

Mycology should be recognized as a field in biology at eye level with other major disciplines – a memorandum

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Abstract Fungi are key players in terrestrial ecosystem functions. They are not only indispensable symbionts of most of the terrestrial plants, but can also interact with almost all organisms and are the major decomposers of organic matter. Indeed, they are involved in most ecosystem services, so much that life on earth would not have evolved without them. Competition among fungi and with other organism groups has driven evolution of offensive and defensive mechanisms, including the production of secondary metabolites, which continue to be widely unexplored. In addition, fungal plant parasites threaten the global agricultural production and are therefore of highest relevance for human health and survival. Given the ecological and economical relevance of fungi, advancement of other biological and physical sciences are impeded because mycology—the science devoted to the study of fungi—is insufficiently recognized as a major field of life science and supported in basic and applied research and economic contexts.

Introduction

The term ‘mycology’ dates back in the 18th century. The nascent years of the discipline devoted to the study of fungi were guided by Christian H. Persoon, Elias M. Fries, and later Anton de Bary. While the historical concept of mycology in a broad and positive sense encompassed all biological facets and processes associated with fungi, including pathogens, genetics, physiology, systematics, ecology, biochemical properties, and uses in medicine and food industries, the term nowadays seems to have gained a rather restricted meaning. Mycology, in the current use, is primarily restricted to the organismal biology of fungi, fungal-like organisms and lichens, and mainly focuses on fungal natural history, evolution, and adaptations of their morphological and anatomical traits. In particular, disciplines like systematics, ecology and biodiversity research have become integrated within mycology. In contrast, other dimensions of fungal biology are considered as being model systems studied within the fields of genetics, microbiology, molecular biology and organic chemistry.

In Germany and some other continental European countries, mycology never achieved full appreciation as its own discipline, but largely remained as a subsector of botany, where in some universities it currently remains. As the rapidly exploding field of plant sciences gave rise to a diversity of relatively ‘autonomous’ subdisciplines, barely a handful of chairs represented mycology at the beginning of this century. Consequently, mycology never was perceived as a major discipline in Central Europe, while in the Anglo-Saxon World, mycology was similarly relegated to a minor status. It has been common practice to teach the ‘lower plants’ or so-called ‘cryptogams’ as part of the botany curriculum, and fungi were lumped in with that part of

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that kingdom until only recently. In parallel, biochemical, genetic and physiological dimensions of the fungal world expanded into the field of microbiology.

The total number of fungal species and fungoid organisms is unknown. However, it is clear that only a minor part has been discovered and described so far. The vastness of diversity of fungal organisms and their outstanding importance for the functioning of ecosystems have been revealed only recently, when PCR-based methods for their detection and characterisation became affordable (the early barrier was price, not all labs could afford PCR machines and reagents, and sequencing was done by hand on shared machines). Identification of organisms by molecular methods was developed in bacteriology in the late 1980s and early 1990s (Schleifer et al. 1992; Wagner et al. 1994), followed by the mycologists who adapted the methods for their specialized genetics of eukaryotic fungi (White et al. 1990; Haynes et al. 1995). During the next 10 years, as DNA sequencing became easily accessible to most, promotion of a broad-based DNA barcoding initiative was started as a taxon-independent approach for the identification and classification of all groups of organisms (Hebert et al. 2003; Tautz et al. 2003). The assignment of taxonomic names to research specimens and different kinds of organism voucher specimens will remain essential in the future for multiple and obvious reasons. In addition to the taxonomic challenges imposed by the predicted enormous number of undescribed species, the diversity of fungi is associated with a broad spectrum of ecologically important functions and interactions as antagonists and mutualists of plants, animals, and other major organism groups including prokaryotes. Today, mycology has become an important field of both, basic and applied research. Since the discovery of penicillin, fungi became an important source of antibiotics and therapeutic agents, while in turn, the development and boom of biotechnology boosted the field of mycology. Many fungi, not only *Saccharomyces* and *Penicillium*, are very important in biotechnology. However, as already pointed out, the relevance of mycology for the economy and environment starkly contrasts with the status of mycology as an academic discipline and the public awareness of mycological topics.

Fungal functional diversity and relevance for ecosystem services

Fungi on the one hand are often rather inconspicuous, and their cryptic life obscures our awareness of their presence, yet they permeate all Earth's ecosystems. In fact, only unicellular forms, like yeasts and chytrids, should be regarded as 'microorganisms', because some, like *Armillaria* spp., are regarded to be among the largest and oldest organisms on Earth (Smith et al. 1992). They occur in

all soils, decompose plant litter or live as antagonists or mutualists with other organisms. Their spores contribute hugely to airborne organic matter (Fröhlich-Nowoisky et al. 2012) and also can be found in freshwater and marine environments. From an ecosystem point of view, fungi are known to be highly relevant players effecting the major nutrient cycles. In the carbon cycle, fungal catabolic capabilities dominate due to their wide spectrum of exoenzymes, targeting the spectrum of polysaccharides (cellulose, chitin, etc.), and they are the only life form capable of deconstructing lignin (Paul 2007). The evolution of this latter capacity has changed our planet's history. The advent of white-rot fungal lignin-oxidizing enzymes appears to have contributed to the end the carboniferous geological era (Floudas et al. 2012), and thus the world's fossil fuels are finite. At least quantitatively, they might even outperform the respective capacities of members of the two prokaryotic domains, the Bacteria and Archaea. With regard to C-anabolic processes, their role as mutualistic green plant symbionts (mycorrhizae, lichens) is outstanding. Their capability to mobilize nitrogen and phosphorus from soil and water preconditions them as mutualists for the successful growth and fitness of plants. Most of the fungal interactions therefore shape critical ecosystem functions, and some ecosystem services are exclusively fungal-dependent. There is no doubt that terrestrial ecosystems like deciduous forests or grasslands only exist due to the presence of mycorrhizae and fungal decomposers as they are both essential for the nutritive cycle. Even many of the primary consumers feeding on plant material harbour lignin- and cellulose-degrading fungal symbionts in their guts (Suh et al. 2005). Arthropods like certain ant and termite groups feed on fungi, which they cultivate on plant debris (Mueller and Gerardo 2002). Additionally, direct mineralisation of lignin and cellulose is mediated by highly specialised fungi and recent genomic studies revealed a broad arsenal of enzyme gene families coding for hydrolytic functions (Kües and Rühl 2011). Thus, these fungi and their enzymes have a great potential in bioconversion and biodegradation. Ecosystem functions are also provided by lichenized fungi, which represent functionally central organisms in the driest and coldest habitats on earth. For example, lichens contribute to the mechanical shelter of the soil surface, forming protective 'crusts' against erosion in desert areas, while contributing to the soil nutrient cycle in general and N-supply in particular via their associated nitrogen-fixating cyanobacteria (Belnap and Lange 2005). The enormous richness of secondary metabolites (Laatsch 2012) is a further trait making fungi elite determinants of ecosystem processes. Their capabilities for production of bioactive compounds are only matched by certain bacteria, such as Actinomycetales and Myxococcales. Despite the great importance in the ecosystem functionality, disregard or

inability to measure fungal components and their functions inevitably lead to poorly predictive ecosystem models. Outstanding traits concerning nutrient cycle function and secondary metabolism on the one side and the extreme diversity and omnipresence of mycota on the other, elevates fungal functional diversity to the highest relevance for any kind of ecosystem analysis.

Recent progress in optimizing protocols for direct nucleic acid extraction from soil and other substrates (Peršoh et al. 2008) is opening new vistas for an integrative and comprehensive investigation of fungal diversity. Various DNA- or RNA-based approaches are employed for obtaining fungal biodiversity information, to be classified into fingerprinting (AFLP: Mueller and Wolfenbarger 1999; DGGE: van Elsas et al. 2000; ARISA: Weig et al. 2013), hybridization (NG microarrays; Peršoh et al. 2012) and sequencing methods (including NG sequencing; Wubet et al. 2012; Peršoh 2013). The new RNA-based techniques will gain increasing importance, because transcribed exons are molecular markers for ‘active life stages’ and give information about functions and interactions of the respective organisms. [DNA may originate from diaspores (‘dormant life stages’) and does not necessarily indicate growth, metabolisms and reproduction of the detected organismic genotypes.] By finding their way into mycological research, the metagenome and metatranscriptome RNA analysis techniques open up immense options for hypothesis testing.

However, comparative analyses of the composition and function of whole fungal communities in various kinds of dead and living organic substrates remains challenging. From orthologue metagenome and full metagenome analyses, a considerable part of phylogenetic marker sequences in the dimension of hundreds of thousands will for a long time remain unlinked to known morphologically characterized phenotypes. Orthologue metatranscriptome and full metatranscriptome analyses will result in even much higher numbers of transcript sequence data (going into millions per meta-analysis), only rarely linkable to phylogenetic markers and, as a consequence, to known organisms, with an inconceivable massive production of new data.

In summary, fungi, along with prokaryotes, are—as symbionts of other micro- or macroorganisms and major decomposers—central players in ecosystem functioning. Large- and fine-scale screening projects based on data-driven approaches including metagenomic and metatranscriptomic analyses of fungal diversity and functioning will elucidate patterns of occurrence and cooccurrence of these ‘hidden organisms’ and elucidate the distribution of ecosystem relevant functions in all kinds of substrates and micro- and macrohabitats. Indeed, the high functional diversity and the high ecosystem relevance of fungi will fill severe knowledge gaps in biology on the one side, and the discrepancy between the totals of

estimated and described fungal species numbers on the other (only ca. 2–5 % of the species are assumed to be known so far). Altogether, these are strong arguments, that the research field of mycology with all its partial disciplines badly needs appreciation as a full-fledged discipline of life-sciences. Even more, in the field of ecosystem research, mycology will become one of the leading sciences.

Fungal megadiversity, evolution and symbiology

Rossman (2003) predicted ca. 1.5 Mio species of fungi on Earth, Blackwell (2011) even up to 5 Mio taxa. Chapman (2009) estimated fungi to represent more than 13 % of the Earth’s organisms, this percentage being considered as relatively conservative. The estimated number of fungi approaches—or possibly exceeds—that of the insects, which until now have been considered by far the largest animal group. It is commonly agreed that fungal species diversity far surpasses that of plants. Regarding such megadiversity, it is quite clear that fungi play a dominant role in ecosystems as well as in two- and multi-biont interaction systems (Hawksworth 2001; Chapman 2009).

As heterotrophic organisms, fungi interact with almost all known organisms. They interact as mutualists with cyanobacteria and algae in lichens, as mutualists or parasites with vertebrates and most clades of invertebrates (arthropods, nematodes etc.), but they also occur associated with marine sponges and as parasymbionts or parasites of other fungi, as well as associates of various groups of macro- and microalgae. However, besides being true saprotrophs and antagonists or mutualists of animals and humans, most fungi more or less directly depend on autotrophic organisms. Some extreme environments like glaciers, rocks, deserts as well as habitats in the polar regions are inhabited by different forms of lichens, and some of the early forms of terrestrial life are interpreted as lichens (Yuan et al. 2005). The most diverse fungal interactions, however, are realized between fungi and higher plants. They range from truly mutualistic interactions such as mycorrhizae to parasitic interactions of obligate biotrophic parasites. However, many of the intermediate forms like endophytic or rhizosphere fungi are so far only poorly understood. Obviously, fungi or fungal-like organisms are functionally important components in all ecosystems.

A fungal interaction system of highest economic relevance is the mycorrhizae of plants. Most major crops and all forest trees depend on an active mycorrhizal interaction. Recent research revealed a multitude of basic mechanisms in these systems (Kloppholz et al. 2011), providing key knowledge for sustainable agriculture and agroecology in the future (Gianinazzi et al. 2010). The decline and increased fragility of forests since the late 1980s of the last

century boosted scientific interest in mycorrhiza research, but the patterns of fungal diversity distribution and interaction types in soil remained poorly known. Recently, with new methods and approaches like next generation sequencing and new discoveries, such as the root-endophytic species *Piriformospora indica* promoting the growth of plants (Weiß et al. 2011; Oberwinkler et al. 2013), the mycorrhizal fungi regain major attention as a subject of symbiology research.

Plant pathology has long been a sister discipline of mycology. The parasitic interactions between fungi and plants are of prime agro-economic interest because they are the ‘number one’ threat of crop yield. Not only is the importance obvious from the concentration of applied research on fungicides, but it is also illustrated by the support for basic research on virulence mechanisms, pathology and epidemiology at all scales. Plant parasites or plant pathogens are common in all major fungal higher taxa, such as *Armillaria* spp., *Botrytis cinerea*, *Blumeria graminis*, *Fusarium* spp., *Magnaporthe oryzae*, *Mycosphaerella graminicola*, *Phytophthora* spp., and *Puccinia* spp. are responsible for epidemics and may cause yield losses up to 100 % in certain years (Dean et al. 2012). The recognition of the *Puccinia graminis* strain Ug99 as the causal agent of a recent wheat stem rust outbreak, exhibiting strong virulence on previously resistant hosts, again illustrates the importance of research on host specificity, virulence factors and their evolution in fungal populations (Singh et al. 2008).

Although not an economically relevant pathogen in Europe, *Ustilago maydis* is a model organism for studying the genetic basis of interaction, virulence and resistance (Martínez-Espinoza et al. 2002; Kahmann and Kämper 2004) as well as basal genetics of mating (Kellner et al. 2011). Currently, the smut fungi (Ustilaginomycotina and Microbotryales) are the best-studied model group with respect to their phylogenetic structure, host specificity and evolutionary biology (Begerow et al. 2006; Kemler et al. 2012). There is little doubt that investment in this kind of research results in better knowledge about selectivity and mechanisms of host–parasite interactions. This will have considerable impact on the reduction of fungicide application worldwide, leading in the long run to a residue-free, yet sustainable agriculture (Tikhonovich and Provorov 2011).

Many fungi are human pathogens and cause so-called ‘mycoses’, like the symptoms of candidosis, aspergillosis and cryptococcosis. These diseases are highly important in medicine and have resulted in the specialized discipline of medical mycology. With the advent of immune suppression treatment as part of cancer chemotherapy and transplant medicine plus the rise of immune deficiencies as consequences of diseases like HIV-related fungal infections, the situation has escalated as more and more fungal taxa are recognized, having the potential to establish themselves as

opportunistic human pathogens. To meet this challenge, expertise from biodiversity research within mycology is urgently required. Common respiratory allergy symptoms, such as asthma and rhinitis, can be a result of airborne fungi. The main allergens found in the outdoors are pollen grains and fungal spores. Spore concentrations at times may be 100- to 1000-fold that of pollen, depending on environmental factors (Horner et al. 1995). It has been estimated that about 5 % of the general population will suffer at some time an allergy caused by fungi, and about 20–30 % of the patients suffering from respiratory allergy are sensitized to fungal spores (Kurup et al. 2000; Gioulekas et al. 2004; Bush et al. 2006). Finally, fungi might have had an important impact in the evolution of mammals, as a force of selection for homeothermy as mechanism to avoid fungal infections, because most of the fungal species cannot grow at 37 °C (Casadevall 2012).

The aforementioned symbiotic interactions take place under strong competition among different fungi and often under antagonistic relations to plants or animals. This obviously led to two major facts: a) Mutualism and parasitism together with the short generation time span of fungi and fungal organisms resulted in their enormous radiation and diversity. b) Due to their immobile life form, fungi have adapted defensive strategies by producing a great array of antibiotic secondary metabolites. Thus, they frequently outcompete rival associates, or protect their habitats against invading organisms. Examples of such ecological associations mediated by chemical defense are the *Neotyphodium*–ryegrass symbioses (Schardl et al. 2004), where ‘seedborne’, vertically transmitted endophytic fungal species produce toxic alkaloids in sufficient concentrations to efficiently protect the fungus–plant consortium against herbivores.

Summarizing, basic research in symbiology, pathology and evolution of fungi is urgently required as fungi are one of the Earth’s largest groups of organisms and one of the players with major impact on human health and survival. A better understanding of fungal diversity and plant–fungus interactions will offer key understanding for the sustainable use of mankind’s environment. Given the modern techniques of comparative genomics, the information on the genomic potential of fungi is growing rapidly. In addition, more experimental proof and extension of previously gathered patchy data will lead to a real understanding of biotic interaction functioning, which also includes the field of medical mycology. For instance, better knowledge of parasitic interactions on a mechanistic level would enable new target discovery leading to much more specific fungicides. So-called ‘holobiont’ analyses of multipartite organismic aggregates (e.g., Cardoza et al. 2008) will deliver new insights in the world of organisms living in plants and animals (e.g., insects guts) and will lead to the detection of fungal

genotypes which are evolutionarily distant to known species. With all this background in mind, it is difficult to understand why—outside mycology—the relevance of fungi is received with such little enthusiasm. Their role in evolution and symbiology are often neglected in biological textbooks and not reflected well enough in university structures and scientific advisory boards.

Metabolic products and steps towards meta-metabolome analysis

The fungi are at the forefront of eukaryote comparative genomics with hundreds of completed and ongoing genome projects. These studies are constantly yielding substantial evidence for a richness of SM pathways among the major kinds of fungi well beyond that imagined to date, and the number of sequenced genomes will grow exponentially in the near future. Next-generation sequencing and automated gene prediction can preview the biosynthetic menu of a fungus and anticipate the pathways for known and unknown antibiotics. To develop a perspective for the future, a brief review on the state-of-the-art regarding previous accomplishments on secondary metabolite discovery from fungi appears practical.

As judged from queries in commercially available comprehensive natural product databases (e.g., Laatsch 2012, Chapman & Hall's Dictionary of Natural Products¹), about 20,000 biologically active fungal metabolites are estimated to be known to science. However, over 95 % of all fungal genera are not represented at all in these databases, or only a single compound has been reported from them. On the other hand, several dozen new metabolites have occasionally been discovered from a single species. Accordingly, it may be safely assumed that no more than 1 % of all known fungal species have been studied thoroughly with respect to secondary metabolite production and other potentially beneficial properties, and even among these known metabolites, their applications have hardly been tested beyond those that leading to their original discovery. Many fungal metabolites have natural functions as a means of signalling, virulence or defence, the most prominent examples being the antibiotics. The discovery of antibiosis and its therapeutic value is often attributed to Alexander Fleming, who detected penicillin in 1928. However, the first fungal antibiotic identified was mycophenolic acid from another *Penicillium* species, and its antibiotic effect was already discovered by Gosio (1896). Interestingly, based on slight chemical modifications, this 'ancient' antibiotic was recently repurposed into two potent immunomodulatory drugs (mycophenolate mofetil, by

Roche and mycophenolate sodium, by Novartis). The discovery of penicillins and cephalosporins (i.e., the beta-lactam antibiotics), however, has marked the onset of the Golden Era of antibiotics. Annual sales of this class still add up to ca. 15 B \$US, which is equivalent to ca. 65 % of the total market for antibiotics, even over 70 years after their initial discovery (Elander 2003).

Whereas most of the antibiotics discovered in the second half of the 20th century were derived from actinomycetes or other prokaryotes, more recently introduced compound classes, such as the antimycotic lipopeptides (caspofungin, etc.) and the antibacterial pleuromutilins were derived from fungi. Pleuromutilins belong to the most 'innovative' molecules that have made it to the market. They are the first terpene antibiotic drugs from cultures of basidiomycetes, had already been discovered in the 1950s, but the development of semisynthetic derivatives with improved properties that could be approved as drugs took decades. In view of the present 'antibiotic crisis', the prolonged time span between discovery and market launch calls for sustained studies including screening projects for detecting potential alternative fungal antibiotic producers.

Routine screening for drug leads and early stage pharmaceutical development has declined severely in most large pharma companies. Instead, research groups in scientific infrastructure institutions and universities are expected to develop new approaches for discovery and exploitation of novel bioactive compounds. These groups have to be interdisciplinary and should include mycologists. They need to have the chance to expand in size and number, and to incorporate up-to-date methods and capital infrastructure for structure elucidation and for determining the genetic basis of metabolic pathways. In the era of intensive genome and transcriptome research, sophisticated molecular genetic methods need to be applied to elucidate biosynthetic pathways for optimising the production of known bioactive molecules. However, the techniques that were developed for model organisms like *Aspergillus nidulans* often transfer poorly to other fungal groups. The first biosynthetic genes for terpenoids from basidiomycetes have only recently been characterised (Engels et al. 2011). Genome mining and epigenetic techniques are beginning to demonstrate that it is possible to wake silent biosynthetic genes (Bergmann et al. 2010; Smith et al. 2012).

So far, two examples of therapeutically useful agents from endophytes have resulted to date in pharmaceutical development. They were originally isolated from xylariaceous fungi. Both are antiparasitic drugs. Aside from cyclodepsipeptides of the 'PF-1022'/emodepside type (Scherkenbeck et al. 2002), which are already marketed by Bayer, nodulisporic acid from an endophytic tropical *Nodulisporium* species was developed by Merck & Co. (Meinke et al. 2002). This study proved that molecular phylogenetic data and secondary metabolite

¹ Comprehensive database distributed by CRC Press, see <http://dnp.chemnetbase.com/intro/index.jsp>

production in endophytic fungi are strongly interrelated. On this background, it appears feasible to study endophytic fungi at large scale by an hitherto unprecedented combination of genetic barcoding and secondary metabolomics, paired with classical methodology of natural product drug discovery. Employing classical isolation procedures combined with new surface sterilization methods of apparently healthy plant tissues (Unterseher 2011), this approach will likely result in the discovery of new potential producer organisms relevant under 'bioeconomical' aspects. Endophytes have also provided new fields of applied research, such as the application of mycofumigants that are being evaluated in biocontrol, owing to their capability to produce volatile antibiotics, or even biofuel production (Stadler and Schulz 2009).

Endophytes and other fungi showing an interesting ecology, such as the manifold invertebrate-associated and mycophilic clades, can now be studied in their natural environments, using modern highly sensitive analytical methods such as HPLC-DAD/MS (Bitzer et al. 2007), which allow for detection of the bioactive compounds in nanogram amounts. Structure elucidation of new compounds can now be accomplished with 50 µg, with the availability of high field cryo LC-NMR techniques. 'Meta-metabolomics' techniques have already been successfully employed in medicine and medicinal microbiology to detect certain biomarkers that are present in larger amounts. Their adaptation to environmental samples will probably constitute a great challenge, owing to the vast diversity of metabolites encountered in the environment and the lack of reliable standards. Direct detection of secondary metabolites in the environment is still only possible under certain circumstances, and may require selective sample preparation. Still, the progression of secondary metabolite production in fungi can be studied throughout the vegetation period, revealing the genetic networks underlying the development of reproductive structures and resulting in detection of numerous new compounds (Stadler et al. 2006). Moreover, certain quantitative real-time PCR methods are already being used for specific detection of the expression of biosynthetic genes. Measuring gene expression in situ will in all likelihood shed further light on the natural functions of those metabolites that are not overproduced in vitro. Finally, even slow-growing strains, such as those of mycorrhizal basidiomycetes, may be examined for secondary metabolites, if biodiversity exerts joint forces with molecular geneticists and use expression of biosynthetic genes encountered during genome mining in heterologous hosts.

Assessing metabolite expression as an antibiotic-producing fungus switches among growth forms as it explores, captures, or defends its substratum is technically feasible. This can be accomplished either by metabolite extraction followed by direct MS analysis, as mentioned above, or by RT-PCR monitoring transcription of key

secondary metabolite pathway genes, as has been done with the model fungi *Podospora anserina* (Espagne et al. 2008) and *Sordaria macrospora* (Nowrousia et al. 2010). High-throughput mRNA deep sequencing could also map and quantify transcriptomes while overcoming the limitations of hybridization-based approaches because sequencing not only detects transcripts corresponding to known genomic sequences, but also unknown genes from non-model organisms. Thus, the method would be suitable for evaluating fungus-fungus and fungus-bacterium interactions and gene expressions, even when dealing with novel microorganisms.

In summary, the -omics techniques have been substantially refined by both the applied and the basic sectors of mycology, but during the past 20 years, the respective sub-disciplines have been drifting apart. Now is the time to encourage them to rejoin forces by placing high priority respective funding for interdisciplinary research in this field. The mycological communities in Germany and Europe are already preparing for such endeavours in a kind of bottom-up approach. In scientific networks such as the Basidonet² and the COST Action FA1103³, biodiversity researchers have consolidated forces to consider cooperative projects involving both basic and applied mycology. Additionally, members from chemical and engineering sciences and industry have joined these networks.

Current challenges for mycology in Germany

Within the last 20 years, mycology has had to face two paradigm shifts. The first was—like in all other subdisciplines of biodiversity research—a dramatic transition from morphoanatomical and chemical analysis towards the use of DNA markers for reconstructing taxon phylogeny and the evolution of characters in monophyletic groups. During the last 10 years, DNA sequencing developed further towards a high-throughput technology. Recently, mycology—along with bacteriology—has needed to face a second paradigm shift with the opportunity to apply 'meta-omics' approaches, mainly concerning metagenomics, meta-transcriptomics, and meta-metabolomics. To confront this challenge, mycologists have had to make exceptional efforts establishing suitable protocols for quantitative nucleic acid isolation and elaborating or adopting rapidly evolving bioinformatics tools and algorithms to process mass sequence data. For some individuals, their efforts to retool entailed partial renouncement of their research and publishing, based on established traditional methodology. In principal, such a transition is a highly welcome situation for the scientific

² <http://www.basidionet.uni-hannover.de>

³ <http://www.endophytes.eu/>

community, as new approaches and methods trigger innovative science.

During the past 5 years, a small number of mycological research groups in Germany played a key role in laying the groundwork for a sufficiently high technological level to fill out the concept of ‘meta-omics’ with real content, i.e., research activities and useable data output. Various methodological approaches within meta-omics, being tailored to each other, allow the gathering of information layers at different scales. The option to ‘see’ and ‘understand’ functional diversity of whole microbial or fungal communities now actually exists and has to be of major interest for all biologists and geo-ecologists involved in ecosystem research. The use of established adequate meta-omics methodology on a large-scale will allow the ‘mapping’ of whole landscapes with regard to functional microbial community patterns, including seasonality and spatial shifts and obtain totally new information layers concerning biodiversity and function in a given area. Such data-driven approaches will revolutionise ecosystem research completely. Hopefully, even more mycologists will adopt and apply these new methods in plant pathology, evolutionary biology as well as applied mycology for detecting genes encoding fungal enzymes responsible for the production of secondary compounds. With the availability of their own validated protocols and methods as well as specific research topics, mycology indeed has emancipated itself from the neighbouring disciplines like botany and bacteriology.

Regarding the biological research communities in Germany and other European countries, they seem still remain unprepared to adapt to this situation as corresponding research programs and projects for omics-research in mycology are still lacking. Frequently, mycologists are not even invited to participate in traditional ecosystem research projects with a focus on plants and animals diversity and function. It is a fact, that in Germany, several of the pioneers in establishing molecular tools and developing further meta-omics protocols and prototype analyses in mycology, now lack funding. The undervaluation of mycology as an essential discipline is also reflected in the overall lack of university structures, such as explicitly designated chairs or professorships in mycology.

Although the mycological community is small, the number of Ph.D. students is significant, and several promising mycologists with Ph.D. degrees are employed in short-term postdoctoral positions. They have successfully developed and pushed forward (meta)omics methodologies in mycology, and are therefore the most experienced scientists in this field. It is of great priority that the best of them will be enabled to continue their career for having a chance to transfer their know-how to the upcoming student generation. A loss of this expertise in Germany could not be compensated in the future. Unfortunately, the uncertain perspectives in mycology are communicated to the younger students.

Together with the lack of doctoral programs and other financial support for Ph.D. students, this entails a migration of students with master degree in mycology to neighbouring disciplines in ecology or genetics. This efflux of young scientists from mycology needs to be averted to remain competitive in the future. Only projects with a primary focus on fungal functional diversity will bring adequate mycological results needed in ecosystem research and will guarantee the inclusion of fungal (meta)-omics information layers essential for any kind of ecosystem analysis.

There is no doubt that mycology needs a much broader and more influential lobby. It is interesting to see that this lack of influence also is reflected in the role of living collections. Although in general, fungi are much easier to handle compared to plants and animals, there is only one internationally recognized culture collection in Germany, the DSMZ. Nevertheless, mycologists at natural history collections have shown to be highly effective. Although less than ten scientists are employed as curators in fungal bio-systematic reference collections (‘fungal and lichen herbaria’), Germany hosts the only Global Biodiversity Facility (GBIF) participant node explicitly devoted to fungi and lichens worldwide.

Conclusions

Outstanding traits of fungi include their (1) omnipresence, (2) phenotype and genotype hyperdiversity, (3) essential nutrient cycle functions and ecosystem services, (4) mega-rich secondary metabolism, (5) benefits and hazards to human health, (6) threats and benefits to agriculture and alimentation. These traits provide fungi with the highest relevance for mankind's health and survival. Considering the insufficient personnel and financial resources in the field of academic and applied mycology in most European countries, it is high time to consolidate the various and dispersed subdisciplines working with fungi into one discipline at eye level with other major fields in biology like botany, zoology, and microbiology. The major global challenges of the next decades like renewable energy, consequences of climate change, sustainability of agriculture, human health and nutrition or soil erosion will not be solved as long as fungi are neglected as major ecosystem players. Thus, an enhancement and reinforcement of mycology is urgently needed. The time for pushing is highly opportune now, considering the new methodological approaches from which mycology in special and in consequence functional biodiversity and ecosystem research in general can profit. In summary, a number of measures (a) by the mycological science community in particular, (b) by the biological community in general, and (c) by funding organizations are urgently required:

- 1.- Research and teaching: A major issue for mycologists is realising a more effective networking and cross-linking of their subdisciplines (e.g., ecology, phylogeny, physiology, genetics, and metabolomics, nutrition science, infection biology). The challenges of the future can only be mastered by establishing new collaborative projects with combined approaches from various fields/directions. By this method only can synergetic effects emerge. In addition, teaching mycology at all educational levels is a very important mission, which should include courses for undergraduate and graduate students, and also citizen scientists and the general public as well.
- 2.- Staffing and capacity building: Mycology, however, also needs support from its neighbouring disciplines in life sciences. Faculty members should be convinced that strong efforts are necessary, and that professorships and equivalent positions working with fungi should obtain the formal designation 'mycology'. Although labels seem trivial, it is the only way to change the perception of the relevance of mycology as an important biological discipline.
- 3.- Funding: Major changes are also needed at the level of research institutes and funding agencies. The lists of funding criteria and disciplines need to be adapted so that decisions on mycological concerns and reviews of grant proposals from mycology are deputized primarily by referees from mycology.

We therefore appeal to colleagues from inside and outside of mycology to exert their influence to launch the emancipation of mycology.

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