CLASSIFICATION AND DIVERSITY OF LIFE FORMS

Alessandro Minelli
Department of Biology, University of Padova, Padova, Italy

Giancarlo Contrafatto
School of Life and Environmental Science, University of Natal, Durban, South Africa

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Summary

Conservation and sustainable utilization of biological resources rely on sound knowledge of biodiversity. Because biodiversity is vast (c.a. 1.8 million described species), a universal system of classification is a necessity in order to store and retrieve in a cogent manner the great wealth of available biological information. Presently, four similar hierarchical systems of progressively more inclusive categories, all based on the Linnean binomial system, are in use and are controlled by the four codes of Bacterial, Botanical, Viral and Zoological nomenclatures. This reflects an intrinsic difficulty, due to the sheer mass of available data and scientific names, in creating an integrated classification system, as recently attempted by the BioCode. Such a difficulty is compounded by the existence of countless folk taxonomies, each expressed in a different language, but all useful from medical, veterinary and other practical perspectives. Although the definition of biodiversity encompasses genetic, species and

ecosystem diversities, the most common and readily available means of global assessment is by species counts. However, present species inventories are far from being satisfactory because various areas of the world have been, and are being, poorly sampled (i.e. deep oceans) and because of difficulties in sampling even small, but species-rich areas (i.e. forest canopy). Therefore, the number of undiscovered, and hence undescribed, species is unknown and its estimates can introduce wide variation into available species inventories. Areas of the planet that are peculiarly rich in taxa (endemic areas) are object of intensive investigations as they may hold the key to understanding 'evolutionary success', which is presently explained in terms of adaptation and the diversity of Earth's environment. This knowledge has been given impetus by a number of methodological developments that took place in the second half of the XX century, such as the application of biochemical, cytogenetical and molecular techniques to taxonomic work. These have been successfully supported by contemporary analytical methods, such as phenetics and cladistics, which may facilitate the goal, within the XXI century, of a congruent phylogenetic classification of all life.

1. Natural vs. artificial classifications

Conservation and sustainable utilization of biological resources are critically dependent on a sound knowledge of biodiversity and the evolutionary mechanisms whence biodiversity derives. Therefore, systematic biology holds a pivotal role in the elaboration of methods and policies concerning sustainable development. Inventories of species diversity carried out during the first two years of the XXI century, place the number of described extant species at between 1.7 and 1.8 million. However, because many more species are as yet undiscovered, various methods of estimating the likely number of undescribed species have been devised. These estimates have generated figures of species diversity that range widely, from 11 to 107 million. Nevertheless, regardless of estimation methods, we are dealing with great numbers of species. It should be self-evident, therefore, that such a great array of biological entities can be handled intelligently only through a classification, a procedure that consists in arranging living and fossil organisms into meaningful classes.

Therefore, we can state that a general purpose of a classification is to allow us to store and retrieve information concerning the classified organisms. The process of classifying goes hand in hand with the process of naming organisms and is the domain of the science of taxonomy. Besides being an obvious practical necessity, the taxonomic process is needed also because names and categories act as receptacles of biological information. This information, in turn, can be used in order to protect, or to sustainably exploit, the organisms associated with it or the habitats associated with the organisms. Upstream of this, however, the usefulness of a classification rests with its potential to express patterns of relationship among classes of organisms. These patterns should also allow unequivocal identification of category members (species) and, in doing so, become predictive by allowing us to deduce some of the properties of the members of any given category.

Hence, a goal of Systematic Biology is to understand and describe the nature and biology of species, populations and their gene pools. In doing so the patterns of phenotypic and genotypic variation, both, geographic and temporal, can be understood.

This allows for a better understanding of the evolution of species. Taxonomy, in turn, uses this intelligence in order to generate a classification that best reflects organism diversity. Such a classification should be an unambiguous system of names, which can be integrated with existing information, including ethnic biological knowledge, and provide analytical keys to facilitate identification of diversity. Because such analytical keys can be based on meaningful biological characters, they provide a synthetic description of living organisms. Therefore, the eventual outcome of a successful classification would be a complete description of Earth's biodiversity within a coherent and universal system.

Many ways of classifying organisms are possible. We could simply arrange a series of specimens by alphabetical order: if, for example, quick retrieval and storage of collection specimens is all we are interested in, then this classification may be perfectly acceptable and functional. We know exactly where to find all specimens in the letter 'A' class and we can retrieve them quickly because, presumably, we also know where to find the cabinet assigned to the letter 'A'. However, if our collection is to serve a more complex function, this may not be an ideal way of creating classes. Class 'A' may include a number of specimens of the genus *Arvicanthis* (a rodent), as well as specimens of the genus *Alytes* (a toad), and these may be mixed with samples of *Ascaris* (a worm) and, possibly, cultures of the mould *Aspergillus* and the cyanobacterium *Anabaena*. An unwary molecular biologist planning to extract DNA from museum specimens in order to study some aspects of small mammal biology, may be justifiably discouraged by the prospect of searching our collection for useful material. On the other hand, we may choose to classify organisms on the basis of some useful properties they may have, or threats they may represent to human life and activities, such as the case of most folk taxonomies. All early people had some such classifications in place. The ones that featured most prominently in historical times, perhaps, are those that classified plants according to their medicinal properties (herbals). Among such systems, the Chinese *Pen Ts'ao* - written some 4 800 years ago and listing almost 360 species of medicinal and agricultural utility - or the Ebers Medical papyrus from Egypt (3 500 YBP) and the Assyrian Herbals (1 700 YBP), may be mentioned (see *Systematic Botany*).

This type of classifications, whose historical value to humans may be exemplified by the public garden called *'Giardino dei Semplici'* in the city of Florence, have not been abandoned because, by their very nature, they serve some useful purpose. One of the most recent examples of such a classification, is represented by Bergey's Manual of Determinative Bacteriology, which has provided a useful service to microbiology practitioners throughout the second half of the XX century and beyond. Bergey's manual classifies bacteria according to a great number of features, but more prominently by cell-shape, Gram stain reaction, flagella and respiration type, which are undoubtedly useful in identifying bacterial cultures and/or clinical specimens in a laboratory but, do not always reflect the 'natural order' of the procaryotic world.

Because all these classifications have been devised with some specific purpose in mind, they use somewhat arbitrary assortment criteria thus, usually, grouping unrelated organisms into more or less artificial classes. Therefore, such classifications may be regarded as artificial as they describe relationships that do not necessarily exist in nature, or that do not reflect kinship.

The major shortcoming of artificial classifications is that, by definition, they do not meet the requirements we set out above, for a consistent and universal classification of all life on Earth. Because, ultimately, we want to be able to describe the nature and biology of species, we tend to prefer natural classifications, which attempt to fully describe the nature of species and are based on biologically meaningful characters. Such characters should allow species to be grouped together according to their affinities as seen in nature which, in turn, should reflect their phenotypic and genotypic relatedness. In this way, natural classifications acquire the power of describing and, ultimately, predicting evolutionary patterns of biodiversity.

Although rooted into Aristotelian taxonomy, the first examples of natural classifications only occurred in the XVIII century, due to the efforts of botanists such as, Carolus Linnaeus, John Ray and Bernard de Jussieu. Indeed, this is the type of classifications that, with due modifications and refinements, is still in use today. Most telling in this respect is that fact that, useful as Bergey's manual is, since 1989 its publication has been paralleled by that of its sister manual: Bergey's Manual of Systematic Bacteriology. The latter then, takes into account genetic diversity, as measured by molecular methods, to express the natural affinities among procaryotes in the form of a classification that is more natural than that followed by its older sister manual. It should be noted further, that the publication of the determinative manual has not been discontinued. Its purpose is still fulfilled because of its ability to aid bacterial identification for practical, laboratory or medical purposes. By the same token, the existence of a future universal classification must not be taken to mean that folk taxonomies, for example, are no longer useful. It simply means that a more powerful and congruent classification will be available to integrate and supplement, rather than displace, existing ones.

2. Classification vs. system

As mentioned above, a long tradition, rooted in the structure of folk taxonomy as well as in the Aristotelian logic, gave shape throughout the centuries, to what eventually evolved into the Linnean classification of animals and plants. Following Linnaeus (see *Historical Review of Systematic Biology and Nomenclature*), we are currently using, as a reference system for the diversity of living beings on Earth, a hierarchical arrangement whose levels are called *taxonomic categories*. The basic taxonomic category is the *species*. A group of closely related species is termed a *genus*. Above the genus, further categories are recognized, such as the *family*, the *order*, the *class*, and the *phylum*, in ascending order, up to the *kingdom*, which is the top taxonomic category. Whenever necessary, intermediate ranks are introduced, such as the subfamily, the superfamily, the suborder, and so on. All classificatory units, at whatever level they might be placed, are termed *taxa* (singular: *taxon*). For example, the human species, the wolf, and the date palm are three species-level taxa, whereas rodents, bats and carnivores are three order-level taxa.

Nothing forbids the recognition of taxa below the species level. Indeed, infraspecific diversity may be very important, both for theoretical and for practical reasons. Many species comprise a number of geographically distinct populations, or groups of populations, which are unambiguously distinct, despite the fact that they can still interbreed. If geographical isolation lasts long enough, and the populations do not go extinct in the meantime, these geographical isolates may evolve into distinct species. But there is no need to wait for such a process to be completed before we give these geographical forms their distinct identity within the classification. There are, however, different traditions in the different subdisciplines of biological systematics. Zoologists do not recognize more than one infraspecific level, the *subspecies*, whereas botanists accept more than one (e.g., *subspecies*, *variety*, *form*), especially in the case of cultivated plants. In the latter case, a commonly used varietal category is the *cultivar*.

Despite its consolidated use in all branches of biological science and its obvious usefulness as a reference tool for arranging our knowledge on the diversity of living beings, the Linnaean hierarchy has not escaped criticisms. A first objection is that traditional classifications take a branched topology of the tree of life for granted which, however, is not necessarily true in all instances. In particular, the origin of the eucaryotic cell (see *Biological Science Fundamentals*), i.e. an event which is at the origin of most of today’s living world, was quite probably due to a stabilized symbiotic event, that is, to a fusion (anastomosis) of two, or possibly three previously distinct branches of the tree of life. Many more anastomoses of the same tree are produced by hybridization, an event that is all but rare, in the plant world especially. Of a completely different nature is the objection that we cannot find a reliable criterion for assigning a given taxon an absolute rank. For example, what is the meaning of classifying both Carnivores and Beetles as orders, within the Mammals and the Insects respectively? Why do we treat these two groups as ‘equivalent’? When we have reconstructed a phylogeny, we can obviously recognize relationships of inclusion (e.g., the genus *Canis* (dog, wolf) within the Canids, and the Canids within the Carnivores, and the Carnivores within the Mammals, and so on). Therefore, the rank of Mammals is higher than the rank of the Carnivores, and the rank of the Carnivores is higher than the rank of the Canids, but this is only matter of relative, rather than absolute, ranking. From the fact that both Carnivores and Rodents are included within Mammals it does not follow that Carnivores and Rodents should both assigned the same rank, as in traditional, so-called Linnean classifications. According to several modern authorities, we should dispose outright of formal taxonomic ranks and replace the *classification*, and its hierarchical arrangement of taxa, with a *phylogenetic system* exactly mirroring the topology of the phylogenetic tree. No absolute ranks, in this system, but only orderly relationships of inclusion of rankless lower taxa within rankless higher taxa.

3. Nomenclature

3.1. The international codes of nomenclature

The need for a stable and universally accepted nomenclature of animals and plants was first recognized long ago. Indeed, the works of some Renaissance naturalists, especially those of botanists, such as Caspard Bauhin, a Swiss author of the XVII century, were full of lists of names. These were equivalent to what we would call today synonymic lists, including for each species the ‘valid’ accepted name, and a list of all other names used for the same species but, for whatever reason, recommended for exclusion from common use. It was not until the end of the XVII century, however, that the need for an adequate set of nomenclatural rules was explicitly recognized.

Carl Linné, or Linnaeus (1707-1778) is usually credited with the status of father of the modern zoological and botanical nomenclature. In fact, Linnaeus was preceded in this endeavor by a few botanists such as the German August Quirinus Bachmann (=Rivinus), but it is only through the sound example of two successful works of Linnaeus (*Species Plantarum* and *Systema Naturae*) that the still current way of naming animals and plants was finally established.

The advent of the binomial nomenclature, however, did not guarantee, *per se*, the stability of names. For example, nothing could avoid two different species of animals or plants being called (for a while at least) by identical names, or two different nomenclatural traditions being established and maintained by two opposite schools of researchers. With the increasing volume of zoological and botanical literature developed by the pupils and imitators of Linnaeus, the scientific community came to realize the need for a set of sound and internationally agreed rules of nomenclature. Efforts in this direction affected zoology as well as botany. In the former area, the first important document is the so-called Strickland Code (1842), produced by a British team of which the young Charles Darwin was a member; in the latter, the most significant early work is Alphonse de Candolle’s (1806-1893) *Lois de la nomenclature botanique* (1867). Despite their intrinsic merits, however, these sets of rules obtained a limited success, because of a lack of really international support. It was only around the turn of that century that the first international codes of nomenclature were produced, more or less directly under the responsibility of the international congresses, of zoology and botany respectively. Such are, for example, the *Règles internationales de la nomenclature zoologique* issued in 1905, the first document eventually produced by the International Commission on Zoological Nomenclature, the body still in charge today of ruling on nomenclature on behalf of the zoological community.

Today, biological nomenclature is ruled by four main codes, the *International Code of Zoological Nomenclature* (ICZN), the *International Code of Botanical Nomenclature* (ICBN), the *International Code of Nomenclature of Bacteria* (ICNB) and the *International Code of Virus Classification and Nomenclature* (ICVCN).

The long history of biological nomenclature has witnessed several efforts to harmonize, or even to combine into a single set of rules, the provisions of the zoological and botanical codes. These efforts, however, always failed to achieve a workable result. The last effort in this direction (last decade of the XX century) saw lively discussions around a draft BioCode, aiming to solve at least problems such as the very numerous cross-kingdom homonyms (there are thousands of names of animal genera identical to names of plant genera, e.g. *Pieris*, both a butterfly and a plant of the heather family) and the controversial nomenclature of ambiregnal organisms, those groups of protists which have been sometimes regarded as animals (protozoans) and named according to the ICZN, sometimes as plants (unicellular algae) and named according to the ICBN. The main difficulty that no project on unified nomenclature seems to be able to overcome is the sheer existence of some million names that have been created and are currently used following the rules of the existing codes; rules that would cease to apply, in part, with the eventual adoption of a single code. Therefore, it seems difficult to see how a possible unified code could have rules suitable for the past as well as for the new names.

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Bibliography

Carpaneto, G.M. and Germi, F.P. (1989) The Mammals in the Zoological Culture of the Mbuti Pygmies in North-Eastern Zaire. *Hystrix*, 1:1-83 [An informative account of central African vernacular nomenclature]

Forey PL, Humphries CJ and Vane-Wright PJ (ed.) (1997) Systematics and Conservation Evaluation. Oxford: Oxford University Press. [Interesting essays at the crossroads between phylogenetic systematics and conservation studies]

Gaston KJ (ed.) (1996) Biodiversity: a Biology of Numbers and Difference. Oxford: Blackwell Science. [Useful chapters on biodiversity, mostly on methodological issues]

Groombridge B (ed.) (1992) Biodiversity: Status of the Earth's Living Resources. London: Chapman and Hall. [A precious detailed collection of quantitative data on biological diversity on Earth]

Heywood VH and Watson RT (eds) (1995) Global Biodiversity Assessment. Cambridge: Cambridge University Press. [A very important, bulky collection of critical essays evaluating current stand, prospects and possible management policies of biodiversity]

Hillis, D.M. and Moritz, C. (eds) (1990). Molecular Systematics. Sunderland, Massachusetts, Sinauer Associates Inc. 588 pp. [An invaluable collection of essays and detailed laboratory techniques for measuring genetic diversity. Includes biochemical and cytogenetical techniques]

Mayr, E. (1982) Systematics and the Origin of Species. New York: Columbia University Press. (Originally published 1942) [Mayr's original presentation of the 'Modern Synthesis' or 'Neo-Darwinism', as a follow-up to Dobzhansky's 'Genetics and the Origin of Species', with an introduction by Niles Eldredge]

Minelli A. (1993) Biological Systematics: the State of the Art. London: Chapman and Hall [An overview of problems, methods and current knowledge in biological systematics]

Reaka-Kudla ML, Wilson DE and Wilson EO (eds) (1997) Biodiversity II. Washington DC: Joseph Henry Press. [A collection of insightful essays on biodiversity and its management]

Biographical Sketches

Alessandro Minelli, born 1948, is full professor of zoology at the University of Padova (Italy). President (1995-2001) of the International Commission on Zoological Nomenclature. His major research interests are the evolution of arthropods and the evolutionary developmental biology of segmentation, together with theoretical and historical aspects of systematic biology.

Giancarlo Contrafatto, born 1948, is a graduate in Biological Sciences from the University of Turin (Italy) and has obtained his Ph.D. from the University of Natal Durban (South Africa). His research interests are isolation mechanisms related to speciation of small mammals. Recipient of the 1976 British Association Medal, from the South African Association for the Advancement of Science, G. Contrafatto has been on the staff of the University of Natal since 1983, and is responsible for the courses of Microbiology, Immunology, Comparative Immunology, Systematics and Evolution.