no energy is lost in muscle movement, suggesting that there were no *vital forces* necessary to move a muscle. These empirical results led to the abandonment of scientific interest in vitalistic theories, although the belief lingered on in non-scientific theories such as homeopathy, which interprets diseases and sickness as caused by disturbances in a hypothetical vital force or life force.

Definitions

It is still a challenge for scientists and philosophers to define life in unequivocal terms. Defining life is difficult—in part—because life is a process, not a pure substance. Any definition must be sufficiently broad to encompass all life with which we are familiar, and it should be sufficiently general that, with it, scientists would not miss life that may be fundamentally different from life on Earth.

Biology

Since there is no unequivocal definition of life, the current understanding is descriptive, where life is a characteristic of organisms that exhibit all or most of the following phenomena:

1. **Homeostasis**: Regulation of the internal environment to maintain a constant state; for example, electrolyte concentration or sweating to reduce temperature.
2. **Organization**: Being structurally composed of one or more cells, which are the basic units of life.
3. **Metabolism**: Transformation of energy by converting chemicals and energy into cellular components (anabolism) and decomposing organic matter (catabolism). Living things require energy to maintain internal organization (homeostasis) and to produce the other phenomena associated with life.
4. **Growth**: Maintenance of a higher rate of anabolism than catabolism. A growing organism increases in size in all of its parts, rather than simply accumulating matter.

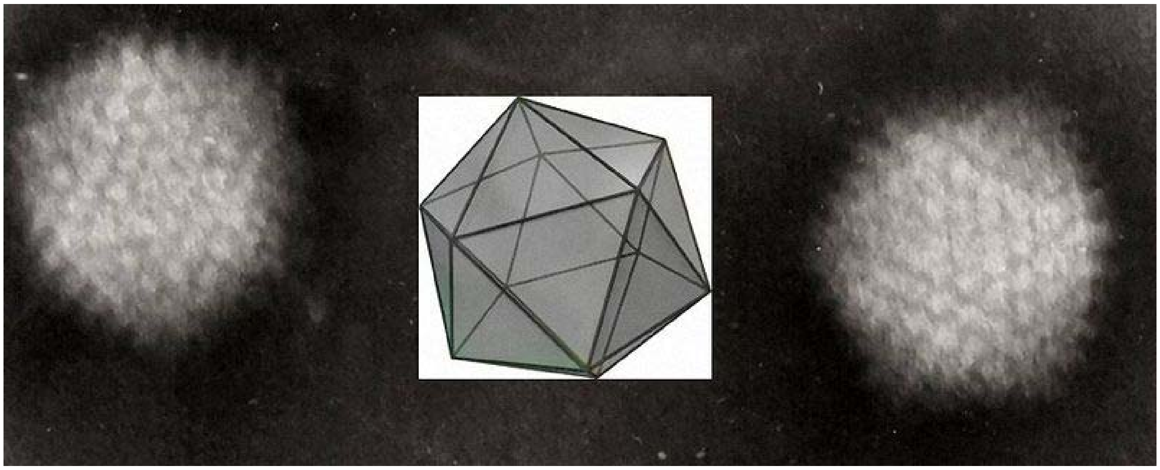
5. **Adaptation**: The ability to change over a period of time in response to the environment. This ability is fundamental to the process of evolution and is determined by the organism's heredity as well as the composition of metabolized substances, and external factors present.
6. **Response to stimuli**: A response can take many forms, from the contraction of a unicellular organism to external chemicals, to complex reactions involving all the senses of multicellular organisms. A response is often expressed by motion, for example, the leaves of a plant turning toward the sun (phototropism) and by chemotaxis.
7. **Reproduction**: The ability to produce new individual organisms, either asexually from a single parent organism, or sexually from two parent organisms.

Proposed

To reflect the minimum phenomena required, some have proposed other biological definitions of life:

- Living things are systems that tend to respond to changes in their environment, and inside themselves, in such a way as to promote their own continuation.
- A network of inferior negative feedbacks (regulatory mechanisms) subordinated to a superior positive feedback (potential of expansion, reproduction).
- A systemic definition of life is that living things are self-organizing and autopoietic (self-producing). Variations of this definition include Stuart Kauffman's definition as an autonomous agent or a multi-agent system capable of reproducing itself or themselves, and of completing at least one thermodynamic work cycle.
- Life is a self-sustained chemical system capable of undergoing Darwinian evolution.
- Things with the capacity for metabolism and motion.
- Life is a delay of the spontaneous diffusion or dispersion of the internal energy of the biomolecules towards more potential microstates.
- Living beings are thermodynamic systems that have an organized molecular structure.

Viruses



Electron micrograph of icosahedral adenovirus

Viruses are most often considered replicators rather than forms of life. They have been described as "organisms at the edge of life," since they possess genes, evolve by natural selection, and replicate by creating multiple copies of themselves through self-assembly. However, viruses do not metabolize and require a host cell to make new products. Virus self-assembly within host cells has implications for the study of the origin of life, as it may support the hypothesis that life could have started as self-assembling organic molecules.

Biophysics

Biophysicists have also commented on the nature and qualities of life forms—notably that they function on negative entropy. In more detail, according to physicists such as John Bernal, Erwin Schrödinger, Eugene Wigner, and John Avery, life is a member of the class of phenomena which are open or continuous systems able to decrease their internal entropy at the expense of substances or free energy taken in from the environment and subsequently rejected in a degraded form (see: entropy and life).

Living systems theories

Some scientists have proposed in the last few decades that a general living systems theory is required to explain the nature of life. Such a general theory, arising out of the ecological and biological sciences, attempts to map general principles for how all living systems work. Instead of examining phenomena by attempting to break things down into component parts, a general living systems theory explores phenomena in terms of dynamic patterns of the relationships of organisms with their environment.

Gaia hypothesis

The idea that the Earth is alive is probably as old as humankind, but the first public expression of it as a fact of science was by a Scottish scientist, James Hutton. In 1785 he stated that the Earth was a superorganism and that its proper study should be physiology. Hutton is rightly remembered as the father of geology, but his idea of a living Earth was forgotten in the intense reductionism of the 19th century. The Gaia hypothesis, originally proposed in the 1960s by scientist James Lovelock, explores the idea that the life on Earth functions as a single organism which actually defines and maintains environmental conditions necessary for its survival.

Nonfractionability

Robert Rosen (1991) built on the assumption that the explanatory powers of the mechanistic worldview cannot help understand the realm of living systems. One of several important clarifications he made was to define a system component as "a unit of organization; a part with a function, i.e., a definite relation between part and whole." From this and other starting concepts, he developed a "relational theory of systems" that attempts to explain the special properties of life. Specifically, he identified the "nonfractionability of components in an organism" as the fundamental difference between living systems and "biological machines."

Life as a property of ecosystems

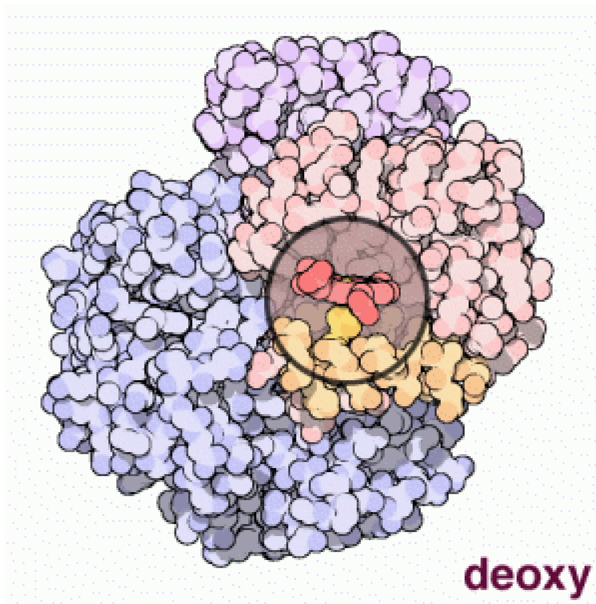
A systems view of life treats environmental fluxes and biological fluxes together as a "reciprocity of influence", and a reciprocal relation with environment is arguably as important for understanding life as it is for understanding ecosystems. As Harold J. Morowitz (1992) explains it, life is a property of an ecological system rather than a single organism or species. He argues that an ecosystemic definition of life is preferable to a strictly biochemical or physical one. Robert Ulanowicz (2009) also highlights mutualism as the key to understand the systemic, order-generating behavior of life and ecosystems.

Origin

Evidence suggests that life on Earth has existed for about 3.7 billion years. All known life forms share fundamental molecular mechanisms, and based on these observations, theories on the origin of life attempt to find a mechanism explaining the formation of a primordial single cell organism from which all life originates. There are many different hypotheses regarding the path that might have been taken from simple organic molecules via pre-cellular life to protocells and metabolism. Many models fall into the "genes-first" category or the "metabolism-first" category, but a recent trend is the emergence of hybrid models that combine both categories.

There is no scientific consensus as to how life originated and all proposed theories are highly speculative. However, most currently accepted scientific models build in one way or another on the following hypotheses:

- The Miller-Urey experiment, and the work of Sidney Fox, suggest that conditions on the primitive Earth may have favored chemical reactions that synthesized some amino acids and other organic compounds from inorganic precursors.
- Phospholipids spontaneously form lipid bilayers, the basic structure of a cell membrane.



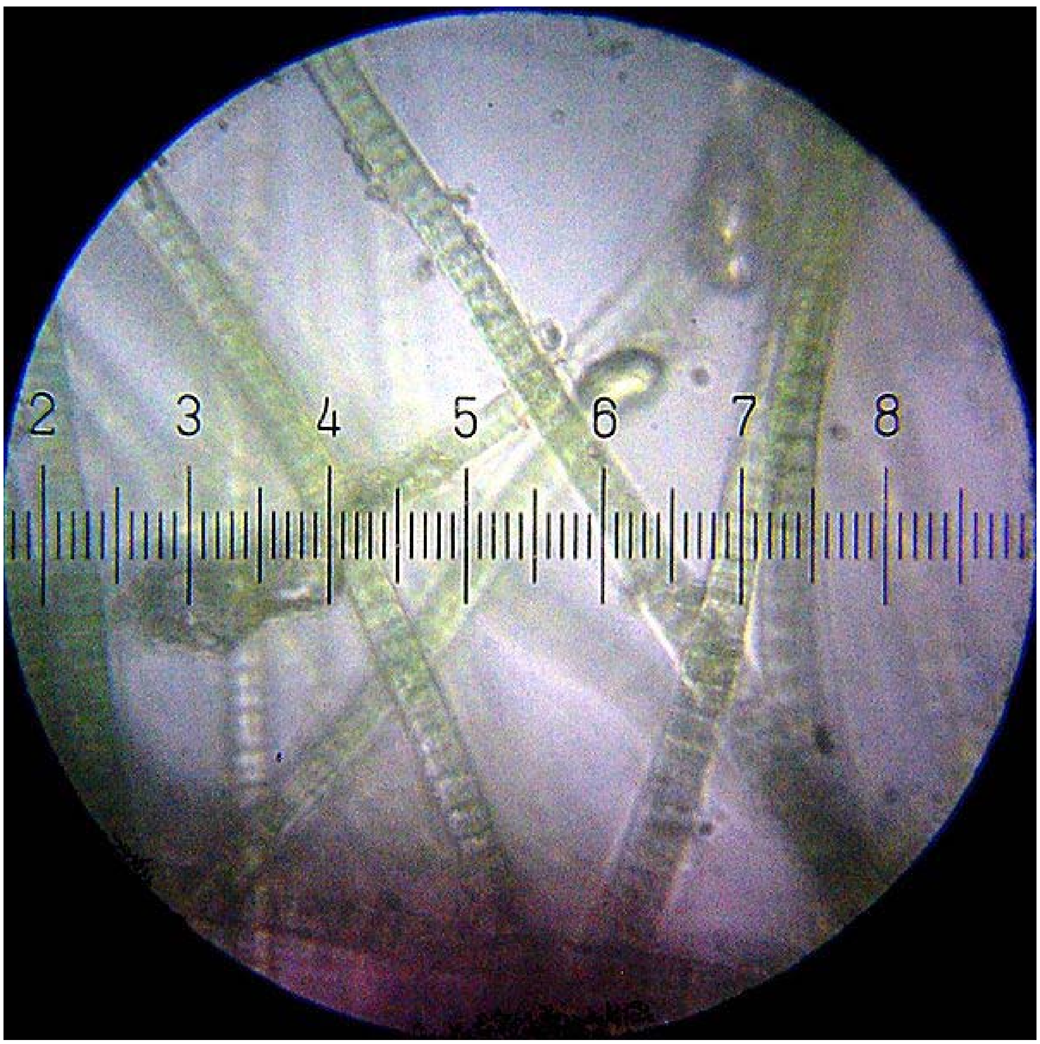
The dynamic structure of hemoglobin protein is responsible for its ability to transport oxygen within mammalian blood.

Life as we know it today synthesizes proteins, which are polymers of amino acids using instructions encoded by cellular genes—which are polymers of deoxyribonucleic acid (DNA). Protein synthesis also entails intermediary ribonucleic acid (RNA) polymers. One possibility is that genes came first and then proteins. Another possibility is that proteins came first and then genes. However, because genes are required to make proteins, and proteins are required to make genes, the problem of considering which came first is like that of the chicken or the egg. Most scientists have adopted the hypothesis that because DNA and proteins function together so intimately, it's unlikely that they arose independently. Therefore, many scientists consider the possibility, apparently first suggested by Francis Crick, that the first life was based on the DNA-protein intermediary: RNA. In fact, RNA has the DNA-like properties of information storage and replication and the catalytic properties of some proteins. Crick and others actually favored the RNA-first hypothesis even before the catalytic properties of RNA had been demonstrated by Thomas Cech.

A significant issue with the RNA-first hypothesis is that experiments designed to synthesize RNA from simple precursors have not been nearly as successful as the Miller-Urey experiments that synthesized other organic molecules from inorganic precursors. One reason for the failure to create RNA in the laboratory is that RNA precursors are very stable and do not react with each other under ambient conditions. However, the successful synthesis of certain RNA molecules under conditions hypothesized to exist prior to life on Earth has been achieved by adding alternative precursors in a specified order with the precursor phosphate present throughout the reaction. This study makes the RNA-first hypothesis more plausible to many scientists.

Recent experiments have demonstrated true Darwinian evolution of unique RNA enzymes (ribozymes) made up of two separate catalytic components that replicate each other *in vitro*. In describing this work from his laboratory, Gerald Joyce stated: "This is the first example, outside of biology, of evolutionary adaptation in a molecular genetic system." Such experiments make the possibility of a primordial *RNA World* even more attractive to many scientists.

Conditions for life



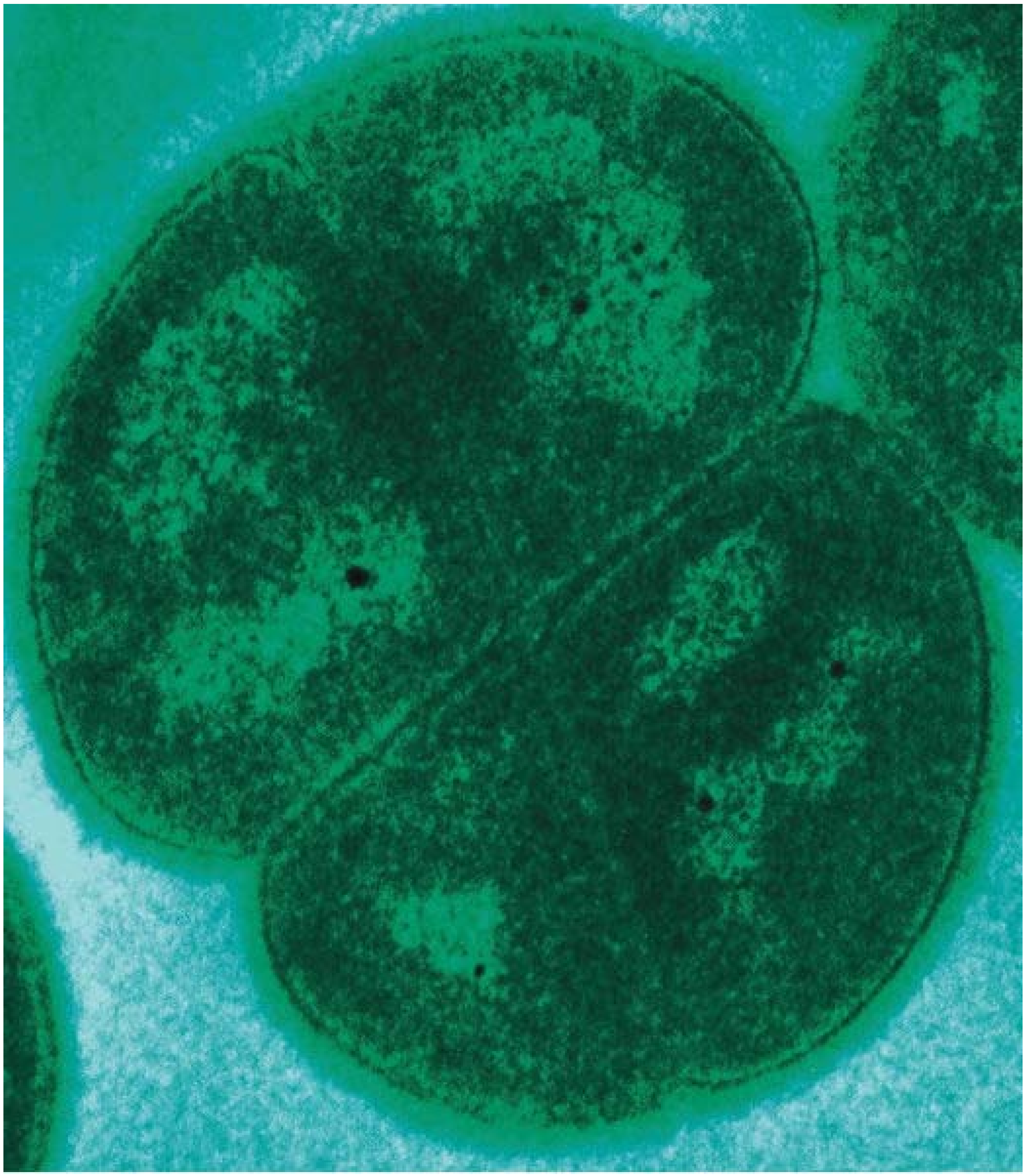
Cyanobacteria dramatically changed the composition of life forms on Earth by stimulating biodiversity and leading to the near-extinction of oxygen-intolerant organisms.

The diversity of life on Earth today is a result of the dynamic interplay between genetic opportunity, metabolic capability, environmental challenges, and symbiosis. For most of its existence, Earth's habitable environment has been dominated by microorganisms and subjected to their metabolism and evolution. As a consequence of such microbial activities on a geologic time scale, the physical-chemical environment on Earth has been changing, thereby determining the path of evolution of subsequent life. For example, the release of molecular oxygen by cyanobacteria as a by-product of photosynthesis induced fundamental, global changes in the Earth's environment. The altered environment, in turn, posed novel evolutionary challenges to the organisms present, which ultimately resulted in the formation of our planet's major animal and plant species. Therefore this "co-evolution" between organisms and their environment is apparently an inherent feature of living systems.

Range of tolerance

The inert components of an ecosystem are the physical and chemical factors necessary for life—energy (sunlight or chemical energy), water, temperature, atmosphere, gravity, nutrients, and ultraviolet solar radiation protection. In most ecosystems the conditions vary during the day and often shift from one season to the next. To live in most ecosystems, then, organisms must be able to survive a range of conditions, called "range of tolerance." Outside of that are the "zones of physiological stress," where the survival and reproduction are possible but not optimal. Outside of these zones are the "zones of intolerance," where life for that organism is implausible. It has been determined that organisms that have a wide range of tolerance are more widely distributed than organisms with a narrow range of tolerance.

Extremophiles



Deinococcus radiodurans can resist radiation exposure.

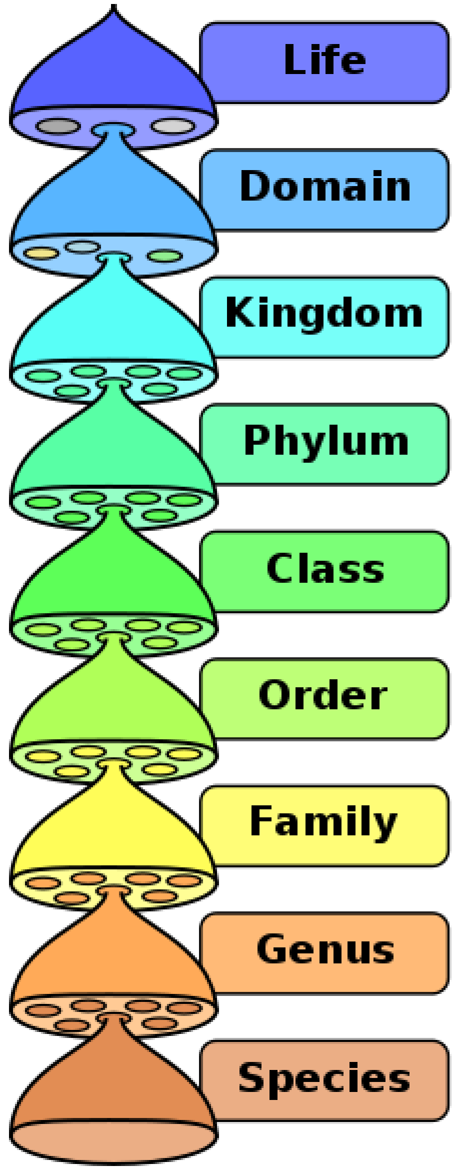
To survive, some microorganisms can assume forms that enable them to withstand freezing, complete desiccation, starvation, high-levels of radiation exposure, and other physical or chemical challenges. Furthermore, some microorganisms can survive exposure to such conditions for weeks, months, years, or even centuries. Extremophiles are microbial life forms that thrive outside the ranges life is commonly found in. They also excel at exploiting uncommon sources of energy. While all organisms are composed of nearly identical molecules, evolution has enabled such microbes to cope with this wide range of physical and chemical conditions. Characterization of the structure and metabolic diversity of microbial communities in such extreme environments is ongoing. An understanding of the tenacity and versatility of life on Earth, as well as an understanding of the molecular systems that some organisms utilize to survive such extremes, will provide a critical foundation for the search for life beyond Earth.

Chemical element requirements

All life forms require certain core chemical elements needed for biochemical functioning. This list of core life elements usually includes carbon, hydrogen, nitrogen, oxygen, phosphorus, and sulfur—the "Big Six" elemental macronutrients for all organisms —often represented by the acronym CHNOPS. Together these make up nucleic acids, proteins and lipids, the bulk of living matter.

However, alternative hypothetical types of biochemistry have been proposed which eliminate one or more of these elements, swap out an element for one not on the list, or change required chiralities or other chemical properties. For example, the recently discovered GFAJ-1 bacteria in Mono Lake, California may be able to partially substitute phosphorus with arsenic, which is toxic to most forms of life.

Classification of life



The hierarchy of biological classification's eight major taxonomic ranks, which is an example of definition by genus and differentia. **Life** is divided into domains, which are subdivided into further groups. Intermediate minor rankings are not shown.

Traditionally, people have divided organisms into the classes of plants and animals, based mainly on their ability of movement. The first known attempt to classify organisms was conducted by the Greek philosopher Aristotle (384–322 BC). He classified all living organisms known at that time as either a plant or an animal. Aristotle distinguished animals with blood from animals without blood (or at least without red blood), which can be compared with the concepts of vertebrates and invertebrates respectively. He divided the blooded animals into five groups: viviparous quadrupeds (mammals), birds, oviparous quadrupeds (reptiles and amphibians), fishes and whales. The bloodless animals were also divided into five groups: cephalopods, crustaceans, insects (which also included the spiders, scorpions, and centipedes, in addition to what we now define as insects), shelled animals (such as most molluscs and echinoderms) and "zoophytes." Though Aristotle's work in zoology was not without errors, it was the grandest biological synthesis of the time and remained the ultimate authority for many centuries after his death.

The exploration of the American continent revealed large numbers of new plants and animals that needed descriptions and classification. In the latter part of the 16th century and the beginning of the 17th, careful study of animals commenced and was gradually extended until it formed a sufficient body of knowledge to serve as an anatomical basis for classification.

In the late 1740s, Carolus Linnaeus introduced his method, still used, to formulate the scientific name of every species. Linnaeus took every effort to improve the composition and reduce the length of the many-worded names by abolishing unnecessary rhetoric, introducing new descriptive terms and defining their meaning with an unprecedented precision. By consistently using his system, Linnaeus separated nomenclature from taxonomy. This convention for naming species is referred to as binomial nomenclature.

The fungi were originally treated as plants. For a short period Linnaeus had placed them in the taxon Vermes in Animalia. He later placed them back in Plantae. Copeland classified the Fungi in his Protoctista, thus partially avoiding the problem but acknowledged their special status. The problem was eventually solved by Whittaker, when he gave them their own kingdom in his five-kingdom system. As it turned out, the fungi are more closely related to animals than to plants.

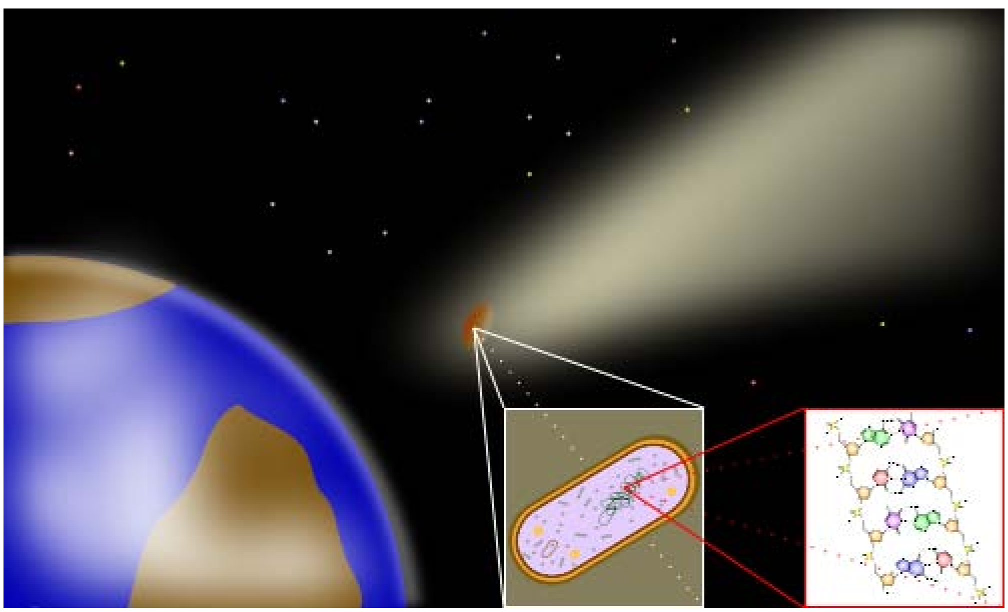
As new discoveries enabled us to study cells and microorganisms, new groups of life were revealed, and the fields of cell biology and microbiology were created. These new organisms were originally described separately in protozoa as animals and protophyta/thallophyta as plants, but were united by Haeckel in his kingdom protista, later the group of prokaryotes were split off in the kingdom Monera, eventually this kingdom would be divided in two separate groups, the Bacteria and the Archaea, leading to the six-kingdom system and eventually to the current three-domain system. The classification of eukaryotes is still controversial, with protist taxonomy especially problematic.

As microbiology, molecular biology and virology developed, non-cellular reproducing agents were discovered, such as viruses and viroids. Sometimes these entities are considered to be alive but others argue that viruses are not living organisms since they lack characteristics such as cell membrane, metabolism and do not grow or respond to their environments. Viruses can however be classed into "species" based on their biology and genetics but many aspects of such a classification remain controversial.

Since the 1960s a trend called cladistics has emerged, arranging taxa in an evolutionary or phylogenetic tree. It is unclear, should this be implemented, how the different codes will coexist.

<table>
<tr><th>Linnaeus 1735
2 kingdoms</th><th>Haeckel 1866
3 kingdoms</th><th>Chatton 1925
2 empires</th><th>Copeland 1938
4 kingdoms</th><th>Whittaker 1969
5 kingdoms</th><th>Woese et al. 1977
6 kingdoms</th><th>Woese et al. 1990
3 domains</th><th>Cavalier-Smith 2004
6 kingdoms</th></tr>
<tr><td rowspan="4">(not treated)</td><td rowspan="4">Protista</td><td rowspan="2">Prokaryota</td><td rowspan="2">Mychota</td><td rowspan="2">Monera</td><td>Eubacteria</td><td>Bacteria</td><td rowspan="2">Bacteria</td></tr>
<tr><td>Archaebacteria</td><td>Archaea</td></tr>
<tr><td rowspan="5">Eukaryota</td><td rowspan="2">Protoctista</td><td rowspan="2">Protista</td><td rowspan="2">Protista</td><td rowspan="5">Eukarya</td><td>Protozoa</td></tr>
<tr><td>Chromista</td></tr>
<tr><td rowspan="2">Vegetabilia</td><td rowspan="2">Plantae</td><td>Plantae</td><td>Plantae</td><td>Plantae</td><td>Plantae</td></tr>
<tr><td>Protoctista</td><td>Fungi</td><td>Fungi</td><td>Fungi</td></tr>
<tr><td>Animalia</td><td>Animalia</td><td>Animalia</td><td>Animalia</td><td>Animalia</td><td>Animalia</td></tr>
</table>

Extraterrestrial life



Panspermia hypothesis

Earth is the only planet in the universe known to harbor life. The Drake equation, which relates the number of extraterrestrial civilizations in our galaxy with which we might come in contact, has been used to discuss the probability of life elsewhere, but scientists disagree on many of the values of variables in this equation. Depending on those values, the equation may either suggest that life arises frequently or infrequently.

The region around a main sequence star that could support Earth-like life on an Earth-like planet is known as the habitable zone. The inner and outer radii of this zone vary with the luminosity of the star, as does the time interval during which the zone will survive. Stars more massive than the Sun have a larger habitable zone, but will remain on the main sequence for a shorter time interval during which life can evolve. Small red dwarf stars have the opposite problem, compounded with higher levels of magnetic activity and the effects of tidal locking from close orbits. Hence, stars in the intermediate mass range such as the Sun may possess the optimal conditions for Earth-like life to develop. The location of the star within a galaxy may also have an impact on the likelihood of life forming.

Panspermia, also called exogenesis, is a hypothesis proposing that life originated elsewhere in the universe and was subsequently transferred to Earth in the form of spores perhaps via meteorites, comets or cosmic dust. However, this hypothesis does not help explain the ultimate origin of life.

Death

Death is the permanent termination of all vital functions or life processes in an organism or cell. After death, the remains of an organism become part of the biogeochemical cycle. Organisms may be consumed by a predator or a scavenger and leftover organic material may then be further decomposed by detritivores, organisms which recycle detritus, returning it to the environment for reuse in the food chain.

One of the challenges in defining death is in distinguishing it from life. Death would seem to refer to either the moment at which life ends, or when the state that follows life begins. However, determining when death has occurred requires drawing precise conceptual boundaries between life and death. This is problematic, however, because there is little consensus over how to define life. The nature of death has for millennia been a central concern of the world's religious traditions and of philosophical inquiry. Many religions maintain faith in either some kind of afterlife, reincarnation, or resurrection.

Extinction

Extinction is the gradual process by which a group of taxa or species dies out, reducing biodiversity. The moment of extinction is generally considered to be the death of the last individual of that species. Because a species' potential range may be very large, determining this moment is difficult, and is usually done retrospectively after a period of apparent absence. Species become extinct when they are no longer able to survive in changing habitat or against superior competition. Over the history of the Earth, over 99% of all the species that have ever lived have gone extinct; however, mass extinctions may have accelerated evolution by providing opportunities for new groups of organisms to diversify.

Fossils

Fossils are the preserved remains or traces of animals, plants, and other organisms from the remote past. The totality of fossils, both discovered and undiscovered, and their placement in fossil-containing rock formations and sedimentary layers (strata) is known as the *fossil record*. Such a preserved specimen is called a "fossil" if it is older than the arbitrary date of 10,000 years ago. Hence, fossils range in age from the youngest at the start of the Holocene Epoch to the oldest from the Archaean Eon, a few billion years old.

Chapter 9

Type (Biology)

Type specimen for *Cimbrophlebia brooksi*, a fossil scorpion fly. By convention, the red label denotes a type specimen.

In biology, a **type** is one particular specimen (or in some cases a group of specimens) of an organism to which the scientific name of that organism is formally attached. In other words, a type is an example that serves to anchor or centralize the defining features of that particular taxon.

A taxon is a scientifically named grouping of organisms with other like organisms, a set that includes some organisms and excludes others, based on a detailed published description (for example a species description) and on the provision of type material, which is usually available to scientists for examination in a major museum research collection, or similar institution.

Type specimen

According to a precise set of rules laid down by the ICZN and the ICBN, the scientific name of every taxon is almost always based on one particular *specimen*, or in some cases specimens. Types are of great significance to biologists, especially to taxonomists. Types are usually physical specimens that are kept in a specially designated *type collection* in a museum research collection, or are a particular plant sample in a herbarium. Usually types are a physical example of the taxon, but failing that, an image of an individual of that taxon can be used. This material is the "type" or "types" of that taxon. Describing species and appointing type specimens is part of scientific nomenclature and alpha taxonomy.

When identifying material, a scientist attempts to apply a taxon name to a specimen or group of specimens based on his or her understanding of the relevant taxa, based on (at least) having read the type description(s), preferably based on an examination of all the type material of all of the relevant taxa. If there is more than one named type that all appear to be the same taxon, then the oldest name takes precedence, and is considered to be the correct name of the material in hand. If on the other hand the taxon appears never to have been named at all, then the scientist or another qualified expert picks a type specimen and publishes a new name and an official description.

This process is crucial to the science of biological taxonomy. People's ideas of how living things should be grouped changes and shifts over time. How do we know that that that we call "*Canis lupus*" is the same thing, or approximately the same thing, as what they will be calling "*Canis lupus*" in 200 years time? It is possible to check this because there is a particular wolf specimen preserved in a museum somewhere, and everyone who uses that name--no matter what else they may mean by it--will mean that particular specimen.

Depending on the nomenclature code applied to the organism in question, a type can be a specimen, a culture, an illustration, a description, or a taxon.

For example, in the research collection of the Natural History Museum in London, there is a bird specimen numbered 1886.6.24.20. This is a specimen of a kind of bird commonly known as the Spotted Harrier, which currently bears the scientific name *Circus assimilis*. This particular specimen is the holotype for that species; the name *Circus assimilis* refers, by definition, to the species of that particular specimen. That species was named and described by Jardine and Selby in 1828, and the holotype was placed in the museum collection so that other scientists might refer to it as necessary.

Note that at least for type specimens there is no requirement for a "typical" individual to be used. When describing new species, this is often impossible to tell anyway until more research has been done. Genera and families, particularly those established by early taxonomists, tend to be named after species that are more "typical" for them, but here too this is not always the case and due to changes in systematics *cannot* be. Hence, the term name-bearing type or onomatophore is sometimes used, to denote the fact that biological types do not define "typical" individuals or (in zoology) taxa, but rather fix a scientific name to a specific operational taxonomic unit. Type specimens are theoretically even allowed to be aberrant or deformed individuals or color variations, though this is rarely chosen to be the case, as it makes it hard to determine to which population the individual belonged.

The usage of the term *type* is somewhat complicated by slightly different uses in botany and zoology. In the *PhyloCode*, type-based definitions are replaced by phylogenetic definitions.

Types in botany

In botanical nomenclature, a *type* (*typus*, *nomenclatural type*), "is that element to which the name of a taxon is permanently attached."

A botanical name, by itself, is only a phrase (of one to three words). For a name to be meaningful it is necessary to be sure what it applies to. A type fixes a botanical name to a taxon. In botany a type is either a specimen or an illustration. A specimen is a real plant (or one or more parts of a plant or a lot of small plants), dead and kept safe, "curated", in a herbarium (or the equivalent for fungi). Notable cases of where an illustration may serve as a type are (this is not an exclusive listing):

- A detailed drawing, painting, etc., depicting the plant, from the early days of plant taxonomy (as we now know it). In those days a dried plant was difficult to transport and hard to keep safe for the future: many specimens that famous botanists looked at have since been lost or damaged. However, there were devoted botanical artists who upon assignment by a botanist (or naturalist) could make a faithful and detailed work of botanical art, for inclusion in a costly book.
- A detailed picture of something that can be seen only through a microscope. A tiny 'plant' on a microscope slide makes for a poor type: the microscope slide may be lost or damaged, or it may be very difficult to find the 'plant' in question among whatever else is on the microscope slide. An illustration makes for a much more reliable type (Art 37.5 of the *Vienna Code*, 2006).

Note that a type fixes only a name to a single representative of the taxon. A type does not determine the circumscription (therefore a taxon is independent of its type species or specimen) of the taxon. For example, the common dandelion is a controversial taxon:

some botanists consider it to consist of over a hundred species, although most botanists regard it to be a single species. The type of the name *Taraxacum officinale* is the same whether the circumscription of the species includes all those small species (*Taraxacum officinale* is a 'big' species) or whether the circumscription is limited to only one small species among the other hundred (*Taraxacum officinale* is a 'small' species). In this case the name *Taraxacum officinale* is the same and the type of the name is the same, but the extent of what the name actually applies to varies strongly. Setting the circumscription of a taxon is done by a taxonomist in a publication.

Miscellaneous notes:

1. Usually, only a species or an infraspecific taxon can have a type of its own. For a new taxon (published on or after 1 January 1958) at these ranks a type should not be an illustration.
2. A genus (almost always) has the same type as that of one of its species. Because the mere name of the species is considered equivalent to that species's type, this species is frequently called the type specie, a phrase that has no standing under the *ICBN*.
3. A family has the same type as that of one of its genera (that is, almost always the type of a species). The term type genus for the same reason "type species" is.
4. The *ICBN* provides a listing of the various kinds of type in Art 9, the most important of which is the holotype. Note that the word "type" appears in botanical literature as a part of several terms that have no status under the *ICBN*: for example a clonotype, an herbarium specimen vegetatively propagated from (and thus a clone of) the same plant from which a type specimen was made that is used for documenting the type collection.

Types in zoology

In zoological nomenclature, the type of a species (or subspecies) is a specimen (or series of specimens), the type of a genus (or subgenus) is a species, and the type of a suprageneric taxon (e.g., family, etc.) is a genus. Names higher than superfamily rank do not have types. A "name-bearing type" "provides the objective standard of reference whereby the application of the name of a nominal taxon can be determined."

Definitions

- A type specimen is a vernacular term (not a formally defined term) typically used for an individual or fossil that is any of the various name-bearing types for a species. For example, the type specimen for the species *Homo neanderthalensis* was the specimen "Neanderthal-1" discovered by Johann Karl Fuhlrott in 1856 at Feldhofer in the Neander Valley in Germany, consisting of a skullcap, thigh bones, part of a pelvis, some ribs, and some arm and shoulder bones. There may be more than one type specimen, but there is (at least in modern times) only one holotype.

- A type species is the nominal species that is the name-bearing type of a nominal genus or subgenus.
- A type genus is the nominal genus that is the name-bearing type of a nominal family-group taxon.
- The type series are all those specimens included by the author in a taxon's formal description, unless the author explicitly or implicitly excludes them as part of the series.

Use of types

Although in reality biologists may examine many specimens (when available) of a new taxon before writing an official published species description, nonetheless, under the formal rules for naming species (the International Code of Zoological Nomenclature), a single type must be designated, as part of the published description.

When a single specimen is clearly designated in the original description, this specimen is known as the holotype of that species. The holotype is typically placed in a major museum, or similar well-known public collection, so that it is freely available for later examination by other biologists. Type illustrations have also been used by zoologists, as in the case of the Réunion Parakeet, which is known only from historical illustrations and descriptions.[:24]

A type description must include a diagnosis (typically, a discussion of similarities to and differences from closely related species), and an indication of where the type specimen or specimens are deposited for examination. The geographical location where a type specimen was originally found is known as its type locality. In the case of parasites, the term type host (or symbiotype) is used to indicate the host organism from which the type specimen was obtained.

Zoological collections are maintained by universities and museums. Ensuring that types are kept in good condition and made available for examination by taxonomists are two important functions of such collections. And, while there is only one *holotype* designated, there can be other "type" specimens, the following of which are formally defined:

- **Paratype** – Any additional specimen other than the holotype, listed in the type series, where the original description designated a holotype. These are not name-bearing types.
- **Neotype** – A specimen later selected to serve as the single type specimen when an original holotype has been lost or destroyed, or where the original author never cited a specimen.
- **Syntype** – Any of two or more specimens listed in a species description where a holotype was not designated; historically, syntypes were often explicitly designated as such, and under the present Code this is a requirement, but modern attempts to publish species description based on syntypes are generally frowned upon by practicing taxonomists, and most are gradually being replaced by lectotypes. Those that still exist are still considered name-bearing types.

- **Lectotype** – A specimen later selected to serve as the single type specimen for species originally described from a set of syntypes.
- **Paralectotype** – Any additional specimen from among a set of syntypes, after a lectotype has been designated from among them. These are not name-bearing types.
- **Hapantotype** – A special case in Protistans where the type consists of two or more specimens of "directly related individuals representing distinct stages in the life cycle"; these are collectively treated as a single entity, and lectotypes cannot be designated from among them.

The various types listed above are necessary because many species were described one or two centuries ago, when a single type specimen, a holotype, was often not designated. Also, types were not always carefully preserved, and intervening events such as wars and fires have resulted in destruction of original type material. The validity of a species name often rests upon the availability of original type specimens; or, if the type cannot be found, or one has never existed, upon the clarity of the description.

The ICZN has existed only since 1961, when the first edition of the Code was published. The ICZN does not always demand a type specimen for the historical validity of a species, and many "type-less" species do exist, perhaps the most notable being *Homo sapiens*. This example is instructive: the current edition of the Code, Article 75.3, prohibits the designation of a neotype unless there is "an exceptional need" for "clarifying the taxonomic status" of a species; as the status and identity of *H. sapiens* is not questioned, there is no exceptional need for clarification, and "any such neotype designation is invalid" (Article 75.2).

Recently, some species have been described where the type specimen was released alive back into the wild, such as the Bulo Burti Boubou (a bushshrike), described as *Laniarius liberatus*, in which the species description included DNA sequences from blood and feather samples. Assuming there is no future question as to the status of such a species, the absence of a type specimen does not invalidate the name, but it may be necessary in the future to designate a neotype for such a taxon, should any questions arise. However, in the case of the bushshrike, ornithologists have argued that the specimen was a rare and hitherto unknown color morph of a long-known species, using only the available blood and feather samples. While there is still some debate on the need to deposit actual killed individuals as type specimens, it can be observed that given proper vouchering and storage, tissue samples can be just as valuable even in case disputes about the validity of a species arise.

There are many other permutations and variations on terms using the suffix "-type" (e.g., allotype, cotype, topotype, generitype, isotype, isoneotype, etc.) but these are not formally regulated by the Code, and a great many are obsolete and/or idiosyncratic. However, some of these categories can potentially apply to genuine type specimens, such as a neotype; e.g., isotypic/topotypic specimens are preferred to other specimens, when they are available at the time a neotype is chosen (because they are from the same time and/or place as the original type).

The term fixation is used by the Code for the declaration of a name-bearing type, whether by original or subsequent designation.

Type species

Each genus must have a designated type species (the term "genotype" was once used for this but has been abandoned because the word has been co-opted for use in genetics and is much better known in that context). The description of a genus is usually based primarily on its type species, modified and expanded by the features of other included species. The generic name is permanently associated with the name-bearing type of its type species.

Ideally, a type species best exemplifies the essential characteristics of the genus to which it belongs, but this is subjective and, ultimately, technically irrelevant, as it is not a requirement of the Code. If the type species proves, upon closer examination, to belong to a pre-existing genus (a common occurrence), then all of the constituent species must be either moved into the pre-existing genus, or disassociated from the original type species and given a new generic name; the old generic name passes into synonymy and is abandoned unless there is a pressing need to make an exception (decided case-by-case, via petition to the International Commission on Zoological Nomenclature).

Type genus

A type genus is that genus from which the name of a family or subfamily is formed. As with type species, the type genus is not necessarily the most representative, but is usually the earliest described, largest or best known genus. It is not uncommon for the name of a family to be based upon the name of a type genus that has passed into synonymy; the family name does not need to be changed in such a situation.

Chapter 10

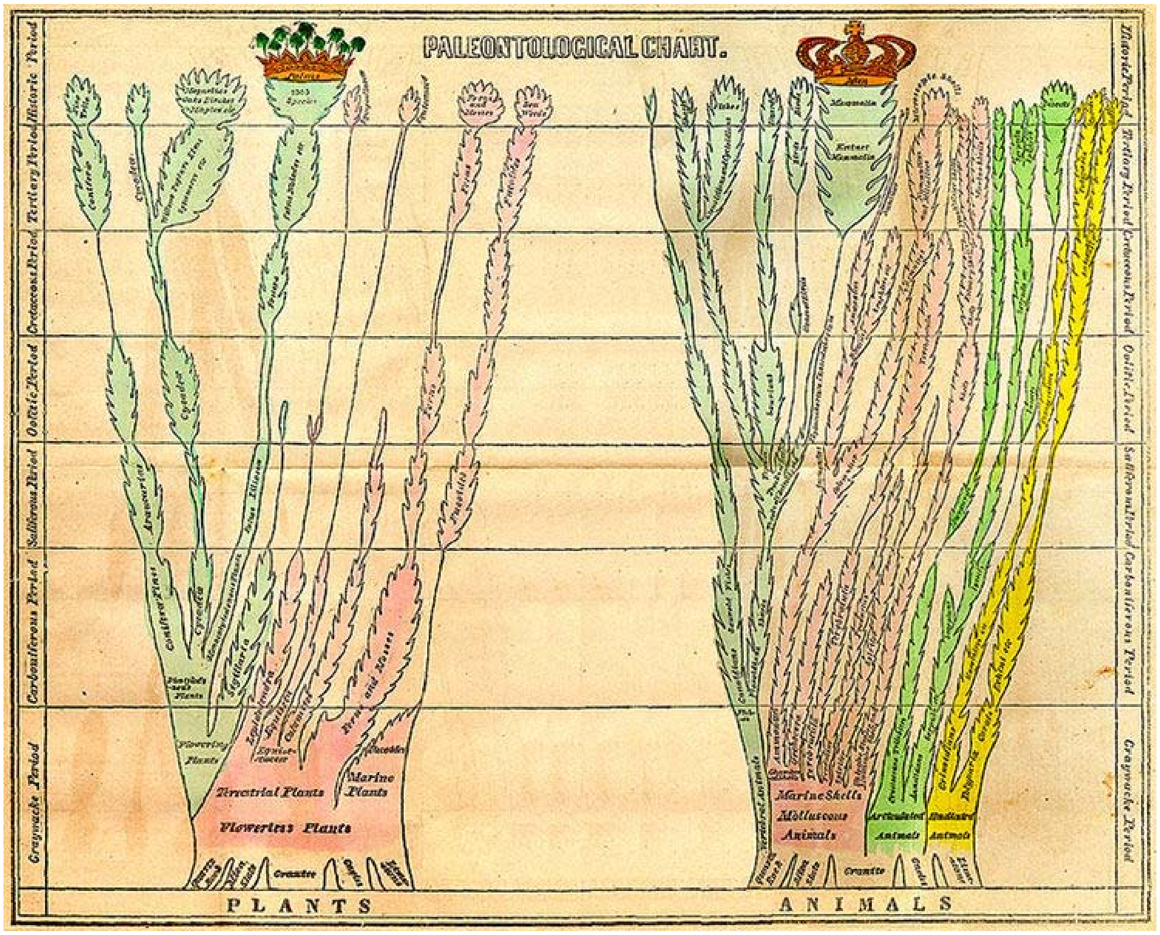
Evolutionary Taxonomy and Phylogenetic Nomenclature

Evolutionary taxonomy

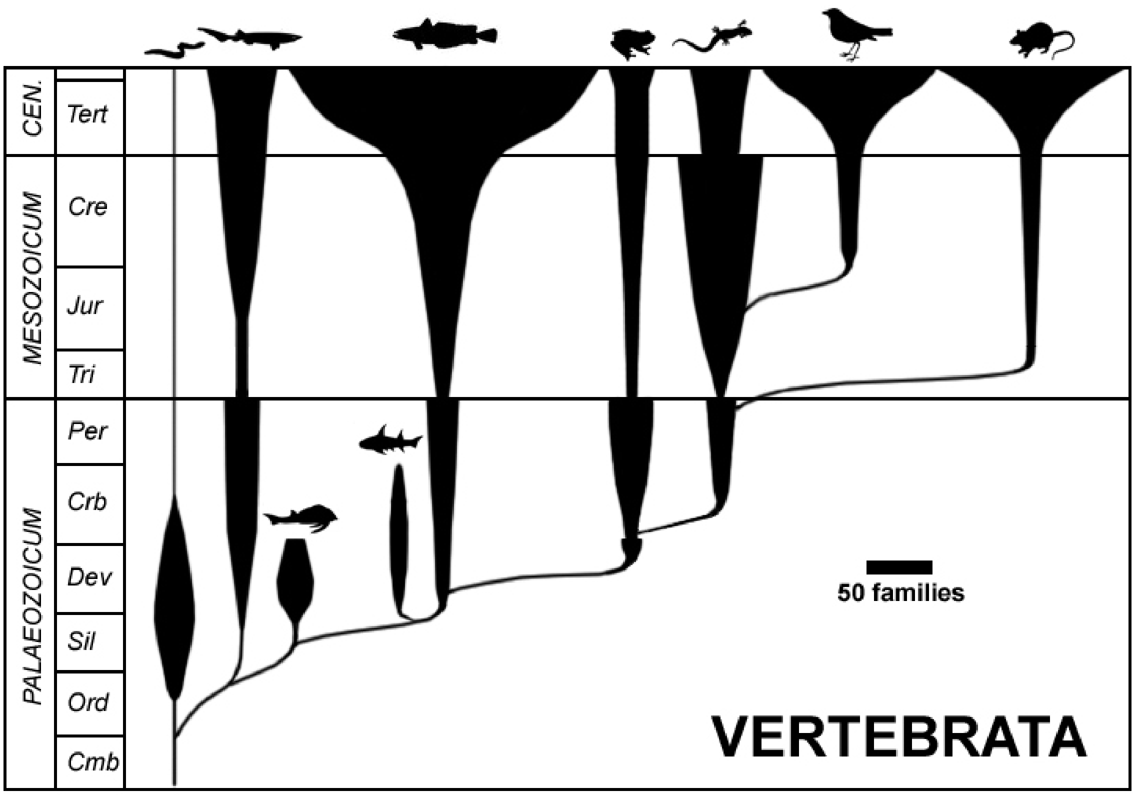
Evolutionary taxonomy, **evolutionary systematics** or **Darwinian classification** is a branch of biological classification that seeks to classify organisms using a combination of phylogenetic relationship and overall similarity. This type of taxonomy considers taxa rather than single species, so that groups of species give rise to new groups. The concept found its current form in the modern evolutionary synthesis of the early 1940's.

Evolutionary taxonomy differs from strict pre-Darwinian Linnaean taxonomy, which produces orderly lists rather than trees. Also, unlike cladism which only maps phylogeny, evolutionary taxonomy also offer a biological classification system.. While in phylogeny where each taxon must consist of a single ancestral node and all its descendants, evolutionary taxonomy allows for groups to be excluded from their parent taxa (e.g. dinosaurs are not considered to *include* birds, but to have *given rise* to them), thus allowing for paraphyletic taxa.

Origin of evolutionary taxonomy



Pre-evolutionary "Tree of Life", 1840. No fossil groups were sufficiently known to allow for a group to evolve from a known ancestor.



Evolution of the vertebrates at class level, width of spindles indicating number of families. Spindle diagrams are a hallmark of evolutionary taxonomy

Linnaean taxonomy was an established discipline when Darwin formulated his theory of evolution. The idea of the Linnaean taxonomy as translating into a sort of dendrogram of the Animal- and Plant Kingdoms was formulated toward the end of the 18th century, well before the *On the Origin of Species* was published. Among early works exploring the idea of a transmutation of species was Erasmus Darwin's 1796 Zoönomia and Jean-Baptiste Lamarck's Philosophie Zoologique of 1809. The idea was popularised in the Anglophone world by the speculative, but widely read Vestiges of the Natural History of Creation, published anonymously by Robert Chambers in 1844.

With Darwin's theory, this thought got a theoretical basis, and Tree of Life representations became popular in scientific works. Very limited knowledge of the fossil record at the time hindered the drawing of specific inferences about the ancestors of modern groups. Bout in *Vestiges of the Natural History of Creation* and *On the Origin of Species*, the ancestor remained largely a hypothetical species, and Darwin was primarily occupied with showing the relationship between living organisms.

One of the first fossil groups to be recognized was dinosaurs, formally named by Richard Owen in 1842. With Darwin's theory of evolution being known, Thomas Henry Huxley used the fossils of *Archaeopteryx* and *Hesperornis* to pronounce the birds descendants of the dinosaurs. Thus, a group of extant animals could be tied to a fossil group. The resulting description, that of dinosaurs "giving rise to" or being "the ancestors of" birds, is the essential hallmark of evolutionary taxonomic thinking.

The Tree of Life

As more and more fossil groups were found and recognized in the late 19th and early 20th century, palaeontologists worked to understand the history of animals through the ages by linking together known groups The Tree of life was slowly being mapped out, with fossil groups taking up their position in the tree as understanding increased. With the modern evolutionary synthesis of the early 1940's, an essentially modern understanding of evolution of the major groups was in place.

These groups still retained their formal Linnaean taxonomic ranks, giving rise to a number of units that were paraphyletic, i.e. where the descendants were considered a part of the daughter group rather than that of the ancestral group. Particularly on the level of orders and classes, most of the traditional vertebrate systematic units are paraphyletic, representing natural evolutionary grades rather than clades.

Difference from cladistic taxonomy

The two approaches differ in the use of the word *monophyletic*. For evolutionary systematicists, monophyletic means only that a group derives from a single common ancestor included in the group, whereas for cladists it also means that the group includes all species descended from that group. The term *holophyletic* has been proposed for the latter meaning.

The product of evolutionary systematics is a division according to Linnaean taxonomy (which can then be used to form tentative conclusions about phylogeny); the product of a cladistic classification is a cladogram, which can then be used to recommend a taxonomy.

Cladistics collects character data only from the taxa being classified. It does not consider the inferred characters of ancestors.

Evolutionary systematics also differs in method from cladistics. Cladistics involves collecting data and feeding it into a computer program. Evolutionary systematics involves a researcher following flexible guidelines which consider various kinds of evidence (which need not be represented as discrete alternatives).

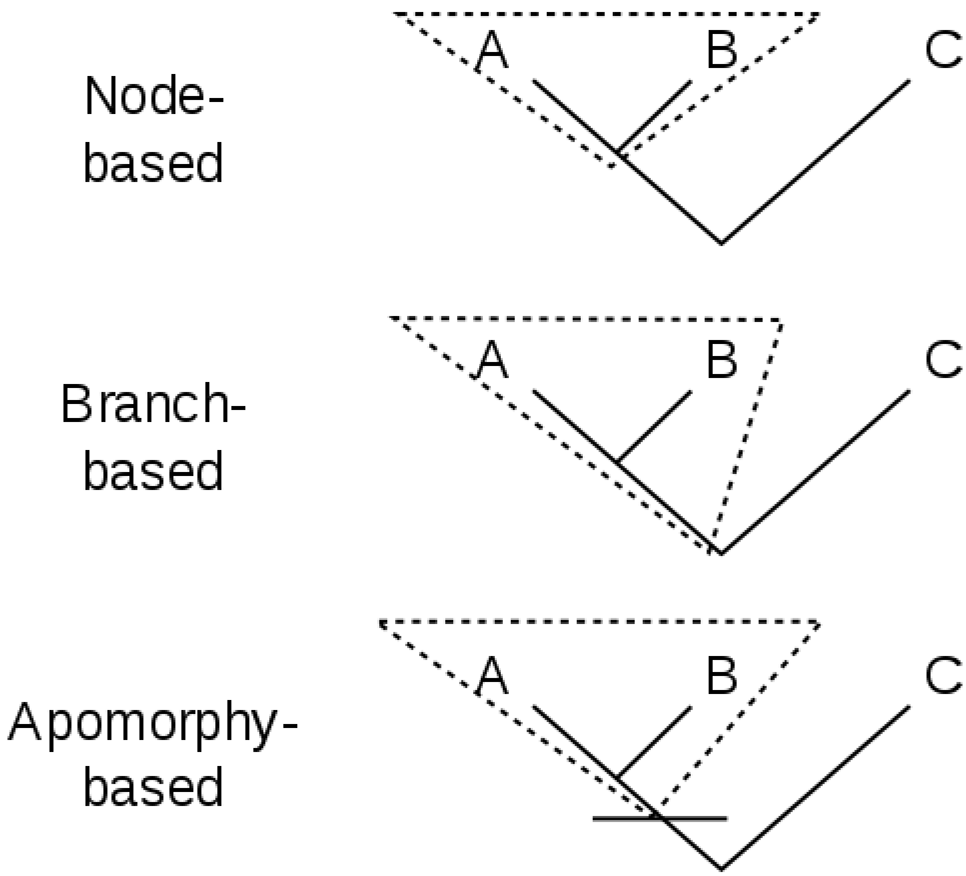
Other debates between evolutionary systematists and cladists are not about the underlying approach, but on details. One is whether there is a danger of artificial classifications when preparing a classification using molecular phylogeny based on only a single gene or part of a gene. Another is whether it is sufficient to study DNA from chloroplasts, mitochondria, and ribosomes, as opposed to non-ribosomal nuclear DNA.

Phylogenetic nomenclature

Phylogenetic nomenclature (PN) or **phylogenetic taxonomy** is an alternative to rank-based nomenclature, applying definitions from cladistics (or *phylogenetic systematics*). Its two defining features are the use of *phylogenetic definitions* of biological taxon names, and the *lack of obligatory ranks*. It is currently not regulated, but the *PhyloCode* (*International Code of Phylogenetic Nomenclature*) is intended to regulate it once implemented.

The terms **cladism** and **cladist** were first introduced by Ernst W. Mayr in 1965. They sometimes refer to cladistics as a whole.

Definitions



Types of phylogenetic definitions. The horizontal bar indicates the evolution of the apomorphy mentioned in the apomorphy-based definition. "Branch-based" was formerly called "stem-based"; the term was changed to avoid confusion with the term "stem group" which means total clade minus crown clade.

Under the rank-based codes of biological nomenclature, names themselves do not have definitions, but are instead usually linked to a type. Some biologists have claimed that this is unsatisfactory and that instability in nomenclature should only reflect instability of our knowledge of phylogeny, not instability in subjective opinions about which ranks should be given to which groups. Phylogenetic nomenclature, on the other hand, uses phylogenetic definitions to tie a name to a clade in such a manner that the meaning of the name is objective under any phylogenetic hypothesis, thus preventing splitting and lumping (unless definitions are changed in the process, which will be allowed under the *PhyloCode* only under carefully restricted circumstances).

Traditionally, groups named in phylogenetic nomenclature are usually monophyletic-that is, they define a natural group made up of all descendants of a single common ancestor. However, it is also possible to create phylogenetic definitions for the names of paraphyletic taxa . Assuming Mammalia and Aves are defined, Reptilia could be defined as "the most recent common ancestor of birds and mammals and all its descendants except birds and mammals". This includes taxa that are not currently named and even taxa that cannot be named under the rank-based codes without seriously disrupting existing classifications, such as "all organisms that share a more recent common ancestor with *Homo sapiens* than with birds and plesiomorphically keep laying eggs". Names of polyphyletic taxa could be defined by referring to the sum of two or more clades or paraphyletic taxa .

Philosophy

Rank-based and phylogenetic nomenclature differ in philosophical outlook. Rank-based nomenclature is linked to classification: it starts with the known species (or subspecies or varieties or even individuals), waits for an act of classification to group them into larger taxa, and then asks how to name these taxa. Phylogenetic nomenclature, on the other hand, starts with the phylogenetic tree of life (as hypothesized by the science of phylogenetics) and asks how and where to tie labels to its branches. Furthermore, phylogenetic nomenclature follows the nomenclature in other sciences in trying to define its terms as precisely as possible, while rank-based nomenclature deliberately keeps its definitions incomplete; for example, Principle 2 of the ICZN is "Nomenclature does not determine the inclusiveness or exclusiveness of any taxon". This is the result of a third philosophical difference: users of rank-based nomenclature commonly start from a name and ask for its meaning (in other words: which taxon the name should be applied to), while users of phylogenetic nomenclature tend to start from a clade and ask what to call it.

Lack of ranks

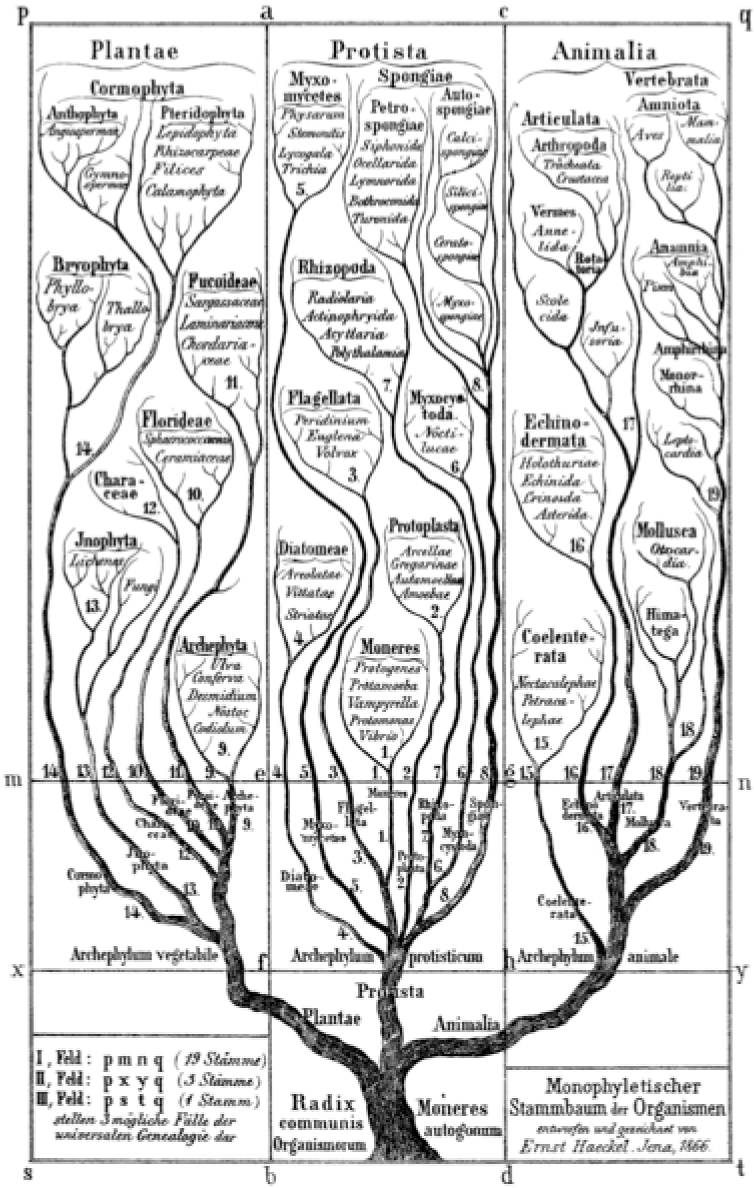
The current codes of biological nomenclature stipulate that taxa cannot be given a valid name without being given a rank. However, the number of generally recognized ranks is limited. Gauthier *et al.* (1988) showed that a classification which uses the common array of ranks, but includes Aves within Reptilia and keeps Reptilia at its traditional rank of class, is forced to demote Aves to the rank of genus, despite the ~ 12,000 known species of extant and extinct birds that would have to be incorporated into this one genus. To reduce this problem, Patterson and Rosen (1977) suggested nine new ranks between family and superfamily in order to be able to classify a clade of herrings, and McKenna and Bell (1997) introduced a large array of new ranks in order to cope with the diversity of Mammalia.

The current codes also each have rules saying that names must have certain endings if they are applied to taxa that have certain ranks. When a taxon changes rank from one classification to another, its name must change its suffix. Ereshefsky (1997:512) stated:

The Linnaean rule of assigning rank-specific suffices [sic] gives rise to even more confusing cases. Simpson (1963, 29–30) and Wiley (1981, 238) agree that the genus *Homo* belongs to a particular taxon. They disagree, however, on that taxon's rank. Acting in accord with the Linnaean system, they attach different suffixes to the root *Homini* [actually Homin-] and give the taxon in question different names: Wiley calls it 'Hominini' [tribe rank] and Simpson calls it 'Hominidae' [family rank]. Their disagreement does not stop there. Wiley believes that the taxon just cited is a part of a more inclusive taxon which is a family. Using the root *Homini*, and following the rules of the Linnaean system [more precisely, the zoological code], he names the more inclusive taxon 'Hominidae.' So for Wiley and Simpson, the name 'Hominidae' refers to two different taxa. In brief, the Linnaean system causes Wiley and Simpson to assign different names to what they agree is the same taxon, and it causes them to give the same name to what they agree are different taxa.

In phylogenetic nomenclature, ranks have no bearing on the spelling of taxon names. Ranks are, however, not altogether forbidden in phylogenetic nomenclature. They are merely decoupled from nomenclature: they do not influence which names can be used, which taxa are associated with which names, and which names can refer to nested taxa (e.g.).

History



"Monophyletic tree of organisms". Ernst Haeckel: *Generelle Morphologie der Organismen,* etc. Berlin, 1866.

Ultimately, phylogenetic nomenclature is a result of Darwin's discovery that the diversity and history of life is best represented in tree-shaped diagrams. This discovery immediately led to changes in the existing classifications. For example, John Hogg proposed the term Protoctista in 1860 for organisms that did not seem closely related to either animals or plants. In 1866, the controversial biologist Ernst Haeckel for the first time reconstructed a single tree of all life (see figure) and immediately proceeded to translate it into a classification. This classification was rank-based, in accordance with the only code of biological nomenclature that existed at the time, but did not contain taxa that

Haeckel considered polyphyletic; in it, Haeckel introduced the rank of phylum which carries a connotation of monophyly in its name.

Ever since it has been debated in which ways and to what extent the phylogeny of life should be used as a basis for its classification, with views ranging from "numerical taxonomy" (phenetics) over "evolutionary taxonomy" (gradistics) to "phylogenetic systematics" (cladistics – today, the term "cladistics" is only used for the method of phylogeny reconstruction, but its inventor, Willi Hennig, regarded this method as a mere tool for the purpose of classification). From the 1960s onwards, rankless classifications were occasionally proposed, but in general the principles of rank-based nomenclature were used by all three schools of thought.

Most of the basic tenets of phylogenetic nomenclature (lack of obligatory ranks, and something close to phylogenetic definitions) can, however, be traced to 1916, when Edwin Goodrich interpreted the name Sauropsida, erected 40 years earlier by Huxley, to include the birds (Aves) as well as *part of* Reptilia, and coined the new name Theropsida to include the mammals as well as another *part of* Reptilia, but did not give them ranks, and treated them exactly as if they had what would today be termed branch-based definitions, using neither contents nor diagnostic characters to decide whether a given animal should belong to Theropsida, Sauropsida, or something else once its phylogenetic position was agreed upon. Goodrich also opined that the name Reptilia should be abandoned once the phylogeny of the reptiles would be better known. The lack of compatibility of his scheme with the existing rank-based classifications (despite agreement on the phylogeny in all but details), and the lack of a method of phylogenetics at this time, are the most likely reasons why Goodrich's suggestions were largely ignored.

The principle that only clades (monophyletic taxa – an ancestor plus all its descendants) should be formally named became popular in the second half of the 20th century. It spread together with the methods for discovering clades (cladistics) and is an integral part of phylogenetic systematics (see above). At the same time, it became apparent that the obligatory ranks that are part of the traditional systems of nomenclature produced problems. Some authors suggested abandoning them altogether, starting with Willi Hennig's abandonment of his earlier proposal to define ranks as geological age classes.

The origin of phylogenetic nomenclature can be dated to 1986, when Jacques Gauthier used phylogenetic definitions for the first time in a published work. Theoretical papers outlining the principles of phylogenetic nomenclature, as well as further publications containing applications of phylogenetic nomenclature (mostly to vertebrates), soon followed.

In an attempt to avoid a schism in the biologist community, "Gauthier suggested to two members of the ICZN to apply formal taxonomic names ruled by the zoological code only to clades (at least for supraspecific taxa) and to abandon Linnean ranks, but these two members promptly rejected these ideas" (Laurin, 2008: 224). This led him, Kevin de Queiroz, and the botanist Philip Cantino to start drafting their own code of nomenclature, the *PhyloCode*, for regulating phylogenetic nomenclature.