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# Principles of Taxonomy and Classification: Current Procedures for Naming and Classifying Organisms

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## Abstract

Taxonomy deals with the naming and classification of organisms and is an integrative part of biological systematics, the science of biodiversity. The information provided by taxonomic research is a fundamental basis for all fields of biology. Current taxonomy focuses on multicharacter integrative approaches, considering all potentially useful sources of information provided by the various fields of biology. The resulting supraspecific classification should be based on the genealogy of organisms, that is, on a phylogenetic analysis, to be objectively testable. However, for pragmatical reasons, a classification based on overall similarity and diagnostically relevant characters might be a heuristically important step in taxonomy and should be perceived as an approximation to a classification tested by phylogenetic methods. The nested levels in a classification of organisms are usually not only named but also ranked, that is, a set of hierarchical terms, like *genus*, *family*, and *class*, is applied to reflect the hierarchical structure of the classification. Assigning these so-called Linnaean categories to a classification is (1) a voluntary action to make a classification notionally more easy to access and (2) a linguistic activity that is done subsequent to obtaining the scientific results of the systematic analysis.

## Introduction

Taxonomy, the science and method of naming organisms, is a fundamental basis for all biological science and its application (Sluys 2013). The primary task of taxonomy is to describe, establish, and give an account of the order that is an inherent property of biological diversity. The order of names provided by taxonomy is arranged as a hierarchical classification, which is considered to portray the hierarchy of species and more inclusive taxa as a result of the continuous chain of species splittings in the evolutionary history of life on earth. Generalizations on organisms as a basic principle in biology are only possible if the infinite number of items in science is classified. Statements about the overwhelming diversity of nature would be impossible without methods for bringing order to this diversity. The world's biota is a vast library of information concerning any aspect of life, and taxonomy is the cataloguing system that everybody must use to access its information. All kinds of biological science and applications link their specific data to species names and use these names for effective communication. As Longino (1993, p. 85) has paraphrased, "... taxonomy is the raw material from which hypotheses of phylogeny are derived." All kinds of comparative biology rely on sound phylogenetic hypotheses, and the reliability of a phylogenetic hypothesis immediately

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depends on the reliability of the underlying taxonomic data. Moreover, society has an increasing need for reliable taxonomic information in order to allow to manage and understand the world's biodiversity (Wheeler et al. 2004; Costello et al. 2013). Until recently, taxonomy was confronted with what Godfray (2002, p. 17) called a new bioinformatics crisis, evidenced "by a lack of prestige and resources that is crippling the continuing cataloguing of biodiversity." Current biological taxonomy quite successfully adopts methods, data structure, and other demands of techniques and theories invented by new entrants to the biological sciences such as the fields of molecular biology (e.g., DNA barcoding; see De Salle et al. 2005). However, all other useful sources of information are simultaneously gathered in modern taxonomy, and this multicharacter integrative approach has been called *integrative taxonomy* (Dayrat 2005; Wheeler 2005; Padial et al. 2010). It allows taxonomists to create new common visions to meet changing demands of a changing global view on global biodiversity and the threats to it (Wheeler and Valdecasas 2005; Wheeler 2008; Polaszek 2010; Wheeler et al. 2012).

## Definitions

Inconsistent terminology is a barrier to communication, results in confusion and misunderstanding, and prevents effective science. The variation in definitions for "taxonomy," "systematics," "classification," and related or derived terms is as complex as it is contradictory. The major problem with these obviously closely allied terms is to differentiate them from each other, and many authors treat them more or less as synonyms, either intentionally or intuitively. In a recent textbook on biological systematics, Schuh (2000) implicitly equated systematics, classification, and taxonomy, when he defined systematics as "the science of biological classification." The opposite view is held by Hawksworth and Bisby (1988, p. 10), who suggested restricting taxonomy to "taxonomic information systems (classification, nomenclature, descriptions, identification aids)" and defining systematics to include "taxonomy in the above restricted sense together with analyses of variation, of phylogeny, evolutionary processes, etc."

Probably, most current scientists would agree that the most appropriate name for the scientific area composed of taxonomy, systematics, classification, and all of their respective concepts, theories, and methods is "biological systematics," or systematics in short.

What are the basic units of systematics? Systematics is not concerned with individual organisms, although these are always studied by systematists as representatives of species or other supraspecific groupings. The simplest and most descriptive statement would be that systematics deals with taxa. What then is a *taxon* (plural, taxa)? Simpson (1961, p. 19) defined it as "a group of real organisms recognized as a formal unit at any level of a hierarchic classification." This definition recognizes groups of organisms as taxa only if they are already formally classified, which is not always necessary or wanted. Newly discovered groups, hypothetical groups that still await confirmation, putatively artificial groups that are still disputed, and many others do not qualify as taxa under Simpson's definition. In the field of phylogenetic systematics or cladistics, the taxon definition is often narrowed even further to monophyletic groups of organisms (Sudhaus and Rehfeld 1992; Mayr and Bock 2002). The final objective of systematics is indeed to include monophyletic groups only, but for a wide variety of reasons, this goal can hardly be achieved right away. Hypotheses on monophyly are created and rejected, groups prove to be nonmonophyletic but are still being discussed, and putatively monophyletic groups are still of unknown position within a certain higher lineage. Other problematic cases are fossil stem groups, like Australopithecinae, which are obviously paraphyletic with respect to Hominidae but can be treated as a heuristically important

grouping in paleoanthropology. All these groupings are best referred to by a generalized term, and taxon is the most appropriate one. Hence, a definition of the term taxon might be: “A taxon is a group of organisms that can be differentiated from other groups of organisms, and that can be described and named.” Other terms to replace the term taxon have been proposed that are considered to carry specific connotations to reflect a specific framework for which they have been proposed. *Terminal taxon*, as used in cladistics, and *operational taxonomic unit* (OTU), proposed by the phenetic school of systematics, are two prominent examples that have been suggested to designate the units of systematics without reference to a particular rank or phylogenetic position. However, the term taxon, as here defined, is sufficient to refer to ranked and unranked groups of organisms.

Biological systematics in fact deals with taxa, that is, biological populations, species, and higher taxa. However, systematics is concerned not only with the taxa themselves and their description and characterization but also with their origin, development, and other kinds of interrelationships. The fundamental and underlying concept of systematics is evolution, and Huxley (1940a, b) regarded systematics as “detecting evolution at work.” Simpson’s (1961, p. 7) classical definition of biological systematics (or just systematics) is still adequate: “Systematics is the scientific study of kinds and diversity of organisms and of any and all relationships among them.” This definition was subsequently simplified to include the modern term “biodiversity,” e.g., Mayr and Ashlock (1991) and Sudhaus and Rehfeld (1992, p. 11): “Systematics is the science of the diversity of organisms.”

Another term that plays an important role in biodiversity research is taxonomy. Taxonomy is not easy to differentiate from systematics, and it has been frequently intermingled with systematics. If separated, taxonomy usually refers to what Hawksworth and Bisby (1988, p. 10) called “taxonomic information systems,” i.e., naming of taxa, nomenclature, descriptions, and identification aids, whereas systematics is widely understood in a general sense of including taxonomy and the analysis of phylogenetic relationships, speciation processes, variation, and others. Since under any definition the terms taxonomy and systematics are closely associated, many authors have simply synonymized them because they consider their separation not to be feasible. The development of a concise methodology and theory of phylogenetic systematics in the last decades has considerably influenced the practice of modern taxonomy. Taxonomy, as understood here, might be treated as a field of systematics, with specific methods, theories, conventions, and terminologies that are different from other systematic fields (Will and Rubinoff 2004). There is, of course, continuous, active transgression of the borders between taxonomy and other branches of systematics, such as phylogeny and biogeography, and the most desired taxonomic revisions are obviously those whose taxonomic decisions are tested by phylogenetic analysis. To summarize, an appropriate definition of taxonomy might be (modified from Winston 1999, p. 9):

Taxonomy is the branch of biological systematics that is concerned with naming of organisms (according to a set of rules developed for the process), identification (referring specimens to previously named taxa), and classification (ordering taxa into an encaptic hierarchy based on perceived characters).

The set of rules that governs the formation and use of taxon names in zoology is provided by the *International Code of Zoological Nomenclature* (hereafter referred to as the *Code*), published by the *International Commission on Zoological Nomenclature* and currently in its fourth edition. The Code and its bearing on taxonomy will be briefly discussed later. The definition described earlier points out that a classification of organisms is based on perceived characters. Any organism consists of innumerable numbers of characters that can potentially be perceived by a biologist, but not all of them qualify as characters helpful in achieving a meaningful classification. The so-called phylogenetic systematics provides the objective framework for evaluating characters according to their meaning for the evolution of a taxon. The most reliable and testable classification is based on the

results of a phylogenetic analysis, which tries to reconstruct the hierarchical structure of organisms as a result of the continuous sequence of speciation events in evolution. This should be the basic goal of all taxonomy. However, for different reasons, phylogenetic relatedness might (still) be unknown, and thus the set of perceived characters for establishing a sound classification might be selected intersubjectively by means of overall similarity and diagnostically relevant characters. A classification based on overall similarity might be a heuristically important step in biological systematics and should be perceived as an approximation to a classification based on phylogenetic hypotheses. In practice, such non- (or pre)phylogenetic classifications might stand for a long time, but they should be regarded as preliminary until tested by phylogenetic methods.

The previously mentioned definition of taxonomy implies that one of its main goals is a classification. As paraphrased by Schuh (2000, p. 15), a “classification represents the codification of the results of [bio]systematic studies.” A general definition of classification might be:

A classification is a set of names that are ordered hierarchically and more and more inclusive. The hierarchy of names is considered to portray the hierarchy of organisms as the result of the evolutionary process.

Again, the hierarchy of organisms should preferably be recovered by means of phylogenetic methods but might be preliminarily but meaningfully approached by the criterion of overall similarity.

Some authors (Griffiths 1974; Wägele 2005) differentiate classification from *systematization* for fundamental reasons. The term classification originates from the term *class* as in use in the philosophical logic and means a group of objects that have a specific set of properties in common. Which property is selected as class-defining is purely subjective and arbitrary, and a classification based on this property is similarly subjective. Thus, a classification, as defined by Wägele and others, is considered to be a strictly conceptual system and is the product of an arbitrary, linguistic activity. In contrast, organisms are the product of the historical process of evolution, which is expressed as a continuous chain of speciation events during the history of life. The sequence of species splittings over millions of years has resulted in a hierarchical structure of the organisms that systematists achieve to *reconstruct*. Thus, this kind of hierarchy is conceptual as well, but it is considered to represent the hypothetically real sequence of speciation events in evolution. This process is called systematization by Wägele (2005). The conceptual representation of the mental order as achieved by the process of systematization is called a *phylogenetic system*. The difference between a classification and a systematization is of fundamental importance but is usually not considered in practical biological systematics. The term classification is used here for both ordering systems, which is in accord with the widely accepted understanding, but the resulting double meaning of classification and the respective subtle differences to systematization must be kept in mind.

A completed classification is a hierarchy of names that denote hypotheses on taxa. It is organized in a more and more inclusive terminological structure of a theoretically infinite number of levels. These levels may bear names, but many of them, particularly in fully resolved cladograms with vast numbers of levels, remain unnamed for practical reasons. After completing a classification and selecting an appropriate number of higher taxa to be named, the hierarchically organized set of named levels can be given relative ranks as individual designations. Such relative ranks are provided by *categories*, such as classes, families, and genera, and this system of categories is well known as the *Linnaean hierarchy* or the *Linnaean categories*. Although the meaning and the current status of the Linnaean categories will be discussed later in more detail, it should be stressed here that an assignment of Linnaean categories to the level of a classification is (1) a voluntary action in order to

make a classification notionally more easy to access and (2) a linguistic activity that is done subsequent to obtaining the scientific results of the systematic analysis.

As has been demonstrated previously, names as linguistic elements are of crucial importance in biological systematics. Names serve as labels to relate to concepts and hypotheses about taxa and their evolution. Names should principally be unequivocal, universal, international, and perpetual. Due to the incommensurably large number of organisms on earth, not to speak of the immense numbers of theoretically possible higher taxa that all could, at least in principle, be named, the need for internationally binding regulations is obvious. The part of taxonomy that is concerned with assigning names to taxa is called *nomenclature*. The sets of regulations that govern the practical application of nomenclature are provided by the International Code of Zoological Nomenclature.

## Taxonomy as a System of Ordering Data

Biologists deal with a remarkable diversity of items. For any scientific procedure in biology, it is of critical importance to differentiate and thus to compare these items. It is one of the intrinsic attributes of a comparative process to arrange the to-be-compared items according to specified properties, that is, to *classify* these items. Mayr (1995) differentiated four different kinds of classifications: (1) special purpose classifications (based on particular features of special importance in the context, e.g., ecologists may divide small mammals into soil dwellers and tree dwellers), (2) downward classification by logical division (starting with the entire animal kingdom, groups are defined on the basis of dichotomous splittings in two less inclusive groups, such as the warm-blooded and the cold-blooded animals, until the species level is reached), (3) upward or grouping classification (items are arranged in more and more inclusive groups according to observed characters), and finally, (4) Hennigian phylogenetic or cladistic system (grouping of species and higher taxa on the basis of common descent). With respect to their nature as ordering systems, the upward classification (3) and phylogenetic systematics (4) do not differ, because in both classifications, species are combined into higher taxa (ranked as genera), these higher taxa are combined into even more inclusive taxa, and so forth. However, phylogenetic systematics is a special kind of upward classification in permitting only one criterion as the basis for the classification, that is, common descent.

Five basic objectives of ordering systems can be differentiated in general and apply to biological systematics as well (Vane-Wright 2001; Mayr and Bock 2002): (1) discrimination (delimiting groups against other groups), (2) information storage and retrieval (the structure of classification systems, based on different criteria that are considered to be informative regarding the group, permits storage and retrieval of a large amount of information), (3) recognizing group affiliations (this is called identification and refers to the process of referring an organism to a previously described taxon, e.g., by the use of a dichotomous key), (4) inferences about not yet studied properties (it is a widely held prediction that many of the characters of a taxon studied will be similar or even identical to those of closely or immediately related taxa), and (5) to serve as a baseline in comparative studies (the validity of comparative studies in biology largely depends on the reliability of the preceding research by which the studied items were grouped). These are basic objectives of that part of biological systematics that focuses on the biological items themselves, i.e., organisms, species, and higher taxa. The scientific treatment of these items requires a scientific terminology to communicate, which is provided by biological nomenclature.



## Taxonomy and Classification Without Phylogeny: An Outdated Remnant or a Practical Necessity?

There is an increasing shift in taxonomy toward modifying the directives on how to name organisms to reflect genealogical relationships. However, despite the fact that most systematists would agree that the hierarchical system of names in biology should be governed by phylogenetic hypotheses instead of by intuitive similarity, the increasing pressure of phylogenetic demands on the naming processes results in intrinsic conflicts in systematics. Phylogenetic analyses have not been conducted for most groups of organisms yet, and it is highly unlikely that many will be undertaken soon. Additionally, new species are rapidly discovered in large numbers, particularly among invertebrates. Since a taxonomic treatment of such new taxa, that is, formal descriptions in taxonomic revisions or even single taxon descriptions, is a prerequisite to any other scientific exploration, new taxa are more rapidly described and made available than phylogenetic hypotheses are worked out. The taxonomic treatment of certain taxa, such as those that are less known, newly discovered, and/or extraordinarily species-rich, is a fundamental first step that opens up the possibility of continuing with subsequent phylogenetic, genetic, behavioral, and other studies.

In practical taxonomy, it is often necessary or at least recommendable initially to leave a comprehensive revision or a phylogenetic reconstruction aside from research projects and the resulting publications. In principle, Mayr and Ashlock (1991, p. 347) are correct that “the isolated description of . . . new species . . ., divorced from revisional or monographic work, is the least desirable form of taxonomic publication.” But Mayr and Ashlock correctly qualify their assertion themselves in stating that it does not hold “in well-known groups.” A well-known group is usually a taxon which is not only well known in terms of scientific research but also which additionally receives extraordinary attention by both the scientific and the general public. It is thus not surprising that isolated descriptions of fossil and recent Primates and large mammals often make their way to the highest-ranked scientific journals (e.g., the description of *Homo floresiensis* by Brown et al. 2004). Obviously, the publicity that results from such publications can be a strong motivation for any scientist to publish a rather isolated description immediately rather than to invest more time to obtain more data for a more comprehensive publication, due to the current system of scientists being under considerable pressure to publish and to compete for limited research money and, finally, jobs.

There are several more potential reasons to conduct *descriptive taxonomy* (Godfray 2002), which may mutually affect each other in most cases. Examples are as follows: (1) it might be desirable to make a new discovery formally available for further studies, which can or should not be conducted at the time of discovery of the new taxon for varying reasons; (2) if a scientist has discovered a new species, and if he intends to describe it formally, this scientist might want to guarantee that the name of this taxon as proposed by him is the first formal description and, thus, has priority over any subsequent name. This might be considered as to imply a connotation of personal rather than true scientific motivation, similar to the argumentation as presented earlier. However, priority is a basic principle of zoological nomenclature, and although it is explicitly thought to be priority of publication without reference to the date of discovery, the publication date here serves as an objectifiable reference point. Hence, priority of publication just replaces the priority of discovery for practical reasons; (3) incomplete knowledge of data might prevent systematists for conducting a comprehensive revision or a cladistic analysis. This might be due to the lack of characters (e.g., in fossils or other incompletely preserved specimens) or material (e.g., modern techniques such as molecular systematics or scanning electron microscopy require fresh or specifically preserved

material, but many rare but potentially informative species are known only from dry museum material, which cannot be fully examined).

Another topic concerns the role of biological systematics in the context of a global biodiversity assessment. The development of global species inventories is considered to be an urgent and vitally important task that is a primary step and fundamental activity for any kind of biodiversity research (Stork and Samways 1995; Purvis and Hector 2000; Wilson 2003). Although it seems to be clearly unrealistic to describe every species of organism on earth, not to speak of the monumental uncertainties as to how many species there are (Godfray 2002), any step toward a global inventory of selected “target taxa” should be achieved as soon as possible.

Phylogenies are inherently hypothetical, simply because they portray historical processes, which cannot be inferred directly. Hypotheses, however, can be of different quality. The reliability of a hypothesis largely depends on the quality of the underlying data, which involves numerous theoretical and methodological aspects. Among these aspects, the *completeness* of the data set is of crucial importance. Completeness of characters is an illusion, since each single organism theoretically consists of an infinite number of characters. Completeness of taxa is, at least in principle, possible. With regard to taxon sampling, the perfect systematic study would include all species of a given taxon, perhaps even both still living and extant. Practically, completeness of taxa is unlikely to be achieved in most groups, except perhaps for some exceptionally well-studied taxa such as birds. However, the reliability of a phylogenetic analysis increases with the increasing completeness of the taxon sampling. Conversely, gaps in the taxon coverage result in considerably less reliable phylogenetic hypotheses. In many cases, phylogenetic analysis should better wait for a more complete species inventory, which, particularly in taxa with many species or with a patchy distribution, can hardly be achieved in one step.

In summary, publications concerned with the taxonomy of a given group are most desirable if their classificational results are based on a comprehensive phylogenetic hypothesis. If at all possible, a systematist should try to interpret his taxonomic data with respect to the corresponding phylogeny rather than relying on an intuitive character evaluation as a basis for a classification. Incidentally, since the hierarchical structure of the organisms on earth is the result of a historically real, continuous sequence of species splittings, the hierarchy of organisms as reconstructed by phylogenetic methods is in the end the only objective base for a classification.

## **Zoological Nomenclature: Governing the Process of Naming**

Biologists are considered with myriad items, and these items need to be named to communicate concepts and hypothesis about these items in the biological sciences. It is not only the millions of species that have to be named. The hierarchical structure of the biodiversity of species and the myriad supraspecific taxa result in an almost infinite number of items that in principle can be named. Since names should be unequivocal in an international perspective, the formation and practical handling of names of species and higher taxa obviously need internationally binding regulations. Nomenclature is the part of taxonomy that regulates how names are assigned to taxa, and the underlying set of formal rules of how nomenclature is applied in practical zoology is the International Code of Zoological Nomenclature.

## **Ranking Hierarchies: Capacity and Limits of Linnaean Categories**

The Linnaean categories are terms that identify the hierarchical level in a classification. Examples for categories are *genus*, *family*, and *class*. A limited number of such categories date back to Carolus



Linnaeus' publications in the eighteenth century, but the number of categories has increased continuously over time, the better to reflect increasingly complex classifications. The rise of phylogenetic methods in the last few decades has resulted in an increasing number of cladograms that depict complex, not directly linear relationships with a seemingly infinite number of potential levels. It is, thus, not surprising that systematists face a myriad practical problems when assigning Linnaean categories to classifications based on cladograms resulting from phylogenetic analysis (Richter and Sudhaus 2004). Even in earlier phylogenetic publications, such as Hennig (1969), the conflicts between phylogenetic results and categories were well known, and in that publication, Hennig replaced the Linnaean categories by a system of consecutive numbers that directly reflects sister group relationships. However, his system received little attention from the beginning, because in less inclusive taxa, single numbers could be confusingly long (such as 2.2.2.2..4.6..1.1. Trichoptera, the sister group of 2.2.2.2..4.6..1.2. Lepidoptera). Hennig's system seems to have disappeared from consideration.

Since that time, various nomenclatural systems have been proposed to eliminate or replace the Linnaean categories, one of the most recent and popular alternative concepts being the *PhyloCode*. It is beyond the scope of this chapter to present the characteristics, the advantages, and the failures of the PhyloCode, but a critical assessment of the capacity and the limits of Linnaean system will be presented instead. It is still the most popular and widely accepted system of taxonomic ranking, and this is not due to the uncritical persistence of antiquated principles but, conversely, for good reasons. The reader should consult one of the numerous papers on the Linnaean categories and their alternatives for more information, such as Cantino and de Queiroz (2010) in the World Wide Web, Pleijel and Rouse (2003) in favor of the PhyloCode, and the rebuttals of arguments for the PhyloCode and its underlying theories by Nixon and Carpenter (2000, 2003), Carpenter (2003), Schuh (2003), and literature cited therein.

Ranking is an inherent property of any hierarchy in biological systematics, whether it is portrayed in a cladogram or by a formal Linnaean ranking scheme. Since ranking is included in any hierarchy, several unambiguous statements can be made concerning the structure of this hierarchy: for example, if taxon A is more inclusive than taxon B and actually includes B, then B does not contain A. However, the taxon names A and B themselves do not carry any reference per se about their relative position in the hierarchy, that is, whether A includes B, or vice versa, or whether A and B are of equal rank. In complex hierarchies, such as the hierarchy of organisms, the user is concerned with an overwhelming number of taxon names of different relative ranks, and he would be lost if any taxon bore an arbitrary name. Instead, communication is considerably more efficient if the ranking information is stated in addition to the taxon name. The Linnaean categories were invented exactly to convey this information by the use of standardized suffixes (for family group names) and binominal nomenclature for species. As an example, the Cercopithecidae, the Old World monkeys, is usually ranked as a family (indicated by the suffix *-idae*) and, among others, contains the subfamily Colobinae (with the suffix *-inae*) (Groves 2001).

The Linnaean ranking system was, and still is, extremely successful, and this is partly because it is easy to understand and to learn. Alternative concepts that have been proposed to replace the Linnaean categories are explicitly rankless. Taxon names still exist, but they do not communicate any information at all about their position in the hierarchy. The user can only understand the hierarchical structure by referring to the underlying cladogram. Hence, discarding Linnaean ranks and the binominal nomenclature results unnecessarily in the complete loss of important information on the taxa. This is not to say that the application of the Linnaean system is always unambiguous. Instead, there are numerous problems involved in taxonomic practice, particularly when portraying

complex cladograms in a hierarchical classification. However, it seems unlikely that “[any] single system of nomenclature can ever possess all desirable attributes” (Schuh 2003, p. 60).

### **Taxa and Categories Are Not the Same**

There is a fundamental difference between a taxon and a category. As defined earlier, taxa are groups of real organisms that can be described and named. They can be monophyletic, nonmonophyletic, or phylogenetically untested. In contrast, categories are terms that can be assigned to taxa to connote a certain rank relative to other, more inclusive or less inclusive taxa. Taxa are the objects of biological systematics, whereas categories are a voluntary, notional tool that improves communication among systematists.

### **Categories and Age**

Linnaean categories contain explicit and helpful information about the relative position of a taxon within a certain lineage. The central question in taxonomic practice is, if there is a hierarchy of names that is supposed to reflect a hypothesis of relatedness (or at least overall similarity), how can this hypothesis be aligned with the Linnaean categories in an objective way? To be honest, the “alignment” of the hierarchy of taxa and the hierarchy of categories is determined by practical considerations, which is in the end a matter of subjectivity. However, there is a long-lasting discussion of how to “objectify” the assignment of categories to a specific level in a classification. Actually, all efforts to do this have failed, and future efforts will probably fail. The reasons are easy to understand. Categories, as indicators of relative rank *within* a phylogenetic lineage of organisms, are inherently subjective, at least in a sense. It is a matter of usefulness for verbal communication and of convention and consistency, if, for example, taxon X is ranked as an order or a class. However, neither the hypothetically real hierarchy of organisms nor the categories themselves provide objective criteria on how to apply them.

However, several approaches to objectify categories have been published. Since phylogenetic reconstruction achieves to reconstruct historical events in the evolution of organisms, it is tempting to try to objectify the assignment of categories to taxa by using age as a criterion. This was already proposed by Hennig (1950, 1966), who discussed the problem of *absolute ranking* of higher taxa in exhaustive details. He suggested that the fossil record allows us to unambiguously define categories by the age of taxa to be classified. His example is the higher-level relationships of insects. Insects are generally considered to be ranked as a class, and since the oldest fossil insects, which belong in the Collembola, have been recorded from the Middle Devonian, the Collembola and their immediate relatives, which must have also been present at that time, would be assigned to what Hennig called a “class stage.” This resulted in the following ranking for Collembola: class Insecta, subclass Entognatha, infraclass Ellipura, and microclass Collembola. Hennig, of course, realized that this approach is impracticable and arbitrary. He suggested to “reserve the well-known category designations (“class” and “subclass”) for the most important and morphologically isolated groups” (Hennig 1966, p. 185), which can hardly serve an objective criterion. Hennig and subsequent workers were well aware that the age criterion of the categories across organisms or at least animals cannot work, simply because the major evolutionary radiations and subsequent diversifications took place in extremely different periods of time. As an example, the major lineages of the placental mammals that are generally ranked as orders arose in the Cretaceous (Murphy et al. 2001) and thus are comparable in age to the major lineages of Hymenoptera (bees, wasps, and ants), which are considered to be of family rank (Rasnitsyn 2002). If categories could be defined horizontally, the categorical hierarchies of Placentalia and Hymenoptera would have to be adjusted to each other, either by “downgrading” Placentalia to family rank or by upgrading Hymenoptera to class rank. This

example clearly shows that a horizontal, *absolute* definition of the Linnaean categories is not only impractical but actually absurd.

However, a *vertical*, relative application of Linnaean categories along a phyletic lineage is a different matter and may be possible as a kind of evidence-based convention. An example is Goodman et al.'s (1998) cladistic analysis of the Primates based on DNA evidence and on extant and fossil morphological characters. Many traditionally recognized taxa appeared to be monophyletic, and their names and ranks as used in current literature were maintained. The ages of these clades were determined using dating evidence as provided by fossils and the model of local molecular clocks. Based on this time scale, clades of roughly equivalent age were assigned the same Linnaean rank. Goodman et al. (1998) analysis resulted in the following dating scheme (category/age [Mio years]/geological period): semiorders/63/early Paleocene, suborders/58–50/late Paleocene to early Eocene, infraorders/45–40/middle Eocene, superfamilies/39–29/middle Eocene to middle Oligocene, families/28–25/middle to late Oligocene, subfamilies/23–22/early Miocene, tribes/20–14/early to middle Eocene, subtribes/14–10/middle to late Miocene, genera/11–7/late Miocene, and subgenera/6–4/late Miocene to early Pliocene.

It needs to be emphasized that an age-related Linnaean ranking might have merits only if applied to clades like the Primates with particular prerequisites. Primates have a widely accepted classificational framework (though the details are still disputed), quite a good fossil record, and cladistic analyses have been published with reliable taxon sampling. If the last common ancestor of the Primates is supposed to be as old as about 63 Mio years, and if the scientific community *agrees* to rank the Primate clade as an order, the highest level of the classification within Primates is defined: clades that arose in the early Paleocene are ranked as orders. Other, younger, fossils can be correlated with a particular rank accordingly. The fossil record, which might include gaps without fossil evidence, is supplemented by the model of the molecular clock, as proposed for Primates. This procedure allows applying the age criterion to any ranking level between the oldest reference point (the putative age of the last common ancestor of the Primates) and the youngest reference points (e.g., the latest splittings to clades generally ranked as subgenera, the youngest fossils).

Approaches like this pretend to be objective in correlating taxa and ranks, at least within the clade they were proposed for. However, it is easy to see that none of the criteria that define the age-rank correlation as proposed by Goodman et al. (1998) leads to an objectively settled ranking. It is a matter of convention if the clade named Primates, which is defined by a set of apomorphies and whose age of origin is defined by a particular fossil, is ranked as an order. Likewise, it is a matter of convention which of the clades within Primates, such as Cercopithecoidea, is assigned superfamily or any other rank. The same arbitrariness applies to the correlation of a clade and an age per se: with respect to the current state of the art in Primate classification, it might be useful to treat the putatively 18-Mio-year-old Cercopithecoidea as a superfamily, but other rank-age combinations might be similarly appropriate if suggested by the total hierarchy within Primates.

Nomenclatural stability is another important issue to be addressed to any classification concept. Stability of nomenclature should minimize changes in the names as they are adopted to changing scientific concepts. Age-defined ranks are, at any hierarchical level, extremely sensitive to the accuracy of the underlying dating of the latest common ancestors. New dating evidence, such as newly discovered fossils or new analytical methods in paleontology or molecular biology, may suggest fundamentally different dates of the origin of particular groups. If, for example, the origin of Primates dates back to 80 Mio years as suggested by Tavaré et al. (2002), the age-related ranking scheme of Goodman et al. (1998) would have to be adopted to the new dating by stretching the ranking range to fit to the longer period of time or by adding more category levels.

The standard approach to calibrating a classification for an age-related application of ranks is to use the earliest known fossils of a particular taxon and to equate their age with the time of origin of this taxon. The resulting age of the taxon under discussion is, obviously, hypothetical and only gives us the so-called *terminus post quem non*, that is, the point of time *after* which the clade cannot have originated. In other words, the fossil record only settles the *minimum* age of the group. This can potentially lead to a serious underestimate of the true time of origin of a clade and, hence, of all other dating results inferred secondarily. As has been pointed out by Martin (2002), this underestimation increases if the fossil record is very patchy. Since this might be the case in many organisms (Tavaré et al. 2002), the oldest fossil of a given clade might be considerably younger than its true stem species. As a result, age-defined ranking schemes are considerably different depending on whether the dating is inferred directly from the fossil evidence, or the dating is indirectly estimated by molecular clock models or estimations of extinction rates and the reliability of the fossil record, is considered.

These applications and problems show that an age-defined, objective correlation of Linnaean categories and clades is as unrealistic, if not impossible, as any other effort toward an absolute definition of ranks. In some cases, such as Primates, age-defined ranks may be useful to some extent, although it must be emphasized that the correlation of ranks and clades even in such cases is at most *intersubjective*, being based on a set of conventions of the respective scientific community. Changing conventions, changing dating evidence, and other factors may considerably alter the putatively objective ranking of Primates. The Linnaean categories are a notional representation of the hierarchical structure of monophyletic taxa representing an inferred, hypothetical sequence of speciation events (or, if a cladistic analysis is still lacking, an a priori assumption of relatedness inferred from overall similarity). As a consequence, the Linnaean system is inherently *relative*, that is, Linnaean ranks denote the hierarchical position of a given taxon relative to other members of the same clade. As has been paraphrased by Schuh (2003, p. 60), “[t]he primary strength of the Linnaean system is its ability to portray hierarchical relationships.” It must, however, be emphasized that Linnaean categories are inherently *subjective* in that the exact correlation of a taxon and its rank is not determined by the taxon or the category themselves.

### **Ranking Fossils**

Fossil and recent taxa are basically treated in an identical way in taxonomy. However, if fossils are included in a cladogram, a number of practical terminological problems arise. Fossils are part of the stem lineage of a given taxon, and each single fossil taxon is considered the sister group of the next, less inclusive, taxon. If sister taxa are given the same rank in the hierarchy, each single fossil species that is considered to be the sister species of a taxon that is ranked as an order must be assigned order rank as well. If several fossil species of a given stem lineage in a continuous sequence of sister group relationships with the next less inclusive taxon are known, each of these single species would have to be given a high rank, which would, for example, result in a proliferation of taxa ranked as orders along a single lineage. In principle, each of the pairs comprising a fossil species and its higher sister taxon could also be assigned a new name.

As a consequence, giving a high rank to each of the fossil species would not only appear to be overblown, but this would also ignore the fact that the exact sequence of fossils along a stem lineage cannot be determined accurately in most cases. As an alternative, Patterson and Rosen (1977) have suggested to order fossils according to their hypothetical phylogenetic position but to leave them unranked. Instead, each of these fossils is named *plesion*. The term *plesion* replaces any rank above the genus level and to tentatively place fossils in cladograms without affecting the hierarchical structure of names and their ranks.



### **Linnaean Categories as a Communication Tool**

Systematists should be aware that the Linnaean categories are a tool for communication. As Griffiths (1976, p. 168) stated, there is no logical reason why taxa *must* be ordered into categories. Linnaean categories do not inherently imply information about the age of a taxon (except if employed within a certain clade by convention, as, e.g., in Primates), the size of a taxon (in terms of species numbers), genetic distinctiveness, or phylogenetic relatedness. The application of a particular rank to a particular taxon is subjective but must fit in the overall hierarchy of the more inclusive taxa.

But Linnaean categories directly mirror the complex, hierarchical relationships in a given clade. Along this lineage, the nestedly ordered categories notionally reflect the nested order of organisms and explicate the relative position of a given taxon to other taxa of the same lineage. The demand for an abolition of the Linnaean categories without substitution involves well-known practical problems and would result in the loss of practical and useful information. There are myriad practical problems involved in the implementation of the Linnaean categories, but this is also the case in any other notional system of ranking. “No single system of nomenclature can ever possess all desirable attributes: i.e., convey information on hierarchical relationships, provide . . . stability in the names . . ., and provide simplicity and continuity in communicating the identities of the taxa and their relationships” (Schuh 2003, p. 60). Since the discussion about the Linnaean categories reflects the problems how best to express scientific contents linguistically, *applicability* is the central criterion to assess the capability of any ranking concept. The search for the “best” biological nomenclature corresponds to the search for compromise between theoretical demands and practical necessities.

### **The International Code of Zoological Nomenclature**

Systematists and, secondly, subsequent users of the results of biological systematics deal with myriad objects: each taxon, if considered a species or ranked as a genus, family, or order, can be recognized as a biological entity, which, to a varying degree, is distinctly different from other such objects. To enable communication about these objects, in principle, requires the application of unique names, which unequivocally refer to the taxa. Even in pre-Linnaean times, the need to point to groups of organisms by names was obvious. However, before Linnaeus, the names given to taxa were thought to be descriptive or diagnostic terms or phrases rather than proper names, as taxon names are seen today. Although easily recognizable organisms might have been given single names (*uninomina*), or if two closely related forms were known, two-word (*binominal*) names were coined. Increasing knowledge of the diversity of forms made complex, descriptive labels necessary to meet the criterion of uniqueness (e.g., the gentian species that is today known as *Gentiana ciliata* was named *Gentiana angustifolia autumnalis, minor floribus ad latera pilosis* by Bauhin (1623) (Mägdefrau 1992); note that Bauhin and other pre-Linnaean authors already employed unique genus names as more inclusive taxa). Linnaeus, however, introduced a strictly formal nomenclatural system, based on a unique binominal species name. The increasing exploration of remote geographic regions made scientists realize that they are concerned with a seemingly infinite organismic diversity. Due to new discoveries and new techniques, taxon names proliferated. However, it was not only the increase in species descriptions that lead to a rapid increase in the total number of taxon names. Inconsistent or even contradictory terminological systems, development of their own rules by many scientists, replacement of already published names that were considered to be inappropriate or incorrectly formed, and other factors resulted in the strong need for general rules of nomenclature.

Beginning with Linnaeus’ works in the eighteenth century, an elaborate body of conventional regulations was developed to provide such general rules. The valid rules of nomenclature in zoology are contained in a judicial text called the International Code of Zoological Nomenclature, here abbreviated as the Code, whose current edition is the fourth. The Code provides a complex set of



rules and aims to cover as much of the complexity of the recent and historical naming process as possible. However, cases might show up in which the strict application of the Code might actually threaten nomenclatural stability, and in such cases, every scientist is free to apply to the *International Commission of Zoological Nomenclature* to set aside priority or other provisions of the Code to increase stability. Many provisions of the Code are the result of compromise between conflicting principles, which partly date back to the very beginning of biological nomenclature. Hence, the rules fixed by the Code are far from written in stone but are under constant development. As has been emphatically pinpointed by Mayr and Ashlock (1991, p. 386), “all good law is living law.”

An exhaustive description of the Code is far beyond the scope of this chapter, but a few basic principles will be considered here.

### **Freedom of Taxonomic Thought**

The Code does not tell anybody how to classify something or how to recognize species or other taxa. These are scientific decisions that are totally under the responsibility of the systematist. The Code provides rules for a system of communication, a “language,” for communicating such taxonomic decisions. This “freedom of scientific thought” is expressly guaranteed in the Preamble of the Code and, indirectly, emphasizes the role of nomenclature in biology as a notional process acting subsequent to the scientific process. As an example, the Code permits a scientist to continue using a name that is considered to be a junior synonym by another author. Conversely, the freedom of taxonomic thought includes also the freedom to make taxonomic mistakes that, as a consequence, do not affect nomenclature. If, for example, a name is erroneously placed in synonymy, its validity is not affected.

### **New Names and Old Names**

The process of naming a newly discovered species properly, that is, in accord with the Code, is surprisingly simple. The Code explicitly provides a set of provisions to be met when describing a species, some of which appear to be commonsense principles. To be usable or, to use the proper term, to be *available*, a name must, first, be *published*. The Codes clearly indicate that distribution “in numerous identical copies . . . for permanent record” constitutes a publication. The use of the 26 letters of the *Latin alphabet* for the taxon name is mandatory, although the descriptive text may also be written using a different alphabet. A name must, of course, in principle be *unique* but on different levels: a species name must only be unique in its own genus (there are several animal species with popular species names like *viridis*, meaning green, but no two species (or subspecies) in a genus may bear this name), whereas a genus name must be unique among all animals. However, it is wise to avoid species names that are already in use in closely related genera. In the future, genera might be combined due to changing evidence, which would result in homonymy of such species names. A new species name “must be explicitly indicated as intentionally *new*,” that is, by adding a Latin term like “new species” to the newly proposed name or an equivalent phrase or abbreviation. The Code also requires the consistent application of *binominal nomenclature*, which does not apply to names of taxa at ranks above the family group. A new species description must also include an explicit fixation of the name-bearing *type specimen(s)*. A type is an individual specimen to which a given name is attached. In cases in which a taxon previously considered a single species is later split into two species, the species to which the type specimen belongs retains the previously given name. This *type method* is important in taxonomy and will be presented in more detail later. Finally, the Code provides a set of mandatory regulations of more linguistic nature, how new names are to be formed. The most important provision is that names must be either *Latin* or latinized or they must be

so constructed that they can be treated as Latin words. Further rules concern practical details such as how names are formed from personal names and other aspects of the correct spelling.

Every scientist who plans to propose a new name for a taxon should consider these simple provisions to be sure that the new name complies with the Code. However, the greater part of the Code is devoted to less simple cases, and most of the problems are caused by names proposed in the past. A smaller part of difficulties systematists face when dealing with previously published names might be caused by the erroneous application of the Code or by erroneous taxonomic decisions. The majority of problems, however, simply portray the continuously changing concepts and applications in the 250-year-old history of biological systematics. Such changes might affect scientific content (e.g., by the invention of alternative species concepts) or might be more formal (e.g., the explicit designation of a name-bearing type was not mandatory at the beginning of biological systematics). As a result, historical names are not only hard to locate in the literature in many cases, they often require time-consuming, elaborate efforts to clarify the correct original spelling, the presence of type material, the identity of the species, the correct date of publication of the original description, and several other potential difficulties. Two of the most common problems that come up when dealing with historical names are *synonymy* and *homonymy*.

The fact that a considerable portion of taxonomic practice is unusually time-consuming when compared to the outcome, i.e., the clarification of a single species name, is part of the legacy of about 250 years of biological systematics. In many groups of organisms, taxonomists are condemned to spend most of their time interpreting the work of pre-twentieth-century systematists. “The past [often] acts as a dead weight on the subject, the complex synonymy and scattered type material deterring anyone from attempting a modern revision” (Godfray 2002, p. 17).

**Validity, Synonymy, and Homonymy** As has been explained earlier, a taxon name must fulfill a set of conditions to be available in terms of Code compliance. Among the available names, only the oldest available name is what systematists call *valid* and has *priority* over the younger names. The valid name of a taxon is sometimes referred to as the *correct* name, which means that open nomenclatural problems have been solved and that a single name retained, which under the provisions of the Code is the only approved one. The date of publication of the original description of a name is thus of crucial importance and must be carefully determined. It must be emphasized that the principle of priority applies to the species, genus, and family levels only but not to levels above the family rank.

In by far the most cases, the valid name is the oldest name. Exceptions occur when the oldest name, in case of a species, is already in use in the genus, resulting in homonymy. Then, the younger of the homonymous names would no longer be valid but must be replaced by the next available name of the same species, if any exists. An example is a subspecies of the common chimpanzee, *Pan troglodytes verus* Schwarz, 1934 (originally described as a subspecies of *Pan satyrus* Linnaeus, 1758, the species name of which was suppressed by the International Commission on Zoological Nomenclature in 1999). The oldest available name of this subspecies is *Simia chimpanse* Matschie, 1904, but despite having priority due to the early publication date, Matschie’s name cannot be used because it is a junior homonym of another species, *Satyrus chimpanse* Mayer, 1856. Since *Satyrus chimpanse* Mayer is considered to be identical to, that is, a synonym of, the nominate subspecies, *Pan troglodytes troglodytes*, the species group name *chimpanse* occurs twice within *Pan*, by Matschie, 1904, and by Mayer, 1856, respectively. This is called *secondary homonymy*, since the two names under discussion were first proposed in different genera and got in conflict after being considered to belong in the same genus. *Simia chimpanse* Matschie was published half a century later than *Satyrus chimpanse* Mayer, and thus the younger of the two names must be replaced. The

next available name is *Pan satyrus verus* Schwarz, published in 1934, which then becomes valid. In many species, however, no name is available other than the originally proposed name. Then, the revising author has the authority to propose a replacement name, which then becomes available with the reviser as the correct author and the date of his publication.

If a single taxon is given two or more names, each of these names is a *synonym*. The earliest published synonym is referred to as the *senior synonym*, even if it is considered to be the valid name. Any other earlier names of the same taxon are called *junior synonyms*. In most cases in practical taxonomy, systematists are confronted with the question if two independently published species names that were based on different name-bearing types actually represent the same species. This kind of synonymy with different types is called *subjective synonymy* because it expresses the scientific conviction of the revising author that the two names refer to the same thing. Names applied to a species on the basis of the same type specimens are *objective synonyms*.

### **Typification: Establishing Objective Reference Points**

The type method is a guiding principle in biological systematics. In taxonomic practice, the identity of species, particularly when described in the past, is often difficult to establish due to insufficient descriptions or illustrations. As a result, historical species descriptions might apply to more than one currently recognized species. Due to new evidence, taxa might be split up into two or more less inclusive taxa. In all such cases, it might be difficult to establish which of the newly separated taxa has to retain the original name and which should be newly named. This problem is solved by the invention of objective reference points, the types. Types in the broadest sense are zoological objects to which a name is firmly tied. The type of a species is always a single specimen, the type of a taxon at genus rank is a species, and finally, the type of a family-rank taxon is a genus. If a previously described species is considered to be actually composed of more than one species, the type specimen fixes the original name to the species, to which it belongs. The same holds for taxa at the genus and family ranks.

The Code permits the use of a few different kinds of types in taxonomic descriptions. At the genus and the family level, only type species and type genera exist, respectively. A *holotype* is always a single specimen, which is either the only specimen available for the original description or it is explicitly selected out of the original series of more than one specimen to give it precedence over the other specimens, which then are called *paratypes*. In current species descriptions, the explicit designation of a holotype is mandatory. Paratypes do not have special standing under the Code but should be explicitly mentioned as members of the original type series by calling them paratypes. If the original describer in older publications mentions more than one specimen but did not select a holotype, all type specimens are the *syntypes*. A syntype series is of little help in conflicting taxonomic situations because they might actually belong to more than one species. In such cases, a revising author has the authority to subsequently select a single specimen from the original type series, which then would be called a *lectotype*. Accordingly, the remaining syntypes would be the *paralectotypes*, which, again, are only of secondary importance. If the type material of a species is considered to be lost, the revising author may select a specimen that was not part of the original type series, as a *neotype*. In some cases, the lack of type material is of minor importance because the identity of the species is obvious. An example is *Homo sapiens* Linnaeus, 1758, for which no type specimen or specimens have ever been settled (Spamer 1999). A neotype must be designated only if this action facilitates nomenclatural stability so that the name is properly and consistently applied. Since a neotype is required in cases with unsettled and problematic nomenclature, one can almost never be completely sure if the neotype and the original types are really conspecific. Thus, designation of a neotype might be risky and should only be done if absolutely necessary. Numerous

other kinds of types have been used in the literature, but only those above are still permitted under the current Code. Examples of types that are not regulated by the Code are allotypes (a specimen of the opposite sex of the holotype, actually simply a paratype) or topotype (a specimen originating from the type locality of the species to which it is thought to belong).

Incidentally, it is a wide held belief that the type specimen or specimens of a newly described species must be dead or should be killed sooner or later to be finally deposited in a museum collection or in another kind of persisting and accessible environment. This means that in most cases, a new species description is based on one or more specimens that are physically available to the scientist during the process of writing the description. The Code requires that the specimen (the holotype) or specimens (syntypes) on which the name is based must be explicitly stated and accompanied by description or diagnosis to differentiate the new taxon. However, this requirement does not include any mandatory provisions about the physical availability, detailed morphological description, or depository of the type specimen (Wakeham-Dawson et al. 2002).

A type specimen need not be especially *typical* for the species to which it belongs. Its function is simply that of a “name bearer” (Simpson 1961). There are several potential criteria for how to select a holotype out of the entire material that is available to a scientist. If the species is differentiated from its congeners by means of complex morphological features of the male genitalia (as is common in invertebrates), it might be appropriate to make a male the holotype. Sometimes, not all type specimens are complete or show the diagnostic characters equally well. It would make sense to choose as the holotype a specimen, which exhibits most or all of the characters that are of diagnostic value at the time of description and with respect to new future discoveries as far as can be predicted.

The description of a new species is always based on all specimens available at the time of description. Since the holotype is just a name bearer, its function is not to serve as the only basis of the original description (except when only a single type specimen is known).

### **Fossils, Fragments, and Heterogeneous Type Specimens**

The Code applies to both living and extinct animals, as is explicitly stated in its Article 1. Thus, the principles of the type method as briefly presented earlier with reference to recent species are equally applicable in paleontology. However, many fossils, particularly complex multistructured organisms, such as vertebrates, inherently lead to practical problems. In most fossil vertebrates, only hard structures are fossilized and thus preserved. In the course of diagenetic processes, soft tissues that connected the hard elements in the living animal are usually decayed so that the resulting skeleton falls apart. In the ideal case, the preserved elements remain in their original position after embedding in a fossilization matrix so that the elements can be easily associated with each other. In many cases, subsequent physical processes might have altered the relative position of the elements or have destroyed parts of the organism.

Fossil hominids are never completely preserved, not even with respect to bones. Sometimes, just a single preserved bone is sufficient to provide evidence for taxonomic identity. If a single bone is the basis of a new taxon, just the bone is referred to as the holotype. An example is the holotype of *Homo heidelbergensis* Schoetensack, 1908, which consists of a complete, adult mandible. There is no ambiguity about the formal basis on which the new species is based. If more than a single element is available, association to individual can be difficult if the elements are not in the original position relative to each other but are more or less dislocated or destroyed. An example is the composition of the types of *Homo habilis* Leakey, Tobias, and Napier, 1964. Several fragments assignable to the new species were available such as mandibles, isolated teeth, parietal and hand bones, and cranial fragments. Due to external evidence, such as the position of the fragments as found during excavation, the fragments could be associated with five individuals. The holotype of *H. habilis*

consists of a mandible with dentition and the associated upper molar and parietal and hand bones, originating from a single juvenile individual.

These examples show another principle of the type method. A type is always a zoological object but is not necessarily something that is or is close to a complete organism. A single tooth, an isolated wing, or any other part of an organism is in principle sufficient to serve as the basis for a new species. In a way, incompleteness is an inherent attribute of most preserved specimens because many preservation techniques result in the loss of some characters. Pinned, that is, dried insects and stuffed, mounted vertebrates have usually lost all or most of their soft tissue. Thus, even if a specimen has lost almost the entire physical structure except for a single tooth, this incompleteness of a specimen does not prevent potential type status. It is, however, wise to associate isolated fragments such as a molar and a mandible to a single type specimen only if the evidence is unambiguous. If subsequent evidence is found that the fragments actually belong to different individuals, this might cause a lot of unnecessary nomenclatural confusion.

## Conclusion

Names can be seen as the key to biodiversity. Names serve as unique identifiers or tags, which unequivocally refer to biological species and higher taxa. Names form the essential language to communicate about biodiversity. The naming process in biology is an intellectual challenge which happens subsequently to the process of scientific discovery and description. New methods and tools for the discovery of the largely unexplored species diversity on earth have been established in the past decades, which have increased the rate of species description in an unexpected amount. In order to fulfill its function as a tool for an effective organization of biological data, a set of rules needs to be followed to make scientific names unique and unequivocal. Modern taxonomy, the science of naming, identification, and classification of organisms, is an integrative approach, which combines a wide range of methods, tools, and theories for both the recent and past diversity.

## Cross-References

- ▶ [Fossil Record of Miocene Hominoids](#)
- ▶ [Historical Overview of Paleoanthropological Research](#)
- ▶ [Neanderthals and Their Contemporaries](#)
- ▶ [Potential Hominoid Ancestors for Hominidae](#)
- ▶ [Primate Origins and Supraordinal Relationships: Morphological Evidence](#)
- ▶ [Species Concepts and Speciation: Facts and Fantasies](#)
- ▶ [The Earliest Putative Hominids](#)
- ▶ [The Species and Diversity of Australopiths](#)
- ▶ [Zoogeography: Primate and Early Hominin Distribution and Migration Pattern](#)

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