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Taxonomy: a discipline on the brink of extinction

Are DNA barcode scanners the future of biodiversity research?

Robert LÜCKING¹

■ Taxonomy once and now

The word *taxonomy* stems from the Greek *taxis*, order, and *nomos*, science. Taxonomy is the science of bringing order into the overwhelming diversity of life. The units defined by taxonomists, the *taxa*, correspond to species (or infraspecies) and groups of species representing higher taxa (genera, families, orders, classes, phyla, kingdoms, domains). These are arranged in hierarchical order according to their relationships. Taxonomy involves two different thought processes: separating operational units into discrete taxa, and bringing them back together by grouping species into higher taxa. If the main purpose of a taxonomist is to describe new species, one refers to this as alpha-taxonomy. Nomenclature sets rules for the correct and formal naming of taxa, and each major domain of organisms (animals, plants and fungi, bacteria) have their specific book of rules called Code, which is updated regularly and can be accessed online.

Until up to the middle of the 20th century, taxonomy was the dominant discipline in biological sciences, with taxonomists attempting to catalogue the diversity of life around the globe. Until then, particularly in the study of fungi and lichens, taxonomy relied heavily on the compound microscope, a technique that had not changed much for virtually a century. The past sixty years saw an explosion of novel methods that also affected taxonomy and systematics and revolutionized our view of the tree of life (<http://tolweb.org/tree>), from electron microscopy, to secondary and protein chemistry, to DNA sequencing. At the same time, the view of taxonomy and nomenclature changed, from a stand-alone discipline to being considered a service tool to other disciplines such as evolutionists, biogeographers, ecologists, and physiologists, and eventually to be viewed as being old-fashioned, outdated and unscientific. Today, a few years into the third millennium, there is the notion that taxonomy, as a discipline, is on the brink of extinction. This view is a dangerous misconception, as it puts into jeopardy a legacy of knowledge and expertise which, once gone, will be irrefutably lost and leave other disciplines without their most important currency: the names of the organisms they work with.

■ Lichens on leaves: the monograph as culminating work of a taxonomist

The word *monograph* stems from Greek and literally means «single writing». In taxonomy, it refers to an all-inclusive revisionary work of a particular taxon or group of organisms. A monograph can comprise just one species, but usually includes hundreds of species, with keys, descriptions, information on ecology and distribution, and a general introductory section. The goal of any serious taxonomist is to provide a monograph of a particular taxon or group of interest. A monograph serves other disciplines, since colleagues will use it to identify taxa within an ecological, biogeographical, physiological, or applied

context. Often the publication of a monograph stimulates further research in a particular group of organisms.

It takes many years to achieve the expertise and assemble all the necessary data to compile a monograph. From early on, my own interest had focused on lichens growing on living leaves of vascular plants, a fascinating group of organisms mostly confined to tropical rain forests (Fig. 1). Rain forests are not usually known for their lichen diversity, but actually have the highest small-scale species richness of lichens of any ecosystem on the planet (Fig. 2). A single hectare of tropical rain forest can harbour up to 600 species of lichens, half of which are

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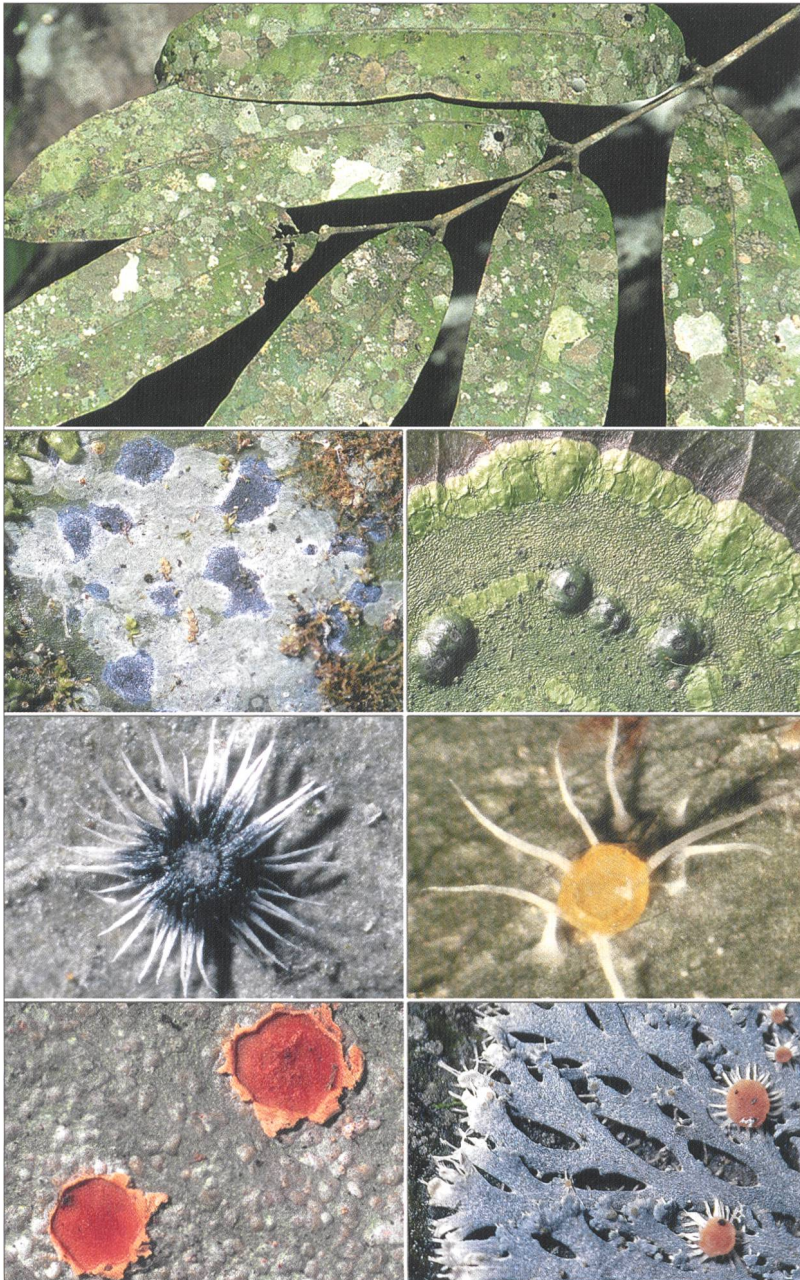


Fig. 1. Foliicolous lichen communities on leaves of a tropical plant and some selected taxa (top to bottom and left to right): *Arthonia cyanea*, *Strigula macrocarpa*, *Trichothelium argenteum*, *Aderkomyces albostrigosus*, *Chroodiscus coccineus*, and *Coccocarpia stellata*.

lichens (Baloch & Grube 2009), and it confirmed species concepts based on our own meticulous analysis of phenotypic features.

Considering its fundamental importance for all areas of biological research, monographic work is rarely appreciated as what it is: first-class science. This is mainly due, especially in North America, to the rating of scientists by the number of publications in high-impact journals. For a scientific career, a two-pager in journals such as *Nature* or *Science* values more than a 500-page monograph. Thereby it is overlooked that high-impact journals select manuscripts by broad appeal and popularity. What they measure is *readability*, in addition to *quality*. Who wants to read a 500-page monograph? A monograph is not a novel, but it is an invaluable source of information. A monograph is almost like a dictionary: you rarely read it, but you use it all the time. It is impossible to publish monographic work in journals with strict page limits, and monograph series such as *Bibliotheca Lichenologica* or *Flora Neotropica* do not achieve high impact factors, because of their specialized audience, due to the fact that they are not cited as often as they deserve, or because they are simply not included in citation indices. Colleagues in other disciplines, who publish in high-impact journals, frequently do not bother to look up or cite monographic references when they work with a particular group of organisms.

leaf-dwelling or *foliicolous* lichens. It took twenty years from collecting my first foliicolous lichen to publishing my monograph on foliicolous lichens of the American tropics, or the *Neotropics*, with over 600 species, in the series *Flora Neotropica* (Lücking 2008). During this time I was able to spend much time in the field and perform ecological, biogeographical, and experimental studies with lichens on leaves (Fig. 3), including interactions with invertebrates feeding on them and the importance of the so-called «drip tips» of tropical leaves (Lücking & Bernecker-Lücking 2005). Foliicolous lichens were the first lichens where re-symbiosis from ascospores was documented *in situ* (Sanders 2002). Pioneering work on genotypic diversity of tropical lichen populations was also done with foliicolous

As a consequence, especially in North America, graduate students are discouraged from doing monographic work or if they do, it is at best considered a «side project». Taxonomy is not viewed as «hot» science, and taxonomists are often seen, by the public and by other disciplines, as dry, boring people with long beards or grey hair who spend their time in-between herbarium cabinets and behind the micro-

scope. This image could not be further from the truth. The taxonomist is a misunderstood human being, and seemingly has been ever since its first appearance (Pennell 1948) and this is in part our own fault, because we do not learn how to promote ourselves and our discipline. One would think that the biodiversity crisis and the increased public awareness towards conservation of natural habitats would give us taxonomists the tools to self-promotion almost automatically. How simple and effective it can be to sell taxonomy was recently shown by the North American lichenologist Kerry Knudsen, who described a new lichen species after US president

Obama and inadvertently brought world-wide attention to lichens (Knudsen 2009; <http://www.sciencedaily.com/~releases/2009/04/090415141217.htm>). Shortly after its publication, the name *Caloplaca obamae* already googled an impressive 38900 online entries. Although probably not intended that way, this was a brilliant move and shows a sense of creativity that many taxonomists lack.

Europe is more conservative in its appreciation of taxonomic work, which is exemplified by the *Augustin-Pyramus de Candolle Prize* given by the *Société de Physique et d'Histoire Naturelle de Genève* for out-

standing monograph in botany or mycology. It is symptomatic that most monographs published in lichenology in the past twenty-five years have been authored by European (and Australian) researchers. Also amateurs often fill the niche of missing professional taxonomists, especially in North America. Of the five lichen monographs published in the *Flora Neotropica* series, only one was authored by a North American lichenologist. Most of the positions of very prolific and outstanding North American lichenologists, such as Mason Hale Jr. (Parmeliaceae, Thelotremataceae), Irwin Brodo (*Lichens of North America*), Thomas Nash III (*Lichen Flora of the Greater Sonoran Desert Region*), Clifford Wetmore (Teloschistaceae), and Theodore Esslinger (Parmeliaceae, *North American Lichen Checklist*), to name a few, have not been, or are not intended to be, refilled with lichen systematists or taxonomists. As a side effect of North America running out of well-trained professional lichen taxonomists, graduate students, post docs, and scientists that are expected to include a taxonomic research component nowadays often have to be recruited from abroad and overseas. The National Science Foundation (NSF) in the United States actually does have rather strong systematic and taxonomic components in its programs, such as PEET (Partnerships for Enhancing Expertise in Taxonomy), but researchers receiving such grants have difficulties to find suitable candidates among US students. For an NSF grant received to do a systematic re-



Fig. 2. Tropical rain forests (above) harbour the highest small-scale diversity of lichens of all terrestrial ecosystems. Tree bases in the shady understory (middle) and upper trunks (below) form distinctive and colourful communities.

vision of a lichen family, we received a total of six applications for a graduate student fellowship. Only one was from the United States. This is of course a great opportunity for candidates from abroad to obtain first-class scientific training, but it shows how far taxonomy is on the decline especially in North America. It also demonstrates how disparate the situation is in North America and Europe: whereas in North America, public funding is recognizing the importance of taxonomy and biotic inventories, but soon there will be no positions to do such work, in Europe there still are strongholds of taxonomic research, but they struggle more and more to obtain financial support for their research projects.

Hypothesis-driven equals science, descriptive does not?

A major problem of taxonomic work in the context of high-impact science is the ill-defined notion that taxonomy is descriptive and not hypothesis-driven and therefore not even science in the strict sense. Supposedly, a scientific study starts out with a hypothesis, based on observations, designs a methodology to test the hypothesis, describes and discusses the results, and concludes whether the hypothesis is supported by the data or not. As a taxonomist, I am often asked by colleagues or students what my hypothesis is, especially when I do inventory work. My answer is: taxonomy is exclusively hypothesis-driven, although this is not obvious to non-taxonomists. A taxonomist always starts out with observations on morphological details of a specimen and upon those observations makes predictions and forms a hypothesis about the identity of the specimen. We then proceed with testing that hypothesis, by looking at anatomical details or by performing a chemical or molecular analysis. The results will either support or falsify the initial hypothesis. Since each specimen is a separate case, taxonomists are doing more hypothesis testing than any other scientific discipline, by several orders of magnitude. Well-trained and talented taxonomists can predict species identities with a high accuracy, which makes taxonomy a more

exact science than any other biological discipline at the organismic, community, and ecosystem level. Species identifications are the most tested hypotheses across biological sciences. No other biological discipline provides such scrutiny.

There is another erroneous concept often associated with taxonomic work not being scientific: intuition. Taxonomists use their *intuition* to formulate a particular concept, and intuition is falsely equated with «gut feeling», which would render taxonomy a non-objective and arbitrary discipline. There are of course



Fig. 3. A solid taxonomy serves as base for advanced and applied studies, such as an experimental approach using artificial leaves (above), interactions with lichen feeders (middle) and the phenomenon of insects mimicking leaves with lichens growing on them (below; photograph by A. Bernecker).

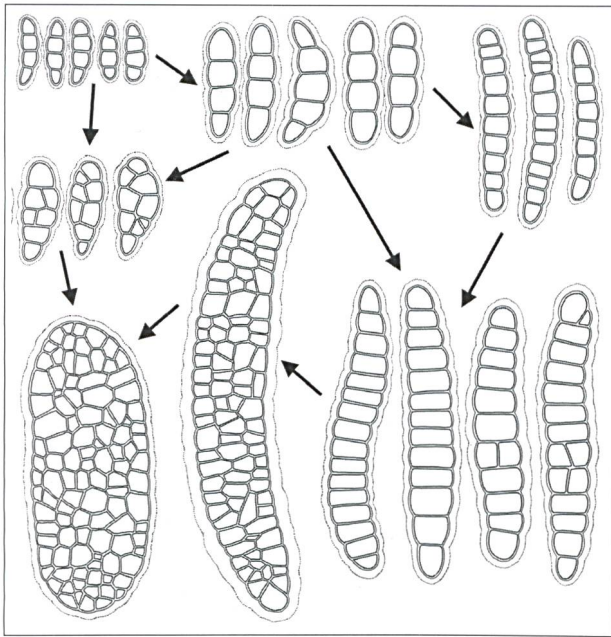


Fig. 4. Variation of ascospore size and septation in the genus *Tapellaria* and possible evolutionary relationships between the different types (after Lücking 2008).

the black sheep among taxonomists who seemingly produce identifications by rolling a dice, but these are the exception. A taxonomist's intuition is not a feeling. It is actually the capability of recognizing patterns, of having a photographic memory, of being able to filter structure from noise in the data, without recurring to computer software. An «intuitive» taxonomist can recognize patterns for which others would have to run a multivariate analysis first. Intuitive taxonomists have made remarkably accurate and often bold predictions about phylogenetic relationships between taxa that only recently have been «detected» by DNA sequencing. The Swedish lichenologist Rolf Santesson was the first to predict that species with different ascospores but otherwise similar characters, so-called sporomorphs, form closely related series. Originally illustrated by the foliicolous lichen genus *Tapellaria* (Fig. 4), this concept remained long ignored by taxonomists and systematists, but has been confirmed by molecular data in the genus *Thelotrema* (Fig. 5). One of the outstanding lichenologists of the 20th century, Aino Henssen, suggested thirty-five years ago that the apothecial lichen genus *Coenogonium* might be related to the perithecial genus *Porina*, because of similar ontogenetic features, whereas others maintained those genera separated in different classes of Ascomycota. Molecular data show that *Coenogoniaceae* and *Porinaceae* are sister lineages. The late Czech lichenologist Antonín Vezda, undoubtedly the most outstanding modern lichen taxonomist, placed the lichen genera *Aulaxina*, *Echinoplaca*, and *Gomphillus*, in the same family, an idea hard to

digest because the genera seem to have little in common except for certain anatomical details (Fig. 6). How important these details are was shown only recently, when Vezda's concept was confirmed by DNA sequencing (Lücking *et al.* 2004a). The 2004 *Augustin-Pyramus de Candolle Prize* winner, Bettina Staiger, in her monograph on the lichen family *Graphidaceae*, redefined the genus *Glyphis* to include species with disparate fruit body morphology, but all with a chocolate-colored cover on the fruit bodies (Staiger 2002). The genus was later confirmed as one of the genetically most distinctive lineages in the family (Staiger *et al.* 2006).

These examples show that a good taxonomist does not only need training but also talent. Techniques and tricks can be learned, but the intuition, the capability of recognizing patterns, the photographic memory, the means of filtering structure from noise,

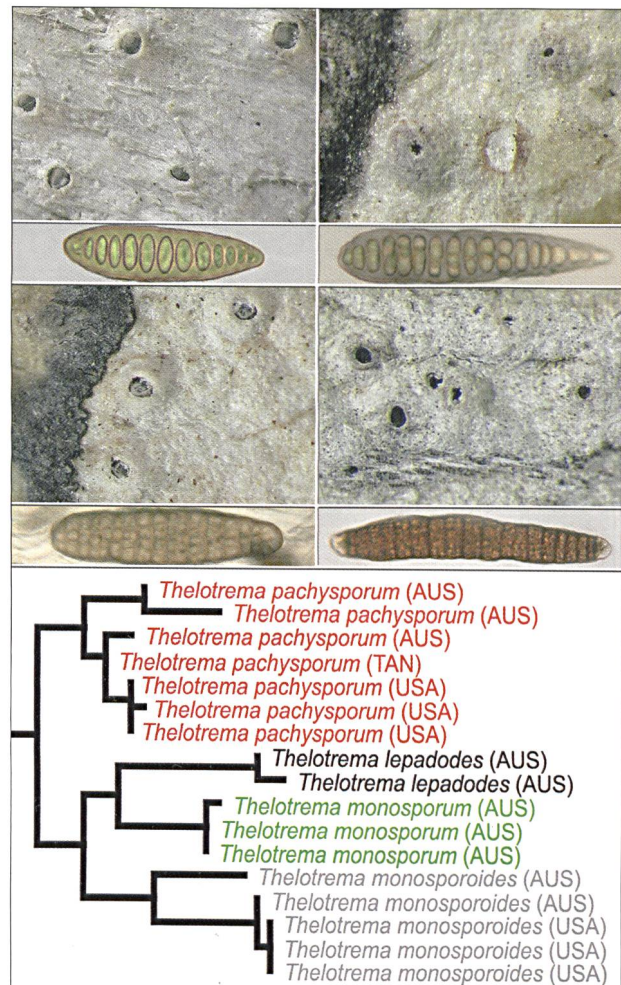


Fig. 5. The concept of sporomorphs shown with the genus *Thelotrema*. The four species depicted differ in the size and septation of their ascospores but are otherwise morphologically identical. The cladogram based on mitochondrial and nuclear genes separates the species well (after Lumbsch *et al.* 2008).

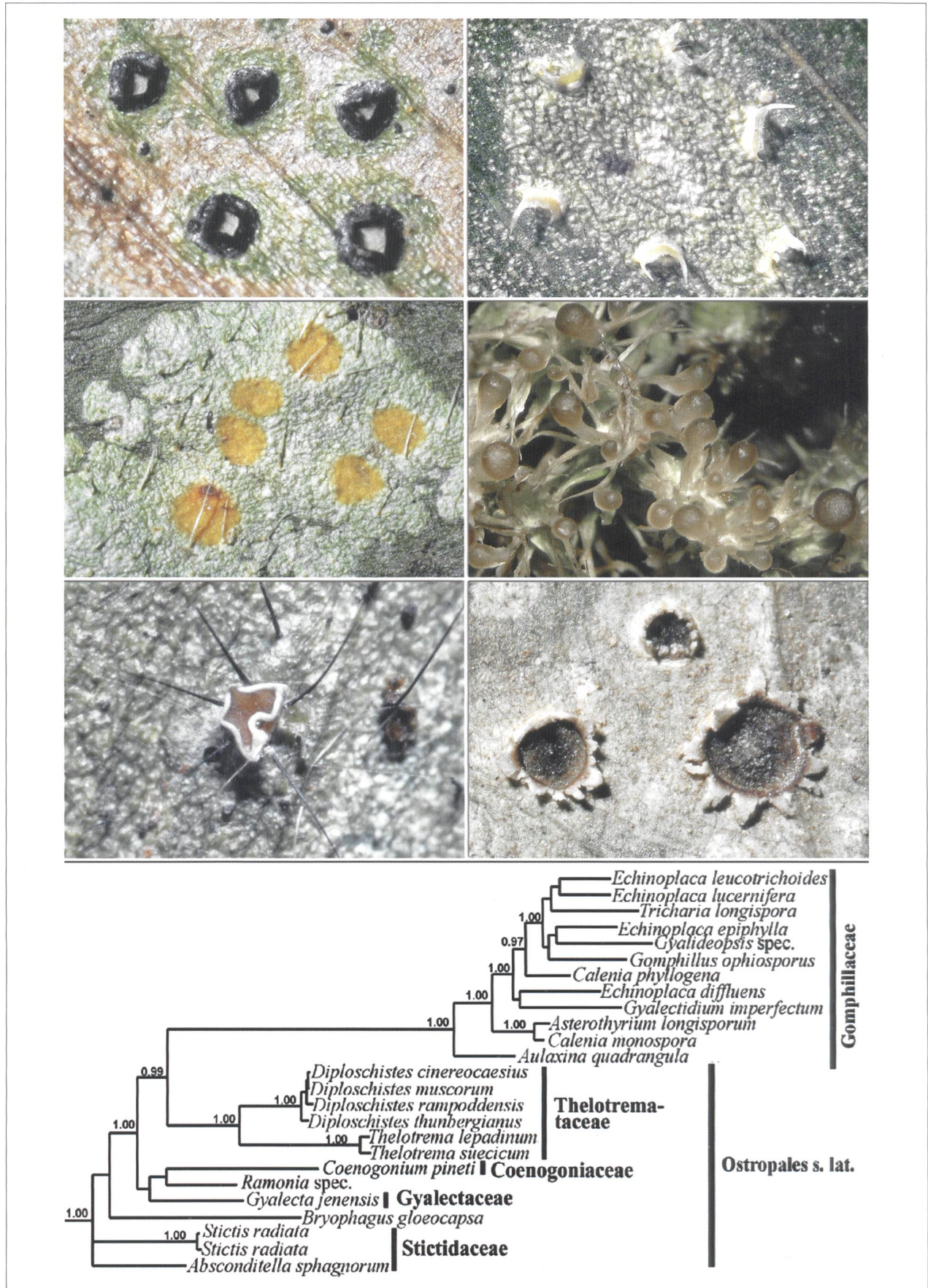


Fig. 6. The lichen family Gomphillaceae is composed of morphologically disparate elements, such as *Aulaxina*, *Gyalectidium*, *Echinoplaca*, *Gomphillus*, *Tricharia*, and *Asterothyrium* (top to bottom and left to right). Molecular phylogenetic analysis confirms that the family is monophyletic and genetically quite unique (from Lücking et al. 2004a).

is something that is pre-wired in the human brain. Discovering and nurturing such talent is of utmost importance. Interestingly enough, the same talent is necessary for the most critical step of molecular phylogenetic analysis: the sequence alignment. In sequence alignment, individual sequences of a gene for different taxa are compared against each other to determine homologous positions, an indispensable prerequisite for correct phylogenetic analysis. Such alignments are nowadays performed automatically by computer applications, such as *Clustal W*, but have to be carefully hand-inspected to detect errors (Fig. 7). Without the talent of visual pattern recognition, a photographic memory, and filtering structure from noise, this is a very difficult task.

Taxonomy and nomenclature in modern research

In the past two decades, and specifically in the past five to ten years, biological sciences have shifted significantly from organismic research towards molecular and applied approaches, with focus on evolutionary mechanisms and medical applications. Integrative disciplines such as systematics, ecology, and biogeography, going strong in the second half of the 20th century, are not considered «hot» science anymore, unless they have a significant molecular component. There is a strong tendency to move from studying entire organisms and communities to looking at molecules and their metabolism, in the hope that these can eventually explain everything. Especially in North America, there appears to be no desire anymore to train new generations of students in a holistic way, including solid taxonomy and nomenclature (Dunn 2003). In typical university committee meetings, it is often not important whether the student has assembled a broad knowledge and field experience of the group of interest, or has spent effort to produce a correct sequence alignment. What

seems to matter is the number of new DNA sequences generated, a task easily performed by a lab technician and for which no graduate student training is necessary. This requires students to spend countless hours, in fact most of their thesis work, in the lab, instead of diversifying their training efforts into all possible directions, including taxonomy.

As a consequence, the typical student, once graduated, may have a profound knowledge of phylogenetic methods, from DNA extraction to producing cladograms and hypothesis testing, but often has not seen the organisms in the field or has no idea of their taxonomy. A colleague was once asked by a recently graduated student to look at a phylogenetic tree in which a particular genus of lichenized fungi appeared to be polyphyletic: the three species sequenced, A, B, and C, fell within three different, unrelated lineages 1, 2, and 3. The colleague knew the genus well and realized that there must have been something wrong with the cladogram and therefore suggested to have a look at the sequenced specimens. As it turned out, only A belonged to the genus in question and came out correctly in the tree, whereas B and C each belonged to completely different genera and actually came out right where they were expected to, in clades 2 and 3. The stu-

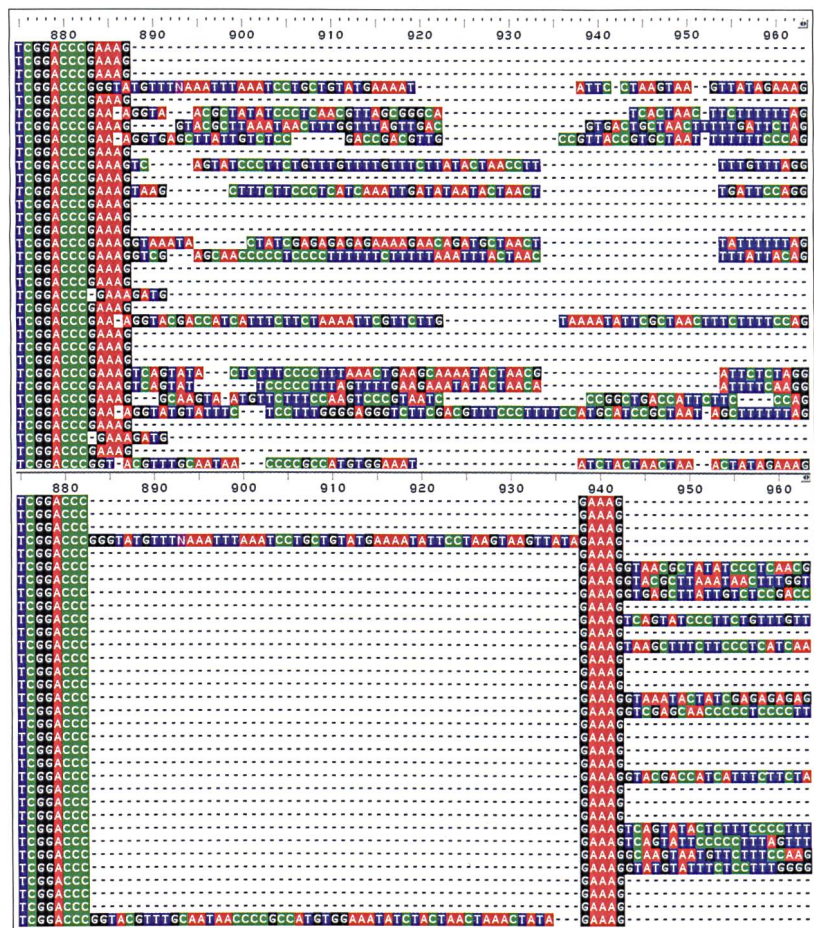


Fig. 7. Automated sequence alignment after applying Clustal W (above) and the same alignment after additional manual inspection and correction (below). Especially in intron-rich regions such as the one shown here, automated alignment programs perform poorly and their manual correction requires the skills and patience of a good taxonomist.

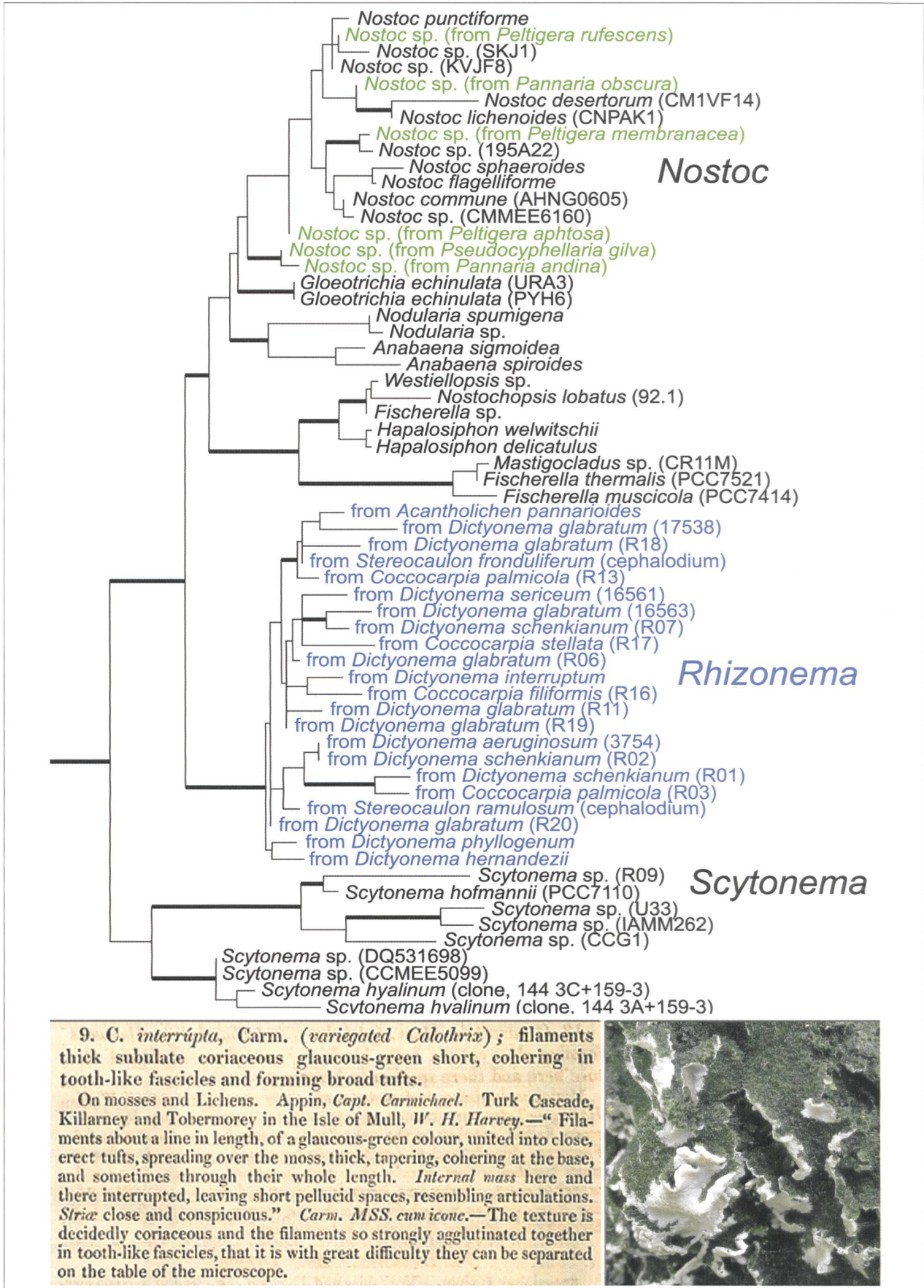


Fig. 8. Molecular phylogeny of cyanobacterial lichen photobionts, showing the novel clade named Rhizonema. Below on the left a portion of the original publication of the type species of Rhizonema, *Calothrix interrupta*, and on the right a species of the basidiolichen *Dictyonema* which contains Rhizonema photobionts (after Lücking et al. 2009).

dent had not bothered to check the specimens sent by other colleagues and might not even have realized that they were erroneous, because the person did not have much of a taxonomic training.

While this is probably an extreme case, it illustrates the general problem, which is also underlined by the fact that a large proportion of sequences deposited at GenBank are wrongly or not at all identified and that individual correction of these other than by the original submitters is not possible at present (Nilsson *et al.* 2006; Pennisi 2008). Phylogeneticists and systematists download such sequences blindly and create trees that often have taxa at odd places. A good taxonomist spots such errors quickly, but in many cases good taxonomists are not at hand or are not consulted. Phylogenetic trees are then interpreted wrongly or valuable sequences are discarded. In one of our ongoing research projects, we downloaded all available sequences (over 300) from GenBank of two different genes of a particular group of lichenized fungi and, after an initial alignment and analysis, went on to check all identifications. We found that about 50% of the sequences were incompletely or wrongly identified at the genus and/or species level. While in many cases, the voucher specimen from which the sequences are derived can be tracked and checked, in other cases this is not possible and the sequences have to be discarded. This means that a large number of sequences deposited at GenBank is worthless unless critically checked by experienced taxonomists, especially when it comes to lower-level phylogenies such as the delimitation of genera and species. If no experienced taxonomist is at hand in such a case, sequences are either interpreted wrongly or discarded all together. Fortunately, collaborative efforts such as the AFTOL initiative have recognized this, and multiple involvement and authorship of large-scale phylogenetic studies (Lutzoni *et al.* 2004; Hibbett *et al.* 2007; Schoch *et al.* 2009) guarantee at least a certain level of taxonomic correctness.

With taxonomy on the decline, most phylogenetic studies nowadays lack a solid taxonomic component and often fail to formalize their conclusions. In a recent study of the basidiolichen genus *Dictyonema*, we sequenced its photobiont, believed to belong in the cyanobacterial genus *Scytonema*. To our surprise, the photobionts of *Dictyonema* and other tropical cyanolichens such as *Coccocarpia* turned out to belong to a previously unrecognized, entirely new lineage of cyanobacteria (Lücking *et al.* 2009). A typical phylogenetic study would have stopped here, presenting the new clade and perhaps giving it an informal clade name. Being familiar with nomenclature, we performed some detailed detective work, looked

up historical literature, and revised the rules of the International Code of Botanical Nomenclature (ICBN 2006). In the course, we made some surprising discoveries and came up with the name *Rhizonema* for this clade (Fig. 8). Lab-trained graduate students would have been unable to do this, because their education suggests taxonomy and nomenclature to be unscientific, boring, and superfluous. Yet, a solid taxonomic and nomenclatural component is what makes a phylogenetic study round and complete. Symptomatically, while our study was accepted for publication in a high-impact journal, reviewers suggested to shorten or eliminate(!) the nomenclatural part (which we successfully refused to do).

This problem finds parallels in disciplines other than molecular phylogeny. In ecological studies, it is common practice to leave taxonomy aside in favor of data analysis. Not rarely is there a publication in which sophisticated analytical methods have been thrown at a dataset in which, if at all, the organisms are identified as Genus spec. A, Genus spec. B, Genus sp. C. This happens even more so in applied studies, especially in developing countries, where students and researchers are forced to invent a use for their organisms before they actually know them well. It is not rare to see a study on the use of lichens as bioindicators of atmospheric pollution, without the species being identified, or identified correctly. While applied studies are important, without a sound taxonomic component the data are practically worthless, unless a non-taxonomic method is specifically applied. The National Institute of Biodiversity in Costa Rica (INBio) is currently conducting extensive biological screening essays using tropical lichens, in collaboration with Harvard Medical School, the University of Michigan in Ann Arbor, the Broad Institute, the Novartis Institutes for Biomedical Research in Cambridge, and The Field Museum (Dalton 2006). Our knowledge accumulated during the Costa Rican lichen biodiversity inventory, TICOLICHEN (Lücking *et al.* 2004b), enabled us to make precise predictions where to collect particular species and which groups might yield results, thus making the screening much more effective compared to a blind search.

■ DNA barcode scanners versus taxonomists: reality or utopia?

Are we able, one day, to simply point a device, a DNA «scanner», towards a tree, an insect, a mushroom, a lichen, and get its correct name displayed on a screen? Honestly, the answer to this question is: yes. It is in the nature of taxa, from the level of species to the level of kingdom, that their DNA has signature sequences unique for the taxon and uniform in all mem-



Fig. 9. Sixty selected species of animals, plants, and fungi that represent a tiny fraction, in fact 0.0002 to 0.0006 percent, of the diversity of life on our planet (all photographs by the author).

bers of it. If that were not the case, molecular phylogeny would not be able to resolve relationships between taxa. It is thus possible to define a signature sequence for each taxon and use this as reference to identify the taxon by means of DNA analysis, without actually having any taxonomic background. This is the idea of the *International Barcode of Life Project Initiative* (iBOL; <http://www.dnabarcoding.org>; <http://www.barcoding.si.edu>), the «barcode» being the signature sequence (BOLD; <http://www.barcodinglife.org>).

Promoters of this idea state that this could quickly, and entirely, replace traditional taxonomy. Not so fast! First of all, there are numerous technical and logistic problems involved which will eventually be resolved, but not as quickly as believed. It will take years to make this technique reliable, and many more years to make it cost-effective, and surely decades to create a hand-held device that could be used in the field like the crew of the Enterprise used a tricoder. The first problem to be solved is the definition of reliable signature sequences for each taxon. The initial hope that this could be a single gene locus for all organisms quickly faded, and now the search is on to find specific signature sequences for different taxa at different levels. Eventually, this will require to comparatively sequence entire genomes across a variety of taxa, an expensive and time-consuming effort. It took 13 years and \$300 million to sequence the human genome of 3.1 billion base pairs (about 10 cents per base pair), and we are just a single species. Although sequencing costs are rapidly declining and sequencing an entire human genome now costs only about \$10 000(!), there are an estimated 10 to 30 million species on Earth, and we would probably need entire genomes from each major lineage to identify the most reliable signature sequences.

The second problem is the cost and time involved in routine sequencing. Including work and materials, to sequence a single specimen presently costs about \$20 on average and takes several days to come up with a result. And this does not take into account that, depending on the group of organisms, sequencing fails to a certain percentage. It does also not consider that, for many organisms, fresh samples are required, which poses logistic and administrative challenges as to collecting the material. Many countries now require very specific permits if collected material is to be sequenced, much more difficult to obtain than «normal» collecting permits. The obvious advantage of molecular screening is that it provides information beyond phenotype taxonomy, such as disentangling species complexes, detecting cryptic diversity, and providing identifications for different life stages of the same species. However, at present, large-scale DNA screening for the purposes of rou-

tine identifications is cost-prohibitive, and it will take significant technological progress to make this approach competitive. A typical ecological community study, such as one involving lichens, deals with thousands of specimens. Sequencing a single gene of a thousand lichen specimens to provide routine identifications would cost \$20 000 including labour and would probably take three months to complete, not counting potential failures. A well-trained taxonomist could do the same work in about a month, with a comparatively small amount of technology, and if well-paid (most taxonomists are not, or even provide their services for free), it would cost somewhere around \$5 000 or less. With respect to futuristic DNA «scanners», it might be impossible to circumvent the step of DNA extraction, especially for plants and fungi. A technique that could scan a specific DNA signature sequence *in situ* in the living organism, without interferences from the organisms metabolism, requires technological advances that are not imaginable at this point.

Even if we assume that all technological problems can eventually be surpassed, there is one major issue that tends to be overlooked: even the best technology is worthless without a complete reference database of correctly named signature sequences for all living organisms. This is an enormous task that can only be accomplished by well-trained taxonomists, and only by a large number of them (Ronquist & Gärdenfors 2003). Just as in diagnostic medicine, names are the currency of biological research, the language scientists speak to each other and to the public, and the language has to be correct. Current estimates count the number of possibly existing species on Earth at between 10 and 30 million (Fig. 9). Generating 30 million signature sequences is doable. In relatively short time, GenBank has amassed over 100 million sequences and a concerted global effort could provide 30 million signature sequences relatively quickly. However, who is going to collect the specimens in a targeted effort? And who is going to attach the correct taxonomic names to these sequences before they are entered into a database? Of the 10 to 30 million estimated species, only about 2 million have been described. This is the result of more than 300 years of taxonomy. Even if we assume that modern taxonomy did not commence before late into the 20th century, and if we equate the 2 million described and catalogued species to 50 years of work, it would take the same amount of taxonomists between 200 and 700 years to describe the remaining 8 to 28 million species! And this does not take into account the notion that molecular research suggests the existence of many more species where previously only one species was recognized, another challenge that requires meticulous taxonomic work.

And this refers only to the formal description and cataloging of new species, a task that is huge but can be streamlined to make it more effective than it currently is. The major problem is the application of the correct nomenclature to species that have already been described, most of them in the 18th and 19th century. This requires the comparison of sequenced specimens to authentic original type material, a task that is time-consuming and can only be performed by well-trained taxonomists with profound knowledge in nomenclature. Since most of the 2 million known species have been described historically, this task applies to a large proportion of names. A significant time of a taxonomist's work deals with this issue. Since there were virtually no «trained» taxonomists until the second half of the 20th century, we are faced with a nomenclatural mess that has to be dealt with every time a taxonomist revises a group of organisms. Unless we completely disregard the work of taxonomists until the middle of the 20th century, and just describe all species as new, which would be indeed much faster, we will need a multitude of taxonomists for many decades to come to complete the task of having correctly identified reference sequences for all living organisms. Sadly enough, this endeavour might be made more simple by the fact that we are destroying our natural environment at an accelerated rate and many of the 8 to 28 million undescribed species will become extinct before we can catalogue and sequence them.

■ Taxonomists: back to where they belong

Taxonomists are currently being treated the way Linnaeus treated lichens in his groundbreaking work *Species Plantarum*: as the *rustici pauperrimi*, the «poor trash». Positions held by taxonomists, across the globe, are either eliminated, once the person retires, or converted into positions focusing on molecular research or microbiology. In North America, practically an entire generation of prominent lichenologists, including Mason Hale Jr. (Smithsonian Institution), William Weber (University of Colorado), Irwin Brodo (Canadian Museum of Nature), Clifford Wetmore (Minnesota State University), Richard Harris (New York Botanical Garden), Thomas Nash III (Arizona State University), Robert Egan (University of Nebraska), and Theodore Esslinger (North Dakota State University), is going to retire or disappear without a next generation following in their footsteps. Taxonomy cannot be learned from books, it requires training by experienced personnel. If the current trend continues, no such personnel will be available within a few years. In Europe, at least some hotspots of lichen taxonomy remain across the continent. Still, public institutions that once con-

tributed significantly to biodiversity research, such as the University of Utrecht and the CBS Fungal Biodiversity Centre in the Netherlands, are either eliminating taxonomic positions or closing their herbarium collections. Many other public universities in North America and Europe have been or are doing the same. This leaves private natural history institutions, such as The Field Museum in Chicago and the National Institute of Biodiversity in Costa Rica, with the task of documenting and studying biotic diversity, a task that should be substantially supported by public funds, as it is of public interest.

In developing countries, the situation is even worse, particular with regard to lichen taxonomy. In Latin America, there has never been a taxonomic tradition in the first place, except for extratropical areas such as central and northern Mexico (UNAM), southern Brazil (e.g. the reknown Institute of Botany in São Paulo), Chile, and Argentina. The only exception is Cuba, which however remains isolated from the international scientific community for reasons a scientist can hardly understand. Scientific policies in Latin American countries, if at all in place, do not support taxonomy as valid science worth pursuing a career. The Neotropics are assumed to harbour over 7000 lichen species (Lücking & Rivas Plata 2009), many of them unknown; yet, the number of well-trained and knowledgeable lichen taxonomists in the region is less than a handful. There are many promising talents, but they are caught in a conflicting situation where either their talent is not properly recognized or their future does not hold a paid position with a predominantly taxonomic focus. On top of that, the infrastructure is often not functional, and such simple things as air-conditioned rooms with steel cabinets for scientific collections are often missing. It is a paradox that these countries are proud of their biodiversity and promote and use it in different ways, from ecotourism to pharmaceutical research, but do not support their own taxonomic studies and biotic inventories. The annual gross domestic product (GDP) of Latin America all together is over three trillion dollars. With a population of 570 million and an average family size of three or more children, this amounts to nearly \$10 000 per potentially working adult per year. Academic salaries in Latin America are ridiculously low, often below \$10 000 per year, but at this level, entertaining a sufficient number of well-trained taxonomists would cost an insignificant amount of money. This is money well spent considering the fact that biodiversity is a primary resource which attracts tourism and industries. Compared to all other biological sciences, taxonomy is cheap! The same applies to industrialized countries. The GDP of the United States and Europe together is ten times the amount of all of Latin America, but with a

population of just 800 million, that amounts to over \$60 000 per working adult per year. Yet, the population of professional taxonomists is rapidly reaching non-sustainable levels.

In order to prevent a taxonomy-crisis, and to have a solid taxonomic and nomenclatural framework for cataloging our planet's organismic diversity and specifically for the *International Barcode of Life Project Initiative*, the following strategy will be necessary in the short and mid term (the next five decades):

Both industrial and developing nations will have to provide substantial and sustainable support to biotic inventories, chiefly in providing permanent staff positions at public or private research institutes for scientists primarily dedicated to taxonomy. The number of such positions depends on the estimated biodiversity of the area and the state of knowledge. Strong quality control involving international peer-review should be in place to ensure that such positions are occupied by talented and well-trained personnel. For example, a tropical country the size and diversity of Costa Rica should have at least three vascular plant botanists, one bryologist, three mycologists, and one lichenologist, who are first-class and full-time taxonomists and systematists and, besides their research, provide training to students.

The quality of taxonomic work, and the quality of journals publishing taxonomic work, must be judged by its own merit criteria, not by the criteria set up by high-impact journals or providers of citation indices. Researchers applying for positions with an organismic component (evolution, biodiversity, conservation) should be judged by their overall, holistic approach to science, not only by their ability to generate and analyze DNA sequences or write computer programs. This should include, by all means, a strong taxonomic component.

Concerted efforts by taxonomists of a given group world-wide must be undertaken to streamline biotic inventories and monographic revisions. Instead of individuals doing revisionary work, future monographs should adopt the style of the *Tree of Life* project, such as AFTOL, in which many individuals contribute at different levels to a monographic revision. This will not only dramatically increase effectiveness and value of taxonomic work, but will also have a strong positive feedback in participating developing countries.

Projects such as the *Encyclopedia of Life* (<http://www.eol.org>) must realize that, in addition to receiving large amounts of money for developing computer applications for online data presentation, a

significant portion of the money has to go those who provide the actual data, those who do the basic work to make such initiatives a success. This includes manpower and capacitation for taxonomy and nomenclature, as well as for databasing.

Last but not least, we taxonomists must learn to sell ourselves much better than we have done in the past. There are many creative ways to do so, and it is an error to believe that our discipline and our work is self-explaining. If we are not able to reach a level where we can potentially be considered *National Geographic* material, then we are doing something wrong.

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