



Leopoldina
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Challenges and Opportunities of Integrative Taxonomy for Research and Society

Taxonomic Research in the Era of *OMICS* Technologies

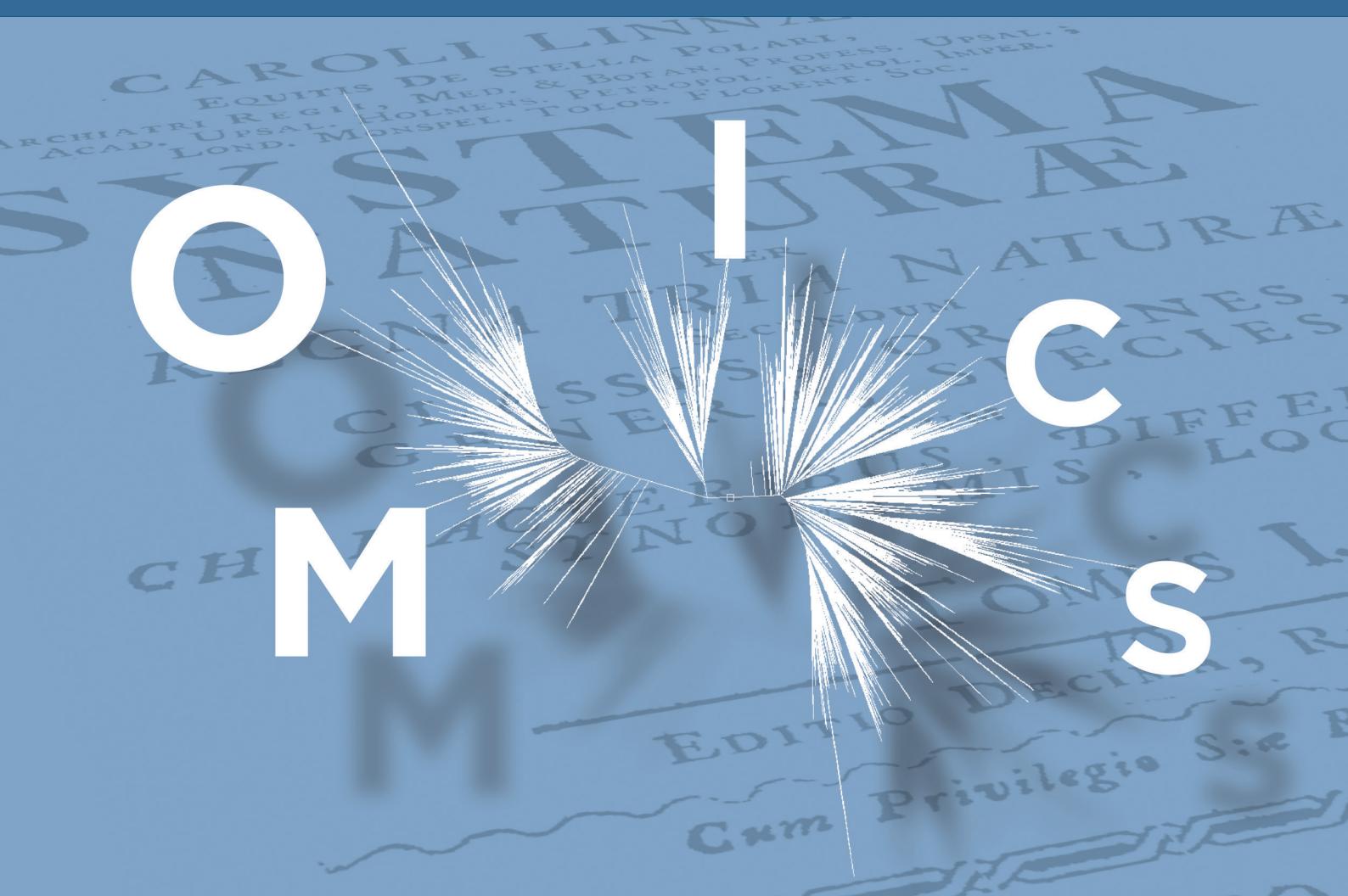
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OMICS Technologies are high-throughput methods used for the complete acquisition of molecular biological information. Such high-throughput methods generate huge amounts of data in a very short time. These data are stored in databases and can be analysed with bioinformatics tools. The term *OMICS* is derived from the common suffix of the individual technology-driven research areas: acquisition of the complete genetic information of an organism is known as gen*OMICS*, acquisition of the complete set of RNA molecules is known as transcript*OMICS* and that of the proteins present in the cells is known as prote*OMICS*.

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Challenges and Opportunities of Integrative Taxonomy for Research and Society

Taxonomic Research in the Era of *OMICS* Technologies

Foreword

Describing and classifying the multitude of species around us represents the beginning of scientific research on organisms. In his manuscript *Systema Naturae* published in 1735, Carl von Linné's ideas for a new method of organising nature unleashed a revolution that shaped biology for a long time. Almost 280 years later, taxonomy, which is the science of cataloguing, describing and classifying our world's biological diversity, provides important basic principles for nearly all research areas in the life sciences.

Present-day taxonomy is currently experiencing profound changes; it uses modern high-throughput analyses to obtain molecular information, thus widening to an unprecedented degree our understanding of previously hidden, complex relationships within our environment. More than ever before, a modern taxonomic science is emerging that has an integrative character. However, these changes present immense challenges that both science and society will have to face to fully exploit the available potential of modern taxonomic research.

In this statement, the Leopoldina presents an overview of taxonomic research in Germany and proposes how it can maintain and improve its position on the international stage. These recommendations are intended not only for politicians and research sponsors, they also provide ideas on how the scientific community itself can appropriately strengthen integrative taxonomy and provide sustainable development in the future.

June 2014

A handwritten signature in blue ink, appearing to read "Jörg Hacker".

Prof. Dr. Jörg Hacker
President
German National Academy of Sciences Leopoldina

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Summary

Taxonomy, the science of identifying, describing and classifying living organisms, is currently experiencing a technological revolution. The rapid development of molecular biological high-throughput methods, so-called *OMICS* methods, for sequencing and analysing genetic information, proteins and metabolic products, opens completely new dimensions for the biosciences. The rapid pace at which these data as well as phenotypic traits of the species can be automatically generated enables taxonomists to come tantalisingly close to their major goal – cataloguing our planet's entire range of biological diversity.

Along with the molecular biological possibilities, the importance of integrative taxonomy is greatly increasing – for basic research and for answering socio-political questions. Approximately 1.8 million species are known today, and our existence is essentially dependent on this biodiversity. Foods, medicines, as well as clean drinking water and fertile soils are created by living organisms. At the same time, species are disappearing irretrievably every day. How many this involves and the potential we are losing due to this extinction is almost impossible to quantify. This is an important task for taxonomy.

German university institutes that engage in taxonomic research, and particularly major museums of natural history and state collections, are already important centres of international research. They store millions of objects, some of which were collected over 300 years ago. These are a natural resource of inestimable value. Such collections of known global biodiversity belong to the most ex-

tensive in the world and contain essential information that can be used to answer current scientific issues arising in various disciplines. These collections serve as a reference point for the question of how species diversity has altered due to phenomena such as climate change, and are a treasure chest for new active substances.

Not only research questions, but also international political protection commitments require access to taxonomic data. These commitments include the Convention on Biological Diversity (CBD), the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and the German National Biodiversity Strategy (NBS). Developing and monitoring models of our ecosystems is only possible if we have the necessary knowledge of species and are able to properly utilise taxonomic methods and compare our findings with the past. For this purpose, the collections have committed themselves to the mammoth task of converting their objects into digital form using the most advanced techniques, such as 3D scanners, and making them available to researchers around the globe in open online databases. Knowledge of classical methods of describing and classifying is just as important as the application of modern *OMICS* methods.

Our taxonomy is thus in a good position to become an internationally recognised leader in the current transition phase. However, increasing cutbacks in taxonomic education and research at universities in recent decades is not commensurate with such a goal. Particularly during the current phase of technological

development that taxonomy is undergoing due to *OMICS* methods, existing institutions and organisational forms must adapt to the new requirements. Improved networking of university and non-univer-

sity research and teaching, as well as specific training and application of *OMICS* methods is essential if German research institutions are to play a key role in cataloguing global species diversity.

Recommendations

Improved integration of taxonomic expertise in science and society:

In recent decades, taxonomic research in Germany has increasingly shifted from the universities to the major natural history museums and state collections, which has had negative consequences, particularly in education. The ‘Integrative Taxonomy’ Working Group of the Leopoldina holds that the *OMICS* revolution in the life sciences represents an opportunity to reverse this trend, and that improved integration of taxonomy will strengthen Germany as a science and business location. Such a goal requires a collective effort by universities and non-university research institutions, by research policy-makers and sponsors, as well as society in general. Taxonomy is indispensable for the protection of species and for the sustainable development of our environment.

Reforming taxonomy by prioritisation, networking, strengthening education, establishing a research infrastructure and internationalisation:

National capacity and performance can be improved by the following five actions:

1. Prioritisation at selected locations:

Universities at suitable locations must promote integrative taxonomy in research and education, and also place greater emphasis on cooperation with non-university institutions.

2. Establishing a Competence Network for Integrative Taxonomy:

The taxonomic competences of university and non-university institutions in Germany should be linked together by means of a ‘Competence Network of Integrative Taxonomy’. This network should serve as a direct contact partner for politics and society, identify core research areas in a coordinated manner and take an active role in developing standardisation processes at the national and international levels.

3. Establishing ‘Schools of Taxonomy’:

Internationally-oriented ‘Schools of Taxonomy’ should be established at the priority locations that offer combined master’s and doctoral programmes in integrative taxonomy that include *OMICS* technologies.

4. Establishing internationally-competitive research infrastructures:

At the priority locations (e.g. Berlin, Bonn, Frankfurt, Munich; and Braunschweig for microorganisms), the existing *OMICS* facilities in the research museums and state collections should be expanded and made available to university research at these locations, as well as research collections and universities at other locations.

5. International networking:

An integrative taxonomy using state-of-the-art methods and technology will foster international exchange of taxonomic data within the context of interdisciplinary research topics. Germany should maintain its high level of commitment in the UN Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) and in international projects to catalogue the biodiversity and provision of biodiversity data (GBIF).

Archiving and processing data:

Permanent storage and provision of taxonomic information is a central task. An umbrella structure could support the existing decentralised data infrastructures and combine them virtually, optimise their linkages and interoperability, and also ensure international compatibility.

Open access for taxonomy:

The Competence Network for Integrative Taxonomy should actively contribute to making taxonomic information even more freely available internationally. Existing scientific journals at the priority locations should be converted to the open access standard. The aim is to make current as well as older species descriptions available as cheaply as possible or even free of charge while maintaining high quality standards.

the development of plant and animal species. Here, the GBoL ('German Barcode of Life') project, which is sponsored by the German government, is a starting point. The description process for such an extensive task must be significantly accelerated through automated techniques.

Internal revisions of collections:

The inventories of museum collections represent a data archive of inestimable value for many interdisciplinary research topics. This requires them to be inventoried, catalogued, digitalised and made accessible as fully as possible. German research collections should be put in a position to review their collections according to the standards of integrative taxonomy.

Further development of taxonomy:

The application of sequence-based *OMICS* methods can overcome the historically developed delineations between the taxonomic sub-disciplines for plants, animals, algae, fungi, unicellular organisms and microorganisms. Taxonomy is thus approaching the other sub-disciplines of biology. Formulating *OMICS*-based standards is recommended. The international nomenclature rules governing naming in taxonomy should be increasingly adapted to cross-organism application. They should thus be adequate to the requirements of integrative taxonomy.

Recommended research projects

Description of all species in Central Europe:

Even in Germany, we do not know the full range of biodiversity. The description of all species occurring in Germany should be an objective for the society because this is the only way to completely measure and understand any changes to the environment. This should include algae, fungi, unicellular organisms and microorganisms because these also play a key role in environmental adaptations and in

1 Introduction

The enormous diversity of species on our planet is the fascinating result of millions of years of evolutionary biological processes that have shaped life on Earth. This biodiversity alone is an immense treasure trove. The preservation and sustainable use of this biodiversity is thus not only of extreme scientific, economic and socio-political relevance, it is also our ethical obligation. Prerequisite for this is the taxonomic cataloguing of this treasure.

Taxonomy is the scientific study of biological species and is thus a fundamental sub-discipline of biology. Taxonomists catalogue, describe and classify species, compare their traits in order to name species and categorise these species according to their natural phylogenetic relationships. Such classifications are one of the most important basic principles of the life sciences.

Integrative taxonomy follows a multidisciplinary approach and combines classical methods of taxonomic research with other methods, such as molecular *OMICS* technologies.

Taxonomy is the science of cataloguing, describing and classifying biological species diversity.¹ New methods and approaches from *OMICS* technologies are prompting a quantum leap in the study of species diversity – from biotic communities to the molecular level.

***OMICS* technologies** refer to high-throughput methods for complete acquisition of molecular biological information. Such high-throughput methods generate vast amounts of data in a very short time. These data are stored in databases and can be analysed with bioinformatics tools. The term *OMICS* is derived from the common suffix of the individual technology-driven research areas. Current research is focussing on four major *OMICS* technologies: acquisition of the complete genetic information of an organism is known as gen*OMICS*, acquisition of the complete set of RNA molecules present is known as transcript*OMICS*, and acquisition of the proteins present in the cells is known as prote*OMICS*. Finally, metabol*OMICS* determines the metabolic products in a cell or a tissue or even an organism.

Due to the *OMICS* revolution, taxonomy is in a transition phase that promises both a solution to key biological, medical or farming issues, as well as efficient and precise ecological monitoring, which is necessary to achieve the goals set by the UN Biodiversity Convention (CBD) or the requirements of intergovernmental agreements. It is important for Germany to exploit current opportunities and to achieve an international pioneering role. Furthermore, the *OMICS* technologies are integrative and link further fields of the life sciences by overcoming the limitations of various disciplines using different methods.

¹ Lohrmann V, Vohland K, Ohl M, Häuser C (eds.). 2012. Taxonomische Forschung in Deutschland – Eine Übersichtsstudie. Museum für Naturkunde Berlin, 122 pp. Available at: <http://www.biodiversity.de/images/stories/Downloads/taxo-studie-2012.pdf>, accessed on 01.06.2012.

International obligations – taxonomy in the political sector

By signing the United Nations Convention on Biological Diversity (**CBD**, December 1993), the Federal Republic of Germany committed itself to identifying the components of biodiversity, to monitor changes by means of regular analyses of samples, and to reduce the rate of species loss. These aims are anchored in the ‘*Nationale Strategie zur biologischen Vielfalt*’ (German National Strategy on Biological Diversity). Knowledge of taxonomy is the basis of this.

The **Nagoya Protocol** of the CBD (October 2010) regulates the framework under international law for access to genetic resources and for the fair and equitable sharing of benefits between the countries of origin and their users. Identifying genetic resources requires taxonomic research.

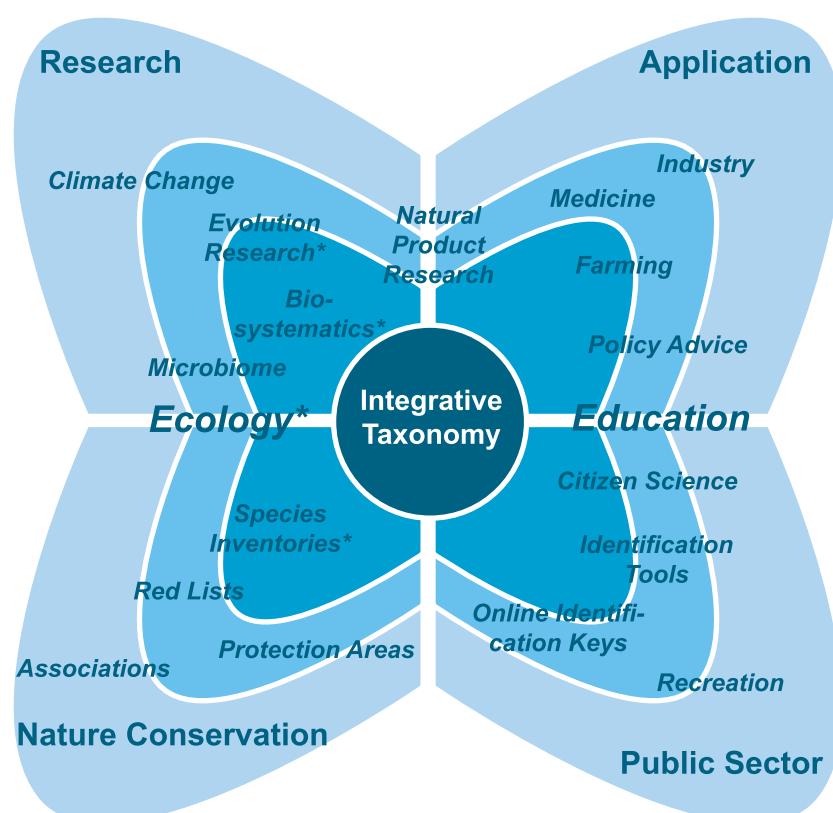
The Intergovernmental Platform on Biodiversity and Ecosystem Services (**IPBES**) is based in Bonn. Similar to the Intergovernmental Panel on Climate Change, the IPBES compiles status reports and issues forecasts on the development of biodiversity. As such, IPBES relies extremely on taxonomic data.

1.1 Taxonomy in research

Only a small fraction of the world’s bacteria, fungi, algae, unicellular organisms, plants and animals have been scientifically discovered and described. Thus, documenting and understanding the extinction of species is currently only possible for this known fraction of the overall biodiversity. In this regard, **OMICS** technologies have made a major contribution to improving the documentability of species, and thus our understanding.

We probably know only a fraction of the world’s pathogens and our knowledge is generally limited to humans and to some crops and livestock. However, if we consider that many epidemiological events may be traced back to still unknown pathogens, the significance of a comprehensive analysis of the microbial diversity becomes obvious. More detailed knowledge of the pathogens as well as their intermediate hosts creates new opportunities for early detection and

Figure 1: Integrative taxonomy is present in many areas of everyday life. This illustration shows the relevance of integrative taxonomy in the context of research, application, nature conservation and society. Disciplines marked with an asterisk represent biodiversity research as a whole. Diagram by Sonja Kreft and Carsten Lüter (Museum für Naturkunde Berlin).



improves our estimation of their risk potentials. Advances in genome sequencing and bioinformatics approaches provide a faster and more accurate taxonomic classification of microorganisms.

In the field of infection medicine, the results of taxonomic research can directly affect the diagnosis and treatment of patients. One example relates to amoeba that cause severe bloody diarrhoea (amoebic dysentery) and life-threatening complications (amoebic liver abscesses), but which in many cases can also colonise without any symptoms. In the 1990s, researchers used molecular biological methods to successfully differentiate *Entamoeba histolytica*, an amoeba species that cannot be differentiated morphologically (i.e. by its physical appearance), into two species. One of these species, *Entamoeba histolytica*, is a human pathogen and is responsible for the aforementioned diseases, whereas the second species, *Entamoeba dispar*, does not cause any illnesses. Based on these results, diagnostic methods have been developed that now enable treatment of only the pathogenic species. Every year, this research result saves many thousands of patients a stressful course of therapy (see also the example of *Aspergillus*, p. 15).

Genome analysis is becoming increasingly important in biology and medicine. It provides a new understanding of evolutionary processes, particularly the questions of how species evolve and why they differ. Genes mutate and reproduce themselves over time, which can lead, for example, to new structures such as wings in insects or to adaptations such as antibiotic resistances in bacteria.

With the aid of comparative genome analyses, the history of the association of pathogens with humans can be analysed. Particularly well-known examples of this are *Yersinia pestis*, the pathogen that caused the plague ('Black

Death'),² the carcinogenic gastric bacterium *Helicobacter pylori* or the tuberculosis pathogen *Mycobacterium tuberculosis*.^{3,4,5} Genome analyses also provide very detailed information on outbreaks. One example of this is the widespread outbreak due to enterohaemorrhagic *Escherichia coli* (EHEC) O104:H4, which led to more than 3 500 infections and 54 fatalities in the spring of 2011, mainly in Northern Germany.⁶ In the near future, genome sequencing will very probably become the standard method of fine grained typing of pathogens used in expert opinions or in forensic applications, and will supersede other typing methods.

Expedited by OMICS technologies, new active substances and constituents are discovered almost every day in bacteria, fungi, plants, sponges, sea squirts and other organisms. The natural functions of these active substances are frequently unknown; they may have signalling or defensive functions and originate from adaptations of the individual species to their habitat. The discovery of these new active substances is of great significance, also economically, for pharmacology, medicine, physiology and the ecology. These active substances can only be accessed if the corresponding species has been correctly identified.

² Morelli G, Song Y, Mazzoni CJ, Eppinger M et al. 2010. *Yersinia pestis* genome sequencing identifies patterns of global phylogenetic diversity. *Nature Genet* 42:1140-1143.

³ Alm RA, Ling LSL, Moir DT, King BL et al. 1999. Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen *Helicobacter pylori*. *Nature* 397:176-180.

⁴ Falush D, Wirth T, Linz B, Pritchard JK et al. 2003. Traces of human migrations in *Helicobacter pylori* populations. *Science* 299:1582-1585.

⁵ Roetzer A, Diel R, Kohl TA, Ruckert C et al. 2013. Whole genome sequencing versus traditional genotyping for investigation of a *Mycobacterium tuberculosis* outbreak: a longitudinal molecular epidemiological study. *PLoS Med*. 10:e1001387.

⁶ Mellmann A, Harmsen D, Cummings CA, Zentz EB et al. 2011. Prospective genomic characterization of the German enterohemorrhagic *Escherichia coli* O104:H4 outbreak by rapid next generation sequencing technology. *PLoS ONE*. 6:e22751.

Identifying organisms accelerated by *OMICS* technologies also provides new opportunities to evaluate our environment. The quality of soils in forests and the agricultural landscape, the water quality of lakes and rivers, the state of our coastal seas and the survival probability of threatened species can only be evaluated when the organismal composition contained in environmental samples has been determined so that any changes can be detected. This includes identifying rust fungi and other pests on fruit trees and cereal crops, but also non-native animal and plant species that are currently spreading, promoted by global warming (see the example of *Ambrosia*, p. 14). Of particular relevance for humans are the unknown viruses carried by primates.

We are often confronted with massive changes in the natural species communities, which have direct consequences for our living conditions and are mainly due to human activities. For example, global trading has introduced invasive species that supplant indigenous species and can alter the environment (see e.g. identification of invasive species, p. 16). Documentation and reaction to these changes in our environment are only possible on the basis of taxonomic research. The use of *OMICS* technologies in this case can offer the possibility of analysing the current status of the species composition, of reconstructing former statuses and comparing the two. This enables us to predict future changes so that any necessary actions can be promptly initiated.

Numerous organisms in soils and surface waters particularly bacteria, but also algae, fungi and unicellular organisms – have not yet been successfully cultured in the laboratory. Thus, information on these organisms has been difficult to obtain. By using genomic approaches, it will be possible to catalogue the biotic communities of complete biotopes (metagenomics). The genetic information

of non-culturable organisms can be filtered out of this data, which provides entirely new possibilities for modern taxonomy to characterise organisms with special traits via their genetic information and to compare them with other organisms.

Microbiomes of both animals and plants are largely unknown and thus represent promising new research areas for integrative taxonomy. The term microbiome refers to the total population of microorganisms and their genes that interact with a higher organism, for example in a human intestinal tract, on the skin of an animal, or around the roots of a plant. In humans, there are about ten times as many microbial cells as body cells. We are only just beginning to understand the composition, dynamics and function of this microbiome – the ‘second genome’ of each human, plant or animal. The human microbiome is highly dynamic and is very important for our health and diet.⁷ Detailed taxonomic knowledge of microbiomes enables e.g. early identification of the sources of potential pathogens for humans as well as for livestock or crops. The description and functional analysis of the microbiome in a human intestinal tract is starting to deliver not only a new understanding of a healthy human diet, but also provides insights into the interaction of the individual microbiome with the immune system.

1.2 Taxonomy in the 21st century

Both *OMICS* technology and taxonomy have undergone considerable development and modernisation in recent years. Taxonomic research in particular is becoming increasingly integrative with respect to its methods and approaches. Molecular biological datasets, new imaging methods, networked online databases and various bioinformatics analysis

⁷ see e.g. Smith MI, Yatsunenko T, Manary MJ, Trehan I et al. 2013. Gut microbiomes of Malawian twin pairs discordant for Kwashiorkor. *Science* 339:548–554.

methods are now regarded as being as equally important as classical morphological methods and object collections. The ongoing digitalisation of collection information that can be freely accessed in online databases greatly facilitates automated analyses. Meanwhile, botanical and zoological species descriptions can now be published electronically. Taxonomic research is booming in many newly industrialised countries with large species diversity, thus providing promising opportunities for international cooperation and knowledge transfer.

With respect to the taxonomic development process for urgent applications, it will be necessary to establish modern research infrastructures for morphology⁸ as well as *OMICS* technologies, and to help develop a wide body of methodological expertise. Herein lies immense potential for the profile establishment of the research community in Germany. Networking between universities, non-university institutions and research collections is a basic requisite for fully exploiting the huge potentials for taxonomy in Germany. Using combined master/doctoral programmes, it would be possible to educate a new generation of life scientists who are familiar with taxonomy and its most modern techniques. This would contribute to profile building for the respective universities.

Taxonomic research has always been associated with research collections. In particular, historical objects in research collections offer an enormous opportunity for using *OMICS* methods to understand changes in species composition under shifting ecological conditions. Such collections have the essential task of archiving research objects and its associated data. These collections also help identify previously discovered organisms and obtain or verify new data.

⁸ such as digital electron microscopy, confocal microscopy, computer tomography (μ CT), 3D methods, morphometry and their combinations

This is all the more important because due to international agreements such as the Convention on Biological Diversity (CBD), it has become more difficult to import new collections, particularly from tropical regions. Innovative taxonomic biobanks are used to store a rich trove of specimens (hides, bones, preserved material, deep-frozen tissue, cells, DNAs, RNAs, etc.) that researchers can immediately access and analyse with *OMICS* technologies.^{9,10} In addition to the objects themselves, the corresponding metadata are also becoming more important, so the research collections are acting increasingly as open access information sources. To cover the requirements of all users, professional and defined standards must be developed for these taxonomic biobanks that are similar to those already used for medical biobanks.

Integrative taxonomy is a modern science that is equipped to face important societal challenges. Together with a corresponding strategy for institutional networking and continued methodological development, integrative taxonomy can become a key driver of the biosciences in the 21st century.

⁹ Bi K, Linderöth T, Vanderpool D, Good JM et al. 2013. Unlocking the vault: next-generation museum population genomics. *Mol Ecol* 22:6018–6032. doi:10.1111/mec.12516

¹⁰ Droege G, Barker K, Astrin JJ, Bartels P et al. 2014. The Global Genome Biodiversity Network (GGBN) Data Portal. *Nucl Acids Res* 42 (D1):D607–D612.

How quickly is the highly allergenic common ragweed spreading?



Figure 2: *Ambrosia artemisiifolia* at a building site near Munich.

Photo: Bernhard Dickoré.

The pollen of common ragweed (*Ambrosia artemisiifolia* L.) is highly allergenic. Molecular data has been used to show that this North American species has reached Europe through several independent pathways. Ragweed's current gene pool in Europe is more diverse and mixed than that of the natural North American populations.¹¹ In order to efficiently combat this species, it is necessary to determine how quickly it is spreading and which measures are effective for controlling it. In Southern Germany, the species is being introduced together with sunflower seeds and is thus being spread further.^{12,13} Inspections of seed mixtures marketed within the EU are both difficult and costly, but *Ambrosia* seeds can be efficiently differentiated from the seeds of similar-looking Asteraceae using OMICS methods.

¹¹ Genton BJ, Shykoff JA, Giraud T. 2005. High genetic diversity in French invasive populations of common ragweed, *Ambrosia artemisiifolia*, as a result of multiple sources of introduction. Mol Ecol 14:4275-4285.

¹² Klotz J. 2006. Zur Verbreitung von *Ambrosia artemisiifolia* bei Regensburg. Hoppea 67:471-484.

¹³ Klotz J. 2009. Breitet sich *Ambrosia artemisiifolia* im Raum Regensburg weiter aus? Hoppea 70:97-104.

Filamentous fungi (*Aspergillus*) can be both 'good' and 'bad'

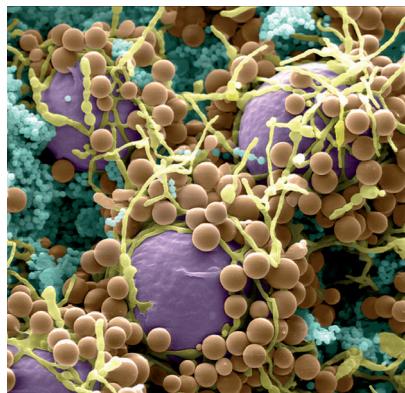
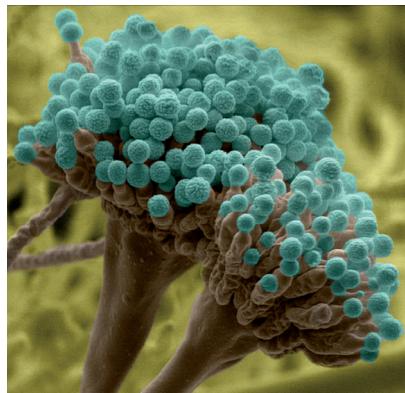


Figure 3 a and b: The filamentous fungus *Aspergillus nidulans* can occur in an asexual form (top) and a sexual form (below). The form with sexual fruiting bodies (purple; diameter approx. 0.5 mm) overwinters and classical taxonomy named it *Emericella nidulans*. Images: O. Bayram and G. Braus, Universität Göttingen.

More than two thirds of all *Aspergillus* species have no known sexual reproduction. However, the remaining third can form sexual fruiting bodies, which has recently led to a reclassification of the genus. Thus, the illustrated *Aspergillus nidulans* (top) is also called *Emericella nidulans* (below) when it forms fruiting bodies. Not even ten years after the first publication of *Aspergillus* genomes (2005),¹⁴ OMICS technologies have revealed numerous new insights into this important fungal genus. However, major similarities in the genomes of *Aspergillus* moulds do not automatically mean similar characteristics. Most pathogenic representatives have harmless relatives. For example, the biotechnologically used and harmless *A. oryzae* is a domesticated form of the toxic species *A. flavus*; their genomes are 99.5% identical.

Aspergillus fungi have also been referred to as the 'Dr. Jekyll and Mr. Hyde genus' of fungi. The name originates from the carriers of asexual spores that are spread by air throughout the globe. These filamentous moulds influence human life in very different ways. For example, *Aspergillus fumigatus* affects patients with a weakened immune system and is thus regarded as the 'most expensive' fungus treated by our Central European healthcare system. *Aspergillus flavus* contaminates numerous agricultural products and forms aflatoxin, an extremely carcinogenic toxin. *Aspergillus sydowii*, on the other hand, is a serious threat to the coral system in the Caribbean. On the 'Dr. Jekyll side', *A. niger* is used to produce citric acid in many soft drinks, while *A. oryzae* is used in Japan to manufacture their national drink sake, which has earned its own postage stamp.

¹⁴ Galagan JE, Calvo SE, Cuomo C, Ma LJ et al. 2005. Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*. *Nature* 438:1105-1115.

Identification of invasive species using *OMICS* technologies

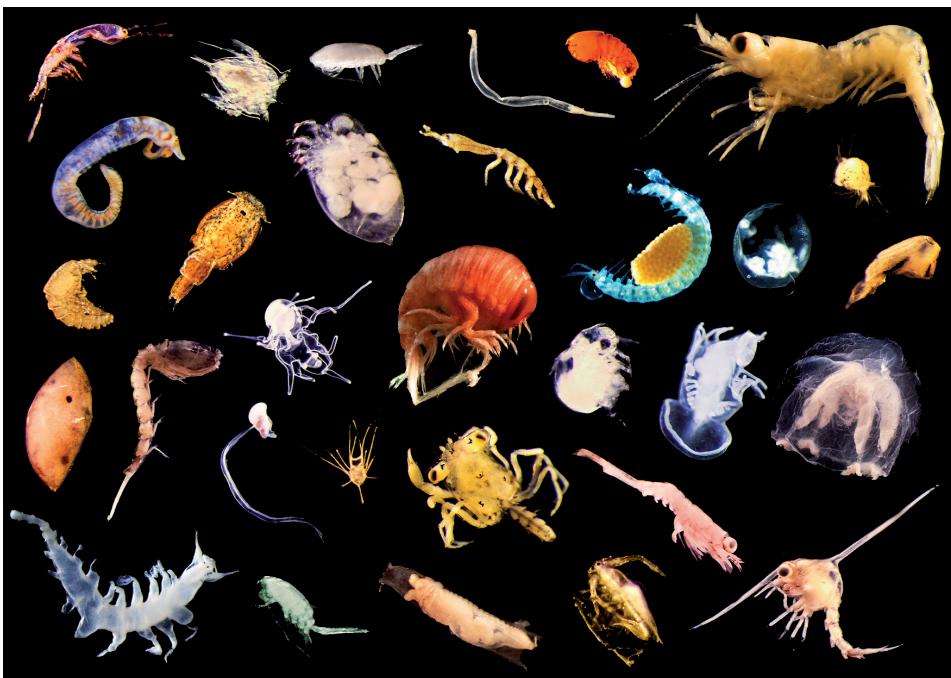


Figure 4: Collage of various zooplankton organisms in the North Sea. Image: Inga Mohrbeck, DZMB/Senckenberg am Meer.

As a consequence of the global movement of goods, more and more organisms are being transported into the North Sea from all over the world, for example larvae swimming in ballast water or attached to the hull of ships.¹⁵ Although most of these alien species (neobiota) perish in their new habitat, some are able to reproduce and establish stable populations. In this context, the foundations of the numerous offshore wind parks represent a hard substrate in the otherwise soft soils in the North Sea and offer a potential new habitat for both native and non-native organisms. Newcomers do not necessarily have negative consequences for the ecosystem, although under certain conditions some of them may supplant indigenous species. Taxonomic expertise is essential for their timely detection and *OMICS* technologies provide new possibilities for rapid and precise monitoring of alien species, particularly for identifying larvae.^{16,17}

¹⁵ Schückel U, Markert A, Neumann H, Kröncke I et al. 2013: Neue Krebse im Vormarsch – Arealverschiebung und Bioinvasionen in der Nordsee. SENCKENBERG – natur – forschung – museum 143 (5/6):152–157.

¹⁶ Thomsen PF, Kielgast J, Iversen LL, Möller PR et al. 2012: Detection of a diverse marine fish fauna using environmental DNA from seawater samples. PLoS ONE 7:e41732.

¹⁷ Thomsen PF, Kielgast J, Iversen LL, Wiuf C et al. 2012: Monitoring endangered freshwater biodiversity using environmental DNA. Mol Ecol 21:2565–2573.

2 Opportunities and challenges for integrative taxonomy

Integrating *OMICS* technologies into taxonomy leads to new opportunities and challenges that necessitate new organisational forms and a clear scientific prioritisation. Specifically, we propose the following four overlapping research topics and then provide recommendations for the necessary organisational forms.

1. Description of all species in Central Europe to protect biodiversity and for basic ecological research

For the first time in the history of taxonomic research it is possible to inventory all groups of organisms using automated high-throughput methods and thus one can determine the status quo as well as changes to the overall level of biodiversity. This represents a quantum leap in diversity research. Studies on the changes of biodiversity in the context of natural and anthropogenic changes would thus receive reliable baseline data that future research could use. This central point of the research agenda should be implemented in close coordination with neighbouring countries, and over the long term also at the European level. An ideal model study would be determining and digitally documenting all species in Central Europe.

2. German taxonomy in the international context: Revisions of collections in close cooperation

With their well-preserved specimens from all parts of the world, scientific collections document the breadth of biodiversity. Modern methods can be applied to existing collections to discover numerous new species. This should be carried out in close scientific coopera-

tion with the corresponding countries of origin and should include a strong university education component.

3. Taxonomy on the timeline: Palaeo*OMICS* and global change

We are currently experiencing both climate change and global biodiversity losses. Urgently needed data are essentially lacking. In the future, automatable high-throughput methods could provide this data for research. Existing collections include organismal specimens that were collected over the last two centuries, and some are even much older. These could be compared to present-day organisms in order to determine changes in the distribution pattern in defined time periods.

4. Taxonomy for the life sciences

With its rapid and precise identification methods, modern integrative taxonomy provides immense opportunities for medicine, biotechnology, farming and nature conservation. The specific requirements of these life science disciplines represent various drivers for the continuous further development of taxonomy. Networked databases with open access are a basic requirement for optimal utilisation of integrative taxonomy in the applied life sciences.

2.1 Description of all species in Central Europe to protect biodiversity and for basic ecological research

Global climate change and the associated extinction of species and changes in the functionality of ecosystems are major

challenges for our society. If such extinction cannot be stopped, it will ultimately reduce the quality of human life. It is thus in our own vital interests to recognise and understand changes in biodiversity. In this case, extensive cataloguing of species (taxonomic census) is an essential requirement because even in Germany we do not know all the species (see the example on new species under our nose, p. 21). This central point of the research agenda should be implemented in close cooperation with neighbouring countries.

In Germany, we know around 70 000 species of animals, plants and higher fungi.¹⁸ If we also consider the lower fungi, algae, unicellular organisms as well as archaea and bacteria, this figure is much higher.¹⁹ The national GBOL project ('German Barcode of Life'²⁰) and the 'Barcode Fauna Bavarica'²¹ initiative are currently determining genetic fingerprints and codifying them into barcodes for the 20 000 most common animal and plant species in Germany. The proposed extension of these projects to all species in Germany, including all algae, fungi and unicellular organisms, as well as the application of an extended spectrum of molecular genetics methods will enable automated and standardised cataloguing of the indigenous flora and fauna for the first time. This will lead to a better understanding of ecological processes and the consequences of human influence.

Such a research programme would for the first time overcome the division of species into uni- and multicellular organisms as well as eukaryotes and prokaryotes

with respect to the cataloguing, description and monitoring of species diversity. This historical and artificial differentiation from the biological perspective is extremely restrictive for the required integrated understanding of aquatic and terrestrial ecosystems.

Considering the diverse patterns of the various organism groups, the methods for completely describing the species in Central Europe must be differentiated. Different marker genes are used for the various organism classes, e.g. mitochondrial 16S rRNA or cytochrome c oxidase sub-unit I (see Section 4.2). When describing a new species, its delineation is validated using additional marker genes and additional morphological, physiological and chemo-taxonomic characteristics.^{22,23} Furthermore, all eukaryotic organisms, i.e. plants, animals, algae, fungi, and unicellular organisms are catalogued using automated imaging methods. The geographic distribution of plants, algae, fungi and animals must also be documented (e.g. in accordance with the directive on the conservation of natural habitats and of wild fauna and flora). Using methods of integrative taxonomy, completely cataloguing all species of prokaryotic and eukaryotic microorganisms has become realistic.²⁴

Once the entire range of organismal diversity has been qualitatively catalogued at selected locations, any changes in biodiversity can be quickly and reliably detected with monitoring programmes. This yields fascinating perspectives, such as understanding how global change

¹⁸ Bundesamt für Naturschutz: Daten zur Natur 2012. Bonn Bad-Godesberg: 358 pp.

¹⁹ Blackwell M. 2011. The Fungi: 1, 2, 3 ... 5.1 million species? *Am J Bot* 98:426–438.

²⁰ GBOL – German Barcode of Life. Deutschlands Fauna und Flora in einer einzigartigen Bibliothek. Wägele W (ed.). Available at: <http://www.bolgermany.de>, accessed on 01.06.2012.

²¹ Barcoding Fauna Bavarica. Erstellung einer genetischen Bibliothek der bayerischen Tierarten. Haszprunar G (ed.). Available at: <http://www.faunabavarica.de>, accessed on 01.03.2013.

²² Richter M, Rossello-Mora R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci USA* 45:19126–19131.

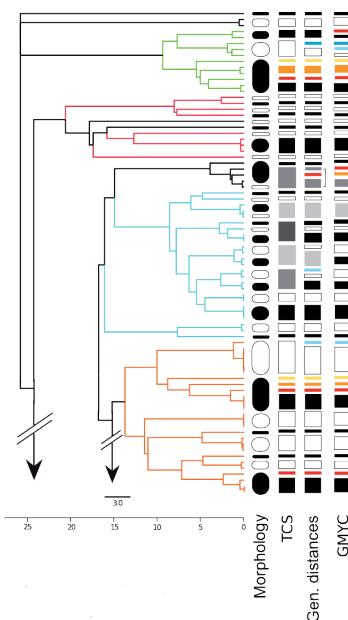
²³ Tindall BJ, Rossello-Mora R, Busse HJ, Ludwig W et al. 2010. Notes on the characterization of prokaryote strains for taxonomic purposes. *Int J Syst Evol Microbiol* 60:249–266.

²⁴ Yarza P, Yilmaz P, Pruesse E, Glöckner FO et al. 2014. Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. *Nat Rev Microbiol* 12:635–645.

influences biodiversity in Central Europe. Status assessments of ecosystems are currently based on a few indicator species and are thus prone to inaccuracies. Completely inventorying the range of biodiversity by means of barcodes enables habitats to be evaluated with respect to the entire organismal community. If it is known which organisms occur in Germany and which organisms produce which genetic signature, these signatures can be detected in different ecosystems using high-throughput methods (metabarcoding) and any changes can be comprehensively identified. Thus, evaluations of habitats that were previously based on individual indicator species can now be placed on a much broader footing (see the example of phylogenetic trees for species identification, p. 20). Alternatively, proteome or metabolome data can be used to precisely characterise species and even identify them in some cases.²⁵ *OMICS* methods can also be used to quickly and efficiently detect changes in the distribution area or in the occurrence of invasive species. This applies, in particular, to invasive species that are difficult to differentiate based on the phenotype.

²⁵ Laakmann S, Gerdts G, Erler R, Knebelsberger T et al. 2013. Comparison of molecular species identification for North Sea calanoid copepods (Crustacea) using proteome fingerprints and DNA sequences. *Mol Ecol Resour* 13:862–876.

Using phylogenetic trees as the basis for species identification



Weevil species from the Cryptorhynchinae sub-family are often difficult to differentiate with the naked eye. They occur, among other areas, in the entire Palaearctic region, including the Canary Islands. The presence of these weevils is often an indication of relatively undisturbed habitats, which makes them an useful tool for nature conservation. Scientists from the Museum Koenig in Bonn have studied the species diversity of this weevil sub-family using classical taxonomic and molecular methods. To achieve a classification that is as biologically relevant as possible, phylogenetic trees based on DNA sequence characteristics were created for these animals. The results showed that, in many cases, animals that cannot be differentiated morphologically do in fact belong to very different and unique genetic lines. Furthermore, forms that are clearly differentiable ecologically do not differ with respect to their molecular sequence characteristics that are used for DNA barcoding.²⁶

Results like these increasingly demonstrate to taxonomists that a biologically relevant species classification is only possible to achieve using an integrative approach based on a variety of methods, for which a phylogenetic tree of the investigated species forms the central starting point. With respect to nature conservation issues, the discovery of cryptic species that are difficult to differentiate is of major importance because only in this way will we be able to reliably describe the species richness and ecological functional structures of many habitats. Many cryptic species differ greatly with respect to their ecological requirements and adaptations. Identifying previously overlooked species thus has major consequences on our understanding of the biological functionality in ecosystems as well as biological, biochemical adaptation phenomena and strategies.

Figure 5 a and b: Weevils of the Cryptorhynchinae sub-family and their assignment to genetic lines, depending on the implemented method. Abbreviations: TCS = Taxon Concept Schema; GMYC = Generalized Mixed Yule Coalescent. Images and phylogenetic tree changed according to 26.

26 Astrin JJ, Stüben PE, Misof B, Waegele JW et al. 2012. Exploring diversity in cryptorhynchine weevils (Coleoptera) using distance-, character- and tree-based species delineation. Mol Phylogen Evol 63:1-14.

New species under our noses – discovering species of diatom algae with the aid of DNA barcoding methods

Diatoms are a species-rich group of unicellular algae that play an important role in oxygen- and primary production in all types of surface waters. It is assumed that diatoms fix 25 % of the globally present CO₂^{27, 28, 29} and contribute up to 20 % to the global net primary production³⁰. Investigation into a single water sample from the Wuhle (D06), a small river in Berlin, revealed a previously unknown diatom species that was first identified by means of molecular biological analyses. This is remarkable inasmuch as the rivers and lakes around Berlin are regarded as the most-studied waters worldwide with respect to diatoms. The new species differs from two already known and very similar diatom species by their different hood-like structures (see Figure 6, right). During the establishment of a taxonomic reference database for the DNA barcoding method, at least 10 % of the identified species from the Berlin surface waters turned out to be new. This clearly demonstrates the knowledge gains that molecular methods produce in taxonomic science.

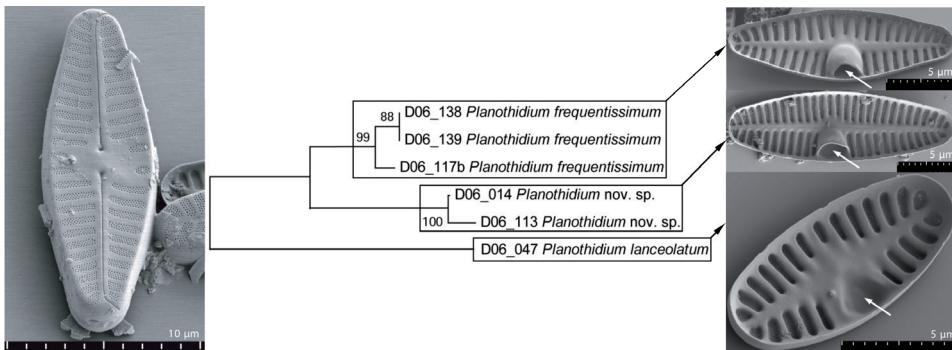


Figure 6: Diatom algae from the Wuhle River in Berlin. Image: Regine Jahn et al., Diatom Research Group, BGBM Freie Universität Berlin.

27 Falkowski PG, Barber RT, Smetacek V. 1998. Biogeochemical controls and feedbacks on ocean primary production. *Science* 281:200-206.

28 Field CB, Behrenfeld MJ, Randerson JT, Falkowski P. 1998. Primary production of the biosphere: Integrating terrestrial and oceanic components. *Science* 281:237-240.

29 Smetacek V. 1999. Diatoms and the ocean carbon cycle. *Protist* 150:25-32.

30 Mann DG. 1999. The species concept in diatoms. *Phycologia* 38:437-495.

2.2 German taxonomy in the international context: Revisions of collections in close cooperation

A considerable fraction of global biodiversity is already preserved in major scientific collections around the world. These collections are indispensable for the discovery and description of the still unknown organismal diversity of the earth because only by comparing with known species can new organisms be identified as ‘new to science’. Collections still contain ‘undetermined material’ in which new species are continuously found. Furthermore, new taxonomic analysis methods are increasingly revealing incorrect classifications that also turn out to be new species. Our centuries-old collections thus represent a treasure trove for the discovery of new species. A critical revision of the major collections could thus make a significant contribution^{31,32} to accelerating global cataloguing of species diversity without having to carry out cost-intensive field work.³³ Such an ‘internal taxonomic revision’ using OMICS methods is one of most urgent tasks facing natural history collections. These revisions can only be carried out properly in cooperation with experts from the (usually tropical) countries of origin. Countries with high species diversity, such as countries in tropical South America, Africa and Southeast Asia, are especially steadily increasing their taxonomic expertise. These experts should be invited to participate in joint research projects based on the traditional collections, and to make the resulting data and findings digitally available for their respective countries’ mutual benefit. The collections in Germany contain many specimens from the 19th and early 20th centuries. The metadata associated with the

objects provide information on the diversity of local ecosystems at the respective period of time. Germany and other countries with traditional natural history collections have a corresponding obligation.

In concrete terms, it is important that the existing body of knowledge relating to biodiversity, taxonomy and systematics is made available internationally in the form of digital, open access publications, linked open databases and training courses, and that they be upgraded to include the new molecular information. This ensures that local data are used in international comparative studies and can thus be made visible. However, this requires open and linked information and education infrastructures. These must be planned by taking account of the equitable distribution of responsibility, accessibility, as well as rights of use. The education courses of these infrastructures can be organised as ‘Schools of Taxonomy’. Furthermore, a central task of these institutions will be the ongoing development of the necessary taxonomic rules to maintain internationally comparable standards, particularly rules to describe new species, and to pass this knowledge on to young taxonomists during their education. At the same time, the basic principles and practices for sustainable collecting must also be passed on to promote establishing and maintaining comparative collections according to international standards. The following tasks thus arise for the major collection infrastructures in Europe and around the globe:

- ‘Internal taxonomic revision’ to accelerate documentation of the global species diversity in already conserved but previously unclassified or incorrectly classified collection units.
- Establishing digital infrastructures (databases, portals, etc.), to promote the exchange of information on biodiversity, taxonomy and collection objects.
- Digital acquisition and making object-based taxonomic data available

³¹ Costello MJ, Coll M, Danovaro R, Halpin P et al. 2010. A census of marine biodiversity knowledge, resources, and future challenges. *PLoS ONE* 5:e12110.

³² Appeltans W, Ahyong ST, Anderson G, Angel MV et al. 2012. The magnitude of global marine species diversity. *Curr Biol* 22:2189–2202.

³³ Bebber DP, Carine MA, Wood JRI, Wortley AH et al. 2010. Herbaria are a major frontier for species discovery. *Proc Natl Acad Sci USA* 107:22169–22171.

internationally to achieve a globally comparable state of knowledge regarding the previously described species diversity that is already preserved in the collections.

- Preparing and defining standards for the description of species.
- Educating young taxonomists and teaching special knowledge associated with the major collections.
- Establishing international networks of taxonomically trained scientists to carry out joint research projects.

(see example on the giant wasp, p. 24). The Indonesian giant wasp is a popular example that illustrates how historical treasures are hidden in the collections of natural history museums. There are large numbers of such ‘undetermined’ objects amongst the invertebrates in particular.

Owing to its scientific tradition and its importance to science in the 19th century – the era of discoveries and founding of the major research museums – Germany plays a key role in dealing with taxonomic tasks. The natural history collections in Germany contain an abundance of materials that, together with the collections in Washington, New York, London, Paris and Vienna, represent the most extensive coverage of the world’s known biodiversity. This means that they, along with their international co-operation partners, play an important role in dealing with cataloguing species around the globe. The most recent efforts of cooperation by the major German natural history museums in Berlin, Bonn and Frankfurt, which are linked together in the Leibniz Biodiversity Network, are indeed pioneering. Further, other museums, the botanical collections and the German Collection of Microorganisms and Cell Cultures (DSMZ) in Braunschweig play just as important a role.

Two key steps in this process of co-operation are intense revision of the collections and making reliable, object-based metadata available internationally.³⁴ A number of spectacular discoveries have been made during these revisions, including previously unknown organisms

³⁴ Meier R, Dikow T. 2004. Significance of databases from taxonomic revisions for estimating and mapping the global species diversity of invertebrates and repatriating reliable specimen data. *Conserv Biol* 18:478–488.

'Monster wasp' discovered in Berlin's Museum für Naturkunde



Figure 7: Giant wasps look imposing. Male giant wasp (top) next to a female worker of a common wasp from Berlin. Text and photos: Michael Ohl (MfN Berlin).

When Gerd Heinrich, an explorer and expert on birds and ichneumon wasps, caught two giant wasps on the Indonesian island of Sulawesi in 1930, he probably gave them little attention. He was more interested in the little-known diversity of birds and ichneumon wasps on the island. Thus, both giant wasps were added to the collections of the Berlin Museum für Naturkunde, along with hundreds, if not thousands, of other insects as 'by-catches'. They remained undiscovered for more than eighty years.

While examining unidentified specimens of digger wasps during extensive research projects on the diversity and phylogeny of these animals, museum curator Michael Ohl discovered the two male wasps that were conspicuous due to their enormous body size. Comparisons with previously identified collection materials and the corresponding literature soon proved not only that this was a previously undescribed species, but that these wasps also had to be assigned to a new genus.

Almost at the same time, Lynn Kimsey, an US American wasp researcher, found examples of a spectacular wasp on Sulawesi during an insect cataloguing project in cooperation with Indonesian scientists. Kimsey sent digital images to Michael Ohl, who recognised that they were the same species of giant wasp that Gerd Heinrich had already collected eighty years previously. After publishing a paper describing the new species, which was co-authored by Lynn Kimsey and Michael Ohl,³⁵ the publishing house, the Museum für Naturkunde as well as the University of California, published press releases on this unusual find, which was cited by hundreds of newspapers around the globe as a 'monster wasp' or 'giant wasp'.

³⁵ Kimsey LS, Ohl M. 2012. *Megalara garuda*, a new genus and species of larrine wasps from Indonesia (Larrinae, Crabronidae, Hymenoptera). ZooKeys 177:49–57.

2.3 Taxonomy on the timeline: PalaeoOMICS and global change

Global change is altering the living conditions of humans, and climate change has received the most attention so far. The loss of biodiversity is a particularly dramatic component of this change because it is irreversible; extinct species are lost forever. In order to measure, understand and counteract the mechanisms of this diversity loss, it is necessary to obtain data on the composition and status of species communities both today and in the past.

PalaeoOMICS deals with high-throughput analyses of ‘ancient’, mostly degraded (fragmented) DNA from museum specimens, which are often hundreds of years old or are even taken from fossils. As early as the 1980s, genetic material from the quagga, an extinct species of zebra, was successfully analysed with conventional methods³⁶ and conclusions were drawn regarding its evolutionary relatedness to present-day species. Using OMICS technologies, it is now possible to analyse not only short sections of genetic information, but also entire genomes, quickly and relatively inexpensively. The significance of such complete datasets is impressively illustrated by the example of human evolution: only by sequencing the complete genome of modern humans as well as our extinct relatives, the Neanderthals³⁷ and Denisovans³⁸, was it possible to prove, in contrast to earlier hypotheses, that modern humans repeatedly interbred with related species (see the example on the evolutionary history of modern humans, p. 26). The history of human evolution must therefore be rewritten. In the case of pandemics of infectious diseases such as the plague,

leprosy, Spanish influenza or the Irish potato blight, analysing ancient DNA using OMICS technologies enables researchers to precisely identify the respective strains and obtain detailed insights into the disease’s variability and adaptation, as well as the dissemination pathways taken by the corresponding pathogens.^{39,40}

Analysing ancient DNA is of great importance for taxonomy and evolutionary research. In some cases it is even possible to detect evolutionary changes in defined time periods, and thus reconstruct evolutionary processes. This also includes extinct populations and species such as the thylacine, cave bear, mammoth or *Sicyos villosum*,⁴¹ a gourd that was collected by Darwin in 1835 on Galapagos and which now only exists as museum specimens or fossils. Biodiversity research also depends on the analysis of ancient DNA. With the aid of genetic samples from existing tiger populations in India, and from museum specimens, it was recently shown that the genetic variation within these populations has greatly declined over the last 60 years.⁴² OMICS-based analyses of deep-frozen genetic material, which has thus been protected against decomposition, obtained from sediment deposits of permafrost soils in the Arctic have provided completely new insights into prehistoric ecosystems and our climate history. Analysing the DNA of pollen or spores from these samples enables taxonomic classification of the plants or fungi that lived in prehistoric ecosystems several thousand to ten thousand years ago.⁴³

³⁶ Higuchi R, Bowman B, Freiberger M, Ryder OA et al. 1984. DNA sequences from the quagga, an extinct member of the horse family. *Nature* 312:282–284.

³⁷ Green RE, Krause J, Briggs AW, Maricic T et al. 2010. A draft sequence of the Neanderthal genome. *Science* 328:710–722.

³⁸ Meyer M, Kircher M, Gansauge MT, Li H et al. 2012. A high-coverage genome sequence from an archaic Denisovan individual. *Science* 338:222–226.

³⁹ Schuenemann VJ, Singh P, Mendum TA, Krause-Kyora B et al. 2013. Genome-wide comparison of medieval and modern *Mycobacterium leprae*. *Science* 341:179–182.

⁴⁰ Gibbons A. 2013. On the trail of ancient killers. *Science* 340:1278–1282.

⁴¹ Sebastian P, Schaefer H, Renner SS. 2010. Darwin’s Galapagos gourd: Providing new insights 175 years after his visit. *J Biogeogr* 37(5):975–980.

⁴² Mondol S, Bruford MW, Ramakrishnan U. 2013. Demographic loss, genetic structure and the conservation implications for Indian tigers. *Proc R Soc B* 280:20130496.

⁴³ See e.g. Bellemann E, Davey ML, Kauserud H, Epp LS et al. 2013. Fungal palaeodiversity revealed using high-throughput metabarcoding of ancient DNA from Arctic permafrost. *Environ Microbiol* 15:1176–1189.

The evolutionary history of modern humans must be rewritten

Analyses of ancient DNA using *OMICS* technologies provided evidence that, in contrast to earlier hypotheses, anatomically modern humans interbred with related species that are now extinct, such as the Neanderthals and Denisovans. These studies included decoding the complete genetic material of the Neanderthal⁴⁴ and Denisovan hominins,⁴⁵ whose fossils were found in 2008 in a Siberian cave at Denisova, in the Altai Mountains of Central Asia. The Denisovan DNA was obtained from a tiny fragment of finger bone from a juvenile female who lived about 30 000 to 48 000 years ago; this was the only evidence for the existence of this hominid species at the time. A comparison of the Neanderthal and Denisovan genomes with those of modern humans from different geographical populations revealed that the Neanderthals and Denisovans had common ancestors, but after their separation, they interbred locally with modern humans. According to the present state of knowledge, anatomically modern humans migrated out of Africa about 50 000 years ago, and came into contact and exchanged genetic material with the Neanderthals in the Near East. Present-day humans whose ancestors passed through this bottleneck in the Levant carry 1.9% to 3.1% Neanderthal genes. These are not found in humans whose ancestors remained in Africa, south of the Sahara. A similar gene exchange took place between the Denisovans and the ancestors of the inhabitants of East Indonesia, Papua New Guinea, Australia and Polynesia, who now carry about 4.3% to 5.3% of the genetic material from the Denisovans.⁴⁶ These findings, which are based on extensive genetic data, impressively demonstrate the complexity of our own evolutionary history.

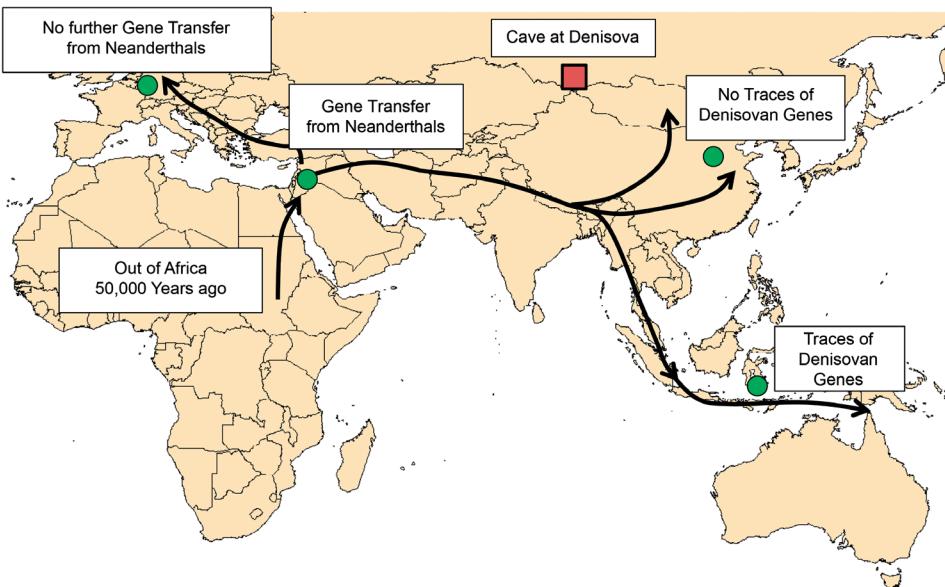


Figure 9: Migration of modern humans and genetic exchange with Neanderthals and Denisovans (from 47; modified according to 48).

44 Green RE, Krause J, Briggs AW, Maricic T et al. 2010. A draft sequence of the Neanderthal genome. *Science* 328:710-722.

45 Meyer M, Kircher M, Gansauge MT, Li H et al. 2012. A high-coverage genome sequence from an archaic Denisovan individual. *Science* 338:222-226.

46 Reich D, Patterson N, Kircher M, Delfin F et al. 2011. Denisova admixture and the first modern human dispersal into Southeast Asia and Oceania. *Am J Hum Genet* 89:516-528.

47 Zinner D, Roos C. 2013. Natürliche Hybridisierung bei Primaten. *Biospektrum* 3/2013:253-256.

48 Stoneking M, Krause J. 2011. Learning about human population history from ancient and modern genomes. *Nature Rev Genet* 12:603-614.

2.4 Taxonomy for the life sciences

Modern integrative taxonomy is an important research field not only on its own account, but it also provides data for applications in medicine, agriculture, biotechnology and food technology, as well as nature conservation. It is thus an important foundation for research in all life sciences. The many existing open databases play a pivotal role in the transfer and accessibility of information.

Medicine

The benefits of taxonomic research for medicine are particularly evident in the case of pathogens. Here, taxonomy helps us to understand their evolution and association with the host, to correctly classify the pathogens, to differentiate between microorganisms that cause diseases from those that are harmless, and to develop diagnostic, therapeutic and preventive (vaccination) strategies.

OMICS technology can be used to trace outbreak events in great detail. During the major outbreak of the so-called enterohaemorrhagic *Escherichia coli* (EHEC) O104:H4 in Germany in the early summer of 2011, the complete genome sequence of the responsible strain was determined less than two weeks after detecting the outbreak. Further, in the case of the cholera outbreak in Haiti after the devastating earthquake in 2010, comparative genome sequencing provided very strong indications that the responsible strain was inadvertently introduced into Haiti from South Asia by UN personnel.⁴⁹

Research into the human microbiome has also developed into a particularly active field of medical research over the last ten years. Indeed, there is an enormous translational potential in the field of health research, especially for the protec-

tion and specific influence of the human microbiome – particularly in the gastrointestinal tract. These advances have greatly stimulated medical interest in the biodiversity of bacteria. In addition to investigating the composition of the microbiome of various regions of the body, attempts are being made to understand the metabolic repertoire of the complete set of bacteria. Microbiome research, however, also provides hypotheses on the roles that individual bacterial species play in key functions of the human body. For example, the results of animal experiments indicate that particular intestinal bacteria play a key role in the human immune system.⁵⁰

Taxonomic work is also indispensable in the search for new active substances to treat diseases. The combined application of different *OMICS* technologies opens new perspectives here as well. For example, metabolic products can be characterised, for which the genome of the organisms contains biosynthesis routes, but which are not expressed under certain conditions, so they cannot be found with other methods.

More than bacteria are medically relevant, however. The aforementioned technologies can also be used to quickly and unambiguously identify parasites that cause malaria, Chagas' disease, sleeping sickness and bilharzia. This also applies to disease carriers such as blood-sucking insects, mosquitoes and horseflies, many of which are difficult to differentiate.

Agriculture, horticulture and agricultural research

Agriculture is the foundation for feeding our continuously growing global population. However, its increasing intensification makes it susceptible to disturbances. Climate change will lead to changes in the types of crops cultivated, many pests will

⁴⁹ Chin CS, Sorenson J, Harris JB, Robins WP et al. 2011. The origin of the Haitian cholera outbreak strain. *N Engl J Med* 364:33-42.

⁵⁰ Kamada N, Kim YG, Sham HP, Vallance BA et al. 2012. Regulated virulence controls the ability of a pathogen to compete with the gut microbiota. *Science* 336:1325-1329.

change their distribution area, and also the ratio between beneficial and harmful organisms will shift. In view of this, agricultural researchers around the globe are currently analysing the genome of rice. Of particular interest are the old wild varieties⁵¹, whose genetic information includes natural resistances against pests or drought and with whose help cultural varieties can be optimised by breeding. But agricultural research also requires reliable identification of the pests. Globalisation is accompanied by the spreading of harmful insects, such as miner flies and moths, fungal diseases and nematodes that damage crop plants. Registration of marker genes of organisms that are difficult to identify in databases will enable their unambiguous classification.

There is a huge potential to increase farming yields by using particular bacteria and soil organisms such as the nitrogen-fixing Rhizobia or bacteria that regulate plant growth. One gramme of soil contains many millions of microorganisms that belong to thousands of different species.⁵² Less than one percent of these soil organisms can be cultivated. Only taxonomic OMICS research is able to identify and characterise them for specific applications.

Integrative taxonomy will also provide important contributions to the evaluation of the fertility and sustainable use of soils. Research into the ‘soil factor’, i.e. the reasons for the enhanced growth of certain crops in certain soils, will be improved in future by open access to taxonomic information and automated inventory of all soil microorganisms.⁵³

⁵¹ Sakai H, Lee SS, Tanaka T, Numa H et al. 2013. Rice Annotation Project Database (RAP-DB): An integrative and interactive database for rice genomics. *Plant Cell Physiol* 54(2):e6(1–11).

⁵² Delmont TO, Robe P, Cecillon S, Clark IM et al. 2011. Accessing the soil metagenome for studies of microbial diversity. *Appl Environ Microb* 77:1315–1324.

⁵³ Bulgarelli D, Rott M, Schlaepf K, van Themaat EVL et al. 2012. Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. *Nature* 488:91–95.

Bio- and food technology

Bacteria and fungi produce numerous bioactive substances that are important for our health. Moulds, for example, produce the antibiotic penicillin,⁵⁴ as well as the immunosuppressant ciclosporine A. The increasing number of decoded genomes has shown that the majority of secondary metabolites and their effects are still unknown. In future, the enormous potential of previously unknown genes for further secondary metabolites in bacteria and fungi can be combined with methods of integrative taxonomy, accessed through synthetic biology and checked with regard to their bioactivity.

Mankind has been using bacteria, yeasts and moulds for a long time to produce foodstuffs such as cheese, yoghurt, sauerkraut, cured sausages and alcoholic beverages. Fermentation processes are initiated by many different organisms. However, microorganisms can also spoil foodstuffs and lead to food poisoning. It is thus important to know the bacteria and fungi used for this. OMICS technologies are finding increasing use in the quality control of foodstuffs, e.g. to detect moulds and to identify microorganism strains (see example of sausage production, p. 30).

For example, complex communities of microorganisms are used in wastewater treatment plants and in biogas plants that generate methane. The biotic community must have the correct composition to ensure that this functions optimally. The corresponding analyses can only be carried out with integrative taxonomic methods. Particular goals in this respect include greater process stability and a causal understanding of the occurrence of unwanted organisms.⁵⁵

⁵⁴ Fleming A. 1929. On the antibacterial action of cultures of a Penicillium with special reference to their use in the insulation of *B. influenzae*. *Br J Exp Path* 10:216–226.

⁵⁵ German National Academy of Sciences Leopoldina. 2012. Bioenergy – Chances and Limits. Halle/Saale, 118 pp.

Conservation science

This topic is closely related to the analysis of global change (see 2.3). Developing effective protection and management strategies requires the most comprehensive knowledge possible of the species that are now present, their characteristics, their habitat requirements and their original distribution area. Particularly in a cultural landscape, there must be clear priorities with regard to nature conservation, not only to find compromises between different interest groups but also for financial reasons. The protection of a species that is only found in a small area generally has a high priority because of its natural rarity and its higher loss potential.⁵⁶ Conservation biology and practical nature conservation are thus especially reliant on correct taxonomic data. The application of molecular methods has led to the discovery of many new species in recent years, which ultimately affects prioritisation in nature conservation. For example, some morphologically and anatomically similar species of South American frogs were originally assigned to one species, which correspondingly increased their distribution area. A fundamental revision of the family of these frogs led to a re-interpretation of the distribution data of many species.⁵⁷ Such a reduction in the area in which the species actually occur can subsequently lead directly to the establishment of new protection areas, as shown by the example of the amphibian fauna of Madagascar (see example of taxonomy for nature reserves, p. 31).

⁵⁶ Steinicke H, Henle K, Gruttko H. 2002. Bewertung der Verantwortlichkeit Deutschlands für die Erhaltung von Amphibien- und Reptilienspezies. Bundesamt für Naturschutz, Bonn-Bad Godesberg, 96 pp.

⁵⁷ Faivovich J, Haddad CFB, Garcia PCA, Frost DR et al. 2005. Systematic review of the frog family Hylidae, with special reference to Hylinae: Phylogenetic analysis and taxonomic revision. *B Am Mus Nat Hist* 294:1-240.

When it comes to making sausages, taxonomy can help



Figure 10: Some staphylococcus strains can cause severe intestinal diseases. *Staphylococcus carnosus*, on the other hand, is a harmless strain that is frequently used to make cured sausages.

Image: © Fotolia.com – Igor Norman.

In addition to lactic acid-producing bacteria (lactobacilli), Gram-positive cocci also participate in the maturation process of raw cured sausages (e.g. fermented, dry salami). These cocci are usually added to the ingredients as starter cultures. German companies produce tons of a coccus used in the manufacturing of cured or fermented sausages. For a long time it was known as *Micrococcus varians*. However, integrative taxonomy has shown that this coccus is not a member of the *Micrococcus* genus, but rather a *Staphylococcus* (*Staphylococcus carnosus*)⁵⁸, which is morphologically very similar to micrococci, but has a very different genotype. In contrast to micrococci, which are all harmless bacteria, some staphylococci can cause food poisoning. Indeed, a German company ap-

plied for approval of a starter culture in the USA shortly after renaming its production strain from *M. varians* to *S. carnosus*. The approval was denied because staphylococci are potentially pathogenic and their harmlessness had to be proven before approval could be granted. The fact that the same production strain had been used as a starter culture for decades in Germany was not adequate evidence for the American authority. If the application for the strain had been submitted under the original name, *M. varians*, there would not have been any difficulties in obtaining approval. The correct nomenclature of a bacteria species thus plays a key role not only in approval applications, but also in patent applications.

⁵⁸ Schleifer KH, Fischer U. 1982. Description of a new species of the genus *Staphylococcus*: *Staphylococcus carnosus*. Int J Syst Bacteriol 32:153–156.

Accelerated taxonomy as the basis for designating nature reserves



Figure 11: Newly discovered species of amphibians, reptiles and primates in Madagascar. More than 400 new species have been discovered in Madagascar in the last 20 years. Images: Vences, TU Braunschweig; Glaw, Zoologische Staatssammlung München; Radespiel, TiHo Hannover.

Lemurs, flat-tailed geckos, frogs and mini-chameleons: Madagascar is famous for the uniqueness of its spectacular animal and plant population. The extremely high deforestation rate is also well known, and is usually due to subsistence farming by the local inhabitants. The fourth-largest island in the world, Madagascar is a natural paradise, but it is also one of the poorest countries in the world. Strategies for sustainable land use are accepted only very slowly. Preserving the biodiversity of this natural paradise is therefore only possible by rapidly prioritising nature conservation issues for clearly-defined natural habitats. This requires precise knowledge of the taxonomy of the affected organisms and their distribution areas.

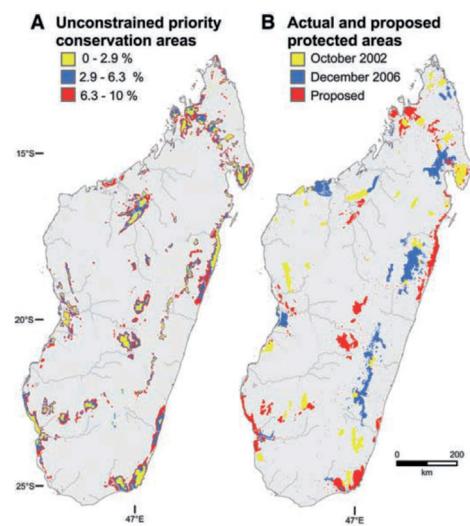


Figure 12: The maps show plans for new protection areas based on the distribution areas of known and newly discovered species. Many of these areas are now under protection. Maps taken from 59.

More than in many other tropical regions, Madagascar's animal and plant populations have been the subject of intensive taxonomic research over the past 20 years. Particularly the establishment of systematic work routines with integrated molecular, morphological and behavioural biological research in collaboration with German research groups has led to singularly rapid advances in the investigation of Madagascan biodiversity.⁵⁹ An apparently paradoxical situation exists: an enormous number of candidate species has been provisionally identified and is still awaiting formal description. At the same time, the state of knowledge on the (described and undescribed) species as a whole is better than in many other biodiversity hotspots. By stringently applying modern methods, the number of known species of amphibians has more than tripled from approximately 130 spe-

cies in 1994 to currently more than 500 species. The distribution data of both the described as well as the undescribed species were used in modelling analyses to define priority regions for nature protection.⁶⁰ As a result, a large number of new protection areas were and are to be established in Madagascar.

59 Kremen C, Cameron A, Moilanen A, Phillips SJ et al. 2008. Aligning conservation priorities across taxa in Madagascar with high-resolution planning tools. *Science* 320:222-226.

60 Vieites DR, Wollenberg KC, Andreone F, Köhler J et al. 2009. Vast underestimation of Madagascar's biodiversity evidenced by an integrative amphibian inventory. *Proc Nat Acad Sci USA* 106:8267-8272.

3 New organisational forms for integrative taxonomy

Implementing the proposed research priorities requires a research structure that is optimally tailored, as well as new organisational forms. Research in the four aforementioned priority topics can only be achieved by interdisciplinary cooperation.

Most taxonomic research in Germany, and internationally, takes place in non-university research institutions. Intensified interlinking of institutes working with taxonomy, in combination with the revitalisation and education potential of the universities, will secure not only the future of the high level of German expertise in this field, it will also lead to enormous synergies. The crucial factor here is to incorporate taxonomic expertise, including full access to the cooperative research infrastructure, in the teaching and research programmes of the universities so that all parties can benefit.

Particular opportunities arise at locations with taxonomic research facilities as well as the major natural history museums and state collections. Here, the experts using modern integrative taxonomy at the international level should be involved to an even greater extent in education and training activities. This ensures that current and accepted methods and standards are incorporated into research and education. Furthermore, research collections and universities at other locations would also profit from these taxonomy priority locations and could thus contribute to modern taxonomic research and training.

On the other hand, these opportunities currently face numerous organisational problems. If non-university scientists

voluntarily teach and thus fulfil the obligations of universities, this leads to problems in apportionment because university teachers cannot fulfil their teaching quota or the undergraduate contingents must be increased. Therefore, involving non-university teaching staff should remain neutral with respect to apportionment.

The Leibniz Association (WGL) includes many high-achieving institutes in the field of taxonomy⁶¹. Collaborations between universities and several non-university institutes are a further possibility. Such collaborations have already been established in other fields, such as biodiversity research, where, for example, non-university institutions from the Helmholtz Association and the Max Planck Society in Leipzig, Halle and Jena are successfully cooperating with nearby universities and are receiving substantial funding from the German Research Foundation (iDiv⁶²). In the field of infection research, a similar collaboration exists in the Hannover and Braunschweig region in which the Helmholtz Association and the Leibniz Association are cooperating with the Technische Universität Braunschweig and the Medizinische Hochschule Hannover.

An important goal of the above-mentioned collaborations is to modernise and revitalise basic education in taxono-

⁶¹ The most important representatives are the Museum für Naturkunde in Berlin, the Museum Alexander Koenig in Bonn, the Senckenberg-Gesellschaft für Naturforschung, with its various locations, and the German Collection of Microorganisms and Cell Cultures in Braunschweig.

⁶² iDiv: Deutsches Zentrum für integrative Biodiversitätsforschung (iDiv; German Centre for Integrative Biodiversity Research) Halle-Jena-Leipzig; <http://www.idiv-biodiversity.de>.

my and to make it attractive to students. The aim is to convey that taxonomy in the 21st century is a modern discipline with a promising future; students frequently recognise its importance only later on in their studies. A further goal is to adapt the curricula of the bachelor's course in biology, including teacher training, by qualitatively modernising the corresponding modules to the current state of research without the necessity of a quantitative broadening. This is not just a question of teaching particular systematics or species lists, but rather the methods and concepts of integrative taxonomy and their significance.

The proposed concept intends to establish future-oriented research and teaching concepts at the prioritised locations. At the same time, it would strengthen the function of these locations as taxonomic competence centres of national and international relevance. These aspects are briefly discussed below under the designations 'Schools of Taxonomy' and 'Competence Network for Taxonomy'. Establishing infrastructures is proposed as a practical implementation for promoting integrative taxonomic research. These infrastructures are dedicated to accelerating species description and its possible standardisation – which is perhaps the greatest challenge for modern taxonomy.

3.1 'Schools of Taxonomy'

Owing to the high degree of specialisation in biology and the increasing profile building of universities, taxonomy is currently taught only superficially and at a decreasing level at many locations. In most cases, teaching is limited to traditional taxonomic fields such as the identification of plants and animals offering determination courses as part of bachelor study programmes. The curricula should be adapted so that students are shown

modern taxonomic research methods at an early stage so that they obtain a broad basic knowledge of integrative taxonomy.

'Schools of Taxonomy' that offer their own master/doctoral study courses should be established at selected locations. The aim here is to combine intensified taxonomic research and teaching at internationally-oriented locations. One requirement for this is to maintain teaching courses based on broad and fundamental topics in taxonomy and systematics at all university locations. The curricula at the 'Schools of Taxonomy' must include not only broad exposure to species and traditional taxonomic methods, but also to *OMICS* technologies, bioinformatics and databases. This would require close cooperation between universities and non-university research institutions. At the state collections and research museums, a wide methodological spectrum of *OMICS* research and excellent taxonomic expertise already exists among their personnel. For the comprehensive education of modern taxonomists, these 'Schools of Taxonomy' must be affiliated with universities because only here is it possible to combine taxonomy with other relevant disciplines such as engineering sciences, informatics, law, philosophy and sociology.

The 'Schools of Taxonomy' would comprise the following components:

1. Graduate schools for integrative taxonomy that require a Master of Science (MSc) in taxonomy should be established at several university locations. These integrated master/doctoral study courses would have a strong international orientation, with English being the teaching language. The curriculum should include all organism groups and a wide range of relevant methods, from classical collection techniques to *OMICS* research. The job market for graduates is global in academia as well

as in industry, NGOs and administrative bodies. Alumni networks should be used to specifically promote lifelong learning.

2. ‘Schools of Taxonomy’ will also be used to develop concepts for technically oriented careers relating to taxonomy (*‘School of Collections Science’*). These schools would further develop and establish job descriptions such as that of a collection manager (*‘natural history collection manager’*) as an academic vocational training ending with a bachelor’s or master’s degree, as already established in the UK and the USA, as well as promote connections with technical vocational training, such as that of a preparator.
3. Attractive and innovative teaching at prioritised locations should not only include developing knowledge of species but also the study of biodiversity and evolution research, including genomic aspects, pattern-based treatments of complex systems, as well as database-based research approaches. The latter will serve to use collection information more intensively as the basis for meta-analyses and modelling global environmental changes.
4. Summer schools and other training possibilities should lead to the expansion of interested target groups, and to the transfer of modern taxonomic teaching and research concepts. These would include courses on collecting samples and specimens for research purposes, expanding taxonomic knowledge, and particularly on applying *OMICS* research methods. Further training courses should be specifically offered to German as well as international participants. Target groups include students and teachers from other universities, researchers from other scientific disciplines, as well as freelance biologists and school teachers the latter again in the sense of lifelong learning.

3.2 Competence Network for Taxonomy

The proposed strengthening of modern taxonomic research and teaching concepts at prioritised locations will create knowledge centres for German taxonomic competence. To utilise this competence more efficiently and fully exploit synergy effects, these locations should be linked into a ‘Competence Network for Taxonomy’ that would also include other university institutions, research collections and research institutions. Such a network would coordinate tasks for long-term archiving of taxonomic data, for taxonomic information portals, as well as provide support for international standardisation processes and quality assurance in taxonomy. None of these central tasks can be fulfilled by an individual institution in Germany.

3.2.1 Long-term data storage, archiving and accessibility

Only a portion of the German institutes working in the field of taxonomy have sufficient competence with respect to data protection, as well as networking national and international databases. The natural history collections are currently faced with the mammoth task of improving the digital accessibility of collection information and its associated research data. In addition to the ongoing work of preserving physical objects and paper-bound information carriers (field notebooks, excursion reports, etc.), there are a number of other tasks, including digitising non-digital collection information, and archiving new ‘native digital’ records from mobile acquisition in the field from images, acoustic or video documents, as well as from molecular and spectroscopic analyses.⁶³ This provides an opportunity to link these databases with the specific databases from *OMICS* research, which are usually based on international

⁶³ see, for example, Specify 6.5: <http://specifysoftware.org>.

data standards (TDWG, Darwin Core, GenOMICS Standards Consortium, etc.) and which are thus suitable for such virtual networking.

It is crucial to secure long-term financing for digital acquisition infrastructures and data storage in natural history collections, including funding for the corresponding qualified personnel. At the same time, a high level of curation must be guaranteed for physical specimens in natural history collections.

In the field of OMICS research, data generation is currently cheaper than data storage. This leads to massive changes in the planning and execution of sequencing projects, which are no longer limited by data generation but rather by data storage and processing.

Establishing a Data Service Centre for taxonomic information could act as an umbrella structure to support existing decentralised data infrastructures and to combine them virtually, optimise their linkages and interoperability and also ensure international compatibility.

Such a centre could fulfil two important functions:

- (1) providing services for networking the existing infrastructure
- (2) stronger centralisation of the decentralised storage infrastructure.

The German Research Foundation (DFG) is providing start-up funding to help establish a national Data Service Centre for biological data in the form of a data warehouse with a highly integrated data pool⁶⁴ so that the data can be networked, for example, with the infrastructures of ecological, taxonomic and medical fields. Service provision and research also include active data maintenance by

curators, extensive access and analysis functions, integration into the Semantic Web, as well as provision of scientific and software tools for meta-analysis and synthesis. However, long-term funding requires different types of additional funding instruments, for example through the Leibniz Association, to which various natural history research museums in Germany already belong. Such an initiative would complement the Pangaea World Data Center for geosciences set up by the Helmholtz Association and MARUM Bremen.

3.2.2 Open access for taxonomic data

The Competence Network fulfils a central task by providing access to all types of taxonomic information within the legal provisions governing the protection of intellectual property and copyrights. The digital acquisition of taxonomic data and their long-term storage is carried out to make them freely available to all users internationally via existing online information portals. In concrete terms, the Academy proposes becoming active in the following fields.

1. Existing descriptions, particularly those of the species occurring in Germany, should be digitally catalogued within the legal framework and new descriptions should be made available in open access journals.⁶⁵ A large amount of existing species descriptions is currently not freely available. Species descriptions may be published in rarely accessed journals, which leads to both redundancy and a loss of information. Microbiology is an exception here, because there is already a curated list of the described species. Since open access journals are frequently associated with costs for the authors, and because voluntary experts play an important role in the field of taxonomy, the

⁶⁴ German Federation for the Curation of Biological Data (GFBIO)

⁶⁵ here, a pioneering role is played, among others, by Pensoft Publishers: <http://www.pensoft.net/journals/>

Competence Network for Taxonomy should enable inexpensive or even free, open-access species descriptions for all species in Germany. This requires the complementary publication organs at the priority locations to be changed to the open access standard.

2. To achieve a deeper level of knowledge on the species diversity that is already conserved in collections, existing objects in the German collections should be digitally catalogued as completely as possible so that they can be made accessible for an international comparison of object-based taxonomic data. This will allow experts around the globe to work with materials in German collections, thereby increasing their value. Digitalised data on collection inventories also form the basis for meta-analyses and modelling of changes in the biological diversity and distribution patterns. Only by using distribution models of precisely determined species is it possible to predict expected changes in biodiversity arising from climate change or socioeconomic changes.
3. A central task of the Competence Network is to increase the compatibility of new taxonomic data. Open access protocols and best-practice guidelines are available for this. These guidelines allow standardised collecting of objects by specialists in various disciplines as well as volunteers (*citizen scientists*⁶⁶). This could also contribute to the standardisation of collection strategies and methods along with their documentation. Conversely, it is also important that ongoing and future *OMICS* projects relating to taxonomy also place specimens in publicly accessible collections. In this case, it is also necessary to agree on protocols for archiving biological environmental samples because they are now being increasingly analysed in metagenome projects. These samples not only deal

with entire biotic communities but also nucleic acid and protein mixtures.

4. Online information platforms provide taxonomic teaching materials for schools and universities as well as for interested non-specialists and citizen scientists. Basic knowledge and taxonomic topics should be taught correctly and innovatively throughout Germany. For example, presentations and course documents from individual members of the Competence Network could be made openly accessible.

3.2.3 Standardisation processes

Taxonomic data are a key and basis for many international agreements. This applies, for example, to the Convention on International Trade in Endangered Species of Wild Fauna and Flora, the Convention on Biological Diversity (CBD)⁶⁷, the Nagoya Protocol of 2010⁶⁸, as well as the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES)⁶⁹. Furthermore, efforts are being made to standardise nomenclature codes for naming organisms and to make registration of new names mandatory. In addition, group-specific standards for describing species must be created and developed further, particularly if molecular genetic data are to be included and the databases are to be networked automatically (*Cybertaxonomy*). This will also accelerate the cataloguing and description of species.

3.2.4 Quality assurance for expert opinions and provision of other services for taxonomy

With respect to the diagnostics of pathogens, the training of medical and techni-

⁶⁶ Bürger schaffen Wissen. The citizen science platform: <http://www.buergerschaffenwissen.de/>, accessed on: 10.12.2013.

⁶⁷ United Nations. 1992. Convention on Biological Diversity. Available at: <http://www.cbd.int/doc/legal/cbd-en.pdf>, accessed on 10.05.2013.

⁶⁸ Secretariat of the Convention on Biological Diversity. 2010. Nagoya protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the Convention on Biological Diversity. Available at: <http://www.cbd.int/abs/>, accessed on: 10.05.2013.

⁶⁹ IPBES – Intergovernmental Platform on Biodiversity and Ecosystem Services. Information available at: <http://www.ipbes.net>, accessed on 10.05.2013.

cal personnel⁷⁰ is regulated by legal and professional stipulations. Laboratories working in the field of pathogen diagnostics are usually accredited, e.g. by the German accreditation body (DAkkS) and must undergo regular compliance audits. Laboratories monitoring foodstuffs, medicines or medicinal products are similarly inspected. Accreditation of a diagnostic laboratory requires regular and successful participation in external quality assurance activities (ring trials) that are offered by similarly accredited ring trial institutions (e.g. INSTAND e.V. in Düsseldorf).

The biological safety assessment and occupational protection of employees against biological substances, as well as protection of the population against infections and poisoning, is essentially based on taxonomic expertise and corresponding quality assurance measures. The Bundesinstitut für Risikobewertung (Federal Institute for Risk Assessment), together with the World Health Organization (WHO), conduct monitoring and research programmes in this field. The various reference laboratories use modern molecular biological methods to determine microorganisms' particular characteristics and associated toxins,⁷¹ as well as to classify them in risk groups and specify safety measures.

Together with taxonomic knowledge, modern technologies also promote compliance with international agreements, e.g. the Biological Weapons Convention.⁷² Under this Convention, the contracting parties are obligated to never, under any circumstances, develop, manu-

facture, stockpile or purchase weapons based on microorganisms and other biological substances or toxins.

It would be expedient to establish quality assurance beyond these fields, including expert opinions on nature conservation. Since both economic and legally important decisions are based on such opinions, the practitioner must possess the relevant expertise. The Competence Network can provide information, for example, on international, cross-border handling of organisms for research purposes (e.g. within the context of the regulation on equitable sharing of benefits arising from the utilisation of genetic resources by the CBD) or information on species for the preparation of environmental expert opinions in the form of inspections and tests. This enables experts from consultancies, environmental agencies and authorities such as environmental protection agencies, to secure their information in specific reference fields by means of recognised processes.

3.3 Species description with high-throughput methods

One of the most fundamental goals and at the same time one of the greatest challenges for taxonomy is to achieve a description of global biodiversity that is as comprehensive as possible. Estimating or even predicting the influence of global change on species diversity and thus of the natural resources that sustain human life requires great knowledge of existing ecosystems. However, the current rate of biodiversity loss is as high or even higher than the description rate of new species.⁷³ Accelerating species description should thus be one of the most urgent goals of integrative taxonomy.

⁷⁰ This includes medical specialists in microbiology, virology, infection epidemiology and laboratory medicine, as well as medico-technical laboratory technicians.

⁷¹ Lebensmittelsicherheit, Mikrobielle Risiken von Lebensmitteln, Biologische Sicherheit. Bundesinstitut für Risikobewertung BfR. Available at: http://www.bfr.bund.de/de/biologische_sicherheit-3981.html, accessed on: 10.05.2013.

⁷² Convention on the Prohibition of the Development, Production and Stockpiling of Bacteriological (Biological) and Toxin Weapons and on their Destruction. Available at: <http://www.unog.ch/80256ED006B8954/%28httpAssets%29/C4048678A93B6934C1257188004848Do/file/BWC-text-English.pdf>, accessed on 10.05.2013.

⁷³ Wheeler QD, Knapp S, Stevenson DW, Stevenson J et al. 2012. Mapping the biosphere: exploring species to understand the origin, organization and sustainability of biodiversity. *Syst Biodivers* 10 (1):1-20.

Such a goal requires not only methodically qualified personnel, but also utilisation and further development of existing technical means. A key step towards accelerating species description lies in the automation of as many fundamental methods as possible, and also requires coupling of scientific approaches with industrial solutions. Such linkages between scientific, engineering science and industrial standards and approaches have already been successfully implemented in other fields; however, for basic biological research in general and taxonomy in particular, this would be a promising innovation that would be unparalleled on the international stage.

Such arrangements serve to integrate functional as well as molecular biological methodological approaches with the aim of discovering and describing new species even faster and to provide access to existing knowledge of described species. The core task here is to expand the high-throughput concept from the molecular level to other levels, for example, by incorporating automated imaging methods to determine the phenotype. In the case of very automated species description, however, it is essential to secure qualitative standards, which requires close involvement of the ‘Schools of Taxonomy’ at the priority locations.

Public-private partnerships offer the possibility of dividing the necessary and considerable capital expenditure for the various resources and their long-term upkeep between a number of parties. One or more such species discovery and description centres should be established at the priority locations of integrative taxonomy; however, they should be open in nature. These centres should thus be made accessible to both smaller institutions as well as the public. Voluntary species experts (*‘citizen scientists’*) would provide a forum for the public and help the centres to act as think tanks facilitating interaction between the public and the scientific community.

Establishing these centres would offer the possibility of institutionalising integrative taxonomy. Such an arrangement would thus serve not only to accelerate the description of new species but also act as a crystallisation point of the Competence Network. It could thus play a key role in the development and implementation of standards, in the self-organisation of the network, and in a fundamental increase in taxonomic efficiency. To fulfil these functions, it is necessary to incorporate various fields, including:

1. Sequencing all known organisms – preferably type material.
2. Ensuring the continuation of specific new collections and making available objects already contained in scientific collections, including DNA sequencing.
3. Generating data from industrial screening of samples (particularly DNA, proteins, biochemical constituents), and from automatic analyses of images and patterns.
4. Analysing data through automatic characterisation and identification of organisms, including a semi-automatic morphological description and graphical documentation.
5. Managing data (in close cooperation with the Data Service Centre) using automatic input of obtained information into international databases (Genbank, CoL, EOL, GBIF, ZooBank etc.).
6. Publishing the results and public relations work.
7. Involving the public (*‘citizen science’*).
8. Training specialist personnel.

However, physically linking these fields is only a central module of accelerating species description. The full innovative potential behind the idea of a ‘species description factory’ can ultimately only be exploited by its comprehensive incorporation into the Competence Network for Taxonomy. The Network would thus become a unique model project that is highly attractive on the international stage.

4 Dynamic further development of classification and nomenclature of organisms

The methodological quantum leap in taxonomy due to *OMICS* combines several independent biological sub-disciplines. Indeed, botany, zoology as well as eukaryotic and prokaryotic microbiology are making increasing use of similar taxonomic methods and characteristics. The dynamics gained from linking these disciplines can be illustrated by the analysis of metagenome data. Enormous datasets such as those obtained from environmental samples may contain gene sequences from very different groups of organisms. The taxonomic expertise required to analyse such datasets can only be generated by close cooperation between the aforementioned sub-disciplines.

This also has consequences for practical procedures such as nomenclature, i.e. the rules used to name organisms. Nomenclature is currently regulated by five international codes that differentiate between botany (algae, fungi and plants), zoology, prokaryotes, viruses and cultivated plants. Closer cooperation between the sub-disciplines could lead to the transfer of proven methods and concepts from the nomenclature rules of the different disciplines, which would simplify naming and describing organisms as a whole and, at the same time, could increase the quality and quantity of the resulting species descriptions.

Reform of the Codes of Nomenclature is recommended. It has recently become possible to publish new species in online journals, botanical species descriptions no longer require a diagnosis in Lat-

in⁷⁴ and a framework for a unified ‘Biocode’ for all groups of organisms has been established.⁷⁵ In spite of their long history, many rules in the Codes of Nomenclature are flexible enough to undergo harmonisation of terms⁷⁶ and re-interpretations of specific rules so that they can continue to serve as the basis for naming organisms. For example, the zoology and botany codes do not specify exactly which traits are to be used for diagnosing and defining a species – and thus molecular data are not excluded.

1. Names are always defined based on reference specimens that are kept in specialised collections. Data on these type specimens and type strains are often insufficient, so ongoing research cannot taxonomically assign many gene sequences owing to the lack of data for comparison. The genomic characterisation of type material can create new benchmarks in this case. If this is not possible for a historical type or if it appears to be too error prone, reference specimens could be identified from the same or a nearby location and added to the collection as an additional specimen (‘epitype’ in the botanical code).
2. In the case of genetic or phenotypic investigations of unidentified organisms as well as in large projects for sequencing

⁷⁴ Knapp S, McNeill J, Turland NJ. 2011. Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you? *PhytoKeys* 6:5-11.

⁷⁵ Greuter W, Garrity G, Hawksworth DL, Jahn R et al. 2011. Principles and rules regulating the naming of organisms. *Bionomina* 3:26-44.

⁷⁶ David J, Garrity GM, Greuter W, Hawksworth DL et al. 2012. Biological nomenclature terms for facilitating communication in the naming of organisms. *ZooKeys* 192:67-72.

ing environmental DNA, a great deal of valuable data is obtained that cannot be catalogued in a standardised taxonomic form at present. In this case, using a provisional status for partially characterised species (Candidate status for prokaryotes, MOTUs for fungi, OTUs for plants and algae, Candidate species in zoology) would allow taxonomy to keep pace with accelerated cataloguing of life forms without reducing the quality of the formal species descriptions.

3. The requirements for registering all newly described taxa and validating their descriptions is regulated differently in the aforementioned five nomenclature codes. Mandatory and automatic database registration of all species descriptions, as well as the associated sets of traits and metadata would enormously improve the availability of nomenclatural and taxonomic data. An agreement on certain validation requirements, such as the publication of new species in peer-reviewed journals would make an important contribution towards securing the quality standards of taxonomy.

4.1 Integrative standards for species descriptions

Taxonomy in the 21st century is integrative. Over the past ten years it has become customary in taxonomy to take account of the observable physical traits and the physiology, as well as genotypic traits. This conceptual standard applies to zoology and botany as well as microbiology. Species descriptions should generally be comprised of sets of traits that are as informative as possible. The development of new standards in this field offers attractive creative freedom in the description of species. Thus, new future-oriented sets of traits can be developed, whereas very time-consuming traits could be omitted for certain groups of organisms if they do not provide an essential gain

in knowledge. Such steps are necessary to substantially speed up the species description procedure. Not only do advances in molecular genetics contribute to this, but so do modern IT technology, robotics and the development of imaging methods (scanners, 3D representations).

In general, the datasets to be integrated should be obtainable as optimally as possible using high-throughput methods, should allow species delineation to be optimised with respect to evolutionary biology, and should enable species to be identified as quickly and accurately as possible.

1. High throughput methods used for determining a wide range of traits open new perspectives for faster and qualitatively improved identification and description of species diversity. This is obvious in the case of genotypic traits considering the explosion of DNA sequencing capacities; however, determination of the phenotype is also undergoing deep-rooted change. A key role here is played by automatic imaging and pattern recognition techniques, as well as methods derived from proteOMICS/metabolOMICS (e.g. MALDI-TOF mass spectrometry, near-IR spectroscopy⁷⁷) that detect the proteins in an organism by spectroscopy, for example, and which can be used as a fingerprint of the proteome.⁷⁸ In this respect, there are some very promising new methods that combine different OMICS technologies (e.g. PCR-ESI-MS).⁷⁹

⁷⁷ Rodríguez-Fernández JI, de Carvalho CJB, Pasquini C, de Lima KMG et al. 2011. Barcoding without DNA? Species identification using near infrared spectroscopy. Zootaxa 2933:46–54.

⁷⁸ Laakmann S, Gerdts G, Erler R, Knebelsberger T et al. 2012. Comparison of molecular species identification for North Sea calanoid copepods (Crustacea) using proteome fingerprints and DNA sequences. Mol Ecol Resour 13:862–876.

⁷⁹ Massire C, Buelow DR, Zhang SX, Lovari R et al. 2013. PCR followed by electrospray ionization mass spectrometry for broad-range identification of fungal pathogens. J Clin Microbiol 51:959–966.

2. From the conceptual perspective, integrative taxonomy provides a better delineation between species that is more strongly based on evolutionary biology and is more comprehensible. An integrative approach allows differences between species to be identified. On the one hand, general genetic differentiation is determinable. On the other hand, in some cases, both genotypic as well as phenotypic data provide inferences to adaptation processes to the environment that are of great interest for species delineation as well as for the various end users of taxonomic metadata.
3. The traits contained in a species description directly influence the methods that can be used during subsequent routine identification. Although genotype-based identification methods offer the greatest potentials (e.g. DNA barcoding), documenting the phenotype, for example using high-throughput imaging as well as spectroscopic and spectrometric methods (e.g. digital electron microscopy, confocal microscopy, computed tomography (μ CT), 3D methods) is very useful in many cases and is decisive for taxonomic continuity. Identifying plants, algae, higher fungi and animals based on their physical appearance continues to be essential for many end users and in future it may even be possible to support this by means of digital pattern recognition software (e.g. apps).

Continuous further developments will also further improve molecular genetic identification methods using DNA barcoding. The complete spectrum of possible developments is not yet foreseeable.

4.2 Genomic markers – parameters for the description of species

Integrative taxonomy profits from genomic data in the following ways: (1) through simple and efficient storage of standardised data in open access databases; (2)

through the large amount of formally readable information in these data for questions at different taxonomic levels, and (3) through the various information levels contained in these data, such as a comparison of the average nucleotide identity (ANI), the average oligonucleotide similarities, phylogenetic reconstructions, or solely the G+C content⁸⁰.

The taxonomy of microorganisms has been using genome-based comparisons for many years to delineate species. Since its beginnings in the 1960s, comparative genomics has become the standard technique in microbiology. However, until recently, routine sequencing of complete genomes in taxonomic research was generally not feasible due to high costs. The development of next generation sequencing (NGS) technologies has opened completely new perspectives for taxonomy. These techniques are now being used for animals, plants, algae and fungi. In the meantime, a human genome can be sequenced for around 1000 Euro and complete bacterial genomes cost only a few hundred Euro. Analysing the resulting data volumes, however, remains time- and cost-intensive. Nevertheless, we can expect that the sequencing of genomes, or at least certain parts of them, will become standard practice in taxonomy to an ever-increasing degree. Genome research and integrative taxonomy will mutually promote each other.

Pairwise genome comparisons to determine the average similarities of nucleotide sequences (ANI) have been proposed as a standard method of species delineation for microorganisms.⁸¹ As a supplement and ultimately as a further development of the current routine sequencing of single gene markers, so-called

⁸⁰ G+C Gehalt: percentage of guanine and cytosine (G+C) in the DNA.

⁸¹ Richter M, Rossello-Mora R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci USA 106:19126–19131.

barcodes, the ANI standard proposed for microbiology can also be applied to higher organisms. This would contribute to standardising taxonomic tools over all groups of organisms. The first steps in this regard were taken by the international *Barcode of Life* Initiative, which is aimed at generating standardised DNA barcodes for all known species. For other, larger organisms, the observable physical traits (phenotype) provide additional information with which the species delineation can be verified. However, analysing marker genes offers the advantage of simpler automation.

Due to the acceptance of molecular methods in the last ten years, taxonomy has made advances towards standardisation. DNA barcoding approaches, in particular, should be mentioned in this respect. The foreseeable development of routine sequencing of at least partial genomes or extensive sets of genes for many species will have a positive effect on the development of integrative taxonomy and genomics without rendering irrelevant the previously performed morphological and molecular work in taxonomic research.

5 Glossary

Archaea

A group of prokaryotic microorganisms that, along with the bacteria and the eukaryotes, form one of the three domains into which all cellular organisms are classified.

Bioactive substances

Food constituents that have a beneficial effect on health but do not have nutrient character.

Biobanks

Combination of one (or more) organised material collection(s) of e.g. body fluids or tissue samples with the associated metadata that are managed in databases.

Candidatus status

A valid description of a bacterial species requires that this species be isolated from the others and can be cultivated. The Candidatus status is assigned to a microbe that, although it can be well characterised, cannot be isolated under laboratory conditions and sustainably cultivated.

CBD

Convention on Biological Diversity: an international agreement of the protection of biological diversity.

CITES

Convention on International Trade in Endangered Species of Wild Fauna and Flora: Washington Convention.
Codes of Nomenclature code (or nomenclature rules)
Rulebook for scientifically naming organisms.

CoL

Catalogue of Life: an international project to catalogue all known species of organisms on Earth.

Cryptic species

A species without discernable differences in morphological traits but which can be identified by molecular methods.

Custody

Position within a museum responsible for maintaining and securing a collection.

Cybertaxonomy

A more efficient branch of taxonomy due to the use of the cyber infrastructure and digital technologies.

Darwin Core

A standard to facilitate the exchange of information of object-related metadata from natural history collections.

Data warehouse

A database containing data from different sources in a standardised format.

DNA barcoding

A method of identifying species based on the DNA sequence of a defined genetic marker (DNA barcode).

Enterohaemorrhagic

Tendency to / causes severe intestinal bleeding.

EOL

Encyclopaedia of Life: an online encyclopaedia written by specialists that aims to include information on all known organisms.

Eukaryotic organisms

(or Eukaryotes)

Includes all organisms whose cells have a nucleus.

GBIF

Global Biodiversity Information Facility: an international network that aims to collate information on species diversity around the world in a digital form from numerous databases in a central internet portal, and to make it freely and permanently available.

GenBank

One of three major DNA sequence databases and part of the National Institute of Health in the United States.

Genome

The complete set of genetic information in a cell or a tissue or an organism.

GenOMICS

Determination of the complete genetic information of a cell or a tissue or an organism using molecular biological high-throughput sequencing methods.

Genomics Standards Consortium

International initiative to standardise the description of genomes as well as the exchange and integration of genomic data.

Genotype

The genetic makeup of an organism that represents its complete genetic constitution and on which the phenotype is based.

Genotypic

See Genotype.

Immunosuppressant

A medicine that suppress the functions of the immune system.

Integrative taxonomy

A taxonomy based on one or more mutually independent systems of traits.

Invasive species

Used in nature conservation to refer to introduced (non-native, neobiota) species that have negative effects on other species, biotic communities or biotopes.

IPBES

Intergovernmental Platform on Biodiversity and Ecosystem Services.

MALDI-TOF mass spectrometry

A method of mass analysis of chemical compounds.

Metabolome

The complete set of all characteristic metabolic products of a cell or a tissue or an organism.

MetabolOMICS

Determination of the metabolic products present in a cell or a tissue or an organism using molecular biological high-throughput methods.

Metagenomics

Study of the complete set of genomic information of all organisms in a specific biotic community or a biotope.

Microbiome

The complete set of genomes of all microorganisms colonising a human or an animal or a plant.

MOTUs

Molecular Operational Taxonomic Units. See OTUs.

NBS

National Biodiversity Strategy.

Near-IR spectroscopy

A physical analytical technique based on spectroscopy that uses short-wave infrared light.

Neobiota

Species that have established themselves in an area in which they were previously not indigenous, either by independent means or by human intervention.

Next generation sequencing

Modern high-throughput sequencing of nucleic acids.

Nomenclature

In biology this refers to the discipline of scientifically naming organisms. It forms the basis for internationally comprehensible and verifiable communications relating to organisms. Owing to its eminent importance, it is regulated by strict rulebooks known as the codes of nomenclature.

Nucleic acids

Macromolecules (DNA and RNA) that are built up of nucleotides. Beside proteins, carbohydrates and lipids, they are one of the four large groups of biomolecules.

Nucleotide

Basic component of nucleic acids.

Oligonucleotide

DNA or RNA molecule made up of a few nucleotides (oligomers).

OMICS technologies

High-throughput methods for determining the complete molecular biological information.

Open access

Free access to scientific literature and other materials on the internet.

OTUs

Operational Taxonomic Units. Taxonomic units delineated by DNA barcoding.

Palaearctic region

A biogeographical region covering Europe, North Africa (up to the southern edge of the Sahara) and parts of Asia (southwards up to the Himalayas), as well as the islands close to these areas.

PalaeoOMICS

High-throughput analysis of mostly fragmented, ancient DNA from museum materials, which are often centuries old or even from fossils.

Pathogen

An infectious agent. Substances or organisms that cause harmful processes in other organisms.

PCR-ESI-MS

Polymerase chain reaction (PCR) electrospray ionization (ESI) mass spectrometry (MS).

Peer review

A process used in the scientific community in which colleagues (peers) review scientific work, particularly publications.

Phenotype

Physical appearance. The set of all traits of an organism.

Phenotypic

See Phenotype.

Phylogeny

Evolutionary history of organisms.

Prokaryotic organisms

Prokaryotes are cellular organisms that do not have a cell nucleus.

Proteome

The complete set of proteins in a cell or a tissue or an organism.

ProteOMICS

Determination of the complete set of proteins present in a cell or a tissue or an organism using molecular biological high-throughput methods.

Rhizobiaceae

Root-nodule bacteria present in root nodules of leguminous plants that are able to bind nitrogen in the air.

Secondary metabolite

A chemical compound synthesised by organisms and which, in contrast to a primary metabolite (sugar, amino acid, etc.), the producing organism does not need in order to live.

Semantic Web

Data in the World Wide Web are linked together by metadata and applications in such a way that they can be retrieved by intelligent systems (e.g. internet portals, search engines). Correct semantics (i.e. the unambiguous description of the meaning of the data) are just as important as a consistent ontology (relationships, correlations or structural interrelationships of data). Data in the Semantic Web can be arbitrarily combined and retrieved, regardless of their source.

Soil factors

Properties of a soil, such as the basic type of rock, water balance, grain size, nutrient supply and soil organisms that affect the composition of plant communities.

Subsistence farming

Type of farming that is primarily based on self-sufficiency whose yields generally remain outside market circulation.

Synthetic biology

An interdisciplinary branch of research that has developed in the boundary region between e.g. biology, biotechnology, chemistry, physics, engineering sciences and information technology, and which is aimed at developing biological systems or organisms with new, defined characteristics that do not occur naturally.

Taxonomy

Branch of biosystematics research that deals with the nomenclature (naming), identification and classification (assignment to a hierarchical system) of organisms.

TDWG

Taxonomic Database Working Group.

Transcriptome

The complete set of RNA molecules (transcripts) produced in a cell or a tissue or an organism.

Transcript*OMICS*

Determination of the complete set of RNA molecules present in a cell or a tissue or an organism using molecular biological high-throughput methods.

Translational

In medicine, this refers to the interface between basic research and application in clinical practice.

Type (specimen)

Selected individual (selected species) that is used as the basis to define and name a taxon.

Type strain

A strain that is used as the basis to describe a species.

ZooBank

Official registry for zoological nomenclature.

6 Methodology

6.1 Reasoning, commissioning and development of this statement

The application of molecular methods has led to pioneering changes in the biosciences and medicine. These changes necessitate reconsideration and adaptation of the structures used in research and teaching, as well as the methodological concepts behind them. Based on the recommendation of the Scientific Commission of Life Sciences of the Leopoldina, the Executive Committee of the Academy decided on 26 October 2011 to establish a Working Group on this topic under the leadership of Professor Rudolf Amann ML.

The Working Group was established during the 5th Max Planck Symposium ‘Biodiversity’ at its first meeting on 7 March 2012 in Berlin, during which

further members were appointed and the procedure for the Working Group was defined. The developments in taxonomy in various research fields were subsequently examined in three thematic workshops in collaboration with external experts:

1. Taxonomy in botany (21/22 June 2012 in Halle/Saale).
2. Taxonomy in microbiology, medical microbiology and mycology (10/11 September 2012 in Bremen).
3. Taxonomy in zoology (13/14 December 2012 in Berlin).

A list of participants at the workshops and the titles of their presentations are provided in the Appendix. The text contributions of the presenters, if available, can be accessed at: www.leopoldina.org/de/TaxonomieSupplement

6.2 Members of the Working Group

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6.4 Review Panel

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6.5 Acknowledgement

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6.6 Presentations in the thematic workshops

Taxonomy in botany (21/22 June 2012 in Halle/Saale)

Regine Jahn, Berlin	Ist der botanische Nomenklatur-Code fit für die Zukunft der taxonomischen Forschung? (Is the Botanical Code of Nomenclature fit for future taxonomic research?)
Wolfram Weckwerth, Vienna	Genomweite Analyse von Inhaltsstoffen und Proteinen für Metaproteogenomik, Annotation von Genomen und Taxonomie (Genome-wide analysis of constituents and proteins for metaproteogenomics, annotation of genomes and taxonomy)
Frank Blattner, Gatersleben	Nutzpflanzentaxonomie, genetische Ressourcen, Genomics und Phenomics (Taxonomy of crop plants, genetic resources, genomics and phenomics)
Birgit Gemeinholzer, Gießen	Datenspeicherung und Vernetzung – Taxonomie und <i>OMICS</i> (Data storage and networking – Taxonomy and <i>OMICS</i>)
Susanne Renner ML, Munich	Molekulare und morphologische Typifizierung und naturhistorische Sammlungen im Zeitalter der - <i>OMICS</i> -Forschung (Molecular and morphological typification and natural history collections in the era of - <i>OMICS</i> research)
Volker Lohrmann, Berlin	TAXON- <i>OMICS</i> – Taxonomie in Deutschland im Zeitalter der ‘- <i>OMICS</i> -Forschung’ (TAXON- <i>OMICS</i> – Taxonomy in Germany in the era of ‘- <i>OMICS</i> research’)

Taxonomy in microbiology, medical microbiology and mycology (10/11 September 2012 in Bremen)

Ulrich Kück, Bochum	Fungal development, fungal biotechnology-teleomorphs and anamorphs in the fungal kingdom
Axel A. Brakhage ML, Jena	Fungal genomics and its impact on secondary metabolite discovery and elucidation of pathogenicity
Ronald de Vries, Utrecht	Fungal biodiversity with respect to carbon utilisation: taxonomic relationships versus parallel evolution
Sebastian Suerbaum ML, Hannover	(Gen-)OMICS and bacterial pathogens: Impact and Potential
Bärbel Stecher, Munich	The intestinal microbiome: role in interaction with human pathogens
Eva H. Stukenbrock, Marburg	A population genomics perspective on speciation and evolution of fungal plant pathogens

Ramon Rossello-Mora, Esporles	Past, present, and future of microbial taxonomy
Rudolf Amann ML, Bremen	Microbiomes and metagenomes in need of professional classification
Jörg Overmann, Braunschweig	Diversification in nonpathogenic bacteria implications for taxonomy, bioinformatics and data repositories
Hans-Peter Klenk, Braunschweig	The encyclopedia of microbial genome sequences
Peter Kämpfer, Gießen	The polyphasic approach in the OMICS era – up to date, or out of date?
Edward Moore, Göteborg	Typing and identification of microorganisms at sub-species levels: considerations for biodiversity, biotechnological, clinical and epidemiological studies

Taxonomy in zoology (13/14 December 2012 in Berlin)

Miguel Vences, Braunschweig	Integrative taxonomy
Christian Roos, Göttingen	Natural Hybridization in Primates
Michael Hofreiter, York	Ancient DNA – retrospective sequencing of types
Wolfgang Wägele, Bonn	GBoL: Overcoming the taxonomic impediment with DNA-Barcoding
Michael J. Raupach, Wilhelms-haven	The use of DNA sequences in animal identification and classification
Christoph Bleidorn, Leipzig	<i>Wolbachia</i> and molecular barcoding conceptions and misconceptions
Axel Meyer ML, Konstanz	Next generation DNA sequencing methods now permit the genetic delineation of extremely young (cichlid fish) species and populations
Bernhard Misof, Bonn	1KITE – 1K Insect Transcriptome Evolution
Thorsten Stoeck, Kaiserslautern	Barcode microbial eukaryotes
Quentin Wheeler, Tempe	The Age of Taxonomy

Further publications (Selection)

Energy- and Research-Policy Recommendations following the Events in Fukushima – Ad-hoc Statement – 2011

Bioenergy: Chances and Limits – Statement – 2012

Animal Experimentation in Research – Statement on the Transposition of EU Directive 2010/63 into German Law – 2012

The Sustainability of the German Science System – Discussion Paper – 2013

Antibiotics-Research: Problems and Perspectives – Statement – 2013

Scientific Freedom and Scientific Responsibility – Recommendations for Handling Security-Relevant Research – 2014

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