

# **Trends in Taxonomy today: an overview about the main topics in Taxonomy**

## **Tendencias actuales en Taxonomía: una visión sobre los principales temas de Taxonomía**

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### **SUMMARY**

Taxonomy is the science of the description and classification of organisms, essential in theoretical and applied biology. About 1.7 million species have been named since Linnaeus and it is estimated that only around 5-10% of the world's biota has been described so far, and, obviously, taxonomy plays the major role in this sense. However, taxonomy is in crisis: funding for taxonomy is inadequate, there is a lack of taxonomists, the recruitment of young scientists into taxonomy and systematics is extremely low, the impact factor of taxonomical journals is very low, and taxonomists have not been able to get the society and other disciplines concerned about the importance of taxonomy. Fortunately, during the last years, several progresses are emerging. The general interest about biodiversity conservation, the advances of internet and web pages, the progress in molecular techniques, the development of statistics in phylogeny, and the new taxonomic funding initiatives and global projects are giving some light: taxonomy is getting fashionable again and topics like Phylocode and Bar Coding are among the most controversial and discussed subjects in taxonomy today. This study represents a major summary about modern trends in taxonomy, and the main concepts and topics in taxonomy today are revised.

## RESUMEN

La Taxonomía es la ciencia de la descripción y la clasificación de los organismos, fundamental en la biología básica y aplicada. Desde Linneo, se han nombrado alrededor de 1.7 millones de especies, y se estima que sólo se ha descrito el 5-10% de la biota mundial; obviamente, la taxonomía desempeña un papel fundamental al respecto. Sin embargo, la taxonomía está en crisis: la financiación no es adecuada, faltan taxónomos, los índices de impacto de las revistas de taxonomía son bajos, y los taxónomos no hemos sido capaces de mostrar a la sociedad y a otras disciplinas la importancia de la taxonomía. Afortunadamente, se ha progresado mucho durante los últimos años. El interés general sobre la conservación de la biodiversidad, los avances informáticos, el progreso de las técnicas moleculares, el desarrollo estadístico en estudios filogenéticos, y las nuevas iniciativas y proyectos para financiar la taxonomía, están arrojando luz: la taxonomía se está poniendo de moda nuevamente y términos como Phylocode o Bar Coding se encuentran entre los más controvertidos y discutidos del momento. Este estudio representa un resumen importante sobre las tendencias en taxonomía y revisa los principales conceptos y temas sobre la taxonomía actual.

## CLARIFYING SOME IMPORTANT CONCEPTS: TAXONOMY, SYSTEMATICS AND PHYLOGENY

The word **taxonomy** is derived from the Greek words *taxis* (= arrangement) and *nomos* (= law). Taxonomy is the science of the description and classification of organisms, essential to the inventory of life on earth (Lincoln *et al.*, 1998; Wägele, 2005). Godfray (2002a) indicates that taxonomy, the classification of living things, has its origins in ancient Greece (with the first basic classification of Aristotle) and in its modern form dates back nearly 250 years, to when Linnaeus introduced the binomial classification still used today. Specific rules have been established for recognising, naming and classifying species to avoid redundant descriptions or the use of the same name for more than one species. These rules were introduced in the late 19<sup>th</sup> century and are continuously monitored by international commission scientists (Tautz *et al.*, 2003). The discipline of taxonomy traditionally covers three areas of stages: alpha (analytically phase), beta (synthetic phase) and gamma (biological phase) taxonomy (Kapoor, 1998; Disney, 2000). Alpha taxonomy is the level at which the species are recognised and described; beta taxonomy refers to the arrangements of the species into a natural system of lower and higher categories, and gamma taxonomy is the analysis of intraspecific variations, ecotypes, polymorphisms, etc. The word **systematics** stem from the Latinised Greek word 'Systema' and can be defined as the classification of living organisms into hierarchical series of groups emphasizing their

phylogenetic interrelationships. It is the science of arranging species' names into an order that reflects their evolutionary relationships. As pointed out by Lincoln *et al.* (1998) the term systematics has often been used as equivalent or synonymous with taxonomy, but a lot of controversy exists about this, and several definitions of taxonomy and systematics have been proposed by different authors to clarify the situation. Kapoor (1998) considers that the relationship of taxonomy to systematics is somewhat like that of theoretical physics to the whole field of physics. In this sense, taxonomy would be just a part of systematics; taxonomy includes classification, but leans heavily on systematics for its concepts, and systematics includes both, taxonomy and phylogeny. The point of view of Wägele (2005) is that, although theoretically, the terms taxonomy and systematics could be synonyms, in practice, however, differences in usage are obvious, and a systematist and a taxonomist can conduct different analyses. Systematists search for a phylogenetic system, but they do not necessarily have to acquire special knowledge on the distinction, validity of proper names, and the numbers of known species. Many systematists study the phylogeny of supraspecific taxa but are not able to identify a new species. This, however, as explained by Wägele (2005) can be done by the specialized taxonomist, who knows the rules of nomenclature and how to describe species. According to this author, the systematist can, but must not necessarily know, the rules of taxonomy. Contrary, the taxonomist should know the logics of phylogenetic systematics in order to be able to systematize new species correctly. In practice, however, it is also possible to describe species without knowledge of the theory of phylogenetics. Scientists proceeding this way are taxonomists, but not systematists. According to Padian (1999), systematics can be seen as the philosophy of organization nature, taxonomy as the use of sets of organic data guided by systematic principles, and **classification** as the tabular or hierarchical end result of this activity. On the other hand, according to renormalization-group philosophy, supported by physics (see Oono, 2003) a natural classification can be possible and objective even when it is not based on phylogeny. Oono (2003) critiqued the present view of the taxonomist, which according to this author, now seem to embrace the conclusion that natural classification not based on phylogeny is impossible in principle. Classification in physics suggests, however, that a natural classification of objects is possible when there are two disparate levels of their description.

On the other hand, as explained by Dubois (2005), taxonomy and **nomenclature** are different disciplines. Taxonomy recognizes classificatory units or taxa, whereas nomenclature attaches a given scientific name to each of these units. Taxonomy is a scientific discipline, whereas nomenclature is a technique.

Strongly correlated (even overlapping) concepts to taxonomy and systematics, are the words phylogeny, phylogenetics and phylogenetic systematics. **Phylogeny** can be defined as the evolutionary history of a group or lineage, the origin and evolution of higher taxa, or the natural process or repeated irreversible splitting of populations (see Lincoln *et al.*, 1998; Wägele, 2005). **Phylogenetics** is the science of the reconstruction of phylogeny, and **phylogenetic systematics** is a method of classification based on the study of evolutionary relationships between groups of organisms, and the integration of proper names of groups of organisms into a hierarchical system which reflects their phylogeny.

### THE IMPORTANCE OF TAXONOMY... IS TAXONOMY IN CRISIS?

It is very important to know the living organisms around us, and careful and accurate identification and classification are of vital importance (Kapoor, 1998). Without taxonomy, nobody would be sure of the identity of organisms they were interested in, or whether they belonged to the same or different species as the organisms studied by others. Without taxonomy, there would be no meaningful genome projects, and medical science, for example, would be seriously compromised. Without taxonomy, we could not begin to understand biodiversity and the related issue of conservation (Nature, 2002). As Kapoor (1998) pointed out, taxonomy is essential in theoretical and applied biology (agriculture and forestry, biological control, public health, wild life management, mineral prospecting through the dating of rocks by their enclosed fauna and flora, national defence, environmental problems, soil fertility, commerce, etc).

About 1.7 million species have been named since Linnaeus and it is generally estimated that only around 10% of the world's biota has so far been described (Wilson, 2000; Disney, 2000). Obviously, taxonomy plays the major role, and its importance as basic science for the remaining sciences should be taken into consideration. However, although society has a growing need for credible taxonomic information in order to allow us to conserve, manage, understand, and enjoy the natural world, support for taxonomy and collections is failing to keep pace (Wheeler *et al.*, 2004) and passing through a world crisis (Boero, 2001). There are several reasons for this crisis and we have compiled here some of the reasons reported recently in the literature.

Taxonomy is suffering from an important lack of funding. Funding for taxonomy is inadequate and largely diverted to studies of phylogeny, while thousands of species are threatened by imminent extinction (Wheeler, 2004; Wheeler *et al.*, 2004). In fact, many authors think that development of theo-

retical and technological advances in phylogeny reconstruction, in combination with advances in molecular biology, have both driven and consumed much of systematic biology in detriment to traditional taxonomy (Wortley *et al.*, 2002). But, as pointed by Godfray (2002a), why can't taxonomy attract large-scale funds in the same way as other big programmes like the Human Genome Project or the Sloan Digital Sky Survey? What do these projects offer that taxonomy does not? According to Godfray (2002a), one reason is that taxonomists lack clearly achievable goals that are both realistic and relevant; the goal of describing every species on Earth is not realistic at present. The second reason given by this author is related to the legacy of more than 200 years of systematics. Many taxonomists spend most of their career trying to interpret the work of nineteenth-century systematics deconstructing their often inadequate published descriptions, or scouring the world's museums for type material that is often in very poor condition.

Furthermore, there is a tendency among young and upwardly mobile ecologists to view museums and herbaria as "dusty" places with old people old-fashioned working on them (see Brooke, 2000). Taxonomists are depicted as postage-stamp collectors (see Gewin, 2002). Species description is seen as an old-fashioned way of doing research. The result is that taxonomical experts retire and are not replaced, zoology and botany disappear from university curricula and new researchers in biodiversity end up being either molecular biologists or ecologists (Boero, 2001). Today, there are only 6000-10000 taxonomists worldwide, few of whom are in the developing countries that contain most of the Earth's biodiversity (Gewin, 2002; Wilson, 2003). As reported by Simonetti (1997) the taxonomic community has a small size, there is a skewed distribution of taxonomic expertise between groups and more than 80% of taxonomists are close to, or older than, 50 years of age. There is a scarce recruitment of young scientists into taxonomy and systematics (Cotterill, 1995; Simonetti, 1997) and the decline in the number of posts in taxonomy in Europe and beyond is well documented (Gaston & May, 1992; Disney, 2000). In many natural history museums around the world, when a taxonomist retires, their position is not filled with a new one. Additionally, as we will comment below in a specific paragraph, the Impact Factor (IF) of most of the journals that publish species descriptions and taxonomic revisions is low or non-existent.

On the other hand, taxonomy often pays insufficient attention to its 'end users': the ecologists, conservationists, pest managers and amateur naturalists who need or want to identify animals and plants (Godfray, 2002a). Ecologists working in the tropics have felt the lack of taxonomic knowledge as an impediment that inhibits their ability to analyze community-level phenomena (see review by Brosnan, 1992), and taxonomy must facilitate,

not obstruct, ecological and biodiversity studies (Wheeler *et al.*, 2004). In this sense, taxonomy also must face up to the ‘species problem’, which is, together with ‘homology’ the main issue in comparative biology, being the subject of continuing discussion and debate (Rieppel, 2004). Species are complex things (Agapow & Sluys, 2005) and, therefore, taxonomy is a dynamic science. But this involves the problem that taxonomic organization of species is constantly changing, and some authors (see Isaac *et al.*, 2004) have asserted that species numbers are increasing rapidly owing to ‘taxonomic inflation’, where known subspecies are raised to species as a result in a change in species concept, rather than to new discoveries, and this has a great influence on macroecology and conservation. Taxonomists are often accused of creating confusion with so many changes.

In fact, one of the main reasons responsible for the ‘bad image’ of taxonomists are we taxonomists ourselves; we have not been able to ‘sell our product’ properly. In spite of the importance of taxonomy, even today we are not able to get society and other disciplines concerned about this, which is, in part, our fault. We have been complaining about our situation in front of our microscopes at our universities or museums, but we have not done very much to try to solve the problem. As pointed out by Boero (2001) the decline of taxonomy is due to taxonomists themselves; specialists in astrophysics are able to convince funding agencies to invest enormous amounts of money to look for extraterrestrial life, and the same people who invest public money in these enterprises are obviously not convinced by taxonomists that it is worthwhile investing money to explore the life of this planet! (Boero, 2001).

However, during the last few years, the situation is fortunately changing, and although we are still in a global crisis and many things need to be improved, some progress is emerging. The general interest about biodiversity conservation, the revolution of internet and web pages, the advances in molecular techniques, the development of statistics in phylogeny, and the new taxonomic funding initiatives and global projects are given some light; taxonomy is getting fashionable again, and we could be witnessing the start of a ‘taxonomic revolution’.

## **BIODIVERSITY AND CONSERVATION: AN INPUT OF OXYGEN FOR TAXONOMY**

### **A lot of taxa remain to be discovered**

Although there is no agreement among scientists about the estimation of the number of unknown species, it is estimated that about 90% of the

world species are still undescribed. The description of the new animal phyla Loricifera in 1983, Cycliophora in 1995 and Mycrognaethozoa in 2000, the possibility that tropical arthropods alone could number over 10 million species, and the fact that over 12,000 new animal species are described yearly, exemplify how little is known regarding the magnitude of global species richness (World Conservation Monitoring Centre, 1992 for an overview; Simonetti, 1997). The smaller the organisms, the more poorly known the group to which it belongs (see Wilson, 2003). About 69,000 species of fungi have been named, but as many as 1.6 million are thought to exist. Of the abundant nematodes, around 15000 species are known but millions more might await discovery. The bacteria and archaeans are the black hole of systematics (Wilson, 2003); although only 6000 have been formally recognized, approximately that many, almost all new to science, can be found only a few grams of rich forest soil. As Wilson pointed out, our ignorance of these microorganisms is vast. For example, the bacteria of the genus *Prochlorococcus*, arguably the most abundant organisms on the planet and responsible for a large part of the organic production of the ocean, were unknown until 1988. Even the largest organisms await a complete inventory. The global number of amphibian species has grown in the past 15 years by more than a third, from 4000 to 5400. The flowering plants could rise from the present 272000 to over 300000.

Unfortunately, we are witnessing, for several reasons (but specifically anthropogenic ones), the extinction of hundreds of species, most of them still undescribed. And it is evident that effective and quick conservation measures must be taken to halt this decline. A decisive moment in biodiversity conservation occurred on 5 June 1992 at the United Nations Conference of Environment and Development in Rio de Janeiro, when the Convention on Biological Diversity (CBD) was launched (Ramos *et al.*, 2001; Taylor, 2004). Most biologists are familiar with the biodiversity crisis, but not with the CBD (Geeta *et al.*, 2004). The CBD recognises that taxonomists have a vital role to play in supporting biodiversity conservation and state that, 'There is an urgent need to train and support more taxonomic experts, and to strengthen the infrastructure required to discover and understand the relationships among the world's biological diversity'. In response to this declaration, the Global Taxonomy Initiative (GTI) was established to ensure that the taxonomic expertise and data needed for biodiversity conservation are in place, and it is funded mainly by the Global Environment Facility. GTI is building taxonomic capacity and making taxonomic information available to help implement the CBD. In this sense, there is an increasing numbers of projects, initiatives and funding programmes, most of them web based, with the purpose of increasing our knowledge of species richness

and make the data available and usable in conservation programmes (see paragraph below: Taxonomy on the web) and the Natural History Museums, as main reservoirs of biodiversity collections, should revitalise and play an important role in this emerging field. As pointed out by numerous authors (see Mace, 2004), traditionally taxonomy and species conservation are often assumed to be completely interdependent activities. Nevertheless, studies of gamma-taxonomy have been successful in order to establish conservational measures on species in danger of extinction (Espinosa & Ozawa, 2006). A shortage of taxonomic information and skills, and confusion about the 'species concept', both cause problems for conservationists (Mace, 2004; Wheeler *et al.*, 2004). Species conservation needs taxonomic solutions such as a set of practical rules to standardize the species units included on regional and global species lists. Related to this, some new terms, such as Phylogenetic Diversity (total amount of evolutionary history represented by a species or group of species) are presently becoming fashionable (Faith *et al.*, 2004; Isaac *et al.*, 2004). The solutions require a new kind of collaboration among conservation biologists, taxonomists and legislators, as well as an increased resource of taxonomists with relevant and high-quality skills (Mace, 2004). However, there is a lack of appreciation by some conservationists of the importance of taxonomic status in identifying conservation targets, and we, the taxonomists need to bridge the gap between taxonomy and conservation (Golding & Timberlake, 2003); without a good, constantly updated taxonomy, biodiversity studies and conservation becomes pure 'number crunching' and 'meaningless' (Valdecasas & Camacho, 2003). These authors stress the need of conducting periodical faunistic studies to properly assess species extinction rates. The training of taxonomists and the creation of new jobs in taxonomy should be a top priority (Ramos *et al.*, 2001).

### **Can parataxonomy be of help?**

Recently, some researches have propagated an alternative to time-consuming full identification in order to provide a more rapid evaluation of regional biodiversity. It is the so called parataxonomy, which consist of sorting out the specimens to recognizable taxonomic units (RTUs) (Oliver & Beattie, 1993; Krell, 2004). The species are not identified, but the specimens are grouped in RTU by non-specialists on the basis of what they perceive that be different. Parataxonomists are 'biological diversity technicians' which are not familiar with the taxonomical groups, but they separate specimens in 'morphospecies' by eye. In Costa Rica the first 'parataxonomists' were established to assist taxonomists in collecting and mounting large numbers

of specimens (Gómez, 1991; Janzen, 1991) and eventually parataxonomists became involved in preliminary sorting of samples to RTUs (Basset *et al.*, 2000). For many authors, 'morphospecies' sorting by parataxonomists with minimum or no involvement of taxonomists has become a widely accepted method in conservation biology and species diversity-based ecology, and many papers present results based on parataxonomic sorting (Oliver & Beattie, 1993; Bolger *et al.*, 2000). As reviewed by Krell (2004), the general opinion is that parataxonomic classification is a reasonably reliable and conservative approach resulting mostly in a lower number of units than the real number of species, because similar species are more often not separated into their constituent true species than variable true species are spread into several units. However, to evaluate this statement, Krell (2004), using published and unpublished literature, compared the outcome of parataxonomic sorting with the result of taxonomic identification of the same samples, and he found overestimates in many cases, indicating that parataxonomic sorting is not necessarily a conservative approach. The error rate was more than 25% in 50% of the examples, and when a low error rate was measured, it was often caused by compensation of underestimates by overestimates within the subgroups. Taxonomy is science but parataxonomy is not; a taxonomic identification to species is the hypothesis that the specimen in question is conspecific with the type of the species (for further details see Krell, 2004). It is true that, often, we cannot expect an ecologist to correctly identify all the organisms he is dealing with. In fact, wrong identification is common in ecological, faunistic and even in taxonomic publications (see Vecchione *et al.*, 2000). This problem is aggravated by the lack of taxonomic experts as we have already commented on; unfortunately we are suffering a significant decline in the number of amateur and professional taxonomists (Hopkins & Frechkleton, 2002). Although parataxonomy can be justified in some cases, its abuse could be dangerous for future studies since RTUs are not described and not named according to the rules, and they are not comparable as they depend on the criteria of the available technician at that time. We agree completely with Krell in considering that applicability of parataxonomic data is limited, but in those fields where they can be used, as in Paleontology for example, they are potentially valuable, because they are often the only way to get results about highly important questions. Parataxonomy can provide useful data for global comparisons of gross species richness and comparisons of species numbers of different habitats, but it is useless in the elaboration of faunistic and floristic inventories, in biogeographical studies at species level, autoecology and area selection in conservation evaluation (Krell, 2004). In synthesis, parataxonomy can help but never be a substitute of taxonomy.

## TAXONOMY ON THE WEB: EVOLUTION, REVOLUTION OR INVOLUTION

Technology has enormously progressed during the last decades, and the birth of the internet has also affected all aspects of science. Today, we can hardly imagine how the previous generations of scientists were able to manage without computers or e-mail! Today, we can easily electronically access a plethora of databases, journals contents, huge amounts of information, we have developed modern apparatus and can use complex statistical models and programmes to process our data, our scientific colleagues all over the world are available at the click of a mouse. Nobody can deny that the technological progress has contributed positively to science. But... can the web be a tool to improve the traditional 'bad concept' of taxonomy? Godfray (2002a,b) was one of the first in proposing that all new taxonomic revisions should be placed on the web, available and accessible to all. He comments that taxonomy is made for the web: it is information-rich and often requires copious illustrations. According to Godfray, taxonomy and systematics have an image problem among funding bodies and the community in general and it is time for a change: taxonomy needs to reinvent itself if it is to survive and flourish. He advocates a unitary taxonomy; all taxonomic information about each group (descriptions, photographs, illustrations, keys) would be on the web and new information could be added, each group being under the administration of an authoritarian body. In this way the information would be more attractive to financial support than taxonomy as presently practised. Major government and private research funders would consider construction and maintenance of a unitary taxonomy. Godfray (2002a) consider that it might also attract new sources of funding 'it surely isn't impossible that a major company might sponsor the web revision of, say, the Lepidoptera, and if it wants to put its logo on the site, then why not?'

Several subsequent papers after Godfray (2002a) have followed this logic. Bisby *et al.* (2002) supported the creative ideas for modernizing taxonomic practices and endorse Godfray's suggestion that species descriptions, images and a platform for publication and debate should be provided on the web. Wilson (2003) imagines an electronic page for each species of organism on Earth, available everywhere by single access on command; the page contains the scientific name of the species, a pictorial or genomic representation of the primary type specimen and a summary of its diagnosis, photographs, pictures, etc, since the page is indefinitely expansible and its contents are continuously peer reviewed and updated. All the pages together for an encyclopedia, the encyclopedia of life (Wilson, 2003). Wheeler *et al.* (2004) insist on the need of taxonomy to accommodate to the new technologies,

'it is time to approach taxonomy as large-scale international science. Gewin (2002) compiled some opinions and views of the pioneers who are trying to turn this vision into reality.

On the other hand, several other scientists did not receive the suggestion by Godfray (2002a) with such optimism. Knapp *et al.* (2002) pointed out that some changes are clearly necessary, but science cannot be replaced by informatics. These authors consider that working within the current enabling conventions is more positive and practical than throwing them out and beginning again; web-based taxonomy is clearly the way of the future, but the technologies needed for this to operate successfully on the scale required are only starting to be available, and quality control is something that also must be addressed (Lee, 2002). Thiele & Yeates (2002) also showed some objections to the Godfray's model, highlighting that a taxon is an hypothesis, not an observation or fact so the proposed solutions for a change cannot be so easily transferred to the domain of taxonomy. According to Scotland *et al.* (2003a), advanced technology does not necessarily result in increased taxonomic productivity, and web-based taxonomy as a technical solution (together with the molecular approach) may provide a tantalising mirage for politicians concerned about conservation of biodiversity, but, in practice, these ideas are largely a red herring, they do little to address the real problem.

## **NEW PROJECTS AND FUNDING INITIATIVES FOR SUPPORTING TAXONOMY**

Although we are not sure yet if the advances of the web will be the solution or not for the taxonomical crisis, we must admit, at least, that the Internet has facilitated various web-based ambitious projects and initiatives. Many Internet taxonomy initiatives exist, perhaps too many, as pointed out by Mallet & Willmott (2003). We have already mentioned previously the importance of the Global Taxonomy Initiative (GTI) and the Convention on Biological Diversity (CBD). Several more exists, *Species 2000* ([www.sp2000.org](http://www.sp2000.org)) and the *Integrated Taxonomic Information System* ([www.itis.usda.gov](http://www.itis.usda.gov)), are two major players in creating an electronic global framework for taxonomy, which joined forces last 2001 in the Catalogue of Life consortium and are now making rapid progress with a catalogue of all known organisms. The 2002 Catalogue of Life now lists 260000 species on CD-ROM and on the Web (Bisby *et al.* 2002). The *Global Biodiversity Information Facility* (GBIF; [www.gbif.org](http://www.gbif.org)) is also a vital step toward accessible species-level information (Blackmore, 2002). The Catalogue of Life and the

GBIF are each funded at about US\$3 million a year and we should see real progress over the next years (Bisby *et al.*, 2002). The *All Species Foundation* was launched, with the goal of cataloguing every species on Earth in 25 years (see e.g. Gewin, 2002; Godfray, 2002a). The *Tree of Life* project ([www.tolweb.org/tree/phylogeny.html](http://www.tolweb.org/tree/phylogeny.html)) is another ambitious project, from a phylogenetic perspective. These are among the largest projects, but more than 50 other web-based projects exist worldwide.

There are also several other interesting initiatives with more discrete and realistic goals focused on restricted geographic areas rather than globally. For example three major European programmes funded by the European Commission: (1) *Fauna Europaea*, which started in 2000 and has the objective of producing a web-based checklist of all European land animals. (2) In 1997 the European Commission funded also another project to compile a taxonomic checklist of marine organisms, and today the *European Register of Marine Species* (ERMS) is now complete in its first edition, available both on the web and in printed format (3) The *EuroMed PlantBase* project has a similar objective for plants. A further objective is to link these European treatments with other systems around the world through the Species 2000 framework. In several countries, separately funded national inventories could be the key to significant acceleration of the biodiversity census (Ronquist & Gärdenfors, 2003). We can use Sweden and the Iberian Peninsula, as examples. The Iberian Peninsula constitutes without doubt, the richest and most diversified region in Western Europe (Ramos *et al.*, 2001). Ten years ago, a nationally funded project, *Fauna Iberica*, was launched, and this project is, without doubt, the most ambitious taxonomic project than ever existed in the Iberian Peninsula and the only one capable at present of bringing together all the necessary resources to produce an inventory of the animal diversity in this area. Seventy-two monographs on animal groups belonging to 11 phyla are already edited, in press or in preparation, representing approximately 20% of the estimated total number of animal species in the Iberian Peninsula and Balearic Islands but, at this rate, more than 75 years will be needed to complete it (Ramos *et al.*, 2001). More taxonomists and more funding are required to save time. The so-called *Swedish Taxonomy Initiative* (STD) provides other example. It was launched in January 2002 and aims to complete an inventory of Sweden's fauna and flora of multicellular organisms within 20 years. Following the tradition of its most famous taxonomist, Sweden aims to be the first country to complete an inventory and pictorial guide to its biodiversity (Miller, 2005).

If most of scientists agree on something concerning taxonomy, it is the lack of funding. Funds are needed to train new taxonomists and to provide facilities and resources to the taxonomists that already exist. We

have also two nice examples to show that, probably, we are moving now into the right direction: The NSF Partnerships for Enhancing Expertise in Taxonomy (*PEET*) developed in the USA, and the Synthesis of Systematic Resources (*SYNTHESYS*) project supported by the European Community. These two funding initiatives, together with others such as PBI (Planetary Biodiversity Initiative) of the US National Science Foundation, the EDIT programme (European Distributed Institute of Taxonomy), the UK-NERC funded CATE (Creating a Taxonomic e-Science) project could serve as appropriate models for future organisations.

The dismissal of taxonomy worldwide possibly originated in the USA and some measures are now being implemented to correct it (Boero, 2001). The National Science Foundation has realized that taxonomy is dying and that the USA cannot have a scientific community which is deprived of taxonomists. This led to the launch of the PEET initiative, which has been training new generations of taxonomists since 1995. This program includes substantial budgets to fund projects, enabling intensive training, targeting poorly known groups of organisms for revisionary or monographic research. The principal investigators of the projects are prestigious taxonomists who train young people from different countries. As shown by Rodman & Cody (2003) many of the PEET trainees have secured employment in the USA and abroad in academic, museums, or government agency positions relevant to systematics.

Synthesis of Systematic Resources (*SYNTHESYS*) is an initiative launched by the Consortium of European Taxonomic Facilities. In 2004, 20 European natural history museums and botanic gardens were successful in securing this integrated infrastructure initiative grant. This programme has two parts, the first one enables European researchers to access the collections comprising more than half of the world's natural history specimens, world-class libraries, facilities for microscopy, physical, chemical and molecular analysis and experienced hosts and trainers at 20 European institutions. The second part is related to networking activities focused on creating a single museum service, an integrated European resource bringing together the collections of the major natural history museums and other institutions in Europe (see [www.synthesys.info](http://www.synthesys.info) for details). *SYNTHESYS* integrates in the same programme some previous similar programmes conducted in each country, such as *SYS-RESOURCE* (Great Britain), *COLPARSYST* (France), *COBICE* (Denmark), *HIGH-LAT* (Sweden), *BIOIBERIA* (Spain) and *ABC* (Belgium).

Natural history museums must play an important role in supporting taxonomy, and they are not only about pure science, but also about educating the public (Brooke, 2000). It is important to bring taxonomy to the gen-

eral public, as society must know the importance of our work. Information from natural history collections about the diversity, taxonomy and historical distributions of species worldwide is becoming increasingly available over the internet. Computerization of collections and development of electronic catalogues are providing new capabilities for curating collections (Graham *et al.*, 2004). Funding programmes should be also addressed to support this type of collection management and to provide more educational activities between scientists and, for example, children, since some of them may belong to the next generation of taxonomists.

## PROGRESS IN PHYLOGENETICS

The main concepts related to phylogeny were already defined above, since phylogenetic ideas are really implicit in the concepts of taxonomy and systematics. In fact, “Nothing in Biology makes sense except in the light of Evolution”, following the famous essay by C. T. Dobzhansky. Consequently, it seems more than reasonable and justified the importance of Phylogenetic Systematics, since classifications should reflect the relationships among taxa in an evolutionary framework. Furthermore, phylogenies are fundamental to comparative biology; there is no doing it without taking them into account (Felsenstein, 1985). Phylogenies provide new ways to measure biodiversity, to assess conservation priorities, and to quantify the evolutionary history in any set of species (Mace *et al.*, 2003). If evolution is the unifying theme of biology, then the tree of life is the framework from which it hangs and reconstructing it should be one of the great scientific goals of the new century (see Baldauf, 2002).

Shortly after the publication of Darwin’s *The Origin of Species*, biologists were enamoured with the concept of phylogeny (Hillis, 1997). In 1866, E. Haeckel (who coined the term “phylogeny”) published a collection of detailed phylogenetic trees that depicted much of what was known about the evolutionary history of life. By the 1940s and 1960s the study of phylogeny greatly diminished, but, fortunately, the reemphasis on phylogenetic perspectives in biology began in the 1960s and 1970s, with the accumulation of new phylogenetic data (especially from molecular biology), the development of explicit and objective methods for phylogenetic inference, and the construction of computer hardware and software sufficient to the task of applying the new methods to the new data (Hillis, 1997). Because no person was present to observe directly the evolution of a group of organisms, biologists must infer phylogenies from the characters of living and fossil taxa (Pagel, 2002).

## Schools of Phylogenetic Inference

Presently there are three main schools dealing with the phylogenetic inference: Evolutionary taxonomy, numerical taxonomy or phenetics, and Phylogenetic Systematics (or Cladistics *sensu lato*).

**Evolutionary taxonomy** is an early school of phylogenetic inference, which recognises that similarity among species could arise either because species were closely related or because of convergent or parallel evolution. The term “evolutionary taxonomy” could be confusing since it seems that only this school explicitly uses the term evolution in its classification system. For this reason, some authors, such as Brusca & Brusca (1990), suggested the name of *orthodox taxonomy*. This school emerged during the middle of the XIX century with G.G. Simpson, E. Mayr, W.J. Bock and P.D. Ashlock and being the main advocates of this school. The traditional classification is mainly based on the evolutionary taxonomy, which accepts paraphyletic groups. Criticism of this school is primarily based on the lack of an explicit and objective methodology. Evolutionary taxonomy is essentially traditional taxonomy with evolution taken into account.

In the early 1960s, a group of statisticians and biologists introduced a new approach, known as **numerical taxonomy** or **phenetics**, initially developed by Sokal and Sneath (1963). This school considers that organisms should be grouped on the basis of overall similarity, independently of whether these groupings represent phylogeny. Many characters are analysed and taxa are arranged using clustering methods based on overall similarity. Numerical taxonomy was popular, however, its use has declined since the clusters do not necessarily reflect true phylogenetic relationships. Some authors talk today about *phenetic cladistics*, in which the treatment of individual characters as units that measure similarity, without evaluation of character quality, is retained (Wägele, 2005).

In 1966, W. Hennig published the book **Phylogenetic Systematics**, giving rise to the highly influential school of systematics known as *cladistics*. This school has common objectives with the pheneticists bringing in objectiveness, but focusses on common ancestry, homologies, synapomorphies (shared derived characters) and monophyly. Only monophyletic groups are considered valid. Phylogenetic systematics is strictly founded on the logic of scientific argumentation in the sense of Karl Popper; hypotheses on homologies and on monophyly can be substantiated and falsified with intersubjectively verifiable criteria (Wägele, 2005). Using the logic of ancestral and derived traits, cladistics construct sets of monophyletic groups to construct phylogenetic trees thought to identify true ancestral-descendant relationships. Hennig’s method has been developed for morphological

characters, but it can also be applied to other discrete characters including DNA sequences (Wägele, 2005).

According to Pagel (2002), by 1980s, statistical and model-based methods for inferring phylogenetic trees began to provide an alternative perspective to cladism. Many authors tend to consider that this new statistical approaches are the basis of a different school, the *statistical school*. There is presently a lot of controversy and different points of view about the exact relationships and interplay between the terms Phylogenetic Systematics, Cladistics, Maximum Parsimony, etc., and numerous questions can be asked: “Is Cladistics really a synonymous with Phylogenetic Systematics?” Cladistics, as defined by Wägele (2005), is the construction of dendrograms from character/taxa datasets using the maximum parsimony method (one of the several available methods, see methods below). According to this, if we are using other methods such as Maximum likelihood or the Bayesian approach to infer phylogenetics, it seems that we are not doing cladistics, but aren't we doing Phylogenetic Systematics?

### **Methods to infer phylogenetics: the statistical domains?**

One of the main problems in inferring phylogenies is that the number of possible phylogenies grows very fast, as the number of taxa increases: for three species there are three choices, but for 10 there are over 34 million, and for 20 there are over  $8.2 \times 10^{21}$  (Quicke, 1997). Phylogenetic trees describe the pattern of descent amongst a group of species. With the rapid accumulation of DNA sequence data, more and more phylogenies are being constructed based upon sequence comparisons. The combination of these phylogenies with powerful new statistical approaches for the analysis of biological evolution is challenging widely held beliefs about the history and evolution of life on Earth.

The three principal methods of phylogenetic inference are parsimony, distance methods, and maximum likelihood, and all draw upon ideas that emerged from the debates among the different schools of phylogenetic inference (see Arnedo, 1999; Pagel, 2002). Parsimony methods are closely linked to cladism, and the maximum likelihood methods arose from the statistical school. Distance-based methods of inference share a number of features with the phenetic school. Beside this, there is also a recent application of Bayesian methods; these methods are not new in the field of statistics [Thomas Bayes's famous formula was published in 1763! (see Lewis & Swofford, 2001)], but are being used recently with phylogenetic purposes. Maximum likelihood and Bayesian have their base in statistics

and these probabilistic techniques represent a parametric approach, while maximum parsimony can be considered nonparametric.

**Parsimony methods** (see Pagel, 2002) seek, out of all the evolutionary trees that could possibly describe the relationships among a group of organisms, the tree that implies the fewest evolutionary changes in the characters being examined, the simplest tree. This most parsimonious tree is taken to be the best estimate of the unknown true tree. The principle of parsimony is based on the ideas of Occam, a fourteenth-century philosopher, who advocated the view that when alternative explanations for an observed phenomenon exist, the simplest (or most parsimonious) explanation is to be preferred. This principle is known as Occam's Razor. One of the main problems of parsimony methods is that they do not use all the available information. To use the information in a more efficient way and have the possibility to choose statistically the best tree Felsenstein (1985) used the new approach initiated by Edwards, the maximum likelihood.

**Distance methods** find phylogenetic trees whose branch lengths most closely reflect the actual "distances" that are observed among all possible pairs of species (see Pagel, 2002 for details). These methods are based on the transformation of discrete characters (as the presence or absence of a morphological character, or the identity of a nucleotide in a homologue region of a gene) in a distance value. Distance methods are also usually more used for molecular data and are based on the comparison of pairs of aligned sequences. These methods constitute the last remnant of phenetics in systematics (they have received much criticism because of this phenetic component), and consequently, the assumptions of these methods are valid in absence of homoplasy. If convergent and parallel changes are rare, then the observed distance between any species will reflect evolutionary events that have occurred since the two species separated from their common ancestor. Dendrograms based on distance can be obtained by (1) searching clusters of most similar sequences based on pairwise distances between sequences (clustering methods such as UPGMA or Neighbour-joining), and (2) seeking the tree whose sum of branch lengths is minimized (minimum evolution methods) (see Wägele, 2005 for details)

**Maximum likelihood** estimation of phylogenetic trees was first introduced by Edwards and Cavalli-Sforza in the early 1960s and Felsenstein implemented the method for DNA sequence data. According to this method, the best tree is the most probable tree. These methods have been developed mainly for molecular data instead of morphological data and most recent advances have focused on the analysis of DNA sequences (Huelsenbeck & Rannala, 1997). One of the drawbacks of these methods is that they requires powerful computers and are very slow to run, and consequently, it is dif-

difficult to analyse large amounts of data as exhaustively as with parsimony methods.

**Bayesian analysis.** An important recent advance in phylogenetic inferences is the application of Bayesian Markov Chain Monte Carlo (MCMC) methods (see Huelsenbeck *et al.*, 2001; Lewis, 2001; Ronquist, 2004). Bayesian methods are also based on a statistical approach, similar to the Maximum Likelihood, but in this case a tree is found with maximum posterior probability, evaluating features in common among the sampled trees. Using Bayesian algorithms one searches the tree or set of trees that maximize the probability of the tree for the given data and the selected substitution model. These methods, by virtue of collecting a random sample of trees from the universe of possible trees, allow one to estimate aspects of the phylogeny. Bayesian inference of phylogeny brings a new perspective to a number of outstanding issues in evolutionary biology, including the analysis of large phylogenetic trees and complex evolutionary models and the detection of the footprint of natural selection in DNA sequences (Huelsenbeck *et al.*, 2001).

Once the trees have been obtained, there are several *a posteriori* criteria that measure the fit between data and topology, such as bootstrapping, Bremer's index and Jackknife percentages (see Arnedo, 1999 for details).

For the past two decades, there has been an ongoing debate within the phylogenetics community over whether model-based approaches for molecular systematics (such as maximum likelihood) should be preferred over the more traditional 'maximum parsimony' approach (Steel, 2005). Some authors (see Thornton and Kolaczkowski, 2005) recommend that those who infer and make use of trees should adopt a pluralistic and critical approach, using both maximum parsimony and maximum likelihood and evaluating the results of both methods cautiously, in the light of the understanding of the strengths and weaknesses of each technique. In fact, as shown by Crisp & Cook (2005) different methods using the same data can give different results. These authors summarised the main advantages and disadvantages of each method; parsimony fails in indicating probability of estimates, while the statistical maximum likelihood and Bayesian inference can fail if the model is unrealistic. Although many authors tend to consider that maximum likelihood and Bayesian methods are really supplanting parsimony methods, Kolaczkowski & Thornton (2004) have recently shown that maximum likelihood and Bayesian approaches can become strongly biased and statistically inconsistent when the rates at which sequence sites evolve change non-identically over time. Maximum parsimony performs substantially better than current parametric methods over a wide range of conditions, specially when evolution is heterogeneous.

Anyway, as pointed by Crisp & Cook (2005), phylogenetic trees are often misinterpreted, so we must be cautious inferring phylogenies. Furthermore, in spite of the progress in statistical models and methodological approaches, there is no magic pill for the phylogenetic error (see Thornton & Kolaczowski, 2005). We still have a long way to try to get the final Tree of Life.

### **Morphology *versus* genetics to address phylogeny**

Misof *et al.* (2005) discuss the recent proposals of DNA taxonomy and summarises some advantages and disadvantages of the molecular and morphological approaches in taxonomy. They do not intend to dismiss DNA based taxonomy, but they emphasise that molecular characters pose completely new problems to taxonomy. DNA taxonomy is currently promoted because of its potential for automation. These authors show that species identification can not be entirely automated since the result of a species description in taxonomy is equivalent to the formulation of a valid hypothesis.

Several papers have been recently published advocating the incorporation of molecular techniques into taxonomic protocols. Tautz *et al.* (2002, 2003) made a plea for DNA taxonomy and indicated that DNA is pointing the way ahead in taxonomy. According to these authors, it's time for DNA's unique contribution to take a central role. DNA sequences are much used in phylogenetic analysis because of the many potential combinations in only a few hundred base pairs. In this sense the genes with the broadest taxonomic coverage currently available are those encoding the ribosomal small subunit sequences, both of nuclear and mitochondrial origin (Tautz *et al.*, 2003). As considered by Misof *et al.* (2005), without any doubt, the incorporation of as many different character sets as possible into a species taxon description will improve the fit between species taxa and real evolutionary units. An issue in recent articles supportive of DNA taxonomy is the emphasis on molecular techniques over morphological approaches; it seems that the new techniques should replace the "old" ones to 'solve' the lack of adequate classifications and effective identification tools. In this sense, after the initial contributions of Tautz *et al.* (2002, 2003) supporting the molecular approach, several critiques appeared fast in the literature (e.g. Lipscomb *et al.*, 2003; Seberg *et al.*, 2003). According to these authors, to relegate taxonomy, rich in theory and knowledge, to a high-tech services industry would be a decisive step backwards for science. Molecular data certainly contribute, but when nothing is known about organisms except their DNA, there are no evolutionarily interesting patterns to explain. According to these

authors, there is no credible reason to give DNA characters greater stature than any other character type. Indeed, they pointed out several problems of the molecular approach: (1) difficulties of aligning sequences of different length, (2) problems of distinguishing paralogs from orthologs, (3) difficulty of selecting appropriate genes for any particular taxonomic study, (4) this new expensive technology would add to the North-South divide in taxonomy, since only the more developed countries would be able to use the new technology and many taxonomists with limited access to sequencing technology would be excluded.

From a phylogenetic point of view Scotland *et al.* (2003b) considered that the increased use of DNA sequence data, relative to morphology, for phylogeny reconstruction is inevitable and well founded. However, curiously, in other article of the same first author, Scotland *et al.* (2003a) reflected a totally different, much more conservative, point of view, and indicated that the lack of taxonomic progress will not be solved by DNA, and that promoting DNA sequences as the central and essential scaffold for all taxonomy would be an extremely inefficient and retrograde step for most groups. In fact they pointed out methodological problems and pitfalls of the DNA approach similar as those reported above by Lipscomb *et al.* (2003) and Seberg *et al.* (2003) The article by Scotland *et al.* (2003b) purporting to examine the value of morphological data in phylogeny reconstruction has been received critically by several systematics. Two of them seem to us especially interesting: Wiens (2004), who explained why we still need to collect more morphological data, and Smith and Turner (2005) who, as a paleontologist, provided a unique perspective in the debate. Wiens (2004) analysed the important role of morphological data in phylogeny reconstruction and reported many reasons to continue to do morphological phylogenetics, in spite of the advances in molecular systematics: (1) morphological data are necessary to solve the phylogenetic relationships of fossil taxa and their relationships to living taxa; (2) for many extant rare taxa, there are no specimens available for molecular studies; indeed many species remain known from a single specimen that was collected decades ago and frequently this scarce material was fixed in formalin, which difficult the DNA extraction; (3) there are many factors that may cause molecular analyses to reconstruct clades that, although statistically well-supported, they are incorrect (i.e. long-branch attraction, deviations between gene and species trees, and even contamination and misidentification of specimens), (4) we are very far from describing all the living species on earth, much less sequencing them. Smith & Turner (2005) supported the ideas of Wiens (2004) and strength the importance of the use of morphological characters in paleontology. In fact, molecular data cannot reconstruct the phylogenetic

relationships of extinct taxa, except for rare cases involving recently extinct forms (Cooper *et al.*, 2001)

Summarising, Mallet and Willmott (2003) pointed out that we might be only one tenth of the way through describing the world's species, questioning when it is sensible to add an extra requirement to the already slow process of describing new taxa, even if funds became available for DNA taxonomy. These authors doubt DNA taxonomy will catch on as a mandatory step for species description in all organisms, and believe that most biologists will prefer to see DNA sequence information as a supplement rather than a required replacement for morphological data.

In our opinion, as concurred by Lee (1999), homoplasy, for example, can contaminate both types of data (morphological and molecular), suggesting that morphological and molecular systematics might have more in common than previously assumed. Both approaches must be used to properly address phylogeny. And not only morphology and genetics must contribute, but also behavioural, ecological, biochemical and physiological data should be also considered. As many tools we will be able to use and integrate, a closer knowledge of the real world we will have. On the other hand, naturalists and molecular biologists often share questions, methods and explanations. In any case, it seems reasonable, that morphology should continue playing a major role in taxonomy: as Dunn (2003) pointed out, it is hard to understand how taxonomy will be taught to students, volunteers, parataxonomists, etc. without starting first with morphology. Quick and accurate identification of species in the field and laboratory based on morphological characters is also critical to many other areas of biology besides systematics (e.g. ecology, behaviour, physiology) (see Wiens, 2004).

### **Supporting a DNA-based taxonomy?: Gen Bank and Bar Coding**

**Genbank** is the genetic sequence data base of the National Institute of Health, and includes collection of all available DNA sequences of published papers. Currently >28,000 million bases from >250,000 species (Harris, 2003) and rising daily. Most journals, before paper publication, require that sequences used in the paper must be registered in data bases such as GenBank, where they are publicly available and can be used by other scientist in further studies. But taking into account that the quality controls depends solely on the original scientists... How reliable are the sequences in the GenBank? Harris (2003) addressed this problem, and indicated that more than half of all published human mtDNA studies contain mistakes, a so high level that geneticists could be drawing incorrect conclusions in

population and evolutionary studies. Much greater controls are needed, both from journals and from individual scientists. Otherwise, all the mistakes will be accumulated in future works and the phylogenetic studies based on DNA sequences will be completely unreliable. Fortunately, some new methods for detecting errors using phylogenetic networks have recently been proposed (see Harris, 2003). Anyway, the best and simplest way to check the quality of published sequences is to re-sequence them, and avoid the use of already published sequences before a previous double checking. Submitters of sequences can maintain the value of GenBank by only including high quality sequences, and scientist including data from databanks need to be aware that the quality of the sequences is not always optimal.

A very nice example of how molecular taxonomy can be applied for species conservation and discovery has been developed by the www.DNA-surveillance project, implemented currently for identification of whales, dolphins and porpoises derived from strandings, fisheries bycatch, regulated exploitation and illegal hunting (Baker *et al.*, 2003). It is a web-based programme which aligns a user-submitted gene sequence of unknown origin against a comprehensive set of reference sequences curated by species specialists. The taxonomy of cetaceans is plagued by the problem of some extremely rare species for which morphological descriptions are often very incomplete. In this case, DNA based taxonomy has undoubtedly helped clarifying issues (Misof *et al.*, 2005). This approach conducted for the single order Cetacea complements a more universal and ambitious proposal: **DNA Barcoding**.

Last February 2005, the First International Barcoding of Life Conference was held in London, convened by the Consortium for the Barcode of Life (CBOL) (see Marshall, 2005). DNA barcoding is now being proposed as a way to catalogue life. This new technology makes use of short but specific DNA tags, or “barcodes” to distinguish one species from another. It uses a small part of the mitochondrial genome, 650 to 750 bases of the cytochrome *c* oxidase I gene (COI) to provide a unique fingerprint for each species. For most eukaryotes, COI variation appears to be lower among individuals within a species than among those from different species (Marshall, 2005). Hebert, considered the “father of bar coding” explained one of the main reasons for the current optimism among those in the field: the price for reading bar codes is dropping. Bar coding all of life would be “relatively cheap in terms of other big science projects”, less than \$1 billion (see Marshall, 2005). But such a project has still big obstacles. Experts are not sure that simple bar codes will work for all species; plants, for example cannot be tracked with the COI gene, and for amphibians, COI gene varies so much from one individual to the next that it cannot be used reliably to mark species. The work of taxonomists provides knowledge of the organisms, not

a few possible unique nucleotides and, in any case, every barcode should be linked with a known, described specimen stored in a publicly available collection. DNA barcoding generates information not knowledge; the vast number of barcodes will tell us what we know, that life is complex (Ebach & Holdrege, 2005). These authors also support the idea that barcoding is in competition with taxonomy for funding. Other authors, however, have the completely opposite idea and indicate that existing DNA barcoding networks have been funded by agencies that do not have a tradition of supporting taxonomic work and that rather than draining support from taxonomy, the DNA barcoding initiative has the potential to inject significant new funding into museums, herbaria, etc. (Gregory, 2005). Hence, the DNA Barcoding project, together with the Phylocode project (see below), is one of the most controversial and debated topics in systematics today and, similar to Phylocode, has seen heated discussions (see also Smith, 2005; Wheeler, 2005; Schander & Willassen, 2005; Hebert & Gregory, 2005; Will *et al.*, 2005). In our opinion, barcoding as a tool can be helpful in some aspects, as is the case with cetaceans, but we should not forget that science is not a supermarket where all items are marked with a bar code. If we go to the countryside to study, identify or just to enjoy and learn about birds, insects or plants, we will not find a label stuck in each species showing the barcode. In this case genotypes will not be useful and we will need expertise in taxonomy, identification keys and field guides based on morphological characters, etc. to distinguish phenotypes which can help us to learn about organisms “in situ”. We agree completely with Dunn (2003) in his claim that it is difficult to see how a set of DNA sequences could be used to aid students in learning flora or fauna, in the identification of living or herbarium specimens, or in other fieldwork. Dunn is not a systematist, he is a botanic garden and part-time educator. From his point of view, it is clearly ludicrous to expect that botanic gardeners, plant explorers, and other garden staff will use DNA sequences in making decisions as to which taxonomic group a particular plant belongs. As Ebach & Holdrege (2005) pointed out, DNA barcoding is no substitute for taxonomy.

### **“Phylocode” or the traditional Linnaeus nomenclature: that’s the question**

For more than 200 years the binomial system described in *Systema Naturae* (1758) by the Swedish botanist Carolus Linnaeus has been the adopted classification and nomenclature system. As we have already commented above, nowadays phylogenetics is getting a main role in the play

of classification, and the possibility of a reform of the rules are currently under debate. Are the traditional nomenclature rules threatened with extinction? The new system, known as the “PhyloCode”, has brought controversy among scientists (see Bryant & Cantino, 2002). This new naming system is based more explicitly on evolutionary relationships. Instead of being grouped into ranks, such as genus, family and order, organisms are assembled into “clades”, defined as any set of organisms with a common ancestor. More specifically, a clade is a monophyletic taxon. In this sense, within a system of phylogenetic taxonomy, some authors (see Pleijel & Rouse, 2000) believe that taxon names should refer to monophyletic groups only and that species should not be recognized as taxa. To distinguish the smallest identified taxa, these authors introduce the least-inclusive taxonomic unit (LITU). LITUs imply nothing absolute about inclusiveness, only that subdivisions are not presently recognized. Under the PhyloCode approach, genus level names might be lost and species names might be shortened, hyphenated with their former genus designation, or given a numeric designation. As Pennisi (2001) pointed out, these ideas were developed in several publications during the early 1990s (see De Queiroz & Gauthier, 1994), and then introduced to the wider biological community at a symposium held during the 1995 meeting of the American Institute of Biological Sciences (AIBS). Interest was strong enough that K. de Queiroz, one of the main PhyloCode’s developers, and other supporters organized a workshop at Harvard in August 1998. P.D. Cantino became one of the PhyloCode’s strongest advocates and helped de Queiroz to elaborate the rules, which were posted on the web for comments (see <http://www.ohiou.edu/phylocode>). The first International Phylogenetic Nomenclature Meeting, which took place in Paris in July 2004 was one of the final steps towards the proposed implementation of the PhyloCode: the inauguration of the International Society for Phylogenetic Nomenclature (ISPN) was inaugurated. Currently, the voluntary PhyloCode only governs clade names; in the future, it will consist of two parts: a clade part and a species part (Dayrat, 2005). Although the main focus of the Paris meeting was clade names, significant progress was also made towards initiation of a code for species names (Laurin & Cantino, 2004). Indeed, Dayrat (2005) support the advantages of naming species under the PhyloCode and show an example of how a new species of Nudibranchia may be named under these new rules. The major rules of this proposed phylogenetic nomenclature are eloquently summarised in Wägele (2005) and its logical basis can be found in Sereno (2005). But this initiative has not very well received by other scientists such as J. Davis, F. Ferrari, K. Nixon, K.J. Niklas or M.J. Benton (see Benton, 2000; Pennisi, 2001; Niklas, 2001; Wheeler, 2004). For example, Niklas (2001), editor-in-chief of the American Journal of

Botany, points out that the Linnean system is anything but antiquated or inadequate. It provides stability, flexibility, and a high degree of structure that facilitates communication, information retrieval and editorial sanity; in contrast, the precepts of the PhyloCode appear to rest on the currently unstable bifurcate hierarchies of seemingly endlessly revised cladograms, whose nodes may bring nothing to bear on the hierarchy of taxonomic ranks or their biology. Despite the strong and somewhat rancorous controversy portrayed by Pennisi (2001), the Smithsonian Institute, for example, (staff members of which advocate on both sides of the debate) is opening the channels of communication between the proponents of the Linnaean system and the PhyloCode system, who claim to have Darwin on their side (Kress, 2001). Anyway, as pointed by Wägele (2005), the PhyloCode has some weak points: (1) it is highly improbable that the scientific community will give up binomial species names; (2) the number of taxon names would increase dramatically because names are linked with specific definitions and cladograms; (3) all valid names that are currently being used (about 3 million) have to be defined and registered, and for decades taxonomists will discuss the correct circumscription of established names, and (4) many will not accept that a small committee will play the role of a nomenclature police and take decisions for each proposed taxon name. In our opinion, the new approach seems interesting in many ways but we must take into account that the phylogenetic relationships among plant and animal taxa are still not clear, and changing at this moment in time would create even more confusion. As mentioned by Niklas (2001) until the phylogenetic relationships become reasonably well stabilised through scientific consensus, the use of the PhyloCode could thus lead to endless revision of plant and animal names, with ensuing instability of names. Without any doubt, we must try to consider phylogeny in our taxonomical descriptions, and go towards definition of monophyletic groups, but, in our opinion, this is one thing, and other different thing, a little bit dangerous and worrisome at the moment, is try to change the classification system. We must be cautious and go step by step. In fact, there are also many other problems to solve related to taxonomy and nomenclature; the scientific names of higher-ranked taxa (above the superfamily) of animals are not regulated by the International Code of Zoological Nomenclature (ICZN), but by “consensus” among workers (Dubois, 2005). When there is no real consensus, a frequent situation, some criteria must be used to establish which *nomen* should be considered valid for any given taxon. Dubois (2005) in a detailed revision and reflection has recently proposed some rules for the incorporation of nomina of higher-ranked zoological taxa in the ICZN. In this interesting work, he discusses detailed approaches to several problems altogether, general ques-

tions, concepts and terms of biological nomenclature, including a strong and well-balanced criticism of the “PhyloCode” project.

## TAXONOMY AND IMPACT FACTORS

As pointed out by Boero (2001) and Minelli (2003), the impact factor (IF) of the journals in which scientists publish, is, nowadays, a fundamental (or sometimes the only) criterion for scoring the performance of researchers and for assigning resources and opportunities in today’s academic market; if you have a low IF, your future is dark. Unfortunately, most of the journals in which taxonomists publish are not included in the ISI Journal of Citation Reports (which means  $IF=0,00$ ), and if they are included, the IF is very low when compared with other journals. Krell (2000, 2002) used several arguments to explain that the IF, as calculated by the ISI, is inapplicable in taxonomy: (1) the number of taxonomists is declining, so the average age of references in taxonomic publications is much higher than those in other scientific disciplines; most of the cites are old and it is pointless to use the ISI method of analysing citations over the preceding two years; (2) the relevance of descriptive publications in taxonomy remains the same over time and, consequently, original descriptions have to be referred to for ever, independent of the paper’s quality; (3) for some taxonomical groups there are just a few specialists working on, so the chance to be cited by colleagues is rare compared with other fields, and this is not related at all with the quality of the paper (some excellent papers have to wait a generation to be cited); (4) taxonomical papers provide identification keys which are often used also for non-specialists, but these keys are usually not documented in the references section of papers and, consequently, this impact is missed for the ISI system. We mostly agree with these strong arguments given by Krell (2002), and, surely, alternative systems should be developed to measure the real impact and quality of taxonomical papers should be developed. It is true that, nowadays, we give probably too much importance to the IF and we do not take into account the quality or the importance of the paper itself. Here, an example which could seem ridiculous but which it is not, according to the IF. Imagine that there is a position X available at the University Y and there are two applicants, A and B. Applicant A has 10 papers published in different journals with IF, but each of these papers includes only a single description of a new species; applicant B has also 10 papers, very long papers in this case, all of them including extensive revisions of genera, descriptions and redescriptions of abundant new taxa, ecological and phylogenetic information, etc, but these

papers were published in several museum's journals, very good taxonomical journals but with IF=0.00 since, unfortunately, they are not covered by the *Science Citation Index (SCI)*. Which applicant deserves the position? We would say, applicant B, of course. But, according to the present system of punctuation in many universities and/or research centers, applicant A would have probably more chance to be selected because he/she would have higher score. On the other hand, the IF system is contributing to the extinction of  $\alpha$ -taxonomists since many of them are changing to new techniques and tools who can let them have access to the IF system. Consequently, urgent measures should be taken to provide scientific recognition to those working in aspects which are not considered by the IFs. But, meanwhile an alternative system is developed, we should continue trying to get our taxonomical results published in journals with IF; on the other hand, these journals have usually more diffusion and are easier to locate than other journals, since it is more common that universities, museums and research centers' libraries have electronic access to ISI journals rather than to others not included in the ISI system. And today, it seems that, there is, fortunately, an increasing interest to promote journals devoted to taxonomy. In zoology, for example, the journal *Zootaxa* (presently covered by the *SCI*) has come out as a rapid international journal for animal taxonomists and publishes quality papers regardless of the length of each paper/monograph. Anyway, it is true that the IF of taxonomical journals is low when compared with others. In this sense, when IF is used as a parameter to provide research positions, funding, etc., some institutions have tried to minimise comparative problems by not considering the number IF itself, but considering the position of the journal, according to the IF, in a list of journals of the same topic or category (first, second, third or fourth quartile of the list, or first half vs second half of the list). In this way, the important point is that the journal should be included in the list of journals with IF, but the absolute value of the IF is not so relevant.

Another possibility, in which zoologists and botanists might find a radical solution to the shortcomings of the current taxonomic practice and publishing, could be lighted by the example of bacteriologists (see Minelli, 2003). Bacteriologists are free to publish a scientific taxonomic paper in any journal, but, a new name is considered officially recognised only if it is registered in the *International Journal of Systematic Bacteriology*. Consequently, the bacterial code already has a unitary taxonomy, with a new starting date for nomenclature of 1980 (<http://www.dsmz.de/bacnom/bactname.htm>). As pointed out by Minelli (2003) this bibliographic reference tool could be enhanced with all additional information, making it a functionally complete archive of the legal documents related to new nomenclatural acts. Publish-

ing in the same journal all papers dealing with Zoological taxonomy, for instance (descriptions of new taxa, genera revision, etc.) would represent some advantages (all new taxa compiled together, only one value of IF and probably higher than previously), but the journal would be overwhelmed and the editorial would need many people working on, different sections, etc., and, on the other hand, probably, many taxonomist would not be willing to publish all their work in the same journal. The possibility that a few specialists might monopolize nomenclature was among the worries that led botanists to reject calls for a central registry of names at the International Botanical Congress in 1999; similar proposals were also rejected in the 1999 Zoological Code. In addition, because many name changes are due to differing species concepts rather than to confusion about name priority or identity, stability of names would be unlikely to result even if a single registry became mandatory (Mallet & Willmott, 2003).

## CONCLUSIONS

- (1) Taxonomy, the classification of living things, is essential in theoretical and applied biology (agriculture and forestry, biological control, public health, wild life management, mineral prospecting through the datation of rocks by their enclosed fauna and flora, national defence, environmental problems, soil fertility, commerce, etc.). However, this discipline is presently in a crisis: there is a lack of funding for taxonomy, the number of taxonomists is dramatically decreasing and taxonomical studies have a low impact factor.
- (2) Fortunately, the emerging interest for biodiversity and conservation is representing a vital input to taxonomy. It is estimated than more than 90% of the world species are still unknown and undescribed, and even new animal phyla are still being described. We are witnessing the extinction of thousands of species, most of them still undescribed. Obviously, taxonomy plays a major role in the sense of biological conservation. Parataxonomy, consisting in sorting out the specimens to recognizable taxonomic units (RTUs) is being proposed as a useful tool in assessing biodiversity evaluations, but has obvious limitations.
- (3) Can the web contribute to improve the traditional 'bad concept' of taxonomy? Some authors insist on the need of taxonomy to accommodate to the new technologies, considering that taxonomy is made for the web since it is information-rich and often requires copious illustrations. These authors advocate an encyclopaedia of life and/or web-based unitary taxonomy; all taxonomic information about each

- group (descriptions, photographs, illustrations, keys) would be on the web and new information could be added, each group being under the administration of an expert. Other scientists have not welcomed this proposed with so much optimism.
- (4) Fortunately, the number of new projects and funding initiatives for supporting taxonomy have recently been increasing, at global scale (e.g. Species 2000, Integrated Taxonomic Information System, the Global Biodiversity Information Facility, All Species Foundation, Tree of Life), or on more regional scale (e.g. Fauna Europaea in Europe, Fauna Iberica in Spain or the Swedish Taxonomy Initiative in Sweden). Two programmes, the Partnerships for Enhancing Expertise in Taxonomy (PEET) developed in USA, and SYNTHESYS, supported by the European Community, are two interesting funding initiatives which should serve like models for future; these programmes are destined to train new taxonomists and to provide facilities and resources to the taxonomists which already exist.
  - (5) The emphasis on phylogenetic perspectives in biology began in the 1960s and 1970s, with the accumulation of new phylogenetic data (especially from molecular biology), the development of explicit and objective methods for phylogenetic inference, and the construction of computer hardware and software sufficient to the task of applying the new methods to the new data. In this sense, bayesian inference of phylogeny brings a new perspective to a number of outstanding issues in evolutionary biology. Both, morphological and molecular approaches should be the two sides of the same coin in systematics. And not only morphology and genetics must contribute, but also behavioural, ecological, biochemical and physiological data should be considered.
  - (6) DNA barcoding is now being proposed as a way to catalogue life. This new technology makes use of short but specific DNA tags, or “barcodes” to distinguish one species from another. It uses a small part of the mitochondrial genome, 650 to 750 bases of the cytochrome c oxidase I gene (COI) to provide a unique fingerprint for each species. Despite the potential benefits of DNA barcoding to both the practitioners and users of taxonomy, it has been controversial in some scientific circles. A few scientists have even characterized DNA barcoding as being “anti-taxonomy”.
  - (7) The new proposed nomenclature system, known as “Phylocode” has also brought controversy among scientists. This new naming system is based more explicitly on evolutionary relationships and, instead of being grouped into ranks, such as genus, family and order, organisms are assembled into “clades”, defined as any set of organisms with a

common ancestor. Although “Phylocode” is strongly supported by many scientists, this system has also some weak points (e.g. the number of taxon names would dramatically increase, all valid names currently being used should have to be defined and registered, and, taking into account that the phylogenetic relationships are not clear for many taxa yet, the establishing of this new system right now would increase the confusion instead of clarification)

- (8) Taxonomy is now in at one important cross-roads in its long history, and we must decide to go into one direction or another. New approaches have emerged and technological progress is demanding, sometimes without understanding. There are many topics under debate and many different points of view. Several authors (see Wheeler & Valdecasas, 2005) are proposing challenges to transform taxonomy such as establish a federation of taxonomy societies and institutions, increase kinds and levels of outreach and education, undertake species inventories, expand identification tool chest, etc. This is, obviously, positive since, as pointed by Bisby *et al.* (2002), the excellent news is that the interest in taxonomy is reawakening. But we must be careful and not lose our way, we must join our efforts to have clear objectives to show them to others, specially those who can provide funding. Taxonomy needs time and money to face the crisis, but we must first know how to use them and for what. We must go to the Renaissance and not to the Tower of Babel. To understand the world around us, we must understand all the species which live with us on it, and until now we only know the 5-10% of them. We must focus our efforts convincing about the importance of taxonomy as a basic science for understanding our lives, the skeleton of hundreds of disciplines. And phylogenetics, DNA progress, the web, the new statistic methods should be the tools to support taxonomy not the weapons to eventually kill it. Taxonomy is taxonomy, and must survive as taxonomy for ever.

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