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## Introduction to Botanical Taxonomy

Alessandro Rapini

### Abstract

Botanical taxonomy delimits groups of plants and describes and names taxa based on these groups to identify other members of the same taxa. The circumscription of taxa is directed by the principles of classification, and the name assigned is governed by a code of nomenclature. However, changes in the principles of classification and information accumulated from different sources affect taxon circumscriptions and, consequently, the meaning of scientific names. This process is continuous but, by governing the application of names, nomenclature has enabled the construction of a sizable body of plant knowledge. Taxonomic works store botanical information, and scientific names permit the access to and linkage of this information synergistically, thus enhancing the knowledge regarding plants and disseminating it in space and time.

**Key words** Classification, Description, Identification, Naturalists, Nomenclature, Phylogenetics, Plant systematics, Scientific names

“Nature produces individuals, and nothing more. She produces them in such countless numbers that we are compelled to sort them into kinds in order that we may be able to carry them in our minds. This sorting is classification—taxonomy.” [1]

Ethnobiology investigates the folk knowledge of human interactions with organisms [2]. Traditional societies are intimately dependent upon local environment where they have found material to supply most of their demands—food, shelter, clothing, implements, utensils, medicaments, instruments, etc.—for a long time [3]. Therefore, ethnobiology can provide critical knowledge in assessments of biodiversity and sustainable conservation and is currently considered a priority area in biological sciences because traditional knowledge and biological diversity are both being rapidly lost [4].

Although folk classifications are structurally arranged following general principles [5], a plant may have different local names and a vernacular name may be used as reference to different plants.

Consequently, common names cannot substitute scientific names, and appropriate procedures for recording plant species should be followed to reach best practice and guarantee high standards of scientific works in ethnobotany: first, a voucher specimen identified by the local informants should be collected and placed in a herbarium to be used as reference to this record; second, the herbarium specimen should be identified by a competent botanist; and third, the correct scientific name of the plant and its author(s) should be mentioned in the article as well as the voucher specimen and the botanist responsible for its scientific identification [6]. Therefore, the accuracy, reliability and quality of plant information to accomplish the best practice in Ethnobotany rely essentially on the taxonomy, which is a basic requirement to any biological science.

Taxonomy is the discipline responsible for ordering the diversity of life: it provides a synthetic method to classify and designate organisms, allowing efficient communication. The discipline of taxonomy arises from the combination between the principles used to arrange biodiversity and the procedures established to name its components. As an inductive method by which we organise the universe, classifications are anthropocentric constructions devised with particular interests and assumptions: they group objects and create classes (intention) based on their properties in such a way that other objects (extension) of that same kind will also belong to those classes. In taxonomy, the organisms are the objects, and taxa are the classes [7] or natural kinds of a sort [8]. Taxa are concepts or statements defined by common properties or the relationships of their members: they are created but do not have physical existence; they can be modified but do not evolve; they can be abandoned but do not become extinct [9].

The function of taxonomists is to delimit, describe and name taxa in such a way that organisms are identified by their conformity to these taxa. The primary role of taxonomy, therefore, is to circumscribe taxa and create a hierarchical system of classes. These classifications can be constructed with different aims. Some are only operational and are designed to be simple and stable, whereas others favour the empirical content, synthesising the knowledge of groups or investing in predictions. Lastly, some classifications are theoretical and represent entities in action or the result of natural processes. Considering that plants are highly diverse and widespread and also that they have long been used by humans in different parts of the world and with different purposes, it is not surprising that different systems have been proposed to classify this group. In this chapter, botanical taxonomy is introduced considering three integrated components of the systematisation of plant diversity: (1) the principles of classification, (2) botanical nomenclature and (3) description and identification.

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## 1 Systems and Principles of Plant Classification

Although Aristotle is widely known as the first naturalist, Theophrastus (371–287 B.C.), his pupil, is recognised as the father of Botany (important events for the history of plant taxonomy since then can be found in [10, 11]). Theophrastus described approximately 500 plants. He was the first to name plants and contemplate how they should be ordered by using characters, such as their habit (herbs, sub-shrub, shrubs and trees) and their utility for humans (wild and cultivated plants), as criteria for their grouping. After the books in Alexandria had been burned, Theophrastus' contribution became largely ignored for more than 1,500 years, until his *Enquiry to Plants* was translated back into Latin by Teodoro of Gaza in the fifteenth century from an Arab manuscript discovered in the Vatican library.

Theophrastus was followed by Dioscorides, a Greek physician who produced a field guide of useful plants, particularly for medicine, and by Pliny, a Roman lawyer who compiled most of the natural history information that had accumulated up to his lifetime. Dioscorides' *Materia Medica* (approx. 600 plants) and Pliny's *Natural History* (approx. 800 plants) were published almost at the same time (60–80 A.D.) and became the main botanical references during the Middle Ages (fifth to fifteenth centuries A.D.). In Medieval times, Arabian contributions to plant knowledge were restricted to innovations in agriculture and medicine, in addition to reproductions of earlier manuscripts.

Natural history was reborn during the Renaissance. The German herbalists Brunfels, Bock, Cordus and Fuchs produced their own botanical-medical books, and the herbals spread to Holland, France and England. With the great exploratory travels during this period, many curious new plants arrived in Europe from the Orient and the New World, and in the sixteenth century, universities began to devote attention to the study of plants. Plantsmen were also interested in describing plants and not merely their uses, as most herbalists did. In Italy, Luca Ghini set up the first European botanical garden in Pisa, and his student Andrea Cesalpino prepared a herbarium (collection of dried plant specimens) in Bologna, now housed in the Natural History Museum in Florence.

Cesalpino renewed Theophrastus' search for order and advocated for a method to organise plants according to their affinities. He also used plant growth, a character recurrently employed in several systems, from Theophrastus (approx. 300 A.D.) to Hutchinson (the 1970s), but associated it with the properties of fruits and seeds. Cesalpino's method for plant classification was further improved by John Ray. Ray had included more than 18,500 "species" of plants in his *Historia Plantarum* (1686–1704),

therefore a method for the arrangement of these plants was needed. Ray employed plant growth as a primary criterion, associating it with the number of cotyledons, a character influential in subsequent systems. According to Ray's *Methodus Plantarum Emendata* (1703), the method of classification should be suggested by the plants and not imposed to them: groups should be ordered according to their affinities, and they should be clearly recognised and stable enough to avoid confusion. Ray was establishing a new scientific discipline for plantsmen: Taxonomy (a term only introduced by Augustin Pyramus de Candolle more than a century later), thus establishing a course for Linnaeus' contributions.

In *Species Plantarum*, published in 1753, the Swedish botanist Carl Linnaeus named 5,890 species of plants and 1,097 genera from different parts of the world. Linnaeus was the first to apply Latin binomials consistently and to use a hierarchical system of classification considering five categories—species, genera, orders, classes and kingdoms; most previous treatments used polynomial tags describing diagnostic features and scarcely recognised categories above genus. His concept of species was derived from John Ray, whereas his concept of genera was based on the nearly 700 genera considered by the Frenchman Joseph Pitton de Tournefort in the 1700s. The simple standardisation promoted by Linnaeus for naming taxa has been incorporated in botany since and is still in use today. His sexual system was one of the first to emphasise floral features in classification, recognising 24 classes based on the number and arrangement of stamens and subdividing these classes into orders according to the number of pistils. Nevertheless, Linnaeus was not strict with his own artificial method and eventually included species with different numbers of stamens in the same genus, species that otherwise would be treated as different classes [12]. Following Ray, Linnaeus also thought that characters should be designated by taxa, and not the contrary, and believed that natural groups existed, though it was impossible for these groups to be revealed at that time. An advancement in this direction would have to wait for *Genera Plantarum*, which was published by the Frenchman Antoine Laurent de Jussieu in 1789.

Describing genera and orders (currently, termed families) and grouping them into classes (now, orders), de Jussieu's work on 100 families is the basis of our current system. He recognised groups with more than 1 and less than 100 members, a reasonable range to favour memorisation. Similar to the earlier Frenchman Michael Adanson, de Jussieu also proposed a synthetic system based on general similarities, defining groups based on a combination of different characters; however, unlike his fellow countryman, he considered the features within groups to be invariable. De Jussieu's system was followed by other natural systems. The Swiss professor of Botany Augustin Pyramus de Candolle, for instance, initiated the Herculean effort to describe all vascular plants in his

*Prodromus Systematis Naturalis Regni Vegetabilis*. This work was started in 1824 and was continued by his son and grandson, Alphonse and Casimir de Candolle, respectively, not to have the dicotyledons completed until 1873. By this time, the number of species was approaching ten times the number that Linnaeus had considered. Natural systems were also constructed by, for instance, the Englishmen Bentham and Hooker, who prepared the 3-volume *Genera Plantarum* (1862–1883), and later, by the Germans Engler and Prantl in their 23-volume *Die Natürlichen Pflanzenfamilien* (1887–1915).

Although artificial systems are based on a single or few characters selected a priori, such as in the sexual system of Linnaeus or in herbals in which plants are often arranged according to their uses and effects, natural systems are polythetic: they are based on many characters, grouping plants with a large number of correlated attributes. Accordingly, a natural classification is expected to be more useful and informative than an artificial one and to offer a higher predictive value [13]. However, different from what has been largely disseminated since the mid-twentieth century [10, 14–16], these pre-evolutionary systems were not essentialist. They used exemplars (or types) as references to associate other members according to their overall resemblance. Therefore, groups were formed around these models and not defined because of essential features found for Platonic types [17]. In fact, evolutionary principles had little effect on taxonomic methods; what changed was the way classifications were explained [12].

Darwin was aware that taxonomic categories were constructions defined by convenience and that classification was a logical process that synthesised much information in few words [18]. However, he did not agree with the natural systems of his time because they did not consider genealogical relationships in their classifications. For him, degrees of similarity should be used only to reveal descendant from a common ancestral stock upon which taxa should be based [19]. Although Darwin was already appealing for a type of phylogenetic classification, more than a century would be required for it to become consolidated in botany.

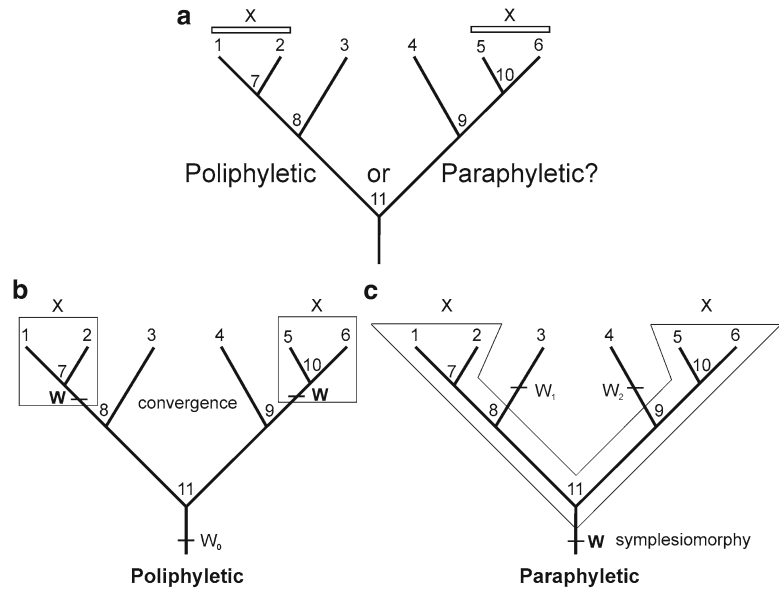
In 1915, the American Charles Bessey, a student of Asa Gray, proposed an influential system, in his *Phylogenetic Taxonomy of Flowering Plants*. Despite the title, his system was evolutionist. Following Ray and de Jussieu, Bessey also employed the number of cotyledons as an important character, and most subsequent evolutionary systems to the end of twentieth century, such as those proposed by Armen Takhtajan, Arthur Cronquist, Robert Thorne and Rolf Dahlgren, continued to divide flowering plants into dicots and monocots. These evolutionary authors employed an enormous amount of information, from phytochemistry and anatomy to ordinary morphology and ecology, to infer evolutionary relationships. Taxa were then constructed based on groups, as revealed

by a combination of common evolution and degree of similarities and differences.

Given the complex mosaic of features, evolutionary authors devote particular attention to different parts of the plant. Weights are usually given to some characters, and classifications depend greatly on the author's judgment. Consequently, evolutionary systems also address a high degree of subjectivity and are usually supported based on the authority and experience of their proponents rather than on their utility or objectivity. As a reaction, a numerical taxonomy [20] emerged. Because plant features can be observed but ancestral relationships can only be inferred, some authors advocated for classifications objectively based on the amount of similarity; they were calling for repeatability and more objectivity in systematics.

Although the German entomologist Willi Hennig published the book *Phylogenetic Systematics* in the mid-1950s, phylogenetics only became popular in botany decades later. Introduced by Bremer and Wantorp [21], the phylogenetic approach soon changed the way plants were classified. In a phylogenetic system, classifications must consider only monophyletic taxa (also treated as "holophyletic" by some). Monophyletic groups (or clades, then cladistics) are those that include a common ancestor and all its descendants; consequently, these groups are recognised by synapomorphies, i.e. features shared because of their common ancestry. Therefore, a phylogenetic classification requires, before anything else, hypotheses of ancestral relationships, which are usually depicted in a phylogenetic tree: a branched diagram composed of internal nodes, representing hypothetical ancestors, and terminals, representing organisms. Similar to an artificial system, phylogenetic classifications are also based on a single property of their members, also established a priori: common exclusive ancestry, even though many characters are usually considered to reconstruct this relationship.

Both evolutionary and phylogenetic systems recognise only groups derived from a common ancestor, thus preventing the recognition of polyphyletic groups, those recognised by homoplasies (convergences or reversions), i.e. features that appear more than once independently. Nevertheless, in addition to clades, evolutionary systems also recognise grades (paraphyletic groups), which are conveniently decoupled from the immediately nested clades because of their degree of dissimilarity. Grades are recognised by symplesiomorphies (or the absence of synapomorphies), i.e. features that were present in their common ancestor but derived in some of its descendants (Fig. 1). Grade members are not necessarily closely related to each other and may share a more recent ancestor with members of another group. By accepting only monophyletic groups, phylogenetic systems reduce the subjectivity of recognising grades based on the amount of their similarity. Nonetheless, many alternative clade classifications are also possible based on a



**Fig. 1** Phylogenetic tree, with the terminals (1–6) and internal nodes (7–11) numbered. Taxon X is recognised by the feature W and includes terminals 1, 2, 5 and 6 (a). Through this information, it is possible to conclude that X is not monophyletic. However, to decide the phylogenetic nature of a taxon, it is necessary to ascertain whether the common ancestor of its members (11, in this example) is included, which can be accessed only by convention or by understanding the evolution of taxon intension (W, in this example). If feature W appeared twice independently (convergence), then Taxon X is polyphyletic (b). However, if feature W appeared only once, Taxon X is recognised by a feature present in the ancestor but not in all its descents (symplesiomorphy); that is, X is recognised by the absence of  $W_1$  and  $W_2$  (c)

phylogenetic tree. Thus, secondary principles of classification must be considered to assist taxonomic decisions; among them, Backlund and Bremer [22] listed the general stability and phylogenetic content and confidence (support) and diagnosability of clades.

Although different assumptions, analyses and data sources can be used to reconstruct the phylogeny of a group, nothing can guarantee that the true phylogeny will be completely revealed. Adding data and improving analytical procedures are obvious strategies to achieve results that are close to the correct ones, and progress in our knowledge of plant relationships directly affects the taxonomy of these groups. Up to the 1980s, most phylogenetic studies with plants included few terminals and were mainly based on morphological data using parsimony. According to the parsimony criterion, when presented with alternative hypotheses, the simplest should be preferred; phylogenetically speaking, this means trees with less homoplasy. However, parsimony is a philosophical criterion and not a biological one: nature is not necessarily simple,



and parsimony, in several situations, can be inconsistent [23]. Regardless, morphology is an extremely complex source of data, and different authors often interpret it differently. Furthermore, morphological comparisons are not possible for or are questionable between distant groups, and features are often affected by the environment, offering adulterated evidence of relationships. Indeed, trees based on morphology alone are usually poorly resolved, and the few clades are barely supported.

In the mid-1990s, evidence based on molecular data was already surpassing morphology, and this soon became the main source of data in phylogenetic studies, either in combination or not with morphological data. This shift was possible mainly due to molecular sequencing and computational progress and was responsible for important advances in plant systematics. Because DNA is the source of heritability, molecular data are the most direct evidence of ancestral relationships available. Nucleotide sequences are stored in electronic databases, such as GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>), currently with more than 135 million DNA sequences, and can be easily accessed by the scientific community. The task of recognising the four character states of a nucleotide sequence is straightforward, though sequences are not available for every taxon, and their comparisons are not always simple or unambiguous. With the predominance of molecular data, parsimony analyses are also losing space to model-based analyses. Empirical and theoretical advances on molecular evolution favoured the implementation of more reliable models of nucleotide substitution. Currently, most phylogenetic studies in plants use DNA sequences, eventually combined with morphology or, in a genomic approach, considering whole-plastid DNA, and employ maximum likelihood and/or Bayesian inference analyses, often associated with the results from parsimony analyses.

The impact of phylogenetic systematics in botanical taxonomy was enormous. Comprehensive classification systems, such as those proposed for flowering plants [24] and ferns [25], are rooted in phylogenetic results and emerged from consensual collaborative works. Vascular plants were divided into Lycophytina and Euphyllophytina (including seed plants and monilophytes), and the pteridophytes are no longer recognised as a taxonomic group [26]. For monilophytes, the Psilotaceae and Equisetaceae are known to be closer to the eusporangiate ferns Ophioglossaceae and Marattiaceae, respectively [27]. For angiosperms, *Amborella trichopoda* is sister to the rest of angiosperms, forming a grade with Nymphaeales [28], including the graminoid Hydatellaceae [29]. In evolutionary systems (e.g. [30]) *Amborella* (in Laurales) and Nymphaeales belonged to the subclass Magnoliidae of Magnoliopsida (dicotyledons), whereas the Hydatellaceae were treated as Liliopsida (monocotyledons). Traditional groups, such as the dicotyledons, have been abandoned, and informal groups,

such as the eudicots, have been incorporated in classification. The changes at lower levels are also remarkable: some families were disintegrated, including Scrophulariaceae, the members of which were divided into five families [31], whereas others, such as Apocynaceae and Asclepiadaceae, were amalgamated [32]. Most phylogenetic results are absorbed relatively quickly by botanists and are incorporated in textbooks for undergraduates (e.g. [33, 34]).

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## 2 Principles of Nomenclature

Our principles of classification direct how plants should be organised. However, taxonomy would be handicapped if there was not a system to govern the application of scientific names independently of these principles. Botanical nomenclature is constantly being refined to better serve taxonomy. Its function is to offer clarity, universality and stability for plant names. New propositions are discussed every 6 years in a nomenclatural section, 1 week before the International Botanical Congress. Although changes have been gradually incorporated into the nomenclature code [35], the Melbourne code is an example of how such changes can be revolutionary. First of all, rather than *International Code of Botanical Nomenclature*, the new code is titled *Code of Nomenclature for Algae, Fungi, and Plants*. More importantly, since 2012, an electronic publication is effective, as long as it is published in a journal with an ISSN or book with an ISBN and in PDF format, and the diagnoses of new names, in addition to Latin, can also be in English. Previously, a publication would have to be printed and distributed in at least two public libraries to be effective, and a Latin diagnosis or description was mandatory for the valid publication of new plant names [36]. These changes began to work before the publication of the Melbourne code and will certainly increase the rate at which new taxa are described, favouring floristic studies, particularly in megadiverse and still poorly known regions.

The code of nomenclature for plants is composed of articles, recommendations, examples and notes and is independent of the codes for animals, bacteria, viruses and cultivated plants. The names are Latin or Latinised and must be validly published to be recognised; they follow the binomial, hierarchical system, established since Linnaeus, 260 years ago. Taxa are named according to their taxonomic rank. Species names are binomial and composed of the specific epithet following the name of the genus; names above species level are uninomial and begin with a capital letter. Names at the genus level and below are written in italics; those below species also consist of an infraspecific epithet and must have their rank explicitly indicated: subspecies (subsp.), variety (var.) or form (f.). Cultivars can be written in modern language using single quotation marks, e.g. ‘Grape Cooler’. Hybrids are denoted by the

multiplication sign “×” or the prefix “Notho-” and can be written as a formula (or as its own combination), such as *Oenothera bien-nis*×*O. villosa* (or *O.*×*drawertii*). Above the genus level, categories are usually flagged by a suffix denoting their rank. Seven taxonomic categories are mandatory—species, genus, family (-aceae), order (-ales), class (-opsida), phylum or division (-phyta) and kingdom (-bionta)—but others can be recognised at a level between them, usually using the prefix “sub” or “super,” such as subclass (-idae) and superorder (-anae).

Nomenclature does not establish ranking criteria, and taxa are assigned to categories by convention. Categories differ only by their degree of inclusion. When taxa share organisms, those at higher categories are more inclusive unless there is a redundancy between taxa. Circumscriptions of such taxa are broader, and the information is more generalised; consequently, their intensions are more comprehensive than those at lower ranks. Taxa at the same rank are exclusive: they do not share organisms. It is always important to consider that ranks are designed by convention and convenience: they are comparable only by designation and not by any biological or natural meaning [37, 38]. The use of categories has been questioned as a source of instability, and some scientists are accepting only species and clades, as with the Phylocode [39, 40] or “cladonomy” [41]. In the current Linnean nomenclature, however, categories continue to be a requirement for the application of names, as they have informational content and are mnemonic devices that have been successfully and universally applied for a long time [42].

The general principle of nomenclature is that every taxon must have only one correct name; these names must be validly published and legitimated. The discernment between alternative names is taxonomically guided by the type of method and assisted by the nomenclatural principle of publication priority. Since 1958, authors must designate a holotype to validly publish a new name. The holotype is the specimen or illustration designated or used by the author of the species (or a taxon below species) to which the name is attached. Duplicates of a holotype are isotypes. However, types were not always mandatory and, in ancient literature, names were published without an explicit reference to any type specimen. In some of these cases, the holotype can be inferred; but in others, a lectotype must be designated from the original material (syntype) as nomenclatural type. A lectotype must also be designated among the isotypes when the holotype is missing. However, when no original material is available, a neotype must then be designated for the name. Lastly, an epitype can be designated to assist in the precise application of the name when its type is insufficient. Certainly, the type method is central for nomenclature procedure. However, it is important to emphasise that types are designated by

convention and are attached to taxon names only; the taxa themselves do not have any type.

When more than one type is considered in the same taxon, there will be competing names for that taxon. In these cases, the principle of priority must be invoked to discern which is the correct name: the name that was published first has priority and is the correct name of that taxon (equivalent to a valid name in zoology); the names that are published later are heterotypic synonyms. This is an ancient principle of nomenclature that was already formalised in the nineteenth century. However, it can be abandoned in favour of nomenclatural stability. To avoid disadvantageous changes, a widely used name, particularly one with major economic importance, can be conserved, regardless of its priority of publication, whereas others can be rejected. The principle of priority is applicable only at the level of family and below, and names have no priority outside the rank in which they were published.

In botany, tautonymy—species names whose generic and specific names are the same—is invalid. To be valid, names must also be accepted as correct by their authors in the original publication. A correct name of a species or infraspecific taxon is the combination of the legitimate final epithet in that rank and the correct name of the genus or species. The authors of the basionym (original combination of a species) of a later combination appear between parentheses, as in zoology; in botany, however, the author names are followed by the authors of the correct combination. A name can be illegitimate either because it is superfluous, i.e. its type was previously applied to another name, or because it is a posterior homonym, i.e. it was already used for another taxon at that rank. Because a scientific name must be assigned to only one taxon, a posterior homonym requires a substitute new name.

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### 3 Taxonomic Works: From Descriptions to Identification

Classification is a continuous process. Taxonomists may disagree about taxonomic concepts and can always find new evidence to change their own taxonomic opinions. Disagreements may have different causes, and evidence may originate from different sources. For instance, although a taxonomist can consider two morphological variants distinct enough to be recognised as different species, another taxonomist may recognise them as parts of the morphological variation of a single species; in the latter case, the two species will be considered synonyms. Given that a taxonomy based on phylogenetics must reflect ancestral relationships, the discovery of unexpected ancestral relationships may require taxonomic changes, and these changes may affect the circumscription of taxa, potentially changing the name of a species. For instance, a new family can be created or an old one resurrected to comprise individuals of a clade without

requiring any nomenclatural change at the species level. By contrast, a closer relationship of a species with the species of another genus will require its transference and, consequently, a new combination. Changes may also be required in favour of clarity and universality, for instance, when a name is found to be superfluous or a posterior homonym.

Currently, taxonomic changes most frequently result from new phylogenetic information. This is a sign of scientific progress, in contrast to taxonomic stability, which may only reflect ignorance and not necessarily correctness [43]. Taxonomists are responsible for critically evaluating new information and incorporating this information into classifications. As this process often implies taxonomic rearrangements and nomenclatural changes, it is important also to update identifications continuously.

Identification consists of assigning scientific names to organisms of yet-unknown classification. There are several strategies for plant identification [44]. A common procedure is to assign this task to taxonomists, the specialists of the group, as a specialist can best apply his/her experience to provide a rapid and accurate identification. However, taxonomists are not always available; thus, other strategies must be attempted. In such cases, plant identification may also be achieved by consulting specific monographs, technical works that are complete and scientifically accurate. Monographs usually combine complete nomenclatural information, detailed descriptions and high-quality illustrations, comments on taxonomy, phylogenetics, nomenclature, ecology and geographic distribution (usually with maps of occurrence); analytical keys for taxa identification and an initial section introducing the morphology of the group are also included in a thorough monograph. In these treatments, species are arranged in alphabetic order, favouring direct individual queries, or according to their relationships, favouring comparisons of closely related taxa.

When the complete taxonomic and nomenclatural information is included, the correct name of the species is followed by the authors and original reference of the combination. Starting with the basionym, the other homotypic synonyms, with authors and reference, are included in sequence, after the data for the correct name, according to the publication date. Similarly, heterotypic synonyms are included below the correct name header, each starting on a different line, usually listed by the publication date of their basionym. The types of heterotypic names appear at the end of each header, with an indication of whether they were examined by the authors of the work.

Plant descriptions should be standardised and compact but clear and precise. For instance, verbs, articles and conjunctions can be eliminated, but the type of measures must always be specified, even when this seems obvious. The method for description is frequently the same as that used in ancient times, which Winsor [17]

named “method of exemplar”. An initial description is prepared based on an example of the taxon, and the variation is added by including attributes of other exemplars of that taxon. Nevertheless, other methods can be employed, such as the combination of DELTA (DEscription Language for TAXonomy; [45]) format and Lucid software (<http://www.lucidcentral.com>) to construct sharp and parallel descriptions in natural language and consistent keys for identification directly from original databases. Descriptions in taxonomic revisions are complete because these monographs are expected to be more definitive and universal references. In contrast, the intention of a floristic work is to discriminate species from a certain region; their descriptions comprise only the variation found in the study area and should be shorter, long enough only to provide the recognition of those species. The importance of floras in botanical literature is recognised for a long time and they were the first and one of the main sources of plant knowledge for beginners. In the last decades, however, checklists, electronic keys and illustrated guides, rather than classical descriptive floras, have reached a wider audience [46].

Illustrations have been popular in botany since the Juliana book. The work was given to her by the townspeople of Honorata, Constantinople, in 512 A.D. Designed for the illustrations, the book included 383 plants from Dioscorides’ work [11]. Since then, illustrations have become more common, helping users to interpret descriptions and identify plants. Pictures can also be very attractive and helpful, particularly for fresh plant identification and are largely used in field guides. Line drawings are recommended to illustrate diagnostic details; they must bear accurate scales, allowing feedback consultation with descriptions, and legends should be detailed, indicating the specimens used for drawings.

As a scientific work, a taxonomic study must include the material examined by the authors, with the following collection information: locality, date, phenological state, collector and number, and herbaria of duplicates. However, some monographs are based on hundreds of specimens. In these cases, it is recommended to indicate a selected material representing the variation and distribution of the species, and include, at the end of the work, a complete list of exsiccates, only with the collection reference (first collector and number) and its identification (the species number, depicted from its order in the treatment).

Since Lamarck, the characters used in identification keys are decoupled from those used for classification, allowing artificial, pragmatic diagnostic keys designed for the easy identification of taxa in natural (and phylogenetic) classifications. A key consists of pairs of contrasting, preferentially mutually exclusive statements, which are sequentially followed by the user as they best fit the attributes of the specimen to be identified until a taxon is reached. The inclusion of more attributes per statement is preferred, as long

as these attributes are simple and easy to observe. Keys are traditionally dichotomous and can be numbered or indented. In numbered keys, statements of a pair are adjacent, and the next statements are indicated by numbers. In an indented key, statements are organised sequentially, departing gradually from the left, without the necessity of numbers to indicate further statements. Some keys include references to representative illustrations of the attributes; others can be richly illustrated and presented as a diagram.

Different from printed dichotomous key, electronic keys (e-keys) have multiple access, allowing interactive identifications. Users can start at any character and follow different sequences, delaying the use of missing or difficult characters, or they can use a combination of attributes simultaneously (polyclave key). Depending on the material available, morphological information may not converge on a single taxon through the exclusive use of a key. Therefore, additional aspects, such as ecology and distribution, must be considered when comparing the possibilities to decide which taxon best fits the specimen. E-keys permit constant updates and can be accessed through the Internet or distributed in CD format and can also be incorporated in small devices, becoming useful in fieldwork.

Identifications must always be confirmed. A confirmation can be performed initially by comparing the specimen with the description, illustration and comments of the species and later by comparing the material with the specimens in herbaria, preferentially using those identified by a taxonomist with experience in the group. Exsiccates of different species, including types, can also be accessed at synoptic virtual herbaria. If a monograph or a flora is not available, a checklist can help the user to know whether the taxon has been registered in the region; however, its absence in a list cannot exclude the possibility of a new occurrence.

DNA barcodes are another strategy for identification. They consist of short, standardised DNA sequences that are conservative within species but variable enough to discriminate between species. This technology is particularly interesting because it permits identification without conferring with a specialist and is based only on DNA fragments. For animals, the mitochondrial COI gene is used as a universal DNA barcode; however, this region in plants evolves too slowly, and other regions are being tested. To date, the best strategy found is a combination of two plastid regions (*matK* and *rbcL*; [47]). Although this method was unable to identify more than 25 % of the species sampled, when the strategy is used at the regional level, the success of identification is close to 100 %. Considering that the region with most sequences available for plants, the *rbcL* gene, was sequenced for less than 15,000 species and the diversity of plants is approximately 380,000 species, we may understand why DNA barcodes for use in botany is still in its infancy [48].



Taxonomic works are the documentation of our biodiversity. First, publications function like birth certificate of new taxa. They also register new information as data are being collected and join them together in monographs, making the knowledge of plants available to others and enabling its perpetuation between generations. In spite of that, taxonomic work is losing its place in the scientific community. This is because such efforts are time-consuming and publications are used mostly for consulting, scarcely generating citations. However, taxonomy fits well within the Internet, where space is not a limitation, such that data can be continuously accumulated, illustrations can become available in colour without additional costs, and information can be updated and linked to a great assortment of related matters. Websites of plant systematics can be phylogenetically ordered, such as the Angiosperm Phylogeny Website [49], where orders of flowering plants are accessed using an alphabetical index or using a phylogenetic tree. Most orders of the tree are linked to another tree, but of families. By clicking on a family name, users can access updated information of that taxon, such as its diversity, internal arrangements and relationships, characters, and maps.

Currently, there are many websites that can assist plant taxonomy. TROPICOS (<http://www.tropicos.org/>), for instance, provides nomenclatural and taxonomic databases. With approximately 1.2 million scientific names, TROPICOS includes authorship, references and type information, in addition to correct names, synonyms and homonyms. For several names, users are only one click away from the original work, some of which was published hundreds of years ago. Images of types, exsiccates, illustrations and pictures of fresh plants are also available. The website informs about the chromosome number registered for the species and more than four million specimen records. Links to other websites allow the netizen to go directly to different digital collections, such as the virtual herbaria of the New York Botanical Garden (<http://sciweb.nybg.org/science2/vii2.asp>), the *Australian Plant Index* (<http://www.anbg.gov.au/apni/>), and the *African Plant Database* (<http://www.ville-ge.ch/musinfo/bd/cjb/africa/recherche.php>) in Geneva. From TROPICOS, users can also visit the *JStore Plant Science* (<http://jstorplants.org/>), which combines images of exsiccates and the classical literature associated with the species name, and to *The Plant List* website (<http://www.theplantlist.org/>). Many other doors open immediately from *The Plant List*. At this site, the user can often confirm the status of the name, whether it is accepted or not, and continue to other gateways, such as the *Biodiversity Heritage Library* (BHL; <http://www.biodiversitylibrary.org/>) and the *National Center for Biotechnology Information* (NCBI; <http://www.ncbi.nlm.nih.gov/>), with different possibilities of information associated with that taxon, from literature to genetic sequences.



## 4 Final Remarks

Scientific names unite an intricate network of information. They are like seeds travelling in space and time and work like keys for the entire body of literature of the taxa they represent. Taxonomic names guarantee the accumulation of knowledge and its transference between generations, from naturalists to the current phylogeneticists, and have the power to disseminate this knowledge quickly to any country, regardless of the language. However, plant names should have meaning, and this is provided by taxonomy.

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