# Chapter 14
# BONN: Zoologisches Forschungsmuseum Alexander Koenig in Bonn: Transformation of a Classical Natural History Museum of the Nineteenth Century into a Biodiversity Research Institution

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**Abstract** Natural history museums have their origin in times when scientists started to explore unknown landscapes where they collected specimens for scientific study and to demonstrat the general public the wonders of our world. Researchers usually were also hunters and gatherers. The "Zoologisches Forschungsmuseum Alexander Koenig" in Bonn was built on this tradition by a wealthy naturalist at the end of the nineteenth century. Today, this institute has a very different profile. It is a research institute with a focus on biodiversity studies at species level, with a strong taxonomic tradition and a special expertise in molecular studies that are relevant for phylogenetic inference, population genetics, speciation research, and molecular taxonomy. A major challenge for the future is to bridge the gap between knowledge about species taxonomy and biology and the application of this knowledge in ecological research and in applied conservation biology.

In this contribution, we explain the historical background and the use of collections for the case of the bird and reptile departments, the challenges for molecular research, the necessity to build new types of collections (biobanks), the use of collection data for macroecological research, and some examples for knowledge transfer to the general public.

**Keywords** Voucher specimens • Dry collections • Wet collections • Biobanking • Molecular samples • Biodiversity research • Taxonomy

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## 14.1 Research Built on Sugar: Short History of the "Museum Koenig"

In the Rhineland around Cologne, Bonn, and Koblenz, our institute is known as "Museum Koenig." The founder, Alexander Koenig (1858–1940), was a passionate hunter, whose inherited fortune allowed him to dedicate his life to the study of animals, especially birds. The family's fortune had been amassed by his father Leopold Koenig, who owned large estates in Eastern Europe (mainly in Ukraine) to grow sugar beets and several sugar factories located in St. Petersburg and in Ukraine (Hutterer 2008). His enterprise produced about 10 % of the sugar consumed in Eastern Europe. The family possessed several large villas in St. Petersburg, estates in Germany, and the villa later known as "Villa Hammerschmidt" in Bonn, which after the Second World War became Germany's White House. Alexander Koenig went to school in Bonn and as a boy already started hunting and collecting birds. He studied zoology in several German universities and inaugurated in 1900 a small museum close to his parents's villa in Bonn. He never worked to earn money. After his father's death, Alexander Koenig started to construct in 1912 the large museum we know today (Fig. 14.1), enlarging the first building. However, during the Russian Revolution (1917), all possessions in Eastern Europe and the family's main income got lost, forcing A. Koenig to negotiate with the Prussian Government a takeover of the museum, which since then was a governmental institution until it became in 2013 a public law foundation. The Zoological Research Museum Alexander Koenig (ZFMK) is today an institute of the Leibniz Association, jointly funded by federal states and the federal government (via the Federal Ministry for Education and Research). Among German natural history museums, the ZFMK started very early with the implementation of molecular biodiversity research and the informatics needed to analyze sequence data.

**Fig. 14.1** The main building of the Zoological Research Museum Alexander Koenig in Bonn harbors all exhibitions and part of the collections of the Vertebrate Department. The architecture was designed in the first decade of the twentieth century. The institute consists of several buildings, e.g. for the arthropod collection or for the Center for Molecular Biodiversity Research (Photo: © with C. Koch)

Today, the Center for Molecular Biodiversity Research of ZFMK is unique in Germany.

## 14.2 Preparing for the Future: A Transformation Process

Classical natural history museums show the “wonders of the world,” classified into separate collections for animals, plants, fossils, and minerals. The scientific collections are the result of expeditions and of project-dependent research (like a study on the phylogeny of birds in Papua New Guinea). In the future, these museums will be the main providers for information on species, the living components of ecological systems. To understand the consequences of land use, desertification, drainage, climate change, etc., data at species level are needed to model scenarios and predict ecological consequences and the probability that species will survive. This is an essential basis for well-informed responses to the questions policy makers need to answer. To be able to provide this information, the Museum Koenig developed a strategic process that will change the institute’s profile. New tasks are:

- To speed up inventorying in species-rich habitats, new tools for automated sampling and species identification have to be developed. An important aspect is the development of workflows for rapid and cost-efficient barcoding of mass samples.
- To speed up the access to species-specific information, we have:
  - to digitize collection-based data. ZFMK is using the Diversity Workbench (diversityworkbench.net) as repository and to provide data for international databases.
  - to link various databases and to build user-friendly portals (such as BiNHum: wiki.binhum.net) for rapid access to information from different sources.
- To make use of species-specific information for ecological studies. Modeling tools used to predict geographical distribution and dispersal abilities have to be completed with more niche parameters that are relevant for the survival of a species (e.g. biotic interactions and conditions for breeding success).
- Taxonomists have to enlarge their field of activity to document a species’ biology.
- Taxonomists have to be trained to enable them to accelerate species discovery and description.
- To make use of the full potential of available knowledge, it is necessary to bridge the gap between (1) citizen scientists, who possess important data on the occurrence of species, (2) well-funded academic research, and (3) conservation biologists and governmental agencies that have to report on the state of nature.

These are new tasks that should not replace the classical museum. Instead, they require additional resources. *It is a grave mistake to replace taxonomic collections* and research departments with more “modern” working groups. Taxonomy will always be the basis for biodiversity research and for conservation biology. Without the ability to discern species and to protect them, we will transform our planet into a poor and desolate place in the universe.

## 14.3 Linking the Past and the Future: The Ornithological Collection of the ZFMK

A major part of the ZFMK's vertebrate collections, including the ornithological collection, consists of dry-preserved specimens. These specimens comprise study skins (Fig. 14.2), mounted specimens, and skeletons as well as bird eggs and nests. Separately stored and cross-referenced subsamples of organ or tissue material link the dry collections with the museum's alcohol and tissue collections.

Scientific bird collections are available for a wide range of research approaches and methods (faunistics, ecology, molecular systematics, conservation, etc.) of which many were unknown when the collections were established (Joseph 2011; Frahnert et al. 2013). The increasing availability of databased information on collection holdings and associated meta-data facilitates both access to and use of collections for a broad scientific audience. Therefore, the scientific potential even of historic collections is greatly enhanced, particularly with a combination of a continued contemporary extension and scientific advertisement (Viscardi 2013). Using the example of the ZFMK's ornithological collection, it shall be demonstrated how modern research approaches can be implemented in sustainably curated zoological collections.

### *14.3.1 The Bird Collection of the ZFMK*

Dating back to the very beginning of the museum's founder and director Alexander Koenig's private activities in the 1870's, the bird collection, and notably the bird egg collection, became the cradle of the recent Museum Koenig (Rheinwald 1984). Alexander Koenig, an acknowledged ornithologist of his times, invested both his wealth and his personal dedication to the extension of the bird collection and the growth of the museum as a research institution. Hiring able assistants who performed the necessary custodial work as well as assigning major scientific tasks to them, Koenig himself already defined the use of the bird collection primarily for scientific purposes right from the start. Once the museum's public displays and iconic dioramas were finished in 1934 (Hutterer 2015), the focus of the bird collection swung even more into a research direction. The acquisition of the collection of Otto Kleinschmidt in 1935, a huge private bird collection with more than 10,000 study skins, boosted the size and the scientific importance of the bird collection. Subsequently, the overall appearance of the ornithological collection changed from Koenig's aesthetically motivated array of mounted specimens

**Fig. 14.2** The two lectotype specimens of the Canary Island Kestrel (*Falco tinnunculus canariensis*), a taxon described by Alexander Koenig in 1889. They represent an example for the numerous type specimens kept in the ZFMK's ornithological collection, making them a valuable resource for taxonomic research (Photo: © with J.F. Struwe)

(Fig. 14.3) to a more prosaic, yet practical arrangement of a contemporary study skin collection.

The curators succeeding Koenig continuously added scientifically meaningful material to the ornithological collection. There were stages of extensive growth resulting from acquisitions of large private collections, exchange of material, and own collecting activities. Prominent examples are the purchase of the collection of Karl Dernedde in 1944 that contained about 3500 hummingbird skins and the acquisition of a part of the collection of Christian Ludwig Brehm in 1964 by exchanging 2800 European bird skins with the American Museum of Natural History in New York. Currently the ornithological collection holds about 76,000 study skins, 9000 mounted specimens, 3000 skeleton and alcohol specimens, some thousand feather sheets plus Germany's largest egg collection with about 60,000 eggs and clutches, and additional 1700 bird nests. Since a few years, cross-referenced tissue samples, stored in the museum's blood and tissue bank, are taken routinely with every incoming bird specimen. Last but not least, there are numerous type specimens, securing the physical basis of 322 scientific bird names

**Fig. 14.3** Mounted specimen of a Sacred Ibis (*Threskiornis aethiopicus*), collected in 1910. This bird not only exemplifies the fine taxidermic quality of many early bird specimens of the ZFMK but also demonstrates their enduring scientific value because of the meticulous labeling (Photo: © with J.F. Struwe)

(Rheinwald and van den Elzen 1984; van den Elzen 2010). Considering the countless names given by C.L. Brehm, whose collection is held in part at the ZFMK, the total number of types would increase substantially, even though many of these names were never in use to a greater extent.

Although important parts of the present collection are considerably older than the foundation of the Museum Koenig, a striking feature of the ZFMK's bird collection is the high amount of data-rich specimens. This refers not only to skins but, in contrast to many other museums, also to mounted specimens both in the collection and in the exhibition. This holds true also for specimens shown in the dioramas, making them not only historically interesting but also scientifically valuable. Such a high degree of meticulous documentation still allows for outstanding research approaches.

Of particular scientific importance are local specimen series (Fig. 14.4) that represent insightful cross sections of the variation of populations at a certain place and time. For example, in the ZFMK's ornithological collection, there are remarkable local series of North Atlantic seabirds from the early 1900s (coll. A. Koenig) and songbirds from Thuringia collected during the first half of the nineteenth century (coll. C.L. Brehm). Series like these allow comparisons of genetic diversity with extant populations from the very same localities using modern analytical methods.

Another notable part of the museum's bird collection is its large number of eggs and clutches (Fig. 14.5). Compiled and labeled with great care, Alexander Koenig himself made the biggest contribution to this outstanding part of the collection. Because egg collecting has meanwhile ceased due to serious legal restrictions, the egg collection archives unique species records and sometimes even local series of populations that are now becoming of great interest again. Regarding the most recent development in scientific collecting, the ZFMK currently extends its feather collection, mainly through incorporation of bequeathed private material. Feather

**Fig. 14.4** A major strength of the ZFMK's ornithological collection lies in the existence of local series of study skins of many bird species. Being the most requested preparation type in bird collections, study skins are not only useful for a wealth of morphological approaches but have also gained tremendous interest as resources for historical DNA during the last two decades. Combined methods thus form the basis for the current research foci in the Section Ornithology of the ZFMK (Photo: © with J.F. Struwe)

**Fig. 14.5** Clutches of Golden Eagles (*Aquila chrysaetos*). The ZFMK's egg collection is the largest of its kind in German museums. It offers a wide range of study opportunities, including ongoing three-dimensional assessments of intrapopulational size and shape variability in avian eggs (Photo: © with J.F. Struwe)

collections have proved to be valuable for an array of studies, ranging from identification of bird strike remains to stable isotope analyses (Töpfer 2010).

### *14.3.2 Current Research Approaches in Museum Ornithology*

The advent of affordable broad-scale applications of molecular genetics, the profound technical advances in three-dimensional visualizations (e.g. computed tomography), and the accompanied bioinformatics and statistical tools have substantially altered the appreciation of zoological collections. The new techniques have created new demands on the use and treatment of specimens (e.g. destructive sampling). Simultaneously, the self-conception of scientific museums has changed in many places toward becoming multi-methodological research institutions. This trend is in accordance with the current scientific agenda of the ZFMK that defines the museum's main duties in the fields of original zoological research, archiving and collecting physical vouchers of biodiversity and academic teaching.

The section's predominant research strategy is defined as integrative eco-phylogeny, i.e., the study of trait evolution in space and time. Focusing on the population level, integrative methodological approaches allow an up-to-date exploitation of the scientific potential of the collection, and the research outline clearly revolves around the individual bird specimens. By doing so, valuable data can be generated that complement contemporary macroecological approaches. This is particularly interesting because community patterns are influenced by the evolutionary history and the respective adaptations of the taxa involved which can only be disentangled on a fine scale using populational approaches. Taken together, such data sets become highly informative on very different biological levels without losing their intrinsic coherence.

**Fig. 14.6** A glimpse into the collection of Christian Ludwig Brehm held at the ZFMK. These Bluethroats (*Luscinia svecica*) illustrate the enormous scientific value of this collection since most of their specimens were collected close to just a single locality in Thuringia. Compiled in the first half of the nineteenth century, such rare local series allow for unique comparisons of population structures across times scales that usually cannot be covered due to the poor preservation of specimens from these days (Photo: © with J.F. Struwe)

One of the best examples for the multifarious usefulness of bird collections for a wide range of scientific questions and methods can be seen in the bird collection of C.L. Brehm (Fig. 14.6). Compiled between 1808 and 1858, the Brehm collection is an icon of ornithology, representing one of the largest and oldest local collections of birds from those days. Because of their excellent preservation and data richness, the specimens are of paramount relevance for population studies in space and time since they allow a huge variety of modern study opportunities ranging from reflectance spectrophotometry over computed tomography to genomics. In an ongoing project, we make use of the manifold technical possibilities in order to comprehensively compare the structure of selected bird populations over a time span of 200 years.

Moreover, new technologies open up opportunities for the reexamination of natural history objects that were previously considered fully explored. For example, bird egg collections were rarely studied systematically during the last five decades but experienced a revival of interest with the application of reflectance spectrophotometry and molecular methods. One of such new methods employed at the ZFMK is the three-dimensional assessment of egg shape and coloration using a white light scanner. With the aid of highly resolved three-dimensional data, not only size and proportions can be assessed on a very fine scale, but also the absolute and relative distribution of egg shell patterns can be analyzed very well.

However, contemporary museum research is not limited to the museum itself but also includes fieldwork. Regarding the substantial research and collection tradition in Afrotropical ornithology, we currently focus on research in the Horn of Africa. The main interest lies on endemic and often only small-scaled distributed birds of the region. These taxa are studied in the field and in the museum, including molecular population studies. Of course, such research can only be realized in close collaboration with regional partners, ranging from universities to nongovernmental organizations, and it is hoped to establish joint long-term activities.

### *14.3.3 Scientific Perspective and Future Growth*

Regarding the increasing awareness of the importance of voucher specimens for population studies, biochemical or molecular analyses (Clemann et al. 2014), museums might become unable to provide adequate contemporary material in the very near future. In their own interest, museums need to prevent being reduced to merely repositories of past biodiversity. Even if historic collection holdings currently experience a scientific renaissance, the widening gaps in contemporary material will unavoidably impede similar future studies if the current temporal and geographic void cannot be filled immediately. Therefore, coordinated collecting strategies (Viscardi 2013) are needed to strengthen museums as actively working scientific institutions with inevitable research resources of data-rich material.

**Research with Dry Collections**

- Documentation for taxonomy, species descriptions based on morphology and DNA data.
- Voucher specimens for DNA samples.
- Analyses of variations within species (biogeography, evolution of subspecies, sexual variation etc.).
- Comparative morphology of whole organisms, skeletons, structure of feathers and skins, bird egg shapes.

## 14.4 A Taxonomic Collection in Alcohol: Herpetology

It is a tradition to store specimens of fragile arthropods, fish, amphibians, and reptiles in alcohol (Fig. 14.7). It is almost impossible to elucidate a species on the whole only by studying live animals. The herpetological collections of the Museum Koenig in Bonn are a typical example, which is the result of and the basis for intense research. Specimens preserved in alcohol have the advantage that many details can be studied much later after preservation. Besides only documenting the presence of species, collections can be used to describe diversity at many different levels. The examination of voucher specimens stored in alcohol allows researchers to compare the morphology, stomach contents, parasitic infestation and genetic differences, among many other disciplines of science, which would often not be possible with live or stuffed animals.

One of the primary tasks of a scientific collection is a professional and safe storage of primary types. These so called name-bearing specimens are irreplaceable

**Fig. 14.7** A small part of the very large collection of Lacertidae of the Museum Koenig conserved in alcohol (Photo: © with C. Koch)

documents of the registered biodiversity. They are indispensable for the identification of newly discovered species and allow a recheck if results from a study lead to questions about the identification of a specimen/species. Taking recourse of type specimens for comparative studies must be warranted in the long term and at any time (Böhme 2003).

Type specimens together with non-name-bearing voucher specimens document the presence of an animal at a specific place and time and document intraspecific and interspecific diversity.

In the past, diversity has often been overlooked as for identification researchers primarily studied the outer morphology of the animals. In the last years, the use of newer methods such as DNA sequencing or micro-CT scanning resulted in the discovery of higher species diversity in some taxa than previously expected. The application of these methods does not require fresh material and is also possible with voucher specimens stored in a collection for many years, allowing the reassessment of specific diversity.

Collections further allow researchers to assess how populations, species, or communities of animals have changed over time. Some collections have excellent historical series from certain areas and thus are very good representatives of past communities. Those areas can be revisited to see if the same species still exist in the same places, and if so, historical and current information on habitat, morphology, genetics, diet and other traits of the species can be compared.

**Research with Wet Collections**

- Species descriptions based on morphology and DNA data.
- Studies of population genetics with DNA extracted from preserved specimens.
- Comparative anatomy based on X-ray images and 3D-reconstructions of skeletons and soft tissues.
- Analysis of geographical variation (evolution of races, range shifts).

## 14.5 ZFMK's Herpetological Collection

Thanks to the noteworthy collectors such as Herrmann Grün (1892–1963) and Jost H. Jokisch (1881–?) and his first herpetological curator Karl F. Buchholz (1911–1964), ZFMK holds remarkable sample sizes of some Mediterranean squamate species with a particular focus on Portugal, Spain including Balearic Islands, and Greece and most of its islands and islets. This material led to numerous taxonomic revisions and new descriptions (e.g., Buchholz 1954a, b, 1955, 1960, 1961, 1962a, b, 1963, 1964; Gruber 1971; Gruber and Schultze-Westrum 1971; Beutler and Gruber 1977) and was to a large part the basis of studies on the diet (Maragou et al. 1996; Adamopoulou et al. 1999; Perez-Mellado et al. 2011), caudal autotomy (Pafilis and Valakos 2008), reproductive biology (Pafilis et al. 2011), and gastrointestinal parasites of lizards (Pafilis et al 2009; Jorge et al. 2011).

After Buchholz' sudden death in 1967, Ulrich Gruber became the second curator of herpetology at the ZFMK but returned to Munich already in 1971 to become the herpetological curator of the Bavarian State Collection of Zoology (ZSM). Subsequently, only 6 weeks after his oral doctoral examination, Wolfgang Böhme (born 1944) became the third curator of the collection which at that time consisted of only about 9500 specimens. He restructured and reorganized the collection and published the first type catalogue of ZFMK's herpetological collection, representing vouchers for 34 taxon names, including 22 primary types (Böhme 1974). The integration of private collections, together with Böhme's own collecting activities and those of his many diploma and doctoral students led to a massive increase in ZFMK's specimen numbers over the last decades with representatives from every continent. It is especially strong in its holdings from South America (Venezuela, Bolivia, Peru), Africa (Ethiopia, Cameroon, Senegal, Morocco, Mauretania, Guinea, Benin, Kenya, Zambia, Madagascar), and Asia (Caucasus, Cambodia, Iran, Vietnam, Indonesia). Many newly discovered taxa were among the collected material, leading to a considerable increase in type material (Fig. 14.8). The monotypic New Caledonian Skink (*Geoscincus haraldmeieri*), for example, was described by Böhme in 1976 (originally placed in the genus *Eugongylus*), but despite intensive searches at the type locality, it has never been found again and is meanwhile probably already extinct. The two type specimens of the ZFMK seem to be the only existing voucher specimens (Böhme 2014).

The transfer of university-based collections from Kiel, Göttingen, Heidelberg, and Saarbrücken/Trier to the ZFMK further augmented the herpetological material and comprised collections of several historically important zoologists such as Wilhelm F.G. Behn (1808–1878), Friedrich Boie (1789–1870), Heinrich Kuhl (1797–1821), Karl Möbius (1825–1908), Johann Friedrich Blumenbach (1752–1849), Adolph Arnold Berthold (1803–1861), Wilhelm Moritz Keferstein (1833–1870), Moritz Wagner (1813–1887), and Jacques von Bedriaga (1854–1906). The material collected by Paul Müller (1940–2010), formerly stored in the collections of the universities of Saarbrücken and Trier, added about 7.000 Brazilian and 3.000 Tyrrhenian amphibians and reptiles (Böhme 2014).

With these transfers, also some important type specimens (e.g., *Bothriechis schlegelii, Montivipera wagneri*) and other very interesting materials were passed into ZFMK's collection, such as an individual of the draconine agamid *Pseudocophotis sumatranus* which is extremely rare in museum collections. Or a series of the probably already extinct Chile Darwin's Frog (*Rhinoderma rufum*) that could, e.g., be examined in order to determine if an infection with the Chytrid Fungus (*Batrachochytrium dendrobatidis*) is responsible for the decline of the species. The likewise extinct Yunnan Lake Newt (*Cynops wolterstorffi*) was described by the famous European herpetologist George A. Boulenger in 1905, and investigations have shown that the specimen, which ZFMK received through the integration of the Göttingen collection, most probably stems from the same

**Fig. 14.8** Holotypes of some Varanidae described by scientists of the ZFMK. *Varanus yemenensis* (*middle*) was discovered during a television documentary in 1985 (Photo: © with C. Koch)

imported series as the six individuals which were used in Boulenger's original description (Böhme 2014).

Recently Böhme (2014) published a detailed overview of the herpetological activities in Bonn including information on the composition of the herpetological collection of the ZFMK and a critically commented type catalogue. By that time about 97.000 specimens had been catalogued at the ZFMK, and a further about 8.000 specimens are still waiting to be integrated and will bring the entire collection to considerably more than 105.000 specimens.

Turtles and crocodiles play a minor role in the herpetological collection of the ZFMK, whereas amphibians and squamates are well represented, although, as mentioned before, they are unevenly distributed based on the geographical foci. With respect to taxonomic groups, the Lacertidae are by far the best represented group with more than 25.000 individuals, including 41 primary types representing 9 species and 32 subspecies. Among this material are also some large series of certain species representing more than 20 generations and thus being of particular interest for genetic population studies. Altogether, ZFMK's herpetological collection currently houses type material of nearly 670 taxa from more than 70 countries, including 340 primary types representing 244 species and 95 subspecies. One fifth of the primary types (representing 48 species and 16 subspecies) originated from Madagascar, emphasizing the great effort of ZFMK's scientists regarding biodiversity research in this gravely threatened island. With respect to the number of described species within those groups, the Varanidae are especially well represented with 13 primary types (representing ten species and three subspecies). Among these is, e.g., the holotype of the Yemen Monitor (*Varanus yemenensis*, Fig. 14.8) which Wolfgang Böhme accidentally discovered in 1985 while watching a television documentary about the Yemen. Not to be sneezed at is also the number of primary types in the families Chamaeleonidae (16: representing 11 species and 5 subspecies), Agamidae (29: representing 23 species and 6 subspecies), and Gekkonidae (45: representing 27 species and 18 subspecies). Some of the most famous amphibian and reptile species in the world are also represented among the type material, such as two paratypes of the Golden Poison Frog (*Phyllobates terribilis*), the probably most poisonous amphibian and one of the most poisonous animals worldwide, whose poison is used in the hunting darts of indigenous people in the Colombian rainforest. Other examples of spectacular specimens housed in ZFMK's collection are the neotype of the famous Asiatic Reticulated Python (*Malayopython reticulatus*), one of the largest snake species in the world, and the precious holotype of the gecko *Sphaerodactylus dommeli* from the Dominican Republic, which is encased in amber and probably derived from the Middle Oligocene about 25 million years ago (Fig. 14.9).

Most specimens are alcohol-preserved, but the collection also contains about 1500 dry skeletal preparations (Fig. 14.10) which are of value not only for comparative anatomical studies on extant species (e.g., de Buffrénil et al. 2005, 2008) but also in paleontological respect as shown, e.g., in the description of a new snake genus from the upper Oligocene (Szyndlar and Böhme 1996) or in an investigation of evolution of snakes based on the presence or absence of certain skull bones, as supposed homologies among snakes (Palci and Caldwell 2013, 2014). Particularly noteworthy are the about 150 skulls and skeletons of the Galapagos Marine Iguana (*Amblyrhynchus cristatus*) collected and donated by Fritz Trillmich of the

**Fig. 14.9** 25 million-year-old holotype of *Sphaerodactylus dommeli* encased in amber (Photo: © with C. Koch)

**Fig. 14.10** Part of the collection of herpetological dry skeletal preparations (Photo: © with C. Koch)

University of Bielefeld. Some of these preparations were used in a comparative study on differences in the microstructure and the bone compactness values compared to its terrestrial iguanid relatives (Hugi and Sánchez-Villagra 2012). Additionally there are several hundreds of glycerine-stored cleared and stained preparations, which served in numerous studies on comparative osteology of certain reptile and amphibian taxa (e.g., Lang 1991; Glaw et al. 1998; Vences et al. 1998, 1999).

Several dozens of lung preparations in the collection demonstrated species-specific characters and were used to hypothesize the phylogenetic relationship of varanid lizards (Becker et al. 1989).

Furthermore, the collection houses nearly hundred everted and prepared hemipenes of different snake and lizard species which have not only been used as characters for descriptive morphology but also for studies on phylogenetics, sexual selection, and copulatory behavior (e.g., Ziegler and Böhme 1997; Böhme and Ziegler 2009).

**Fig. 14.11** The two-story gallery hall with cabinets for snake specimens plays an important role in guided visitor tours behind the scenes (Photo: © with C. Koch)

Exceptional—compared to other collections and thus worth mentioning—is also the arrangement of ZFMK's herpetological collection, since it is (1) very close to the offices of the scientists who work with the collection and (2) the cabinets with the snake specimens are arranged in an attractive gallery hall on two levels, which is big enough to provide space for visitor groups of 10–15 people for guided tours behind the scenes where visitors can learn much about snakes and herpetological research (Fig. 14.11).

After Böhme's retirement in 2010, Dennis Rödder (born 1979) received the position of the curator of herpetology at the ZFMK. Fortunately and contrary to a recent trend to ax taxonomic positions due to budget cutbacks, a second curatorial position was established in 2014 as a consequence of two main facts: (1) the considerable size of the herpetological collection and the respective scientific output and (2) the fact that amphibians and reptiles belong to different animal classes and were just traditionally grouped together, rooting back to Linnaeus' classification of animals. As Rödder's focus is mainly on the evolution and macroecology of amphibians and reptiles, the second position was filled with Claudia Koch (born 1980), who has a clear focus on taxonomy of amphibians and reptiles.

## 14.6 Molecular Biodiversity Research: Preparing for the Future

Research based on DNA, RNA or proteins is directly linked to biological specimens. Today, transparency, reproducibility, and credibility require the safe deposition of vouchers, samples, primary data, and open access to corresponding metadata. Therefore, natural history museums have to enlarge their scope to include new types of collections and data.

The Center for Molecular Biodiversity Research of the ZFMK was implemented in 2004 and is today one of the leading European centers for DNA barcoding, molecular phylogenetics, genomics, and biobanking.

**Molecular Biodiversity Research at the Museum Koenig**

- Coordination of a genetic inventory of the German fauna and flora based on DNA barcodes (GBOL project).
- Development of new algorithms and software for phylogenetic analysis of sequence data.
- Generation of large transcriptome data sets to study animal phylogeny.
- Genomic research to better understand the evolution of genomes and their relation to phenotypic evolution.
- Molecular phylogenies as a basis for studies on biogeography, speciation, classification.

## 14.7 DNA Barcoding: Securing Taxonomic Knowledge for Large-Scale Ecological Studies

The engagement of the Museum Koenig for large-scale DNA barcoding (Hebert et al. 2003) is motivated by the fact that taxonomy has been losing its anchorage in universities over the last decades, and today most experts able to discern and discover species are surviving among citizen scientists and in natural history museums. In view of both the rapid loss of biodiversity and decreasing number of specialists, taxonomic inventories and monitoring at species level are urgently needed. DNA barcoding is therefore a tool that can improve the availability of data drastically:

- DNA barcode libraries of correctly identified species preserve the taxonomic knowledge of experts and make this knowledge available for everybody and everywhere.
- Linking barcode libraries with databases that offer species-specific information (geographical data, images, biological data) enables rapid identification and access to information.

- Metabarcoding (mass-identification of mixed samples) using automated workflows is currently the only option for efficient and sufficiently precise analysis of environmental samples.
- Barcodes allow the precise characterization of unknown species, even when no taxonomic description is available.

A prerequisite for linking barcodes with already available knowledge is the construction of validated barcode libraries. For biodiversity in Germany, this is currently being pursued in a ZFMK-led consortium of several institutes and many citizen scientists: the German Barcode of Life (GBOL) project. The following table contains data on results of the first 3 years of this project:

| Taxon (examples) | Barcoded specimens (2012–2014) | Barcoded species (2012–2014) |
|---|---|---|
| Vertebrata | 1287 | 173 |
| Coleoptera | 7546 | ~3031 |
| Diptera | 1181 | 577 |
| Lepidoptera | 4758 | 2141 |
| Hymenoptera | 5671 | 2137 |
| Arachnida | 3420 | 670 |

At finalization of the first 3 years, about one third of the German fauna has been barcoded. The completion of the inventory depends mainly on the availability of specimens, which are mostly *provided by qualified citizen scientists.*

## 14.8 A Frozen Bank Within the Museum: The ZFMK Biobank

Within their genomes, organisms contain an immense wealth of information. These genomes have been shaped by billions of years of evolution in changing habitats. They conserve the code to understand, with high granularity and in a unified "language", adaptational processes in a multitude of different life forms. They also lend themselves ideally to identify organisms, comprehend population structures, etc. Today, progress in molecular technologies dramatically speeds up research on genetic biodiversity and finally makes it possible to tap into this rich resource. Consequently, the demand is rapidly increasing for professionally preserved and managed genome-quality tissue, DNA, RNA, and compound samples from throughout the whole tree of life. Evolution, phylogenetics, taxonomy, ecology, and conservation biology are all in need of ample sources of molecular data, as are many other disciplines.

Biodiversity biobanks ('biodiversity' as opposed to human medical biobanks) form an emerging collection type that caters to these needs specifically and complements classical natural history collections. A biobank is "a curated collection/ repository of biological materials that warrants long-term integrity at molecular level, authenticity, availability, and rights management of its samples by adhering to standard operating procedures (SOPs)" (Astrin et al. 2013). While often conveniently associated with "traditional" collections, biobanks are much better suited for modern downstream molecular analysis, as their focus lies explicitly on conserving the molecular structure of their samples. They blend in perfectly into an integrated natural history collection environment, but they contribute a new specialization to the scope of curatorial roles. Biobank curators usually operate with *sub*samples and are very aware of the distinction between specimen vouchers (e.g., morphological vouchers) and molecular vouchers, as of the general importance to deposit tandem molecular *plus* morphological vouchers. They operate in a network of interconnected samples and interconnected data, where the data is expanded by many additional (molecular) data categories and relations, including several public databases. Standardization is of special importance in biobanks due to (1) the fragility of the samples, (2) the influence of preanalytical variables on sensitive downstream applications, (3) the physically challenging environment of ultracold storage, and (4) the increased storage cost. Sample types and formats, storage conditions, labeling, operating procedures, monitoring, security, metadata, and many other aspects are important elements to standardize.

Biobanking is a rapidly growing field, and an increasing number of natural history collections are installing dedicated facilities to serve as repositories for molecular-grade samples. This is an indicator for the globally increased awareness of how relevant molecular data has become in biodiversity studies. From the pragmatic perspective, it is an indicator also for the progressive realization that holding molecular samples in individual laboratories or freezers is a storage form sustainable only for a very short term and that delegating those samples to a dedicated central facility offers a standardized, documented, secure, and sustainable form of storage.

For more than 1.5 decades, ZFMK has placed a strong focus on DNA-based applications. A central biobank for the museum, run by dedicated zmb staff, was established in 2010, building on some of the structures that had been developed since 2007 within a third-party funded project (Gemeinholzer et al. 2011): the "DNA Bank Network." While initially focused on Germany only, it later gathered international partners as well. Its data architecture and philosophy eventually (2011/2012) led into the Global Genome Biodiversity Network, GGBN (Droege et al. 2014), whose secretariat is based at the Smithsonian Institution in Washington DC. GGBN, of which ZFMK is an active partner, aims at virtually unifying the scattered collections of biodiversity biobanks worldwide in order to facilitate centralized sample access and to identify taxonomic or geographic gaps among collections, thus building a global molecular biodiversity resource. GGBN further strives to harmonize biodiversity biobank activities (through various working groups), including the development of standards and best practices.

The ZFMK Biobank archives animal samples, in accordance with the institute's profile. The biobank is structured into a tissue bank (institute and collection code: ZFMK-TIS), a DNA bank (ZFMK-DNA), and soon also an RNA bank (ZFMK-RNA) as well as a molecular compound library (ZFMK-MOL). A biobank curator

**Fig. 14.12** Ultra-frozen DNA samples in the ZFMK Biobank. For each sample, a voucher specimen is kept in the taxonomic collections (Photo: © with J.J. Astrin)

and a curatorial assistant on salaried positions plan and develop the biobank, carry out daily duties, perform experiments to optimize standards, and interact intensively with various biobanking networks and associations.

Sample storage at the time of writing is mostly at −80 °C for buffered DNA and for ethanol-fixed or snap-frozen tissues in 2 ml vials at −140 °C and −180 °C, i.e., below glass transition temperature of water (Fig. 14.12). Temperatures are being monitored externally. While samples are scattered in freezers over five different rooms at the time of writing, a new ZFMK building for molecular biodiversity research is planned and gives hope to unify the freezers and to implement a new infrastructural vision for the biobank.

External users are welcome to donate samples for long-term storage that have been or can be used for molecular analysis. To date, however, most sample depositions result from ZFMK projects. The most copious source of samples so far is the German Barcode of Life (GBOL) project (see above). Accordingly, through this project, a very strong biobank focus lies on species occurring in Central Europe.

The ZFMK Biobank grows quickly, currently containing more than 100,000 samples. Almost 10,000 species are represented.

At the ZFMK, data is kept in the Diversity Workbench database. From there, specimen and molecular data are transferred by wrappers to the GGBN web portal and to the Global Biodiversity Information Facility (GBIF), partly also to the Barcode of Life Data Systems (BOLD) and to EMBL/GenBank/DDBJ (the databases of the International Nucleotide Sequence Database Collaboration).

The website of the ZFMK Biobank can be found at https://www.zfmk.de/en/biobank.

**Research Based on Biobank Material**

- Phylogenetic or evolutionary analyses based on molecular data including complete genomes.
- Population genetics, ecology, and analyses for conservation biology.
- Addition of sequence information to complement earlier studies (e.g. extended ‘DNA barcodes’).
- Validation of previously published data based on the same material, especially in the context of integrative taxonomy.
- Discovery of parasites and symbionts.

## 14.9 Collection Data in Macroecology, Conservation Biology, and Evolutionary Biology

Increasing availability of computation power and of large-scale data sets including both gridded environmental information (e.g., temperature, precipitation, land cover, remote sensing data) and specimen-based data offer nowadays the unique opportunity to integrate very different sets of information to answer exciting novel research questions (Graham et al. 2004; Kozak et al. 2008). Digitalization efforts of natural history collections provide now not only information on the availability of specific taxa in research collections but also snapshots of the spatiotemporal distribution of species, including their biological attributes (morphology, genetics, ecology) (e.g., Graham et al. 2004; Lavoie 2013; Violle et al. 2014, Powney and Isaac 2015). For example, the Global Biodiversity Information Facility (www.gbif.org), a network collecting and providing information from numerous natural history institutions, harbors more than 500 million species records today, >470 million including exact GPS coordinates (as of July 6th 2015). The data availability is steadily increasing. However, digitalization of museum collections is a very time- and cost-consuming process which is still ongoing. Therefore, the utilization of their full value may require allocation of more resources (Johnson et al. 2011). The potential of these data sets is further increased by adding tissue and/or DNA samples and/or morphological data in specialized repositories. This opens novel fields of research and promotes the development of novel methods such as species distribution modelling (SDM) or environmental niche modelling (ENM), which have emerged only during the last decades (e.g., Guisan and Zimmermann 2000; Zimmermann et al. 2010). The popularity of these methods is steadily increasing, and today they represent an integral part of numerous further applications in biological sciences (Ahmed et al. 2015).

By combining georeferenced species records with gridded environmental data, a number of SDM algorithms have been developed to characterize a species’ realized niche in environmental space (e.g., Guisan and Zimmermann 2000; Peterson et al. 2011). Once those environmental combinations, which are likely to provide suitable

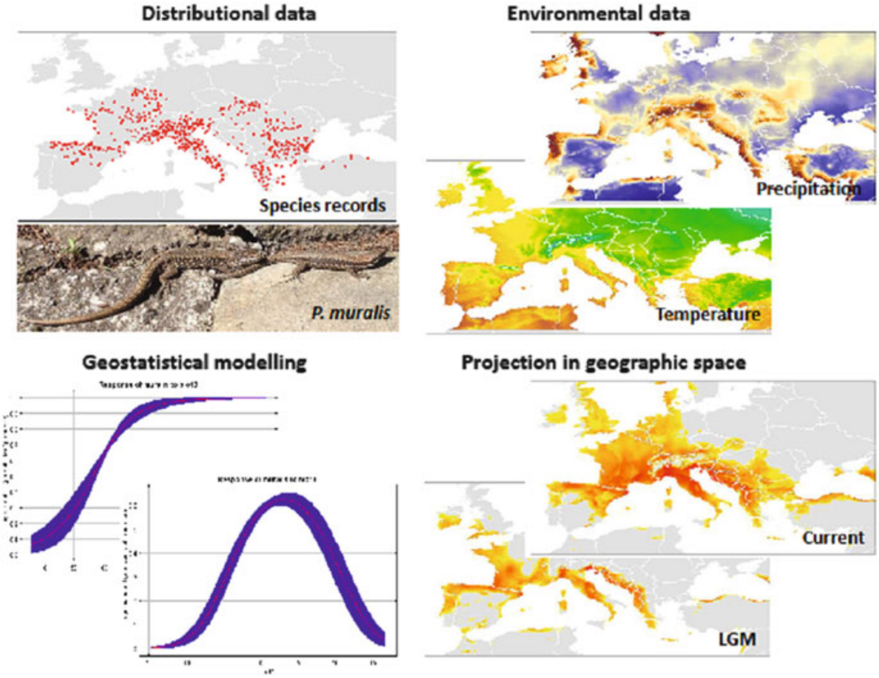

**Fig. 14.13** Generalized workflow of how a species' potential distribution can be estimated based on georeferenced museum specimens. As first step, a comprehensive set of species records is compiled (*upper left*), as well as environmental predictors, which are biologically important for the target taxa (e.g., temperature, precipitation, solar radiation, etc.) (*upper right*). Extracting the environmental conditions at the species records, it is possible to derive statistical relationships between the occurrence probability of the species given the environmental conditions (or combinations thereof) in the general area of occurrence (*lower left*). This model can now be projected from environmental space back into geographic space. Using alternative environmental conditions for model projection, it is also possible to estimate the species' potential distribution for, e.g., the last glacial maximum (LGM, *lower right*) or future climate change scenarios as proposed by the Intergovernmental Panel on Climate Change

conditions for infinite population persistence, are identified, it is possible to project this realized niche space back into geographic space as well as across time in order to assess a species' potential distribution under current, past, and future conditions (for a recent review, see Peterson et al. 2011) (Fig. 14.13). Although the general concepts of correlative SDMs is well settled in the meanwhile, this relatively new field of research is rapidly developing (Ahmed et al. 2015). There are numerous direct applications of SDMs (Powney and Isaac 2015): these comprise the identification of previously unknown populations guiding further field surveys or the identification of potential areas of risk of biological invasion (Peterson 2003). Impacts of past or future environmental changes on biodiversity can be estimated (e.g. Ihlow et al. 2012; Rödder et al. 2013), which in turn can be used for spatial explicit conservation planning and risk management. Furthermore, fine-scale

SDMs can be used to quantify habitat availability and quality to guide landscape management on how to enhance metapopulation connectivity (McShea 2014).

Combined with population genetic and/or phylogeographic information, SDMs provide an independent line of evidence to test alternative hypotheses in biogeographic analyses adding an important aspect, which cannot be captured using molecular methods only (Chan et al. 2011; Habel et al. 2015). For example, on a landscape scale, it is possible to test which landscape features affect the genetic exchange between populations using a multi-model inference approach comparing the observed genetic differentiation between populations and a set of alternative SDMs representing different hypotheses (Engler et al. 2014). Once the most appropriate model is identified, its key parameters can guide the establishment of step stone habitats during landscape planning. In a historical perspective, comparisons of phylogeographic and population genetic information with SDM projections onto climate reconstructions as expected during glacial-interglacial cycles have been shown to be able to reconstruct the origin and spatial distribution of genetic lineages as well to predict events which have led to genetic bottlenecks (Rödder et al. 2013). Facing anthropogenic climate change as predicted by the Intergovernmental Panel on Climate Change, these techniques are pivotal for the identification of areas where strong impacts on biodiversity can be expected and vice versa the identification of safe harbors requiring immediate conservation action (e.g., Keppel et al. 2012). Only biological collections can provide the essential basis for such large-scale analyses.

Information on the morphology of specimens as, e.g., obtained via geometric morphometrics can be combined with georeferenced records of the respective specimens and analyzed in a geographic information system (GIS) framework (e.g., Tomovic et al. 2010). The main advantage using this approach is that spatial interpolation techniques such as kriging allow the identification of areas with significant break points in morphological characters. This information may help to delimit taxa and allows to test for ecological and/or geographic factors leading to diversification, especially when combining them with phylogeographic/population genetic analyses and SDM-based reconstructions of historic changes in potential distributions (e.g., Habel et al. 2015).

In times of ubiquitous data availability and steadily increasing computation power, biological collections including the associated metadata are very valuable. Accumulated over centuries, only data provided by natural history collections allow detailed assessments of temporal changes in global biodiversity. Next to its immense value for basic science, the information stored in natural history collections is crucial to develop effective strategies to mitigate the most pressing effects of habitat loss/modification and climate change to safeguard global biodiversity.

**The New Use of Biodiversity Collections**

- Collections document the presence of species in space and time and are the basis for biological global change research.
- The knowledge of species experts is the basis for biodiversity monitoring and for the sustainable use of biodiversity.
- Collection and monitoring data are the basis for the development of scenarios for the future of biodiversity in a changing world.
- Collections provide a wealth of genomic information for basic and applied research.

## 14.10 The ZFMK as a Partner of the "Bonner Museums curriculum"

The "Bonner Museums curriculum" is an outstanding project that shows the role of collections for teaching and education. In this project, the primary schools of the city of Bonn cooperate with seven museums by developing a program with a variety of modules. These modules are coordinated and built upon each other, combining their contents. An increasing number of schools signed an agreement which ensures that every single class visits one museum in Bonn at least once a year. All partners benefit from their contributions to school education. Depending on how many programs the students have already gone through, at their next visit of a museum, they will carry on with the appropriate lesson.

The Museumscurriculum increases the competence of school staff for teaching and learning incorporating museums. Students and teachers can use museums independently, learning outside the classroom. Furthermore, museums and primary schools improve their image during their cooperation. A continuous progress results from these learning loops, and this process links scholar curricula contents with museum- and collection-based education.

At ZFMK, zoological specimens are used by school teachers as a basis for subjects like evolution, biogeography, species diversity, and conservation biology. However, in the Museumscurriculum, the collections per se are in focus. Young students can learn why and how specimens are preserved. They are able to show initiative and to actively participate in the coursework of collecting and cataloguing. The principles ensuring a consistent acquisition policy in a natural history museum are also mentioned.

### *14.10.1 School Programs at ZFMK*

First grade classes: get to know the museum, its exhibitions and collections. Explore and discover the objects. Learn about the tasks of the museum, such as collecting, preservation, research, and the museum as information provider. The museum is a "castle" for animals. Some parts of the exhibition are older than the founder Alexander Koenig himself. Each century has its own requirements for the documentation of the collected objects. During a guided tour through the museum, students discover different specimens (e.g. vertebrates, insects, or tissues of animals). Also, they get to know all about preparation techniques and learn about the meaning of the objects for the museum.

Second grade classes: experiencing original objects, approach, and methods (Part I). Children will perceive original objects with all senses. As a student, Alexander Koenig was an enthusiastic collector. By exploring a photo album about his life, students are going to find out why the egg collection was on focus for his research and a passion. Furthermore, children discover the egg collection and have the opportunity to experiment with chicken eggs to create their own egg collection, which then opens their view to modern collection methods.

Third grade classes: experiencing original objects, approach, and methods (Part II). The children will describe and compare and discover historical time-varying and content-based relationships. What are the changing tasks of a museum with a growing collection? By playing games, drawing, painting, sculpturing, as well as discovering and comparing original specimens, students learn the methods of identifying organisms to some taxonomic level and determining how they might be related to each other. The pupils will understand common methodologies and guidelines of collection development through educational games and experiments.

Fourth grade classes: work with the exhibits, understand their contents, and present them. Students work with objects and exhibits on their own. Ask employees of the museum: What do visitors expect from an exhibition? What kinds of information about the exhibits are necessary? Students create teams, choose specific objects for shoebox dioramas, and create mediating and easily comprehensible texts with their earned knowledge.

The "Bonner Museumscurriculum" is a trendsetting project for cultural education of children and was awarded with the first prize by "Medienberatung NRW." Classes take around 90 minutes.

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