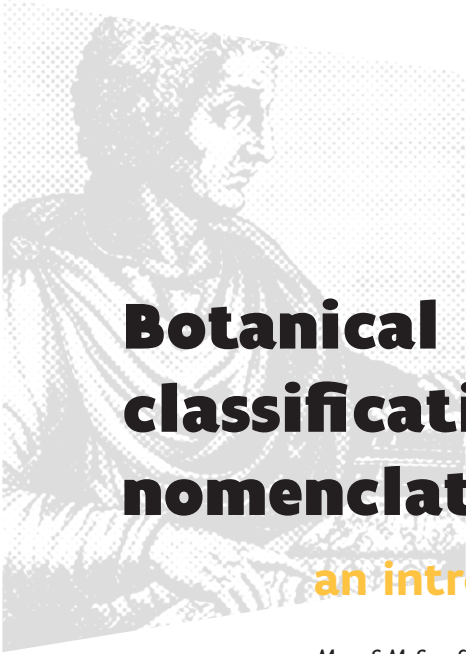


Botanical classification and nomenclature

an introduction –

*Marc S.M. Sosef
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Meise Botanic Garden

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Introduction



Biology is the science that explores the living world around us. To communicate the wonders of nature, names are needed to describe the variety of forms we encounter. This wildly diverse nature may be represented through a hierarchical structure where names are used to indicate groups of organisms at different levels. The classification and naming of organisms is an essential tool for scientific communication. It forms the foundation upon which biological research is based and the discipline is called "**Taxonomy**". Taxonomists explore, describe, name, and classify all living organisms on Earth.

Correctly classifying and naming organisms is crucial to a wide range of biological research fields. Such a framework is also essential to address the topics of sustainable usage and biodiversity management and conservation, including their legal context. This booklet provides an overview of the most important elements and processes of the classification and naming of plants and fungi, hence the field called "**Plant Taxonomy**". We will commence with a historical overview of this discipline. Although we do not deal exhaustively with the methods to reconstruct evolutionary pathways (phylogenetics), we do provide the historical context of its development and some elements that directly influence taxonomic decisions. The aim of this booklet is to provide an introduction and practical guide to this research field. As such, it can be used by those having a specific interest in the classification and naming of plants, but also by those teaching this subject in secondary and tertiary education institutions.

Although the information is general, most examples are drawn from tropical African plant and fungal diversity. Each chapter is followed by an overview of literature and web-based sources related to the subjects dealt with. This is by no means exhaustive, and again focusses on the taxonomy of African plants and fungi.

The authors hope that this publication will contribute to the development of taxonomic expertise, notably in the Central African region. The booklet is produced in English and French, and will be available free of charge (under the CC-BY license) to high schools and universities (both teachers and students), courtesy of Meise Botanic Garden.



**The history of
classification**





THEOPHRASTVS

Any biological study starts with the simple question “What is this?”. Whether it concerns a manager of a nature reserve who needs to know which species grow within the park’s boundaries for setting up a management plan; a primatologist studying the food eaten by chimpanzees; or a plant breeder studying the close wild relatives of the potato in search of a disease resistant gene, all need to be able to identify and name their material. It is preferable that these names are uniformly used and accepted throughout the world.

The need for a uniform system of naming the living world was already recognized by the ancient Greeks and Romans. Names were given to ‘entities’ we now call species that had specific morphological characters and uses. Some produced, for example, edible fruits, or a yellow dye, others had medicinal properties, or were useful for making musical instruments, etc.

In this chapter (largely based on Magnin-Gonze 2009 and Rouhan & Gaudel 2014), we highlight the major historical phases in the development of plant naming and classification. The name for this field of science was coined for the first time in 1813 by the Swiss botanist Augustin Pyramus De Candolle (1778–1841) in his book “*Théorie élémentaire de la Botanique*”. He created the neologism “taxonomy” by combining the words Greek *τάξις* (order) and *νόμος* (law, rule).

1.1 From Theophrastus to the Middle Ages

Even before the invention of written language, c. 5600 years ago, it is likely that an oral plant classification system existed. Initially, names and organisms were not placed into a hierarchical system since the plants were all named following their use such as food, medicines, poisons, or materials (Raven 2004).

The Greeks probably did not just consider plants as being only useful but also as beautiful; the murals in Knossos (1900 BC) not only have useful plants like barley, fig, and olive, but also narcissus, roses, and lilies. The Greek Theophrastus (372–287 BC; figure 1), successor of the great philosopher Aristotle, is especially well known as the first true botanist. Interested in naming plants and finding an order in the diversity of plants, he is the first one to provide us with a philosophical overview of plants. He pointed out some of the important questions that would later define taxonomy, such as “What have we got?” or “How do we differentiate between these things?” Moreover, he was the first to discuss relationships among plant species and to suggest ways to group them. Theophrastus described ca. 500 plants — probably representing all known plants at that time — and classified them as trees, shrubs, subshrubs, and herbs. He also made a distinction between flowering and non-flowering

◁ *Figure 1. Statue of Theophrastus in the botanic garden at Palermo, Italy.*

plants, deciduous and evergreen trees, and between terrestrial and aquatic plants. Even if 80% of the plants included in his works were cultivated, he had realized that “most of the wild kinds have no names, and few know about them,” highlighting the need to recognize, describe, and name plants



◁ Figure 2.
Plinius the Elder.



◁ Figure 3.
Dioscorides.

growing in the wild (Pavord 2005). He soon discarded his trees, shrubs, subshrubs and herbs classes in favour of floral morphology that was better suited to cluster plants into more natural groups. Theophrastus was way ahead of his time, so much so that his botanical ideas and concepts became lost in Europe for many centuries. His works survived in Persia and Arabia, and were translated back into Greek and Latin when rediscovered in Europe in the 15th century. During this long Dark Age for botany, like for all other natural sciences in Europe, the Roman Plinius the Elder (23–79 AD; figure 2) and the Greek Dioscorides (~40–90 AD; figure 3) were two important figures. Although they did not improve the existing knowledge and methods about the description, naming, or classifications of plants, they did compile the available knowledge and their written works were renowned and widely used. For many centuries, the *Naturalis Historia* of Plinius and the *De Materia Medica* of Dioscorides (figure 4) were the only source of information on plants throughout Europe and their works were repeatedly copied. 'Herbalists' tried to link plants they found in France or Britain to those described from the Mediterranean by Plinius and Dioscorides, and one can imagine the problems they encountered. Throughout the Middle Ages, hardly any new knowledge was added to the old works.

1.2 Renaissance, Pre-Linnean period

The Renaissance (late 14th to 17th century) marked a new era for science. Europeans were exploring and discovering America, Africa, Asia and Australia, bringing back many unknown plants to Europe. These were housed in a rapidly increasing number of gardens, the first being created in the early 16th century in Italy. At first, these were called medicinal gardens, later, when the interest shifted towards the study of plants themselves rather than their useful properties, they transformed into the botanical gardens that we know today. Moreover, with the invention of the

printing press (1450-1455), information was more easily shared and distributed, boosting exchange and discussions in scientific knowledge. People became curious about the world surrounding them. Around 1530, in the botanic garden of Pisa,

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Viertes **Reutter**
buech

Darin vil schöne vnd kemb
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vnd außgemacht worden. Welche er nit allain in Hispanien
vmb Aissa vnd in der Prouincia vmb Karthlia sonder auch
in Syria an dem Berge Libano vnd Antilibano auch durch
Arabiam neben dem fluß Euphrate in Chaldea Eßyria
Armenia Mesopotamia vnd andern orten. in seinen mit
Gottes hilfselbbrachten dreijährigen Reisen. mit großer mü-
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the Italian Luca Ghini (1490–1556) invented a revolutionary method for preserving plants by drying and pressing them so they could be studied at any time of the year. The resulting plant specimens were stored in books known as a “hortus siccus” (dried garden), later the term “herbarium” was adopted, and were valuable possessions afforded only by the wealthy (Ghorbanie et al. 2018; figure 5).

This was followed by the era of the great western European herbals, or books describing the plants and their uses. These works were no longer produced only in Latin (the scientific language of the time), but also in the common languages German, English, Dutch and French. This opened up the information on plants to an even wider public. From this period, the herbals

◁ Figure 5. Frontpiece of the Rauwolf herbarium 1573-1575 kept at Naturalis Biodiversity Center, Leiden.

▽ Figure 6. Dodonaeus and two pages from his famous illustrated herbal (Cruydeboeck) printed in 1554.

of Dodoneus (*Cruydeboeck*, 1554; figure 6), Fuchs (*New Kreüterbuch*, 1543) and Gerard (*Herball, or Generall Historie of Plantes*, 1597) are the most famous. Advances in art led to numerous new plant illustrations. These were way superior to those copied over and over from the books of Dioscorides and Plinius, from which the actual species could often hardly be deduced.

A student of Ghini, Andrea Cesalpino (1519–1603), was the first to discuss the work of Theophrastus since the Ancient Greeks. He pointed out that plants should be classified in a





more natural and rational way. His *De Plantis Libri XVI* (1583) describes 1,500 plants which he organized into 32 groups including the Umbelliferae and Compositae. The science of naming plants quickly developed, and in general the plant names comprised a combination of several characteristic features. For example, the

passion flower (*Passiflora edulis*) was called *Flos passionis major* (large passion flower). However, with the rapidly increasing number of species arriving from around the world, more characters were needed to distinguish one species from the other, resulting in ever longer names. In an early catalogue of the Hortus Botanicus at Leiden (The Netherlands) founded in 1592, the same *Passiflora* was called *Cucumis Flos Passionis dictus triphyllos flore roseo clavato* (Cucumber or Passion flower; three-leaved, pink flowered and clavate; the latter possibly pointing to the shape of the styles). In short, the name of a plant also served as a diagnostic summary. The science of botany slowly diversified from the science of medicine to a broader study of the increasing wealth of plants arriving in Europe from all over the world. In 1623, the Swiss Gaspard Bauhin published his *Pinax theatri botanici* describing no less than 5,640 different plants, wild species but also many cultivated forms. Later, the British botanist John Ray published his 3-volume *Historia plantarum species* (1686, 1688, 1704) containing more than 17,000 different 'species' (he also described a very high number of cultivars, monstrosities and other forms). This innovative work was the first to distinguish Monocotyledons from Dicotyledons, and to use text-based dichotomous keys to classify plants. In 1694, the Frenchman Joseph Pitton de Tournefort, developed the concept of genera, which contributed markedly to a better structuration of the classification.

◁ Figure 7.
Carolus Linnaeus.

△ Figure 8. Linnaeus' sexual system to classify plants.

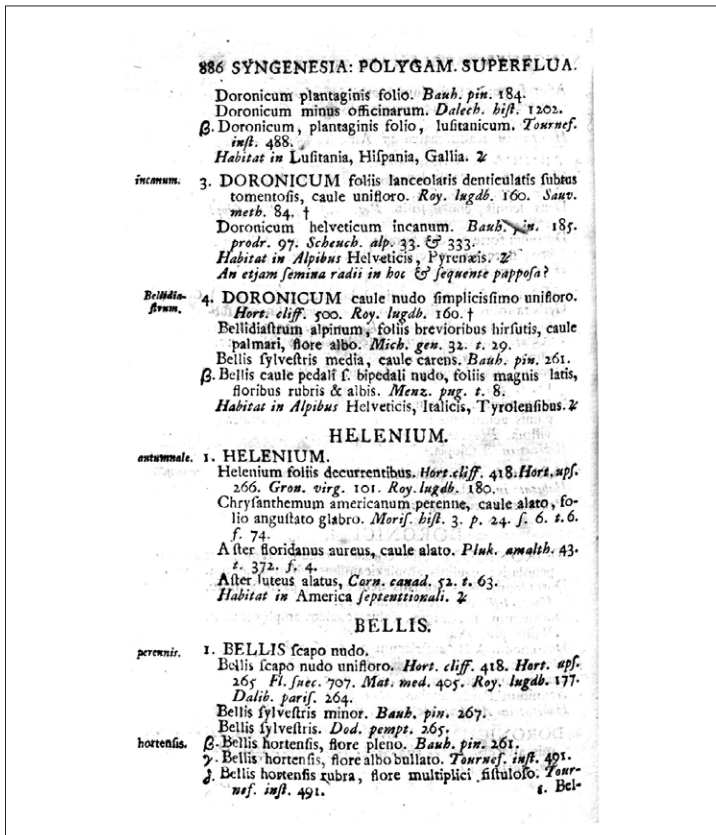
1.3 Linnaeus and the Linnaeans

In the first half of the 18th century, the bright young Swedish botanist, Carl von Linné (figure 7), or Linnaeus in Latin, brought order where there was chaos. While working in The Netherlands, he met famous professors such as Hermann Boerhaave, Adriaan van Royen and Johannes Burmann with whom he discussed several of his new ideas.

First, he created a clear classification system of plants based on the number of stamens and styles in each flower and called it his 'sexual system' (figure 8). He recognized five taxonomic levels, the variety, the species, the genus, the order (\pm equal to our present-day family) and the class. This simple system, although it had a few flaws, worked remarkably well in creating structure.

▽ Figure 9. Page from Linnaeus' famous *Species plantarum*, showing his "trivial names" in the margin.

Second, he suggested to dissociate the name of a plant from its description. In his famous *Species plantarum*, published in 1753, he wrote what he called 'trivial names', a single word, in the margin of each species treatment (figure 9). Preceded by the genus name, that would form a species name



composed of only two words. It was the start of the binomial (two words) nomenclature we still use, a system where a species name is composed of the genus name followed by a word indicating the species, called the **epithet**. Soon, other botanists appreciated the simplicity and genius of the new naming system and adopted it in their own work. Shortly after the success of his *Species plantarum*, Linnaeus, being a keen zoologist as well, introduced the same system for animals in his famous *Systema naturae* (1758).

Linnaeus travelled to England to meet Sir Hans Sloane and Johann Jacob Dillenius, who were both sceptical about his new naming and classification ideas at first, but they came around after several years. In Paris, he met Bernard de Jussieu, who would together with his nephew Antoine Laurent de Jussieu publish their *Genera plantarum*. In that work, they stated that a species, genus, or any other class in the hierarchical classification, which we now call a **taxon** (plural taxa), should group plants showing character constancy within the given taxon, as opposed to the character variability observed among taxa. Since not all characters are useful at the same level of the classification, their principle of subordination led to a character hierarchy: characters displaying high variability should be given less weight than more conserved ones in plant classifications.

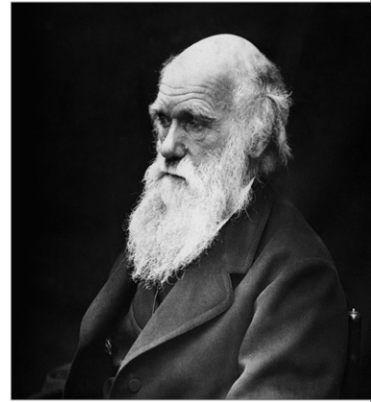
In this period, classification and the study of nature also had a religious implication. Biologists were seen as scientists studying the living things which God has created and placed on Earth. Linnaeus, in his Introduction to his *Species plantarum*, wrote: "In his omnipotent omniscience, God created the theatre of all living beings on earth, and it is our divine task to explore that great creation, served to us as tasty treats, unworthy as we are, and to recognize His hand in it" [freely translated from the Latin]. One can imagine that in this context Darwin's introduction of the novel idea that species were not created by God Almighty, but had evolved from others over a very long period of time, had a tremendous impact on broader society.

1.4 Evolutionary thinking enters classification theory

At the start of the 19th century, new questions arose in the mind of taxonomists. They were not only interested in naming, describing, and classifying organisms, but also in the origin of the observed diversity. In 1809, in his *Philosophie zoologique*, the zoologist Jean-Baptiste de Lamarck proposed a theory where species could evolve and change through time.

It took another 50 years before Charles Darwin (1809–1882; figure 10) published his famous theory of evolution and survival of the fittest in *On the Origin of Species* (1859). Independently, Alfred Russel Wallace (1823–1913) had come to the same conclusion while working in Asia. [In fact, the theory was published already in 1858, in a paper authored by Darwin and Wallace in the *Journal of the Proceedings of the Linnean Society: Zoology*.] Darwin introduced the central concept of descent with modification that later received extensive support and is still generally accepted today. The concept

▷ Figure 10.
Charles Darwin.

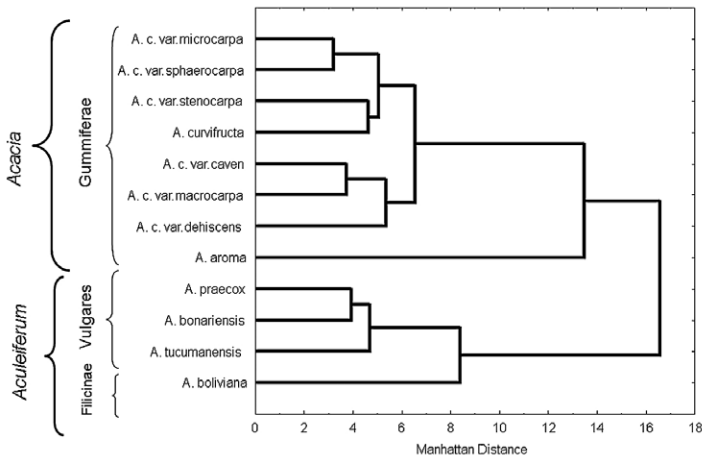


of evolution had a major impact on the development of the theory behind classifying nature, hence the science of taxonomy. Biologists understood that since the history of life is unique, the only classification that is natural is the one reflecting that unique tree of life, the **phylogeny**. The latter word was not coined by Darwin but by Ernst Haeckel (1834–1919) in 1866 in *Generelle Morphologie der Organismen*. Darwin predicted that “our classifications will come to be, as far as they can be so made, genealogies” (Darwin 1859, p. 486). This new theory also implied that characters useful to taxonomy are those inherited from a common ancestor. However, Darwin did not provide any new techniques or approaches to reconstruct the phylogenetic tree for a certain group of taxa or assist practicing taxonomists in their work.

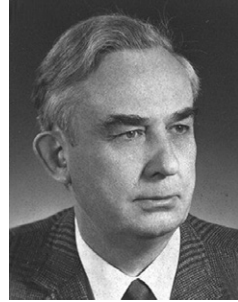
1.5 Phenetics, cladistics and phylogenetics

▽ Figure 11. Example of a phenogram, with a measure of similarity (Manhattan Distance) along the x-axis (from Pometti et al. 2007).

In the early 1960s, a new technique called ‘numerical taxonomy’ arose to produce a tree-like output, or **phenogram** (figure 11), on which one could subsequently base a classification. Notably the work of Sokal & Sneath (1963, and later editions), *Principles of numerical taxonomy*, laid the



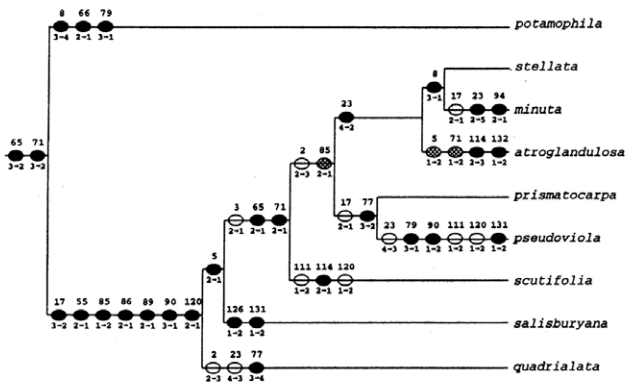
foundation. The technique, also called **phenetics**, was based on a quantitative cluster analysis of overall similarities between taxa, using a characters-by-taxa data matrix - with a mixture of binary characters (stipules present, yes/no), multi-state characters (for example flower colour; with states 1=white, 2=yellow, 3=blue), or continuous characters (for example calyx length in mm) - and resulting in pairwise distances among the individuals or taxa, called OTUs (Operational Taxonomic Units). However, it was soon realized that overall similarity does not necessarily indicate an evolutionary relationship. For example, species may have developed similar features because they adapted to the same environmental stress. As this method was not based on the evolution theory, it could not interpret the observed variation in an evolutionary sense with respect to ancestors and descendants or observed character state changes. Despite the fact it produces tree-like phenograms, these do not represent a natural and evolutionary classification. Nevertheless, this theory flourished for a while, greatly benefiting from rapid advances in informatics.



△ Figure 12.
Willi Hennig.

It was the German zoologist Willi Hennig (1913–1976; figure 12) who fundamentally changed the way biologists reconstruct the evolutionary pathway of a taxonomic group. In 1960 he published his cladistic theory in *Grundzüge einer Theorie der Phylogenetischen Systematik*, but it remained relatively unknown until the English translation *Phylogenetic Systematics* was published in 1966. The primary principle is not to use the overall similarity

▽ Figure 13. Example of a cladogram, showing numbered characters where one may recognize apomorphies (black dots), pallelisms (open dots) and reversals (hatched dots) as well as their character state changes (below each dot).



Cladogram of the *B. potamophila* group. Only more important characters (those receiving a weight of 1 or more with the 'cocode' command) are depicted; black = apomorphy, open = pallelism, hatched = reversal.

among taxa to reconstruct the phylogeny, but to make a distinction between **primitive character states** and those that are derived from them. Only **derived character states**, called **apomorphies**, shared by several taxa then indicate a shared common ancestry, while primitive ones, called **plesiomorphies**, do not. A group derived from a single common ancestor is called a **clade** and the theory behind it **cladistics**. The result of a cladistic analysis is a tree-like figure called a **cladogram** (figure 13), where the branches actually represent one or more character state changes. When, for example, in a group of plants with red flowers an evolutionary change gave rise to blue flowers, 'blue' then is the derived state of the character 'flower colour' and any species having that state is likely to have evolved from the same common ancestor. Having a red flower does not indicate such common ancestry and hence cannot serve as a criterion on which to base a taxonomic group. When, further down the evolutionary history it turns out that a red colour was derived from white flowers, red can still be regarded as a derived character state but at a different level in the phylogeny. And going from white to blue then requires two evolutionary steps rather than one. When a derived state evolves back to the primitive state again, this is called a **reversal**, while the independent evolution of the same character state in two or more different branches of the evolutionary tree is called a **parallelism**.

Furthermore, Hennig argued that every taxonomic decision, from a species definition to a system of higher classification, was to be treated as a provisional hypothesis to be tested by new data or applying other methods. Various algorithms were developed with which a cladogram could be built from a character state/taxon matrix (see also figure 18) and the method benefited from the rapid increase in computational capacity of computers and the development of bioinformatics. New research fields like cytology and chemotaxonomy provided additional character sets. The algorithms aimed to find the cladogram that needed the smallest number of evolutionary changes (or steps). The argument being that those needing the smallest number of changes (or hypotheses) represent the most likely phylogeny. This 'lowest cost' idea was called the **parsimony principle**. The shortest tree then is the most **parsimonious** one.

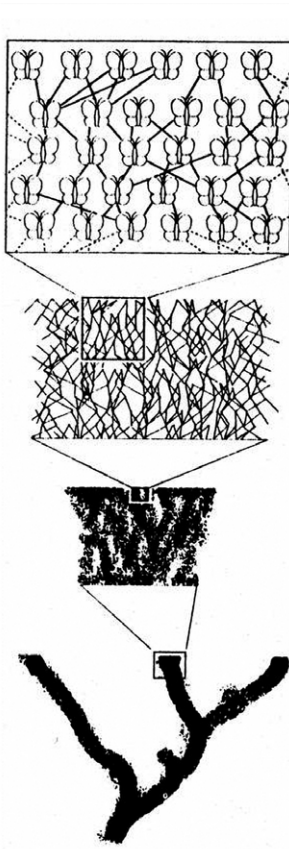
In this new setting, it was felt that a new definition of this biological research field was needed and the term '**systematic biology**' or simply 'systematics' was coined (Michener et al. 1970). It embraced the entire field from describing, naming, classifying, studying the distribution patterns (biogeography), evolutionary relationships, character evolution and adaptations. The term '**taxonomy**' was then restricted to describing, naming and classification. Some, however, treat these two words as synonymous.

The discovery of the double helical structure of the DNA molecule in 1953, by James Watson and Francis Crick, greatly improved our understanding of the evolutionary processes. But it was only after it became possible to target specific fragments of the genome (nuclear, mitochondrial or chloroplast DNA) by selectively amplifying the DNA through the polymerase chain reaction (PCR) (Kary Mullis 1986) that it started to have a dramatic impact on taxonomy and classification. The introduction of DNA sequence data (Meier 2008) offered access to numerous new characters and statistical approaches.

Thus, at the turn of the 21st century, the use of molecular data and new tree building algorithms such as **Maximum Likelihood** and **Bayesian statistics** led to a distinct improvement of our abilities to produce phylogenetic hypotheses. The 'strength' or reliability of each branch in a cladogram can be assessed by using other techniques such as **bootstrapping** (a statistical resampling technique; Holmes 2003) and, again, Bayesian statistics. All these developments led to improved insight into the delimitation of orders and families of flowering plants (Angiosperm Phylogeny Group 2016), as well as a greater understanding of the classification based on evolutionary relationships.

1.6 On natural groups, monophyly, paraphyly and polyphyly

It logically follows from the above that classifying the natural world into species, genera and higher groups has become a search for our best hypothesis on the structure of the evolutionary tree in order to be able to distinguish natural groups. In other words, the cladogram produced by one of various analyses needs to be split into natural parts. However, there are many ways to do this, and requires informed choices.

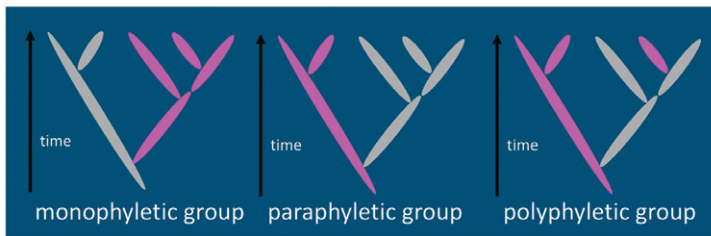


Firstly, we need to understand that a cladogram is not a phylogenetic tree but a schematic representation of the data, showing character state changes (morphologic, chemical or genetic) on its branches (figure 13). Since in systematics we do not aim to classify characters, but rather species (or taxa), we need to transform such a cladogram into a true **phylogenetic tree** showing the ancestor-descendant relationships between individuals, or populations, or species. In a phylogenetic tree, the branches represent the evolutionary relationships between the units involved in the evolutionary process (see figure 14) and hence it can indeed be used to derive a classification from it.

◁ Figure 14. Nature of the branches of a phylogenetic tree, with ancestor-descendant relationships between individual organisms.

Secondly, we need to understand that in our system of nomenclature, rules are such that some categories are mandatory. All species belong to at least a genus, and every genus belongs to a family. When we create a subgenus to accommodate some of the species within a genus, we are forced to make one or more other subgenera to accommodate the remaining species (see also Chapter 3). We have to keep this in mind when applying rules to divide a phylogenetic tree into taxonomic groups that carry a formal name.

The majority of taxonomists will tell you that a classification can only be natural when it is composed exclusively of so-called **monophyletic units**; that is a group of species that includes an ancestral species and all members derived from that one ancestral species (figure 15), also named the most recent common ancestor (MRCA), [Note: a single species can represent a 'group' comprising a single element.] When some, *but not all*, of the species derived from the most recent common ancestor are included, that group is called **paraphyletic** (figure 15). The problem is that while mathematically a cladogram, with taxa represented only at its tips (see figure 13), might be fully chopped up into monophyletic groups (the nodes of the cladogram are said



△ Figure 15. Phylogenetic tree illustrating the meaning of monophyly, paraphyly and polyphyly (further explanation see text).

to represent the character distribution of the potential ancestors), it is impossible to do so when using a phylogenetic tree. Every time a new species splits off from its ancestral one, it may start a new monophyletic group but will always leave behind a paraphyletic remainder (Brummitt 2002, Sosef 1997, Horandl 2006, Podani 2010). Many prefer to only distinguish the 'nicer looking' monophyletic groups, but few seem to realize they subconsciously make the choice to base their classification on a cladogram rather than on a phylogenetic tree. Consequently, such a strict monophyletic classification is not only less natural than one that allows paraphyly, but is often unable to cope with extant ancestral species, fossils, or recently extinct species. An example of the latter is the sabretooth tiger or the mammoth where these species represent the paraphyletic remainder of extant species and thus inevitably lead to non-monophyly. A single extant species can either be monophyletic (when it contains all descendants of a single ancestral origin) or paraphyletic (when it gave rise to a new species) and building a strictly monophyletic classification with such components is mathematically impossible. Some tried to circumvent this 'unwanted' situa-

tion by proposing a convention in which we would agree that all species are monophyletic by definition, clearly a theoretical horror: At one point, a revolutionary new concept of providing names to taxa was developed, called the PhyloCode (de Queiroz 2006), which involved throwing out the idea of any mandatory taxon levels such as genus or family (apart from species). This means that some species may belong to a genus, but others do not and for example only belong to a family. Theoretically, it is probably a better nomenclatural system that would also allow a strict monophyletic classification, but pragmatically systematists did not want to throw the Linnaean binomial system away and adopt such a rigorous new one.

Finally, a **polyphyletic group** is a group of species where the most recent common ancestor belongs to a different group, or where the members arose from more than a single MRCA (see figure 15). When in the past such groups have been recognized as taxonomic entities, it was probably due to species that shared one or more plesiomorphic characters, or one or more characteristics that were not inherited from a common ancestor. For example, non-related species living in a desert might independently develop scale hairs to protect them from dehydration. Such results of parallel or convergent evolution are called **homoplasies**, i.e. a homoplasious character looks the same but has a different evolutionary origin. All agree that such groups are non-natural and should be eliminated from a classification.

After having decided which rules one wants to follow to chop up a phylogenetic tree (or a cladogram) into taxa, there are still many choices one can make that renders the process of classification and naming of taxa partly subjective. "Which part of the tree will I recognize as a genus?" "Or, would it be better to call it a subgenus?" etc. are true questions one needs to answer. Making choices that will cause least perturbation in the existing system is also a valid argument thereby promoting name stability.

General literature on systematics

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**Species
concepts**



2.1 What is a species?

Biologists generally agree that the species is a fundamental natural unit. However, it has proven incredibly difficult to define what exactly a species is! This controversy occurs notably on a theoretical rather than a practical level and has come to be known as 'the species problem'.

One of the most fundamental aspects of the problem is variation. Most, if not all, animal and plant species show variation, every individual often being demonstrably unique. Within a population variation can be continuous (e.g. height or weight) or discontinuous (e.g. sex; having right- or left-spiralled corolla lobes), environmental in origin (e.g. flower colour influenced by the composition of the soil) or genetic (e.g. blood type). Variation can also occur in space between populations (geographical variation). Even when two individuals share exactly the same DNA (clones or twins) they may develop morphological differences under the influence of environment factors; this is called **phenotypic plasticity**. The species problem is, in part, a history of how biologists have tried to address variation. Often, species are thought to represent a natural unit. The most extreme opposing view to this idea, states that only individuals exist in nature. Taxonomic groups, including species, are then seen as man-made abstractions that allow us to conveniently group large numbers of individuals. Few scientists accept this nominalist approach with respect to species, but many believe it does apply to higher taxa (World Conservation Monitoring Centre 1992).

Multiple definitions and species concepts have been proposed. These usually follow the discipline of the author: the taxonomic species concept, the evolutionary species concept, the ecological species concept, the historical species concept, and many more. Species concepts can be divided into two main groups, those concerned with process (evolution, interbreeding) and those concerned with pattern (morphology, ecological preferences). Below are the three most widely known ones:

The biological species concept. This concept defines species in terms of interbreeding. Its biggest advocate was undoubtedly Ernst Mayr, an ornithologist. He defined species as "*groups of interbreeding natural populations that are reproductively isolated from other such groups*". Later, it was refined to "*a population or group of populations whose members have the potential to interbreed in nature and produce viable, fertile offspring, but do not produce viable, fertile offspring with members of other such groups*". It remains the most widely accepted species concept today. It explains why the members of a species resemble one another, and differ from other species. The members exchange genetic material and pass it on to their offspring, but not to other species. Thus, the evolutionary process involves random mutations that remain inside a gene pool that has acquired some form of isolation. Over time these novelties will start to differentiate these populations from other similar gene pools (or populations). Finally, these differences may lead to reproductive isolation, where the isolated gene pools will start acting as species.

In general, zoologists embrace this species concept, however it poses some complications for plants. While hybrids in animals are rare, in plants many species are known to hybridize and produce fertile offspring (Grant 1981, Stace

et al. 2015). Only if such events are rare and the offspring are less viable, can the parent species maintain their unique genetic identity and hence be recognized as distinct species. Furthermore, the concept does not apply to asexual organisms, and in plants for example the occurrence of apomixis would not allow defining a species according to the biological species concept.

The morphological species concept. This concept characterizes a species by morphological distinctiveness and is applied to both asexual and sexual organisms. It can be applied when information on gene flow is unknown e.g. when only herbarium specimens are available. Researchers may disagree on which characters to use to differentiate species which leads to subjectivity.

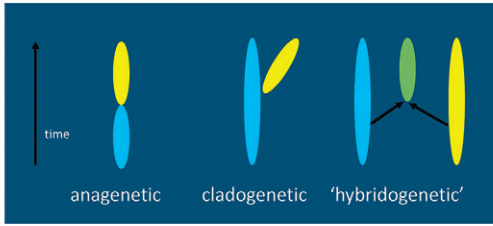
The evolutionary species concept. This concept stresses the importance of a species being an evolutionary unit. It defines them as "*a lineage of interbreeding organisms, reproductively isolated from other lineages, that has a beginning, an end, and a distinct evolutionary trajectory and historical fate*" (Wiley 1978). It is definitely the least practical concept, but does include time as an essential element.

Whatever concept a scientist uses to distinguish a species, the delimitation actually represents a hypothesis about the relationships among the individual organisms belonging to the species. Such a hypothesis about which group of individuals forms a species may be tested using morphological, genetic, behavioural or other types of evidence.

2.2 Speciation

In an evolutionary context, based on progressive change, species are variable in space and will change over time. Such changes may eventually result in the formation of one or several new species. This process generally involves two processes: **isolation**, where one or more individuals of an existing species are no longer able to interbreed and therefore no longer exchange genetic material with the other individuals of the same species, leading to **divergence**. The latter process involves the accumulation of random mutations, gradually or instantly, where the acquisition of new features may cause two isolated entities to become substantially different and be considered distinct species. Both processes may influence each other: Partial isolation, where on rare occasions genetic material is still exchanged, may reduce the speed with which two entities may diverge. Similarly, divergence itself may increase the isolation of a population.

Figure 16 shows three possible processes leading to speciation. The easiest to understand is '**cladogenetic speciation**' where part of an existing species (sometimes comprising a single individual) is separated and becomes isolated. Think of a single seed that is blown across an ocean to a remote island. After arrival, it will be the founder of a new population that will gradually accumulate random mutations and hence diverge from its ancestral populations on the mainland. Note that such a process, also referred to as 'budding', does not alter the nature of the parental species which may continue to exist while the new species differentiates. The second process is '**anagenetic speciation**',



△ *Figure 16. Speciation processes (further explanation see text).*

where a species slowly accumulates random mutations over time and becomes substantially different from its ancestral populations thereby being recognized as something different. In this case, the 'isolation' is through a separation in time. Notably palaeontologists, working with fossils from different time frames, will want to define such groups of individuals as different species. Finally, species may arise instantly through **hybridization**, especially when followed by duplication of the genome resulting in polyploid organisms unable to cross with members of the parental populations. The latter speciation mechanism is rare in animals but fairly common in plants (Grant 1981, Soltis & Soltis 2009).

The speciation process is closely linked to the presence of reproductive isolation mechanisms preventing interbreeding. Below is an overview of such mechanisms, divided into two groups: pre-mating (in plants before pollination) and post-mating (after pollination) isolation mechanisms.

1) **Pre-mating isolation mechanisms** (in plants):

- a) *Geographical isolation.* Individuals occur in different geographical areas separated by a barrier that cannot be crossed by pollen, seed or spores.
- b) *Temporal isolation.* Pollen is not exchanged between species because they flower at different times of the day or in different seasons.
- c) *Ecological isolation.* Individuals occupy different habitats, and therefore pollen is not transferred to other species with different ecological preferences.
- d) *Behavioural isolation.* Related species may attract different animals as pollinators.
- e) *Mechanical isolation.* Physical non-correspondence of flower parts prevents the transfer of pollen to the style, such as in heterostylous flowers.

2) **Post-mating isolation mechanisms** (in plants):

- a) *Gametic incompatibility.* Pollen does reach the style but does not germinate or the pollen tube does not reach the egg cells.
- b) *Zygotic mortality.* The pollen nucleus does reach the egg cell, but the zygote does not develop.
- c) *Hybrid inviability.* A hybrid embryo or plant is formed, but has a reduced viability.

d) *Hybrid sterility*. The hybrid plant is viable, but is sterile and does not produce seeds.

e) *Hybrid breakdown*. First generation (F1) hybrids are viable and fertile, but further hybrid generations (F2 and backcrosses) may be less viable or sterile.

2.3 Intraspecific taxa

Evolution generally is a fairly slow process (apart from some situations involving hybridization). It may take thousands of years before a population that has become isolated will eventually develop into a distinct species. Some DNA mutation may appear, but then disappear again, while others remain although they do not necessarily lead to a phenotypical differentiation. As a result, when we observe the living world, we will see variation at many levels which arises through various processes. We may well witness a time slice in the process of speciation and observe a species in the making. In some cases, when the pattern is discontinuous, we may want to capture such variation in distinct intraspecific taxa. While zoologists only recognize the intraspecific level of subspecies, plants and fungi use subspecies, varieties and formae.

A **subspecies** is defined as a part of a species (one or more populations) that is morphologically or genetically distinct and generally also occurs in a distinct geographical region.

A **variety** is defined as a part of a species (one or more populations) that is morphologically or genetically distinct, but which is generally encountered within the distribution area of the species as a whole. It often occupies a different habitat and is thus ecologically distinct.

A **forma** is defined as a part of a species that is morphologically or genetically distinct, but which represents a mutation that occurs sporadically within a population.

Species concepts

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**Rules of botanical
nomenclature**



Once the character variation within a group has been studied and conclusions have been drawn about which entities, or taxa, need to be distinguished, the question arises as to what the correct names for these entities should be. That is where one enters the realm of botanical nomenclature.

3.1 ICN: the book of law

After 1753, when Linnaeus introduced his binomial system, only some elementary rules for naming plants were developed. Later, in 1813, Augustin de Candolle in his *Théorie élémentaire de la Botanique* provided a detailed set of rules regarding plant nomenclature. However, over time it became apparent that an internationally recognized and accepted system and rules for naming plants was necessary. It was Alphonse de Candolle, son of Augustin de Candolle, who convened an assembly of botanists from several countries to present a new set of nomenclatural rules. In 1867, he organized the First International Botanical Congress (IBC) in Paris, which led to the publication of the so-called Paris Code. Subsequent meetings of the IBC were held in 1892 (Rochester Code), 1905 (Vienna Code), 1907 (American Code) and 1912 (Brussels Code). A general agreement regarding internationally acceptable rules for plant nomenclature was however only reached in 1930 at the IBC meeting in Cambridge. Here, for the first time in botanical history, a Code of nomenclature came into being that was both international in function and name: the **International Code of Botanical Nomenclature (ICBN)**. Today, it is composed of a number of Principles, Rules and Recommendations laid out in 61 Articles, as well as the Provisions for governance of the Code. It looks quite similar to a book of law. Since 1930 many updates of the ICBN have been produced. In 2011, the name changed to "**International Code of Nomenclature for algae, fungi, and plants (ICN)**". It also covers the fossils of these groups (see Turland et al. 2018).

Proposals to amend the Code are published in the journal *Taxon*. Every 6 years, at the start of the International Botanical Congress, during the 'Nomenclatural Session' that may take a full week, taxonomists from all over the world meet to discuss all proposals published during the interim period between conferences. Each institute has a number of votes, depending on their number of research staff. Basically, changes to the rules of botanical nomenclature are decided through a democratic process.

The most important nomenclatorial rules are outlined below. It should be noted that for more detail or more complex cases one should consult the latest version of the Code. Although it may have been translated into several other languages, the English version counts as the only official one.

3.2 From Kingdom to subforma, mandatory categories

Any taxonomic group, be it a family, species or variety, is referred to as a 'taxon' (plural 'taxa'). Names of taxa above the level of species are composed of a single word and those from Subtribe and higher have a specific ending.

Only some of the taxon ranks are mandatory. Below is a list of the most commonly used taxa in plants, algae and fungi, with their specific ending. Mandatory ranks are given in **bold**.

RANK	PLANTS	ALGAE	FUNGI
Kingdom/Regnum	-tae		
Division/Phylum	-phyta		-mycota
Subdivision/Subphylum	-phytina		-mycotina
Class	-opsida	-phyceae	-mycetes
Subclass	-idae	-phycidae	-mycetidae
Superorder	-anae		
Order	-ales		
Suborder	-ineae		
Superfamily	-acea		
Family	-aceae		
Subfamily	-oideae		
Tribe	-eae		
Subtribe	-inae		

Below the level of Subtribe, taxon names do not have a specific ending. The most important ones are (mandatory ones in **bold**):

Supergenus
Genus
 Subgenus
 Section
Species
 Subspecies
 Variety
 Subvariety
 Forma
 Subforma

The names of non-mandatory taxa are composed of a single word that follows the nearest mandatory name above it. The name of a species is com-

posed of the genus name plus the species indication, hence a second word, called the **epithet**. The name of an infraspecific rank is also composed of a single word. The species epithet and all infraspecific names are always starting with a lowercase letter; those of ranks above species start with a capital. Some examples:

Amanita subgen. *Amanitopsis*

Begonia sect. *Scutobegonia*

Poaceae tribu *Andropogoneae*

Monotes rubriglans subsp. *upembensis*

Chlorophytum gallabatense var. *micranthum*

3.3 The type concept

The application of names of taxa at ranks above the family may be determined by the name of an included genus (e.g. Order Asparagales is derived from the generic name *Asparagus*), or may be descriptive names (such as Division Spermatophyta). The application of names of taxa at the rank of family or below however is determined by means of nomenclatural types. A nomenclatural type is the element to which a name is permanently attached, whether that name is the accepted name or a synonym of another name does not matter.

The type of a name of a species or infraspecific taxon is either a single specimen conserved in a herbarium, or an illustration. The type of a name of a genus (or of any subdivision of a genus) is the type specimen (or illustration) of the name of the type species (the first species ever described in the genus or designated as such by the author of the genus). The type of a name of a family (or of any subdivision of a family) is the same as that of the generic name from which it is formed. Note that the nomenclatural type is not necessarily the most typical or representative element of a taxon. More on types can be found in paragraph 3.5 below.

3.4 Valid and effective publication

The original (first) publication of a name is called the **protologue**. In order to be formally accepted as a new name under the rules of the Code, the protologue must fulfil several conditions. When it does not, the name is not accepted by the ICN and is discarded from further processing. The most important condition is that the new name must be both effectively and validly published.

In order to be **effectively** published the name must appear in print and be available in (at least 2) publicly accessible places (like libraries) (Art. 29). From 1 January 2012 onwards, a publication in electronic format (PDF) is also accepted when it has an ISSN or ISBN number.

In order to be **validly** published, a new name (of the rank of genus or below) must be:

- effectively published
- associated with the taxonomic rank it represents (Art. 37), as of 1 January 1953 onwards;
- accompanied by a description or **diagnosis** indicating how it differs from related taxa. Between 1 January 1935 and 31 December 2011, descriptions or diagnoses must be in Latin, thereafter it may also be in English. (Art. 39)
- accompanied by the indication of the type specimen, as of 1 January 1958 (Art. 40.1). After 1 January 1990, the Herbarium where the type has been deposited must also be indicated (Art. 40.7). Herbaria are generally cited by their standard acronym which can be found in Thiers (continuously updated).

In botany, the name of the species epithet cannot be the same as the genus name. In zoology this is allowed (*Bufo bufo* for the Common toad, or *Giraffa giraffa* for the Southern giraffe). Such a name is called a **tautonym** and is invalid under the botanical Code.

Occasionally, it happens that someone publishes a name that is exactly the same as one that was published earlier. Both names are then called **homonyms** and the more recent one is **illegitimate** under the botanical Code.

3.5 Types

Having the correct type specimen linked to a name is essential to plant (and animal) nomenclature. A number of rules have been put in place to deal with situations where the type may be uncertain.

In botany, a plant collection or gathering, is generally indicated by citing the collector and their unique collecting number, for example *Lebrun 1234*. [When a specimen has an associated barcode this can be cited additionally.] In the field, a collector often takes several samples or specimens from the same plant or population where these are given the same collection number (*Lebrun 1234*). Hence, a single collection may comprise several duplicates, which are often sent to various Herbaria in exchange for their duplicate material. The type of a plant name, however, can only be a single specimen, indicated as the **holotype**. Any existing duplicates of the holotype are called the **isotypes**. Although the isotypes can be very useful for research, when it comes to applying the rules of nomenclature only the holotype is considered. Next to a dried plant or fungus, an illustration may also serve as the holotype.

When the protologue does not specifically mention the existence of one or more duplicates, the specimen present in the herbarium where the author worked or one that he or she definitely had access to while preparing the description of the new taxon, may be regarded as the holotype.

All other collections cited in the protologue, but not belonging to the type collection, are called the **paratypes**.

Before 1958, one was not obliged to indicate the type specimen for a new name. As a consequence publications preceding this date regularly have protologues that do not mention a type but rather cite several collections consulted by the author for the new taxon. These are then all regarded as 'original material' and are called **syntypes**. As a name may only have a single type, one must choose a type from amongst this original material (the collections cited and all their duplicates). Such a chosen type is then called the **lectotype**. Duplicates from the lectotype are then called **isolectotypes**. When someone publishes a lectotypification, adding the phrase "*designated here*" is obligatory. Once a type collection is assigned to the name, the remaining syntype material automatically become paratypes.

In a situation where all original material, including any relevant illustrations, has been lost (after proof of an exhaustive search), one is allowed to select a new type that is then called the **neotype**. Duplicates of the neotype then become **isoneotypes**. When creating a neotype, one often tries to select material that was collected at or close to the original type locality, but this is not obligatory. In general, one aims to select a neotype where nomenclatural stability is guaranteed, hence which does not lead to necessary name changes.

Finally, the holotype material may be too scanty to adequately diagnose a taxon (note that the type can also be an illustration where some details may not be apparent). In such a case, one is allowed to select a 'supportive type' known as an **epitype**, so as to leave no doubt about the identity of the taxon concerned. Again, it is important to choose the epitype wisely, so as to guarantee nomenclatural stability.

It is important to note that the Code defines a 'specimen' as being a gathering of a single species or infraspecific taxon that may comprise a single organism, parts of one or several organisms, or multiple small organisms. A specimen is usually mounted on a single herbarium sheet or in an equivalent preparation, such as a box, packet, jar, or microscope slide.

Examples with types

Holotype and isotype citation:

Solanum aculeastrum Dunal (1852: 366). – Type: Afrique du Sud, Cape of Good Hope, eastern part near Morleg, 1500 ft, 1838, Drège s.n. (holo-: G-DC; iso-: AD, BM, K, P).

Explanation: The protologue of the species name *Solanum aculeastrum* has been published by Dunal in 1852. The protologue mentions Dunal saw a single specimen collected by Drège, without a collecting

number (s.n. = sine numero), and states he saw this in the herbarium of De Candolle, which is kept at Geneva. Hence, that specimen (in G-DC) is to be regarded as the holotype. Later, duplicates of this collection have been identified at Adelaide State Herbarium (AD), the British Museum (BM), the Royal Botanic Gardens, Kew (K) and the Muséum national d'Histoire naturelle, Paris (P).

Lectotype designation:

Antheophora elegans Schreb. var. *africana* Pilg. (Pilger 1901: 119). – Type: D.R. Congo, Stanley-Pool, June 1899, Schlechter 12508 (lectotype: B [B 10 0168252], **designated here**; isolectotypes: B [B 10 0168251], BR [BR0000013591571], K [K000281098], P).

Explanation: *Antheophora elegans* var. *africana* was published citing four specimens, Buchholz 1875, Dinklage 464, Dewèvre 120 and Schlechter 12508 which are to be regarded as syntypes and comprise the original material. Since the author worked at Berlin (B), the lectotype should preferably be located there. All except the Schlechter specimen are not present at B and were presumably lost during the 1943 fire. At B, there are two sheets of Schlechter 12508, one of which has no spikelets left, the other with a few spikelets in an envelope glued onto the sheet. The latter is selected as the lectotype, with duplicates located at Meise Botanic Garden, Belgium (BR), Royal Botanic Gardens, Kew (K) and Muséum national d'Histoire naturelle, Paris (P). The barcodes are added to the specimens for which these were available.

Neotype designation (represented by an illustration, also indicated as iconotype, figure 17):

Dracaena sanderiana Sander ex Mast. (Masters 1892: 731). — Neotype (**designated here**): Gard. Chron., ser. 3, 13: 445 (1893), f. 65 (iconotype).

Explanation: *Dracaena sanderiana* was first exhibited by the horticulturalist Sander at the international exhibition in Earl's Court (1892), and published the same year by Masters with a description, but without illustration. Original material of the plant exhibited has not been traced and has probably not been conserved. One year later, *D. sanderiana* was exhibited by Sander in Ghent and an illustration was published in Gard. Chron., ser. 3, vol. 13 (1893). This illustration most likely represents the same plant as originally presented in 1892 and is hence chosen here as the neotype.

3.6 Author names, new taxon names, new combinations

The person publishing a new taxon name is the author of that name, and in formal or official documentation is placed after the taxon name concerned. The author name is often abbreviated, for which a standard abbreviation was

published by Brummitt & Powell (1992) and for which an online database is now maintained by IPNI (at <http://www.ipni.org>).

Sometimes, an author publishes a taxon name within the publication of someone else (either as a chapter in a book, or simply a part of an article accredited to them). In that case, one may cite both authors using the connecting word 'in'. For example, *Verrucaria aethiobola* Wahlenb. in Acharius, Methodus, Suppl.: 17. 1803. The ICN regards the part after Wahlenb. as a bibliographical reference and hence it is not a part of the name.

In other situations, an author may validly publish a taxon name but ascribe it to another person, for example where the person suggested the name (on a herbarium label, or even verbally) but failed to publish it. In that case, the name of the latter is given but is followed by 'ex' and the name of the author who validly published it, e.g. *Acalypha racemosa* Wall. ex Baill. Here, Baillon validly published the name *Acalypha racemosa* that was already coined for that species by Wallich. It is also accepted to omit the name of the first author and simply cite this species as *Acalypha racemosa* Baill.

The fact that an author intends to publish a new taxon name is often indicated by adding the abbreviation **spec. nov.** or **genus nov.** or **subsp. nov.**, etc., behind the name.

When an author moves a species from one genus to another, the epithet is transferred to the new genus while the original author is placed between brackets after it, followed by the transferring author e.g. *Cenchrus purpureus* (Schumach.) Morrone. This species was originally named *Pennisetum purpureum* by Schumacher (1827) and transferred to the genus *Cenchrus* by Morrone (2010). Note that the gender of the epithet has changed in accordance with Latin grammar. The name *Cenchrus purpureus* (Schumach.) Morrone is called a **new combination** (often abbreviated as **comb. nov.**) since it combines the original (protologue) epithet with the name of another genus. The name that provided the epithet for the new combination is called the **basionym**; in this case *Pennisetum purpureum* Schumach.

The same happens when an author downgrades or upgrades a name to a different taxonomic rank. For example, in *Cenchrus polystachios* (L.) Morrone subsp. *atrichus* (Stapf & C.E.Hubb.) Morrone, the name *Pennisetum atrichum* Stapf & C.E.Hubb., the basionym, was transferred to a subspecies of *Cenchrus polystachios* by Morrone. The name *Cenchrus polystachios* (L.) Morrone subsp. *atrichus* (Stapf & C.E.Hubb.) Morrone is not only a new combination (**comb. nov.**, since the basionym was moved to a different genus) but has also given the taxon a **new taxonomic status** or rank, often indicated by adding **stat. nov.** after the new name.



△ Figure 17. The neotype (iconotype) of *Dracaena sanderiana* Sander ex Mast. in *Gard. Chron.*, ser. 3, 13: 445 (1893), f. 65.

3.7 Accepted names and synonyms: the priority rule

The science of taxonomy is dynamic where changes occur often as improvements to the natural classification. This means that a publication may provide new research data that underpin a novel view on the variation present within a species, or on the delimitation of genera, families etc. It is important to understand that such a view represents a new hypothesis, a new opinion, supported by logical arguments. Through this process, the classification, or the taxonomic framework, is ideally improving and evolving towards a stable conclusion. However, some may weigh the supportive data for alternative hypotheses in favour of a different classification. It is then difficult to say which one is 'correct' as we will never be able to fully reconstruct the evolutionary pathways.

When studying a certain group of taxa, an author may consider two or more names to represent the same taxonomic unit. Following the type concept, this basically means that this author is of the opinion that the type specimens of both names belong to the same taxon. For example, Clayton & Renvoize (1982) considered the following species names, in alphabetical order; to represent a single, variable species of grass:

Pennisetum angolense Rendle (Rendle 1899: 189).

Pennisetum giganteum A.Rich. (Richard 1850: 382).

Pennisetum macrourum Trin. (Trinius 1826: 64).

Pennisetum scaettae Robyns (Robyns 1934: 3).

Pennisetum stenorrhachis Stapf & C.E.Hubb. (Stapf & Hubbard 1933: 270).

This implies that all five names are **synonyms**, but the nomenclatural rules stipulate that only a single name can be the **accepted name**; so, which one do we choose? Here we should apply the **priority rule** (Principle III of the Code), which tells us that the oldest synonym has priority over the others. In this case, the correct and accepted name for this species is *Pennisetum macrourum* Trin., since it was published in 1826.

The priority rule applies to all taxonomic levels. For example, in 2010, Morrone published an article in which he merged the genus *Pennisetum* Rich. (Richard in Persoon 1805: 72) with *Cenchrus* L. (Linnaeus 1753: 1049). The priority rule shows the latter genus has priority over the first, and so the genus in its new circumscription should be called *Cenchrus*.

When we follow the view of Morrone (2010), the accepted name for the species *Pennisetum macrourum* Trin. becomes *Cenchrus macrourus* (Trin.) Morrone. Note, that when another author does not agree with this hypothesis and advocates to maintain the genus *Pennisetum*, there are two accepted names for the same species, depending on the scientific point of view.

Further, it is important to know that the priority rule only applies to names of the same taxonomic rank! In the previous example, if the name *Pennisetum polystachion* (L.) Schult. var. *africana* Thunb. (Thunberg 1794: 101) would have

been a synonym of the five other names in *Pennisetum* mentioned above, then it would have been the oldest name available. However, as it is a name at the rank of variety, it has no priority over names at species level. When author Xxx would want to upgrade that variety to the species level (as *Pennisetum africanum* (Thunb.) Xxx) the publication date of that name would be the date this new combination was published. It logically follows that when the taxon *Ixora aneimenodesma* K.Schum. subsp. *kizuensis* De Block has no synonyms and an author Xxx wants to raise it to species level, they have two options: 1) to publish the name *Ixora kizuensis* (De Block) Xxx, or 2) to publish a new species name (e.g. *Ixora congoensis* Xxx), with the subspecies name as a synonym. Option 2 is not considered 'polite' since it removes the original author from the name. However, the name *Ixora kizuensis* may already exist for a different species. In that case, the necessary new combination is 'occupied' and one has to opt for a new name, such as *Ixora deblockiae* Xxx to honour the original author. The necessity to create such a **new name** for a taxon already described before is often indicated by the addition **nom. nov.**

There are two exceptions to the priority rule. The first is that there are eight family names and one subfamily name where one is allowed to choose between two alternatives (ICN Art. 18.5, 19.8). Such names are called **nomina alternativa** (or **nom. alt.**). Below is a list of these allowed alternative family and subfamily names. In a single publication it is advised to use the names of only one of the columns.

Apiaceae	Umbelliferae
Arecaceae	Palmae
Asteraceae	Compositae
Brassicaceae	Cruciferae
Clusiaceae	Guttiferae
Fabaceae incl. subfam. Faboideae	Leguminosae incl. subfam. Papilionoideae
Lamiaceae	Labiatae
Poaceae	Gramineae

Secondly, the strict application of the rules laid down in the ICN may lead to 'unwanted' changes and major instability of the nomenclature within a particular taxonomic group. In that case, one can make a proposal to conserve or reject a specific name. In case of ambiguity related to the correct type specimen, a similar proposal to conserve a specific type can be formulated. Such proposals need to be published in the journal *Taxon* and are then voted on at the next International Botanical Congress. Conserved or rejected names or types are generally followed by the indication '**nom. cons.**', '**nom. rej.**' or '**type cons.**'.

3.8 Hybrids

In the Code, names of hybrid taxa are dealt with in a separate chapter. They can be recognized by the use of the multiplication sign \times or by the addition of the prefix "notho-" to the term denoting the rank of the taxon. A **nothospecies** name, composed of a genus name (or a nothogenus name, see below) and an epithet, indicates a hybrid between two individuals of different species. A **nothogenus** name, a single word, is used when a hybrid has been formed between individuals of species belonging to different genera. It is often composed of parts of the names of the two genera involved.

For example, the hybrid between *Oenothera biennis* L. and *Oenothera villosa* Thunb. can be either indicated by the **hybrid formula** *Oenothera biennis* L. \times *Oenothera villosa* Thunb., or by the nothospecies *Oenothera* \times *drawertii* Renner ex Rostański.

The nothogenus \times *Festulolium* Asch. & Graebn. groups individuals originated from a hybridization event between species of the genera *Festuca* L. and *Lolium* L. The nothospecies \times *Festulolium loliaceum* (Huds.) P.Fourn. indicates the hybrid between *Festuca pratensis* Huds. and *Lolium perenne* L., which can also be indicated by the hybrid formula *Festuca pratensis* Huds. \times *Lolium perenne* L.

3.9 Cultivated plants

Names of cultivated plants are not regulated by the ICN, but rather by the International Code of Nomenclature for Cultivated Plants (ICNCP).

Cultivated forms can be indicated by only three categories, the **Cultivar**, the **Group** or **Cultivar group**, and the **grex**. The latter is used solely in orchid cultivation and indicates the combined hybrid offspring of any cross between the same two entities (taxa or cultivars). A cultivar, abbreviated as **cv.**, is a very specific form derived from any type of selection process and may even have been taken directly from the wild. It is a non-Latin name added after the name of the taxon from which it was derived e.g. *Solanum tuberosum* L. cv. Gogu valley, also written as *Solanum tuberosum* 'Gogu valley'. When it is unclear to which species a cultivar belongs, the cultivar name can follow directly after the genus e.g. *Rosa* cv. Penelope. A new cultivar name can be formally registered by an International Cultivar Registration Authority that needs to be approved by the ISHS Commission for Nomenclature and Cultivar Registration. Each Authority is assigned a specific taxonomic group. After the Authority has formally approved the registration of a new cultivar name, the person who provided the information 'owns' the rights to this name. They can then market both the name and the plants, quite similar to a patent. A Cultivar group, abbreviated as **cv. gr.**, comprises a number of cultivars having a distinct characteristic. One could, for example, create a Cultivar group for all yellow roses. Here it becomes clear that names of cultivated plants are not part of a natural classification, since they need not indicate or reflect common ancestry.

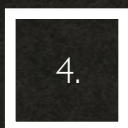
In literature on cultivated plants, one may regularly come across 'variety' or 'form'. Note that these terms should actually not have been used for cultivated plants, as they erroneously refer to the ICN which does not deal with cultivated plants. When possible, such uses of 'variety' or 'form' should be treated as informal descriptions of the variation observed without the intention to create a new taxon name under the ICN.

International Code of Nomenclature for algae, fungi, and plants

- <http://www.iapt-taxon.org/nomen/main.php?>

Scientific names and types

- International Plant Name Index: <https://www.ipni.org>
- Tropicos: <http://www.tropicos.org>
- World Flora Online: <http://www.worldfloraonline.org>
- African Plant Database: <http://www.ville-ge.ch/musinfo/bd/cjb/africa/index.php>
- Linnaean Typification Project: <http://www.nhm.ac.uk/our-science/data/linnaean-typification>
- Global Plants: <https://plants.jstor.org>



**The art
of identification**

In the preceding chapters, we mentioned that the taxonomic science aims to organize the immense diversity of living organisms on earth into discrete units. As such, it provides the essential tools for scientific communication in the form of names and a classification. To be able to perform biological research, protect nature, use plants for medicinal purposes, etc., it is crucial to have access to the wealth of information accumulated over several centuries. Online resources are growing exponentially. However, before one can tap into the information available on certain species or genera, for example, one has to know the name of the particular taxon concerned. As specialists who can identify living organisms by heart are rare, especially in the tropics where diversity is high, taxonomists have developed tools to reliably identify their material.

4.1 Identification keys

An identification key is a practical tool used by both specialists and non-specialists to identify plants, fungi or animals, to the level of family, tribe, genus, species or other. It is often the most extensively used part of a taxonomic publication, and hence deserves the utmost attention of the researcher who creates it!

In order to use an identification key, one generally has to have at least a basic understanding of plant or fungal morphology and terminology. Having a good glossary may be useful. Various good and extensive botanical glossaries exist (see the text box at the end of this chapter).

How to use a key?

An identification key is generally a kind of question-answer 'game' where the user is asked to (carefully!) observe specific characters and report on their state. An identification key may for example use the character 'flower colour', and the user can choose between the states "yellow" or "white". When yellow, continue to question number 2, when white go to question number 10. The first part of the identification key will then look as follows:

- 1. - Flowers yellow 2
- Flowers white 10
- 2. - ...
- ...

In the example above, each question is called a **couplet** of the key, having two **leads**. It is obvious that the two options need to be mutually exclusive, not showing overlap. After having correctly answered a certain number of questions, the user will end up with the name of the plant (or fungus, or animal) at hand.

Generally, the user is given the choice between two options. In such a case, the key is **dichotomous**. Some keys allow the choice between three or even

more options (in the example above, one could add 'Flowers blue', 'Flowers red', for example to arrive at four leads. These are called **polytomous** keys. In general, this structure is deemed less practical and more prone to identification errors. One can easily avoid such choices by combining several states into one lead, such as:

- 1. - Flowers yellow, blue or red 2
- Flowers white 10
- 2. - Flowers yellow 3
- Flowers blue or red 6
- 3. - Twigs spiny *Rosa banksiae*
- Twigs spineless 4
- ...
- 6(2) - Stamens ...
- ...
- ...
- 10(1) - Leaves
- ...

Note that question #3 provides the name of the plant, and that questions 6 and 10 show which previous question pointed to it. The latter is simply assisting the users in keeping track of where they came from, and is generally added only when one has arrived after having made a comparatively large 'leap' in the key.

Basically, there are two forms of dichotomous keys. The form shown above where both leads directly follow each other is called a **bracketed key**. The second form is called an **indented key** and separates the two leads in space. Here is an example of an indented key (adjusted from a key to the species of *Solanum* in Africa, Vorontsova & Knapp 2016):

- 1. Flowers with stamens of different lengths
 - 2. Leaves orbicular to reniform, 1.2-2.5 cm long, wider than long; petioles longer than leaves. Rare in northeastern Somalia *S. cymbalariifolium*
 - 2. Leaves ovate to elliptic or lanceolate, 2-14 cm long, longer than wide; petioles shorter than leaves. Arid eastern and northeastern Africa.
 - 3. Stem prickles dense, acicular; less than 0.5 mm wide at base, pale yellow; fruit fully concealed by the accrescent calyx *S. coagulans*
 - 3. Stem prickles absent or sparse, if present wider than 1 mm at base, yellow to orange or brown; fruit at least partly exposed
..... *S. melastomoides*
- 1. Flowers with all stamens equal in length. Widespread.
 - 4. Flower one per inflorescence, peduncle and rachis absent; corolla pentagonal, lobed for ¼-½ of the way to the base, 0.9-1.3 cm in diameter; Southern Africa *S. supinum*
 - 4. Flower usually more than one per inflorescence, peduncle and/or rachis present in at least some inflorescences; corolla usually stellate, lobed for

more than $\frac{1}{3}$ of the way to the base, or if lobed for $\frac{1}{4}$ - $\frac{1}{3}$ of the way to the base then corolla of long-styled flowers broader than 1.3 cm in diameter; widespread. *S. tuberosum*

When the first lead of couplet 1 corresponds with the plant to be identified, one should carry on to the next question formulated immediately below it (number 2). However, when the second lead of couplet 1 is correct, one continues with the question below, which is number 4. As can be seen, there are no numbers to the right-hand side of the key pointing to the next question. The advantage of an indented key is that the user may more easily derive the way the species are grouped from the structure of the key. A disadvantage is that one has to search for the second lead of the question/couplet concerned. This can be quite far down in larger groups, and in longer keys there will be a lot of unused space on the left side of the page, resulting in a key that needs more printed pages.

Also, note that geographical information may be used in the key. Despite not being a morphological character, it may be deemed helpful. Similarly, ecological or phenological information (flowering/fruitletting period) may be added. It is however advised that these types of characters be used only as supplementary data to morphological features.

How to make a key?

Start by choosing which type of key to construct (see above). Then, think of several clear subgroups that can be recognized within the group concerned. Next, select those groups that can be defined by character states that are well distinct and can be easily observed with the naked eye or when using a 10 \times hand lens. If the first question of a key is about pollen grains, for example, a fair number of users will be immediately stuck and unable to continue. It is also important that any character mentioned in one lead of a couplet, should also be present in the other lead(s)! A couplet like the one below is not to be recommended:

- 1. - Flowers yellow; leaves longer than 10 cm 2
- Flowers white 10

A user having a plant that carries white flowers but also has leaves longer than 10 cm will become uncertain as to what to choose. This brings us to another practical issue. When making a key, one should always try to imagine what a user may have on hand! This is often a single plant, so the key needs to provide exact information. If a couplet states "Flowers big" against "Flowers small", this is a relative concept and the user is unable to judge whether flowers of 1 cm in diameter may be considered 'big' or 'small'.

A single taxon may key out more than once. That may occur when a specific taxon is variable for a certain character. For example, a species may have white as well as occasionally yellow flowers, while most species are constant in that respect.

	Life form			Leaf width			Flowers		Corolla shape			Fruit colour	
	tree	liana	herb	1-5 mm	5-10 mm	10-30 mm	solitary	fasciculate	star	cup	trumpet	yellow	red
Aus a	1	0	0	0	0	1	1	0	1	0	0	1	0
Aus b	1	0	0	0	0	1	1	0	1	0	0	1	0
Aus c	0	0	1	0	1	0	1	0	1	0	0	1	0
Bus x	0	1	1	1	1	0	1	1	1	0	0	0	1
Bus y	0	1	0	0	1	1	1	0	0	0	1	0	1
Bus z	0	0	1	0	0	1	1	0	0	0	1	0	1
Cus m	0	1	1	1	0	0	0	1	0	1	0	0	1
Cus n	1	0	0	1	0	0	0	1	0	1	0	0	1
Cus o	0	0	1	0	1	0	1	0	0	1	0	0	1

△ Figure 18. Example of a species/character data matrix (with fictional taxa Aus a, Bus x, etc.).

Creating a key for a larger group of species (or other taxa) is often greatly facilitated by the preparation of a taxon/character data matrix (see also figure 18). It often helps to get a better overview of the distribution of characters and their correlation. (See also the next paragraph.)

Finally, some advice on key construction:

1. Be practical! Use 100% clear language. Try to avoid characters that need a lot of explanation or are otherwise difficult to understand or even difficult to observe.
2. In a fully dichotomous key, when all taxa key out only once, the number of couplets will always be equal to the number of taxa minus 1. Hence, one cannot influence the number of couplets. However, one can influence the number of questions to be answered before a species is keyed out. The best strategy is to strive for questions/couplets that divide the remaining group of taxa into more or less equal parts.
3. If the species in a group generally do not have flowers and fruits at the same time, it may be wise to present two different keys, one for flowering material and one for fruiting material.

4.2 Multi-entry keys



The keys discussed above, even when prepared with the utmost care, have a serious flaw. The user cannot choose the sequence in which characters are observed. It could be that having red fruits would already greatly reduce the number of potential species, but that fruit colour is only asked in question number 5. In other words, there should be easier ways to identify a plant!

When using a taxon/character data matrix for a selected group of species (see figure 18 for an example), the user could randomly choose a character from the list and fill out the character state observed in the specimen to be identified. Then, this process can be repeated until the specific combination of character states corresponds to a single species.

Before the computer era, taxonomists already tried various multi-entry keys based on similar matrix systems. One would work with a large number of numbered cards, where each card would either represent a character state, or a taxon. Those interested in such **punch card keys** could have a look at figure 19.

Nowadays, such a taxon/character data matrix with its resulting multi-entry key can be processed by several user-friendly software packages e.g. Xper3 (<http://www.xper3.fr/>), DELTA-IntKey (<https://www.delta-intkey.com>) and Linnaeus NG (<http://linnaeus.naturalis.nl/>). The Xper3 and DELTA-IntKey packages even allow you to create a dichotomous key from your data matrix, which can be used in publications. Some have statistical software included that will advise you on the best next character(s) to use in order to render the identification process most efficient.

A different kind of multi-entry key is the so-called **diagnostic key** (also called a synoptic key). This comprises a list of diagnostic or spot characters (typical, remarkable) occurring within a certain group of taxa. Each character is then

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25			
W.A.	B.A.	VIET	N.S.W.	Q'LD	TAS	N.T.	CENTRAL AUST.	A	B	C	D	TREES	SHRUBS OR LIANAS	HALLES	DECIDUOUS E.G. SUM	HELP-BARKED	SPERMATOPHYTES	PERENNIALS OR BULBS	MONOCOTS	OTHER TYPES	CYPERITE	SEBILLE	Mosses- LIMBOSTATE	Lanceolate			
STATE												SUB-DIV.				HABIT				BARK				MATURE LEAVES			
GEOGRAPHICAL DISTRIBUTION												HABIT				BARK				MATURE LEAVES							
NAMES: BOT. <u><i>E. camaldulensis</i> Dehn</u>												BLAKELY No. 197															
SYN. <u><i>E. rostrata</i> Schlecht</u>																											
COMMON <u>River red gum</u>																											
RELATED SPECIES <u><i>E. exserta</i> of Blakely</u>																											
DISTINCTIVE FEATURES <u>Operculum rostrate</u>																											
or conic not cylindroid; no lignotuber																											
NAT. DISTRIB. <u>Riverains; plains subject to</u>												197															
seasonal water logging. Rainfall <u>30"</u>												197															
OPER.												MATURE LEAVES															
INFLORESCENCE												VENATION															
UMBEL												MUCH DARKER															
FRAGILE OR												BULBY PALS															
CONTING												LARGER STIP															
OVER 7%												EVEN SHADE															
MAJINLY												BOTH SHADE															
47%												GLAUCOUS															
BARK												CONTOURS															
IN 2%												FALGATE															
SOLITARY												ONLY CONTOURS															
INTERMEDIARY												PILATE, ETC.															
NEAR DISTINCT												CHATE															
> 80°																											
82-86°																											
< 20°																											
CONSPICUOUS																											
INTERMEDIATE																											
FRUIT																											
MUCH DARKER																											
BULBY PALS																											
LARGER STIP																											
EVEN SHADE																											
BOTH SHADE																											
GLAUCOUS																											
CONTOURS																											
FALGATE																											
ONLY CONTOURS																											
PILATE, ETC.																											
CHATE																											
50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26			

△ Figure 19. Example of a punch card showing the characters (open holes along the edge) for a species of *Eucalyptus*.

followed by a list of all taxa within the group that possess that character. Below is an example of part of a diagnostic key to taxa of Rubiaceae in Central Africa. Note that the taxa indicated are mostly genera, but also tribes and even species.

EXAMPLE OF A (PART OF A) DIAGNOSTIC KEY:

- LEAF

blade linear: *Amphiasma*, *Anthospermum usambarense*, *Cordylostigma*,
Galium, *Knoxia*, *Kohautia*, *Manostachya*, *Oldenlandia*, *Spermacoce*

blade heart-shaped or kidney-shaped: *Geophila*, *Hymenocoleus*,
Pentanisia renifolia, *Rubia*

- FLOWER

unisexual: *Anthospermum*

heterostylous: *Colletocema*, *Craterispermum*, *Gaertnera*, *Knoxieae*,
Lasianthus, *Morinda*, *Mussaendeae*, *Pauridiantha*, *Psychotrieae*,
Sabicea, *Schizocolea*, *Spermacoceae*, *Tricalysia*

4-merous: *Anthospermum*, *Corynanthe*, *Eumachia*, *Galium*, *Heinsia*, *Ixora*,
Keetia, *Knoxia*, *Lasianthus*, *Naudea*, *Otiophora*, *Paraknoxia*, *Pavetta*,
Polysphaeria, *Pouchetia*, *Psychotria*, *Rutidea*, *Spermacoceae*, *Tricalysia*

pleiomorous (with more elements than usual): *Coffeae*, *Gardenia*,
Rothmannia octomera, *Schumanniophyton*

calyx tube long (> 1 cm): *Adenorandia*, *Gardenia*, *Rothmannia*,
Schumanniophyton hirsutum

calyx tube with a lateral slit: *Calycosiphonia*, *Gardenia*, *Polysphaeria*,
Rothmannia, *Sericanthe*, *Tricalysia*

calyx asymmetrical, with highly unequal lobes, or only 1 lateral lobe:
Knoxieae

4.3 DNA barcoding

The most modern method of identification is the use of a unique DNA profile for individual taxa. The idea is that when this unique DNA sequence, or more popularly called the 'DNA barcode' is known for all species and we have the sequence of an unknown organism, we can match it to our data bank to determine the name of the species. Simple in theory; a lot more complicated in practice! Firstly, we need a data bank for all c. 400 000 plant species, c. 10 000 000 animal species, c. 5 000 000 fungi species, etc., which is far from evident. Moreover, as sequencing (obtaining the base pair sequence) the entire DNA content of an organism is still very time consuming and

expensive, we need to find a piece of the genome, a specific part of the DNA, which provides sufficient variation at the desired level (often species). In many animal groups, the cytochrome c oxidase I (COI or COX1) gene is used comprising c. 1500 base pairs. For plants, however it is a lot more difficult. The combination of two chloroplast genes, *rbcl* and *matK*, have been proposed as a suitable candidate. Adding the nuclear non-coding internal transcribed spacer 2 (ITS2) region was proposed to improve 'resolution'. For fungi, the spacer 1 (ITS1) region would be more suitable. Other, possibly better, suggestions are still being debated. Furthermore, it appears that it is not uncommon that these standard barcoding markers show variation within a species. This means that a single sample is insufficient to represent a species in the DNA barcode data bank, as the within-species variation needs to be mapped first before a reliable identification can be made. One cannot, for example, simply state that: "Since my sample differs in 2 sequence positions from the other, it represents a different species", before the variation in the sequence data has been mapped for both species. As a consequence, for each species several samples (minimum 10, preferably more) are needed to build a reliable barcode data bank. Furthermore, each specimen sampled needs to be vouchered; an organism needs to be preserved in order to be able to verify its identity if doubts arise. The data bank will also need to be regularly updated to incorporate changes in taxonomic concepts.

The DNA barcode database needs to be based on a sound and stable taxonomic framework of genera and species. Even for a comparatively well-known group like plants, this framework still has many weak spots. In their turn, the results of DNA barcoding efforts may well assist in making better taxonomic decisions, thereby strengthening the framework.

Despite these challenges, major efforts are done to create a world-wide DNA barcoding database. The activities are coordinated by the International Barcode of Life Consortium (iBOL) together with many regional centres. At present, obtaining a DNA sequence from an organism often takes several days of lab-work. One needs to be patient when using this method of identification. New processes are rapidly evolving, with the development of ever more sophisticated nano-techniques that create the possibility to put together portable minilabs that can be used in the field.

4.4 Identification of herbarium specimens

While identifying living plants in the field can be difficult, trying to correctly identify dried and flattened herbarium specimens is often challenging. Not all characters needed may be directly visible, even with the help of a good 10× hand lens or a stereo microscope (see also paragraph 5.B). The simple question whether the flowers are white or yellow may remain unanswered when the collector did not record this information in the field. Similarly, one may wonder whether this twig with few leaves and nice flowers or fruits comes from a big tree, a liana, a shrub or even a perennial herb? The 3-dimensional shape (notably of flowers and fruits) could be important, but impossible to reconstruct, as is information about underground tubers, rhizomes, smell,

taste, etc. These kinds of information should be noted down in the field by the collector so that the information can be transferred to the label accompanying the specimen. Various publications (Fish 1999, Victor et al. 2004, Bridson & Forman 2010) offer good advice on how to collect plants and correctly prepare valuable dried plant specimens.

When a herbarium specimen has been identified, whether this is at the level of family, genus, species or other; the taxon name is written on a small piece of paper, called an **identification or determination slip**. This also includes the name of the researcher (and affiliation if possible) and the date. It is glued onto the herbarium sheet (when not gummed, use special glue provided by the herbarium curator), preferably somewhere in the lower right corner and always above any previous identifications slips. Make sure only a small part of the slip is glued, so that the remainder can be flipped back to examine any material or written text it may cover. Some herbaria will only allow the use of needles to attach labels and slips to the sheet.

Any uncertainty about the correctness of the identification can be added as well. Preferably use the abbreviations **cf.** or **aff.** The first is short for “confer” meaning “compare with” and is used when a specimen is very close to something else, and may even be the same. The second is short for “affinis” meaning “similar to” and is used when a specimen is similar something else, but is probably different.

Glossaries

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- Jouy A., Foucault B. de (2016) *Dictionnaire illustré de botanique*. Mèze, Biotope.
- Missouri Botanical Garden Glossary: <http://www.mobot.org/mobot/glossary>
- Wikipedia: https://en.wikipedia.org/wiki/Glossary_of_botanical_terms [in French: https://fr.wikipedia.org/wiki/Glossaire_de_botanique]

DNA barcoding

- IBOL (International Barcode Of Life): <https://ibol.org>
- Hebert P.D.N., Cywinska A., Ball S.L., deWaard J.R. (2003) Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences*. 270 (1512): 313–321. doi:10.1098/rspb.2002.2218.



**The art of preparing a
taxonomic revision**



Here, we focus on a taxonomic revision largely based on herbarium specimens. When studying the taxonomy of a plant or fungal group for which field observations are not easily obtained, e.g. tropical species, or simply those from remote places, herbarium specimens are often the only source of information available. Adding field observations to a revision based on herbarium specimens is a big advantage, but it is not a necessity.

Let's assume that it has been decided to prepare a taxonomic revision for a specific group. This is generally because specialists have indicated that the taxonomic framework for a particular group is considered 'weak'. This could be the result of the available identification keys being of poor quality, of unclear boundaries between taxa/species, or of doubts about the correctness of the names applied. It is not uncommon that part of the "weakness" may be due to the presence of undescribed species. Each year, well over 2000 new species of vascular plants are described, as well as some 75 to 100 new genera. This trend has not decreased over the past 15 years (numbers have even risen slightly over the past four years), indicating there is still plenty to be discovered!

A taxonomic revision is often focused on a particular genus, and in the text and examples below we assume it is. When a genus has many species and a large distribution, the study is not seldom restricted to a country, a phytogeographic region, or a continent.

Referring to the depth, thoroughness and practicality of the revision, one can identify four categories:

- *Synoptic revision*, or *Synopsis*: a brief update of the taxonomy of a group (generally provides an identification key, an overview of all accepted species and their synonyms, sometimes including brief morphologic descriptions and some information on distribution);
- *Taxonomic revision*: a standard update of the taxonomy of a group (with identification key, full synonymy, type information, full morphological descriptions, distributional data, often also citing the specimens used);
- *Monograph*, or *Monographic revision*: a very thorough, all-inclusive update of the taxonomy of a group (as detailed as a Taxonomic revision, but often extended with the results of additional anatomical, molecular, ecological or ethnobotanical studies).
- *Flora treatment*: by definition a regional account of a group, generally a critical revision or compilation of existing (published) information. Here, relatively simple problems are addressed, leaving more complicated matters to more detailed future studies. A Flora's primary aim is to provide tools (identification keys, descriptions, illustrations, etc.) to users who want to identify plants.

For all four categories, the scientific process can be divided into seven phases (A–G, see below) which will be dealt with in more detail in the following paragraphs. For the purpose of convenience, we will use the term 'taxonomic revision' in the broader sense, comprising all four categories mentioned above.

The seven phases of a taxonomic revision:

- A. Taxon names and literature study
- B. Herbarium observations
- C. Data basing
- D. Geographical and ecological observations
- E. Taxonomic and nomenclatural decisions
- F. Preparing taxon treatments, descriptions, illustrations and keys
- G. Producing the manuscript and publishing

A. Taxon names and literature study

All scientific studies start with gathering information and data. For a taxonomic revision, it is necessary to gather all the protologues (original publications) for the names concerned. This is a crucial step, especially in phase E when type specimens need to be identified, selected and assigned. The service provided by IPNI (International Plant Name Index; <http://www.ipni.org>) for vascular plants and Index Fungorum (<http://www.indexfungorum.org>) for fungi can generally provide a list of all names within the relevant genus, although some further filtering will be needed for regional studies. Note that IPNI did *not* collect data on infraspecific taxa until 1971! Some may have been entered now, but in general these can only be found through extensive searching (internet and libraries).

From the protologue information, one can now track down the relevant publications by:

- consulting a good, specialized library;
- using web-based services uncovering old taxonomic literature, such as Botanicus (<http://www.botanicus.org>), or the Biodiversity Heritage Library (<https://www.biodiversitylibrary.org>);
- using other web-based resources that link names to their protologues; one of the best is Tropicos (<http://www.tropicos.org>) from Missouri Botanical Garden, but IPNI (see above) also provides this service for many names. Certain families or groups have active communities that maintain specialist websites (e.g. <http://solanaceaesource.org>, <http://www.palm-web.org> or <http://caryophyllales.org>).

Scan or download the relevant pages and file these in an easily traceable system. Also, be sure to note the full reference (see below)! This will be needed when publishing the study.

Next, gather all relevant books and articles that deal with the systematics of the chosen genus. It is also useful to study relevant papers dealing with phylogenetics, biogeography, ecology, etc., as this will give greater insight into the genus and its relatives, especially the evolutionary importance of some of

the characters. Use available internet search engines as well as portals of specialized libraries using the name of your taxon as keyword, along with others such as 'taxonomy', 'revision', 'systematics' etc. Start with the most recent publications, and study the publications cited in their reference lists. Scroll through their paragraph on the taxonomic and systematic history of the genus when available. Also, consult Floras relevant to the study area.

Studying relevant literature should give you a fairly good idea of the position of the genus within the family, which genera are closely related, and which characters are deemed distinctive and informative for species delimitation. Going through identification keys to see which characters have been used to distinguish the species will probably prove to be extremely worthwhile. Nevertheless, it is always important to develop a personal view on the variation of the group studied.

A fair amount of unknown terminology will be encountered when reading the publications, especially the morphological descriptions. A good glossary, explaining these terms, is crucial in this phase. Various good and extensive botanical glossaries exist, see the text box at the end of the previous chapter:

Do not forget to record the full reference when taking notes from publications! It can be very frustrating and time consuming when one cannot remember where one read something.

Here are examples of references for publication types that you are most likely to encounter:

1. *Article in a journal:*

Soreng R.J., Peterson P.M., Davidse G., Zuloaga F.O., Judziewicz E.J., Filgueiras T.S., Davis J.L., Morrone O. (2015) A worldwide phylogenetic classification of the Poaceae (Gramineae). *Journal of Systematics and Evolution* 53(2): 117--137. <http://dx.doi.org/10.1111/jse.12150>

2. *Book:*

Patil J.V. (2016) *Millet and Sorghum: Biology and Genetic Improvement*. Chichester, John Wiley & Sons Ltd. 504 pp.

3. *Chapter in a book or series:*

Clayton W.D. (1989) Gramineae. XXIV. Paniceae. In: Launert E., Pope G.V. (eds) *Flora Zambesiaca* 10(3): 1--192. London, Flora Zambesiaca Management Committee.

Finally, set up a documentation system or data base, where you indicate for each taxonomic name, where the protologue can be found and what its type specimen is. Other authors may have already indicated which specimen is the type, however this should always be checked. The protologue will generally provide the necessary information concerning the type(s), but certainly not in all cases. Searching for type specimens can be a time-consuming activity! This is particularly true for older literature, as it was not obliged to indicate a type. The majority of major Herbaria have scanned and digitized their type specimens. These images are available at the JSTOR Global Plants portal:

<https://plants.jstor.org>, and generally also through the web-portals of the individual institutes. Note that this facility only shows known type material for the various Herbaria. A fair number of types still have to be identified as such by taxonomists. In the course of a revision, it is common to encounter type specimens that had previously gone unnoticed.

b. Herbarium observations

It should be noted that herbarium specimens are valuable and often irreplaceable scientific objects that are brittle and easily damaged! They must be handled with the utmost care. Always ask the appropriate Herbarium Curator about the specific handling instructions.

Practicalities on how to observe plant morphological characters from herbarium material

Plant morphological observations can be performed with a simple hand lens (10×) or with a binocular usually magnifying up to 20(–50)×. The highly brittle material can be made flexible again simply by putting it in boiling water for a short period. Depending on the toughness of the material, it can take 20 seconds to 3 minutes. Always ask the Curator if you are allowed to break off small parts from the herbarium sheet for this purpose. For very tough material add a drop of dishwashing liquid to the water to soften the tissue. An electric laboratory heater, as shown in figure 20, is reasonably safe to use, but a normal, good quality electric kitchen heater and a small steel pot will do as well. You will need a few needles, forceps and petri dishes to handle the material e.g. for dissection under a binocular microscope. Thus allowing the often hidden inside of flowers to be studied, ovaries cut open, and even leaf or wood anatomical features revealed.

After having studied material taken from a herbarium specimen, all elements, also the dissected ones, must be returned to the specimen. Boiled material should be dried again (use absorbent paper to dry it quickly). All parts are then placed in a small bag, which can be glued or pinned to the herbarium sheet of the specimen.

When material, like pollen or a piece of leaf for DNA extraction, is not returned to the sheet (called destructive sampling), the researcher is supposed to add a label to the specimen stating what was removed, for which purpose, by whom and when. Again, ask permission from the Curator before you do!

For your own observations, it is advisable to set up a table where you note all observations and measurements for each specimen (an Excel

table is fine, see below). It is better not to summarize them for a taxon, as specimens may shift between taxa at this stage of your work.

The preparation of fungal specimens for microscope observation is quite specific and detailed in Eyi et al. (2011).

One will need to develop a strategy on how to obtain or consult the majority of the herbarium specimens available elsewhere. Phase A (taxonomic names and literature) has provided you with a fairly good idea of the distribution of the genus, and where most of the species occur. One might consult colleagues to find out which Herbaria contain the vast majority of the relevant material. One can either visit these institutes or have the material to be on loan to your home institute. Herbaria addresses and contact persons can be found on Index Herbariorum (<http://sweetgum.nybg.org/science/ih>). Note that it may take several months for a loan shipment to arrive. Herbaria will generally not send more than several hundred specimens as a loan, and they may have restrictions related to the countries requesting material. An option will then be to visit the institution where the material is housed.

When starting your study, you will need a fair amount of herbarium specimens, so ask for loans as soon as possible. In some cases (i.e. when one already has a fair knowledge of the group concerned), loans can be requested months before the actual start of the revision. Herbaria that house a lot of your material are best visited physically, but this is often expensive. It will generally be far more efficient to visit them once you already have a good knowledge of the species/taxa within your group. So, a good work plan is essential.

Some herbaria have their collections available on-line (see textbox at the end of this chapter). These services often provide some label data and high-resolution scans of available material. These on-line services are extremely helpful, but experience shows that a fair number of sheets need to be loaned to perform more detailed observations on the actual specimens.

▷ Figure 20.
Example of a simple
laboratory device to boil
water in a small cup.



c. Data basing

For taxonomic revisions that concern several hundred specimens or more, it is worthwhile to place the data relating to the specimens in a data base. This can be a simple table in a spreadsheet (e.g. Excel) or a multiple table relational data base (e.g. Access), but many institutes will have their own data base system. These systems may often have many fields one does not need, so consider which fields you need before starting. A minimal set is provided below:

- Barcode
- Main collector (preferably surname and initials in separate fields)
- Additional collector(s)
- Prefix (some collectors add a code or number before the collection number which refers to a research mission, the collecting year or designates a project by its acronym)
- Collection number
- Suffix (any code given after the collection number; see prefix)
- Collecting date
- Country
- Locality
- Latitude
- Longitude
- Habitat
- Altitude
- Uses
- Vernacular names
- Family
- Genus
- Species
- Author(s)
- Intraspecific level (subspecies, variety, forma)
- Intraspecific name
- Intraspecific author(s)
- Identified by
- Identification date
- Herbarium code
- Type of
- Notes

Often, Herbaria that have their specimens digitized will be willing to send their data in a digital format, which can be uploaded into your own data base after some necessary adjustments.

d. Geographical and ecological observations

A species distribution area can vary from small to large, this is generally related to the species having a narrow or broad ecological tolerance. A species restricted to a defined region is said to be **endemic** to that region. A species

can be endemic to a mountain, national park, province, country, continent, etc. (and all species are endemic to the planet Earth!). So, simply stating that a species is endemic without reference to the region is meaningless.

d.1 Mapping

As indicated in Chapter 2 (the paragraph on speciation), information about the geographical distribution and/or ecological preferences may be helpful in making taxonomic decisions. Investigating the distribution of closely related taxa by plotting their recorded localities on a map is a useful exercise.

To be able to plot specimens on a map, one requires the geographical coordinates (latitude, longitude) of the collecting locality. If this is not present on the label, you will need to obtain the coordinates using web-based services (see textbox at the end of this chapter), topographical maps (often historical ones), or even track down field expedition reports. This process is called **georeferencing**. Most contemporary collectors use a GPS (Global Positioning System) in the field, while others may have obtained the lat./long. information from a topographic map. It can be important to add the *precision* of the data. When a collector indicates "15 km West of Nairobi", and knowing that city has a diameter of some 10 km, one may wonder if one should count from the city edge, or from the city centre, and whether one should measure as the crow flies, or along the main road leaving Nairobi in a western direction? Not to mention the fact that some 50 years ago Nairobi occupied a much smaller surface area than today. A coordinate can be accurate at several meters to several kilometres or more.

Note that there are various coordinate systems! These are related to different 'projections', or ways in which the globe has been transposed onto a map. There are also different ways of recording coordinates. The most commonly used coordinate format used by taxonomists is Degrees, Minutes and Seconds, but in some regions the UTM (Universal Transverse Mercator) coordinate system is preferred. Also note that some may use a normal DMS (Degrees, Minutes, Seconds) format, e.g. 15°12'55"N 30°21'32"E, while others prefer DD (Decimal Degrees), e.g. 1.247°N 25.873°E, or DM (Decimal Minutes), e.g. 11°34.75'N 25°21.30'E. A number of online tools (for example <http://www.synnatschke.de/geo-tools/coordinate-converter:php>) allow to easily convert coordinates from the different systems.

One should always be careful when taking coordinates directly from herbarium labels. These are frequently poorly recorded, with no information regarding the projection system used and with wrong coordinate formats, e.g. minutes and seconds values greater than 60. Also, a common error is the inversion of the direction indicators North/South or East/West. These values can be checked against the collecting locality description.

Google Earth is also a useful tool to find the collecting locality, but older collections may have place names no longer in use. For some regions, a published index of plant collecting localities is available, and some websites provide historical maps (see textbox at the end of this chapter). The libraries of many natural history institutes will often have a good collection of historical maps,

collecting registers (collecting notebooks of the collector) or Gazetteers (a book, usually per country, with all place names, including rivers, mountains, etc., with their lat./long. information). On-line gazetteers, like GeoNames (see textbox at the end of this chapter), are also a good way to search for locations as they often have historic names of places as well as allowing “fuzzy” search options. Furthermore, a collector will often have collected several specimens at the same locality and so the specific locality may already have been georeferenced by someone else. Check web-portals providing such data on-line, notably from an institute where you know duplicates from a particular collector were deposited. Some specimen data bases offer the option to create an **itinerary** for a specific number range of a collector which may assist one in finding the right information.

Plotting your specimen data on a map can be done using Google Earth, but when you want to prepare a high-quality distribution map for publication, you should look for other software (e.g. DivaGis, QGIS or ArcView).

D.2 *Ecological observations*

Herbarium specimens will often contain ecological and altitudinal information on the label. However, these are usually fairly coarse habitat descriptions. This data can, at best, be supportive of a taxonomic decision. A person skilled in Ecological Niche Modelling may be able to calculate the environmental niche envelope of a species based on its distribution, and even establish if it is significantly different from that of another species. Such analyses may provide additional support for a taxonomic decision, but are complex and often require additional skills and expertise.

E. **Taxonomic and nomenclatural decisions**

After having performed all morphological, geographical, ecological and possibly other observations, one can group the herbarium specimens into a number of sufficiently homogeneous sets. Each pile of material represents a taxon that differs from the other piles based on your observations. Now, each pile needs to be assigned to a species, subspecies, variety or form using the criteria described in Chapter 2. The resulting list of taxa is your hypothesis for the correct taxonomic framework of the group studied. When this differs from previously published hypotheses, one can and should discuss these differences.

It is often stated that this way of taxon delimitation applies the morphological species concept (see Chapter 2). However, when we think about what modern taxonomists actually do, we may conclude that they are in fact trying to interpret morphological, geographical and ecological data, in terms of a biological species concept based on non-interbreeding populations. When a ‘pile’ of specimens has several distinct morphological characters, one may assume they have arisen from a distinct genetic basis. This can only remain distinct if there is no interbreeding. The same applies to geographical and ecological information. A taxonomist will generally interpret such data within the light of

potential interbreeding. In conclusion, one might state that herbarium-based plant and fungal taxonomy (but also natural history specimen-based animal taxonomy) attempts to apply a biological species concept through interpretation of morphological and other patterns observed. Incorporating the results of molecular studies to determine whether the various species are reproductively isolated is encouraged when available, but that is beyond the scope of this chapter.

It is quite common to find specimens with intermediate characters between taxa. Such intermediates may indicate the existence of gene flow between the morphological groups. In plants, hybrids are not uncommon and therefore do not necessarily disrupt the proposed taxonomic framework. However, when such intermediates are more frequent, this will cast doubt on the correctness of the taxonomic hypothesis and may lead to a re-evaluation. When interpreting patterns of morphological variation, one should keep in mind that we observe only a small time-slice of a larger evolutionary process.

After one has finalized the taxonomic framework, the next step is to establish the correct scientific name for each pile. This is where nomenclatorial decisions have to be made.

Locate all type specimens of all names, species as well as infraspecific taxa, and verify in which pile they are (even those that may not be physically present!). The type specimens in each pile represent the potential names to be considered for that particular taxon. Following the rules of the ICN, as described in Chapter 3, should then lead to identifying the accepted name and its synonyms. Any pile that has no type specimen is a new taxon that will need to be formally described.

f. Preparing taxon treatments, descriptions, illustrations and keys

In a taxonomic revision, the formal treatment of a taxon starts with the nomenclatural part. Firstly, we have the accepted name, followed by its homotypic synonyms in chronological order starting with the oldest name, the basionym, and the data related to the type specimen. Secondly, the heterotypic synonyms follow, if there are any, with their subsequent homotypic synonyms, in chronological order with their associated type specimen data (see example in the text box).

When creating a new taxon, one must meet all requirements of the ICN in order to validly publish the name (see Chapter 3).

The nomenclatural part is generally followed by the morphological description. Any description of a taxon should be clear, precise and sufficiently detailed. It contains the data on which your taxonomic hypotheses are built. The structure of the description is generally uniform for all taxa dealt with in order to facilitate comparison. This means that any character mentioned in one taxon description should also be present in the others. Also, check that all characters used in the identification key (see below) are incorporated as well.

Example of the nomenclatural part of a taxon treatment:

Urochloa dictyoneura (Fig. & De Not.) Veldkamp (Veldkamp 1996: 418). -- *Panicum dictyoneurum* Fig. & De Not. (Figari & De Notaris 1854: 329). -- *Brachiaria dictyoneura* (Fig. & De Not.) Stapf (Stapf 1919: 512). -- Type: Soudan, Kordofan, Fazogl, Figari s.n. (holo-: FI).

Panicum goliae Chiov. (Chiovenda 1914: 43). -- Type: DRC, Catanga, Kayoyo, 20-XII-1911, Bovone 87 (holo-: FI).

Panicum humidicola Rendle (Rendle 1899: 169). -- *Brachiaria humidicola* (Rendle) Schweick. (Hubbard & al. 1936: 297). -- *Urochloa humidicola* (Rendle) Morrone & Zuloaga (Morrone & Zuloaga 1992: 80). -- *Brachiaria dictyoneura* (Fig. & De Not.) Stapf subsp. *humidicola* (Rendle) Catasús (Catasús Guerra 2001: 16). -- Type: Angola, Monino riv., Welwitsch 2678 (holo-: LISU, iso-: K).

One should avoid vague or relative terminology like “rather densely hairy” or “fairly long”. For 2-dimensional shapes, it is advisable to use the standardized set of terms provided by the Systematics Association Committee for Descriptive Biological Terminology (1962). Descriptions follow a logical format, with the various elements being dealt with in a specific sequence: plant – root/stem – leaves – inflorescence – flower – fruit – seed. Within these elements, the sequence is from bottom to the top and from outside to inside. For any organ, a good sequence for descriptive characters is: number of elements – position – overall shape – overall dimensions – base/top/margins – texture – colour and lustre – surface (smooth, rough) – indumentum and/or appendages. For more detail, see the text box below.

For fungi, a description guideline, similar to the one presented in the text box, has been recently published in French (Eyi et al. 2011), and can be freely downloaded from <http://www.abctaxa.be/volumes/volume-10-les-champignons-comestibles-de-l-afrique-centrale>

In a taxonomic treatment, the description is then followed by several paragraphs dealing with distribution, ecology, vernacular names, uses, dispersal etc. Relevant specimens can be cited here or in a separate table as an Appendix or as Supplementary Material. The specific format of these specimen lists varies between authors and journals (see next paragraph). A distribution map can also be added.

Then, notes may be added providing the arguments for the taxonomic decisions and/or the choices made related to the typification of names, etc.

It is advisable to add botanical illustrations to the revision. These are invaluable in the identification process and assist the user in understanding the diagnostic elements of the taxa. One can make these illustrations oneself, but it is usually better to ask a skilled botanical illustrator. Becoming a skilled

Guide to a well-structured plant description

Plant habit, height, distribution of sexes, exudate, other characters shared between different elements, indumentum; bole and branches: diameter; form and structure, indumentum, bark or surface; twigs and/or nodes: as for bole and branches.

Stipules: presence/absence, position, shape, dimensions, base, apex, indumentum, colour.

Leaves: position, simple or compound; sheath: position, shape, dimensions; stipellae: cf stipules; petiole: shape, length, indumentum; when leaf compound: rachis: length, articulations; petiolules: cf. petioles; leaflets: number; sessile or not, shape, dimensions; leaf blade (simple or compound): shape, dimensions, base, apex, margin, indumentum, texture, colour; upper and lower surface; venation type; primary vein: sunken or elevated; secondary veins: number; tertiary venation.

Inflorescence: position, structure, form and/or dimension; peduncle: dimension, indumentum; axes: position, indumentum; bracts: position, form, dimension, indumentum; number of flowers, bi- or unisexual.

Flower: position, symmetry, odour; when flowers unisexual describe male ones first, then female ones; pedicel: dimension, pubescence; bracteoles: position, shape, dimension, indumentum; flower buds: shape, dimensions; hypanthium: shape, dimensions; perianth: number of distinct whorls; sepals: free or number of calyx lobes, position, shape, dimensions, colour, texture, apex, margin, indumentum; petals/tepals: cf. sepals; disk: nectaries or glands, position, shape, dimension, colour; androecium: type, position; stamens: number, position (insertion); filaments: length, colour, indumentum; anthers: insertion, dehiscence, shape, dimensions, colour; connective: shape, dimension; staminodes: cf. stamens; gynoecium: position, number, pubescence; ovary: number, position, shape, dimension, indumentum, number of locules, placentation; ovule: insertion, number; style: position, number, shape, dimension, colour, pubescence; stigma: position, number, shape, dimension, colour.

Infructescence: cf. inflorescence.

Fruit: type, dehiscence type, shape, dimension, colour; surface, indumentum, number of seeds; peri-, exo- endocarp: structure, dimension, colour.

Seed: shape, dimension, colour; surface; arilloid/testa: structure, dimension, colour; endosperm, cotyledons, embryo, radicle.

Characters provided within a genus or family description do not have to be repeated in a species description.

illustrator does not only require talent, but also a considerable investment in time. One may follow specific courses or study relevant books on the subject. In some countries botanical artists have created associations which one may join (e.g. <https://www.botanicalartandartists.com> for England, <https://www.botanischkunstenaarsnederland.nl> for The Netherlands and the Société Française d'illustration Botanique, <http://www.sfib.fr> for France).

Finally, one will need to prepare an identification key to the taxa studied. The key should be practical and assist the user in the identification process. Preferably use characters that are easily observed. For other suggestions, see Chapter 4.

g. Producing the manuscript and publishing the revision

When the taxonomic part of the study (Genus treatment, Key to the species, Species treatments, maps, illustrations, etc.) is finished, one will need to prepare the manuscript for publication. When the revision is meant to be incorporated in a Flora, the taxonomic part is often all that is needed. When, however, one wants to publish the results as an article in a scientific journal, various other paragraphs will need to be added. While some are general, e.g. Introduction, Materials and Methods, others are typical for a taxonomic revision, e.g. the History of the Genus, providing a historical overview of previous studies and their contributions to the taxonomic framework of the genus.

Important factors to consider when choosing a suitable journal to submit the manuscript to are: Impact Factor, regional impact, whether it provides Open Access or not, and publication fees. For taxonomic revisions it is important to check whether the journal accepts specimen citations (and if so in what format). As taxonomic revisions may be quite lengthy, page limitations may apply.

Finally, it is customary to acknowledge all herbaria (and their curators) who have provided access to their collections or have sent specimens on loan. They generally greatly appreciate receiving a copy of the published revision.

Plant collecting

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Historical literature (most useful to retrieve protologues)

- Biodiversity Heritage Library: <https://www.biodiversitylibrary.org>
- Botanicus: <http://www.botanicus.org>
- Taxonomic Literature: <http://www.sil.si.edu/DigitalCollections/tl-2>
- B-P-H: Botanico-Periodicum-Huntianum (Journal titles and their standard abbreviations): http://fmhibd.library.cmu.edu/fmi/iwp/cgi?-db=BPH_2015&-loadframes

Index Herbariorum

- <http://sweetgum.nybg.org/science/ih>

Plant use information

- Plant Resources of Tropical Africa: <https://www.prota4u.org/database>
- PlantUse: <https://uses.plantnet-project.org/fr/Accueil>

Digital herbaria and specimen information

- Global Biodiversity Information Facility (GBIF): <https://www.gbif.org>
- Meise Botanic Garden, Belgium (BR): <http://www.botanicalcollections.be>
- MNHN Paris herbarium (P): <https://science.mnhn.fr/institution/mnhn/collection/p/item/search>
- Naturalis herbarium, The Netherlands (L, U, WAG, AMS): <https://bioportal.naturalis.nl>
- Tropicos, Missouri Botanical Garden, St. Louis (MO): <http://www.tropicos.org>

Georeferencing

- AFRITERRA (historical maps of Africa): <http://catalog.afriterr.org>
- Cartesius (historical maps of Belgium and Central Africa):
<http://www.cartesius.be/CartesiusPortal>
- GEOLocate (A platform for georeferencing natural history collections data): <https://www.geo-locate.org>
- GeoNames (finding place names, also historical ones):
<https://www.geonames.org>
- Google Earth (free software to view the globe):
<http://www.google.co.uk/earth/download/gep/agree.html>

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Figure 1. Statue of Theophrastus in the botanic garden at Palermo, Italy (photo by tato grasso - Own work (personal work), CC BY-SA 2.5, <https://commons.wikimedia.org/w/index.php?curid=3170845>).

Figure 2. Plinius the Elder (from: <https://www.britannica.com/biography/Pliny-the-Elder/images-videos/media/1/464822/234312>, accessed August 16th, 2019).

Figure 3. Dioscorides (from: De Desconocido - <http://huntbot.andrew.cmu.edu>, Dominio público, <https://commons.wikimedia.org/w/index.php?curid=3607187>).

Figure 10. Charles Darwin (from <http://www.charlesdarwin.net/biography.jsp>; accessed august 16th, 2019).



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