# MUSEOMICS SYMPOSIUM 2026

# ABSTRACT BOOK

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**Organizing committee:** Martin Kapun, Luise Kruckenhauser, Andreas Kroh & Elisabeth Haring

**Advisory board**: Anja Palandacic, Martin Schwentner, Tamara Spasojevic & Nikolaus Szucsich

# CONFERENCE PROGRAM:

## 23. MARCH 2026

17:00 **Public lecture** about Museomics (in german)

MUSEOMICS: neue Erkenntnisse aus der DNA von Museumsobjekten
Martin Kapun & Luise Kruckenhauser
(Zentrale Forschungslaboratorien des NHM Wien)

In diesem populärwissenschaftlichen Vortrag bieten uns Martin Kapun, Evolutionsbiologe und Bioinformatiker am Naturhistorisches Museum Wien sowie Luise Kruckenhauser, Leiterin des DNA-Labors, einen Einblick in die Forschung am Museum. Sie zeigen, wie moderne Wissenschaft historische Sammlungsstücke in wahre Schatzkammern neuer Erkenntnisse verwandelt. Im Mittelpunkt steht „Museomics" - ein junges Forschungsfeld, das moderne Genetik mit den einzigartigen Beständen von Museen verbindet. Dabei untersuchen Forschende die Erbinformation, also den „Bauplan des Lebens", von Präparaten aus Museumssammlungen. Mithilfe hochentwickelter Labormethoden und computergestützter Analysen gelingt es, selbst aus sehr altem Material DNA zu gewinnen und zu untersuchen.
Der Vortrag zeigt Beispiele aus der aktuellen Forschung zu gefährdeten oder bereits ausgestorbenen Arten und macht verständlich, wie sich ihre Entwicklungsgeschichte im Erbgut nachvollziehen lässt. So erfahren wir, wie Arten miteinander verwandt sind, wie sie sich im Laufe der Zeit verändert haben – und was wir daraus für die Gegenwart lernen können. Denn die Analyse historischer DNA hilft nicht nur, die Vergangenheit besser zu verstehen. Ohne genetische Analysen biologischer Museumssammlungen fehlten uns wichtige Hinweise darauf, wie Tiere und andere Organismen auf die rasanten Umweltveränderungen unserer Zeit reagieren – und welche Chancen sie haben, in einer sich wandelnden Welt zu überleben.

**Freier Eintritt (ab 16:00) zum Vortrag – Kennwort „Museomics" bei der Kassa nennen**

18:30 **Registration** & **Icebreaker**

## 24. MARCH 2026

08:00 **Registration**

## WELCOME NOTE:

09:00 Welcome note by Katrin Vohland, Director General of the NHMW

## SESSION 1: CHALLENGES AND INNOVATIONS: METHODS IN MUSEOMICS

09:15 - 09:45 **Invited talk**: Carola Greve et al.: Natural history collections as an untapped source of biodiversity genomics: potential, challenges, and the need for interdisciplinarity in long-read sequencing

09:45 - 10:45 **Contributing talks**:

- Bernhard Bein et al.: Benchmarking polymerase amplification for reference genome assembly with ultra-low input HiFi-sequencing
- Katerina Douka et al.: Minimally-invasive biomolecular methods for museum collections

- Sarah Saadain et al.: Rapid and Automated pipeline for quality assessment and processing of Historical DNA
- Daria Shipilina et al.: Museomics for conservation genetics: lessons from a butterfly locally extinct in Sweden

10:45 - 11:30 **Coffee Break**

## SESSION 2: UNLOCKING THE PAST: HISTORIC DNA, NEW INSIGHTS

11:30 - 12:00 **Invited talk**: Alice Petzold et al.: Unlocking wet collections: Museomics for resolving anuran biodiversity

12:00 - 13:30 **Lunch break** and **Poster Session**

13:30 - 14:30 **Contributing talks**:

- Yves Bawin et al.: How coffee conquered the world: tracing the historical spread of Arabica coffee trees using herbarium genomics
- Pedro Frade et al.: 19th century Symbiodiniaceae baselines retrieved from museum collections indicate an increased prevalence of thermotolerant symbionts in present day Red Sea corals
- Zachary Nolen et al.: Species-specific loss of genetic diversity and inbreeding following agricultural intensification
- Ricardo Pereira et al.: The Extended Specimen Approach to Speciation Research: Integrating Genomic, Morphological, and Distributional Data to Reveal the action of Sexual Selection in a Bird Hybrid Zone

14:30 - 15:00 **Coffee Break**

## SESSION 3: MUSEUMS AS BIODIVERSITY ARCHIVES: APPLICATIONS IN CONSERVATION AND POLICY

15:00 - 16:00 **Keynote lecture**: Bernhard Misof: Closing the knowledge-action gap in conservation – The power of natural history collections

16:00 - 16:45 **Panel discussion**: Challenges and opportunities of Museomics

# ABSTRACTS

## KEYNOTE PRESENTATION

### CLOSING THE KNOWLEDGE-ACTION GAP IN CONSERVATION – THE POWER OF NATURAL HISTORY COLLECTIONS

**Author:** Bernhard Misof

**Affiliation:** Leibniz Institute for the Analysis of Biodiversity Change, Bonn, Germany

**Abstract:**

Natural history collections are among our most valuable resources for understanding biodiversity change, yet their potential remains underused in conservation and policy. While they offer unparalleled baseline data on species, ecosystems, and environmental shifts, translating this wealth of information into actionable knowledge remains a persistent challenge. This talk explores how we can close the knowledge-action gap by transforming collections from static archives into dynamic, future-oriented knowledge infrastructures.

I try to highlight the critical role of systematic collecting—both of living and historical material—in preserving biological heritage and enabling the reconstruction of lost biodiversity. Through innovative approaches like museomics, genetic data from museum specimens can now inform evolutionary history, extinction risks, and species resilience. Combined with digital tools and large-scale data integration, these materials fuel predictive models for crisis preparedness and conservation planning.

Despite progress, challenges remain: inconsistent digitization, fragmented data, and limited societal relevance hinder widespread impact. To overcome this, we should advocate for a shift from data spaces to knowledge spaces—where data is not only accessible but interpretable, contextualized, and usable by scientists, policymakers, and the public. International networks like DiSSCo and GBIF are key enablers, fostering collaboration and standardization across borders.

New collection strategies—expanding scope beyond taxonomy to include ecosystem monitoring, climate indicators, and citizen science—further enhance relevance. By embracing digital transformation, open science, and interdisciplinary collaboration, we can unlock the full potential of collections.

Corresponding author: Bernhard Misof (b.misof@leibniz-lib.de)

# SESSION1: CHALLENGES AND INNOVATIONS: METHODS IN MUSEOMICS

## INVITED TALK

### NATURAL COLLECTIONS AS AN UNTAPPED SOURCE OF BIODIVERSITY GENOMICS: POTENTIAL, CHALLENGES, AND THE NEED FOR INTERDISCIPLINARITY IN LONG-READ SEQUENCING.

**Authors:** Greve, C. [1], Gerheim, C. [1], Gscheidel, N. [2,3], Hamadou A.B. [1], Schardt, L. [1], Schneider, C. [4], Chrysostomakis, I. [5], Arantes, L. S. [6,7], Camps, C. G. [8], Brown, T. [6,7], Canesin, L. [1], Yi1, X. [9], Schell, T. [1], Mazzoni, C. J.[6,7], Böhne, A. [5], Winkler, A. [2,3], Bein, B. [1,9], Hiller, M. [1,9]

**Affiliations:** [1] Senckenberg - Leibniz Institution for Biodiversity and Earth System Research, Frankfurt, Germany; [2] Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany; [3] DRESDEN Concept Genome Center, Technische Universität Dresden, Dresden, Germany; [4] Senckenberg Research Institute, Görlitz, Germany; [5] Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig Bonn, Bonn, Germany; [6] Berlin Center for Genomics in Biodiversity Research (BeGenDiv), Berlin, Germany; [7] Department of Evolutionary Genetics, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany; [8] Departamento de Biodiversidad y Biología Evolutiva, CSIC, Museo Nacional de Ciencias Naturales (MNCN), Madrid, Spain; [9] Institute of Cell Biology and Neuroscience, Faculty of Biosciences, Goethe University Frankfurt, Frankfurt, Germany

**Abstract:**

Although samples from natural history collections have great potential for biodiversity research, success in the laboratory using molecular biology techniques has been limited so far. The main problems are: (i) DNA degradation, fragmentation, and chemical modifications; (ii) contamination by environmental DNA, or cross-contamination within the collection; (iii) low quantities of DNA; and (iv) substances that inhibit polymerases and other enzymes. Although snap-frozen samples are the gold standard for long-read sequencing (LRS) technology, they are often difficult to access. In contrast, millions of samples are available in natural history museums. In some cases, they are the only source of DNA available for extinct or difficult-to-access organisms. It is therefore important to examine whether natural history samples can be used in the LRS era. From a laboratory perspective, it is worth testing the DNA of each sample before planning further steps. Often, the DNA is so fragmented that LRS is not possible, and only short-read/target enrichment approaches are the only option. Nevertheless, our results show that sample age is not necessarily correlated with DNA quality and that collection samples can contain unexpected DNA fragments in the kilobase range. Depending on the storage medium, conditions and age, we have developed an approach for using LRS on museum samples. In summary, our results demonstrate that collection samples are a valuable yet underutilised resource for LRS. However, making effective use of natural history specimens requires close interdisciplinary collaboration with curators, companies, and sequencing providers, as well as robust benchmarks using samples from diverse taxonomic groups, in order to develop protocols for successful LRS sequencing.

**Corresponding author:** Carola Greve (carola.greve@senckenberg.de)

# CONTRIBUTING TALKS

## BENCHMARKING POLYMERASE AMPLIFICATION FOR REFERENCE GENOME ASSEMBLY WITH ULTRA-LOW INPUT HIFI-SEQUENCING

**Authors:** Bein, B. [1,2], Gerheim, C. [1], Gescheidel, N. [3,4], Canesin, L. [1], Yi, X. [1,2], Schneider, C. [5], Winkler, S. [3,4], Greve, C. [1], Hiller, M. [1,2]

**Affiliations:** [1] Senckenberg Research Institute, Frankfurt, Germany ; [2] Institute of Cell Biology and Neuroscience, Faculty of Biosciences, Goethe University Frankfurt, Frankfurt, Germany; [3] Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany; [4] DRESDEN Concept Genome Center, Technische Universität Dresden, Dresden, Germany; [5] Senckenberg Research Institute, Görlitz, Germany

**Abstract:**

While PacBio High-Fidelity (HiFi) long-read sequencing has become the one of the preferred methods to obtain reads that can be assembled into highly contiguous and complete reference genome assemblies, many potential samples remain inaccessible to HiFi sequencing because of very small amounts of long DNA fragments available, DNA damage or secondary metabolites inhibiting sequencing performance. Examples include ethanol- or formaldehyde preserved museum specimens as well as small-bodied organisms. We recently showed that amplifying DNA prior to library preparation by long range Polymerase Chain Reaction (PCR) can unlock aforementioned samples for HiFi sequencing by increasing the number of sufficiently long DNA fragments in the final library. However, amplification can introduce systematic biases caused by uneven fragment sampling and GC-content related polymerase dropouts. So far, systematic tests of different polymerase enzymes on an array of samples are lacking. Here, we test 10 enzymes on three different organisms, a collembolan, a sea slug and a bat and assess polymerase bias by comparing resulting assembly completeness, contiguity and polymerase drop-outs in relation to genome-wide GC content. We find that single polymerases perform comparably across samples, indicating that each polymerase has inherent amplification biases. Furthermore, we show that combining various polymerase read sets can increase assembly contiguity, emphasizing that polymerase-specific biases can thus be complemented. We develop guidelines for further polymerase benchmarking and best practices of how to apply our insights to other challenging samples.

**Corresponding author:** Bernhard Bein (bernhard.bein@senckenberg.de)

# MINIMALLY-INVASIVE BIOMOLECULAR METHODS FOR MUSEUM COLLECTIONS

**Authors:** Douka, K. [1,2], Pal Chowdhury, M. [1,2], Papadogianni, A. [1], Sawyer, S. [1,2], van der Sluis, L. [1], Gianni, M., [1], Higham, T. [1,2]

**Affiliations:** [1] Department of Evolutionary Anthropology, University of Vienna, Austria; [2] Human Evolution and Archaeological Sciences Research Network

**Abstract:**

Museum collections of organic remains such as bone and teeth are finite and irreplaceable resources held in trust for future generations. They support research, education, and public engagement, but are also vulnerable to cumulative damage from scientific sampling. While biomolecular techniques such as radiocarbon dating, protein analysis, and ancient DNA research have transformed our understanding of the past, they often require repeated destructive sampling, raising ethical and practical concerns for curators and conservators. In this talk, we present the development of a unified, minimally invasive workflow designed specifically with museum collections in mind. Our approach reduces physical intervention by integrating radiocarbon dating, species identification through palaeoproteomics (ZooMS), and ancient DNA analysis within a single, in-situ, extraction step. Through case studies involving worked bone artefacts, bones and teeth, we demonstrate that reliable biomolecular data can be obtained without compromising curatorial value. The workflow also simplifies curatorial decision-making by reducing the need for multiple sampling requests on the same object. This work is grounded in the recognition that archaeological remains are not expendable laboratory materials, but curated heritage objects with long-term responsibilities attached to them. While minimally invasive approaches may not always maximise analytical yield, they provide a robust compromise to help align museum policies, access and preservation, contributing to more sustainable and ethically responsible heritage science.

**Corresponding author:** Katerina Douka (katerina.douka@univie.ac.at)

## RAPID AND AUTOMATED PIPELINE FOR QUALITY ASSESSMENT AND PROCESSING OF HISTORICAL DNA

**Authors:** Saadain, S. [1,2], Kapun, M. [3], Kofler, R. [1]

**Affiliations:** [1] Institute of Population Genetics, University of Veterinary Medicine, Vienna, Austria; [2] Vienna Graduate School of Population Genetics, Vienna, Austria; [3] Central Research Laboratories, Natural History Museum Vienna, Vienna, Austria

**Abstract:**

The analysis of historical DNA (hDNA) isolated from museum specimens requires specialized computational workflows due to extensive fragmentation and post-mortem damage. We present a fully automated Snakemake pipeline for rapid evaluation of library quality, contamination, suitability for downstream analyses, and alignment to one or multiple reference genomes. As input, the pipeline requires raw sequencing data in FASTQ format and one or several reference genomes to process heterogeneous samples that may require different references. The workflow automatically distinguishes paired-end and single-end data, identifies adapter sequences, performs quality trimming, merges overlapping paired-end reads, applies quality-filtering with optimized parameters for short fragments, merges multiple libraries per sample, aligns reads, and computes quality metrics at each step. Contamination screening is performed prior to mapping, allowing early exclusion of problematic libraries. Outputs include reads aligned to one or multiple reference genomes and extensive quality reports. These provide endogenous DNA content, contamination estimates, damage patterns based on analyses with MapDamage, and read-depth summaries per contig and across non-overlapping genomic windows, offering a genome-wide overview of sequencing depth and coverage. Beyond standard contamination-detection tools, the workflow integrates our novel ECMSD tool, which identifies and taxonomically classifies mitochondrial sequences and applies a Shannon entropy–based index to assess read-distribution uniformity, distinguishing authentic aDNA from contamination and numts. By supporting heterogeneous sequencing libraries from diverse organisms in a fully parallelized and easy-to-install Snakemake-based framework, our tool provides a rapid, scalable, and reproducible solution for an in-depth assessment of contamination, degradation and yield of large-scale museomics datasets.

**Corresponding author:** Sarah Saadain (sarah.saadain@vetmeduni.ac.at)

# MUSEOMICS FOR CONSERVATION GENETICS: LESSONS FROM A BUTTERFLY LOCALLY EXTINCT IN SWEDEN

**Authors:** Shipilina, D. [1,2], Backström, N. [1], Smeds, L. [1], Irestedt, M. [3], Höglund, J. [4]

**Affiliations:** [1] Evolutionary Biology Program, Department of Ecology and Genetics (IEG), Uppsala University, Uppsala, Sweden; [2] Division of Systematic and Evolutionary Botany, Department of Botany and Biodiversity, University of Vienna, Vienna, Austria; [3] Unit of Bioinformatics and Genetics, Swedish Museum of Natural History, Stockholm, Sweden; [4] Animal Ecology Program, Department of Ecology and Genetics (IEG), Uppsala University, Uppsala, Sweden

**Abstract:**

Conservation plans for species reintroduction depend on establishing genetic relatedness between locally extinct populations and potential contemporary donor populations. Assmann's fritillary (*Melitaea britomartis*) was rapidly declining since the 1960s and was officially declared extinct in Sweden in 2018. In response to an initiative from the Västmanland county board, we used museomic and contemporary data with the aim of describing the geographic structure of *M. britomartis* for potential donor selection and quantifying genetic diversity in the Swedish populations before extinction, as low diversity could have contributed to their decline.

We generated whole-genome resequencing data from historical specimens across Sweden and contemporary material from Europe and Asia. Working with museum specimens posed two main challenges: degraded DNA and unexpectedly high sample misidentification. Despite applying multiple sequencing and bioinformatic strategies, data quality and depth remained limited. Moreover, identification of this cryptic species proved challenging and genomic screening revealed that ~10% of the butterflies belonged to several sister species.

After stringent filtering and taxonomic curation, we recovered population structure and showed that historical Swedish populations had low genetic diversity. Our results support careful evaluation of museum and field identifications, ideally combining genomics with genital morphology, and highlight the value and limitations of museomics for reintroduction planning.

**Corresponding author:** Daria Shipilina (daria.shipilina@univie.ac.at)

# POSTER PRESENTATIONS

## DATA CENTRE ‘BIODIVERSITY OF UKRAINE’ – ENTRY POINT TO MUSEOMICS

**Authors:** Rizun, V.B. [1], Hushtan, H.H. [2,3], Hushtan, K.V. [1,4], Yanytsky, T.P. [1]

**Affiliations:** [1] Department of Museum Documentation of Bioresources, State Museum of Natural History of the National Academy of Sciences of Ukraine, Lviv, Ukraine; [2] Department of Biosystematics and Evolution, State Museum of Natural History of the National Academy of Sciences of Ukraine, Lviv, Ukraine; [3] Research Department, Yavoriv National Nature Park, Ivano-Frankove, Ukraine; [4] Separate Structural Department “Lviv Professional College of the Lviv National Environmental University”, Lviv, Ukraine

**Abstract:**

The State Museum of Natural History of the National Academy of Sciences of Ukraine (Lviv) (SMNHL) is one of the oldest and leading natural history research museums in Ukraine. Founded in the mid-19th century, it now ranks among the richest such institutions in Central and Eastern Europe. The museum houses approximately 400,000 scientific specimens representing all major fields of natural science, including palaeontology (Cambrian–late Cenozoic, with internationally significant mammoth and woolly rhinoceros remains from Starunia), botany (vascular plants and bryophytes from Ukraine, the Caucasus, and Central Asia), diverse invertebrate groups, including entomology and molluscs, and vertebrates, with numerous type specimens. The SMNHL established the open-access Data Centre “Biodiversity of Ukraine” (DCBU; https://dc.smnh.org/), a national biodiversity information system currently containing 12,958 species and 86,760 specimens (17,500 digitised), including about 1,900 protected taxa. The DCBU supports searches by taxonomy, geography, habitat, conservation status, and time period, and enables the generation of species lists for specific territories, endemics, and protected groups. Together, the SMNHL collections and the DCBU form a strong foundation for museomic research integrating historical, taxonomic, and spatial data. The DCBU enables targeted specimen selection for sequencing, reconstruction of historical species ranges, and comparison of regional populations, while linking inventory data, localities, dates, and publications to minimise misidentifications and ensure reliable interpretation of historical DNA. The feedback of museomic results into the DCBU enhances the scientific and applied value of the collections, supports evidence-based decision-making, and integrates Ukraine into the global museomic infrastructure.

**Corresponding author:** Habriel Hushtan (habrielhushtan@gmail.com)

# STRONG LONG-TERM ECOPHYSIOLOGICAL RESPONSES OF PLANTS TO ELEVATED CO2 BUT NO SUPPORT FOR PROGRESSIVE NITROGEN LIMITATION IN CENTRAL EUROPE: A ROBUST HERBARIUM-BASED EVIDENCE ACROSS SPECIES AND HABITATS

**Authors:** Mráz, P. [1,2], Hanzelka, J. [3], Danihelka, J. [4,5], Jandová, K. [3]

**Affiliations:** [1] Herbarium collections, Faculty of Science, Charles University, Prague, Czechia; [2] Department of Botany, Faculty of Science, Charles University, Prague, Czechia; [3] Institute for Environmental Studies, Faculty of Science, Charles University, Prague, Czechia; [4] Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czechia; [5] The Czech Academy of Sciences, Institute of Botany, Průhonice, Czechia

**Abstract:**

Herbarium samples can provide an import insight on long-term responses to increasing atmospheric CO2 concentrations and N depositions. Using specimens repeatedly collected at the same sites, we tested the long-term effects of increased CO2 on plant physiology in the context of the progressive nitrogen limitation hypothesis. We determined foliar carbon (C) and nitrogen (N), their stable isotope compositions (δ13Cleaf and δ15N), intrinsic water-use efficiency (iWUE) and C:N ratio in herbarium specimens of ten vascular plant species collected in 1806–2017 at five natural sites in Central Europe. We found a strong decline in δ13Cleaf and δ15N, while iWUE increased considerably and C moderately over time. By contrast, N did not significantly decline either across the dataset as a whole, nor in any single species. Despite these overall patterns, responses were frequently species specific and were determined also by habitat conditions. Our results show that despite a widespread response of plants to rising CO2, we have no evidence for nitrogen limitation but rather an alternation of N source. Our study emphasizes a need to consider local environmental conditions and species identity when projecting future impacts of global change on plants and plant communities.

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## RECONSTRUCTING ANCIENT GENOMES FROM PALEOLITHIC MOLLUSK SHELLS

**Authors:** Hummer, P. [1,2], Saadain, S. [1,2], Cheronet, O. [3], Pinhasi, R. [3], Kofler, R. [1]

**Affiliations:** [1] Institute of Population Genetics, University of Veterinary Medicine, Vienna, Austria; [2] Vienna Graduate School of Population Genetics, Vienna, Austria; [3] Department of Evolutionary Anthropology, University of Vienna, Vienna, Austria

**Abstract:**

It has been shown that DNA can be preserved in mollusk shells for a very long time and a few studies have published sequence data (Der Sarkissian et al. 2017). We recently obtained shells of two marine gastropod species, Littorina littorea and Patella vulgata, that were collected from various anthropogenic shell middens in caves in northern Spain and dated to the Upper Paleolithic (10,000–17,000 BP). Due to an exceptional combination of favorable conditions, these shells are expected to preserve substantial amounts of ancient DNA.

Pilot sequencing confirms this: Several individuals exhibit an unexpectedly high amount of endogenous DNA, reaching up to 33%. This suggests that (partial) nuclear genome reconstruction is feasible—which to our knowledge has not previously been achieved for mollusks from the Paleolithic. Currently, we are deep sequencing our most promising individual of each of the two species, as well as sequencing a high number of individuals to a low coverage. This data will support the reconstruction of demographic history through haplotype networks, as well as guide the selection of additional individuals for deep sequencing. Additionally, we will also be testing if the extraction process can be improved by the use of density separation.

Reconstructions of ancient genomes are a valuable resource for evolutionary research and will—among other questions—enable us to investigate long-term dynamics of transposable elements. Pianezza et al. (2025a, 2025b) have shown that the Dipteran *Drosophila melanogaster* has experienced 12 TE invasions in ~200 years. In contrast, our material offers the opportunity to reconstruct transposable element histories on a much greater timescale, which would be a major contribution to the understanding of transposable element invasions in mollusks.

**Corresponding author:** Philipp Hummer (philipp.hummer98@gmail.com)

## INVITED TALK

### UNLOCKING WET COLLECTIONS: MUSEOMICS FOR RESOLVING ANURAN BIODIVERSITY

**Authors:** Petzold, A. [1,2], Loader, S. [3], Rödel, M.-O. [2], Thrane, C. [4], Scherz, M.D. [4]

**Affiliations:** [1] Institute of Biochemistry and Biology, University of Potsdam, Potsdam, Germany; [2] Museum für Naturkunde – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany; [3] The Natural History Museum, London, United Kingdom; [4] Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark

**Abstract:**

Natural history collections represent treasure troves of biological information, housing specimens from across the world and capturing an unparalleled breadth of spatial and temporal diversity. Once primarily valued for studies of morphology and anatomy, these collections are increasingly recognized for their potential as molecular archives. Recent developments in museomics now allow the retrieval of highly degraded DNA from archived specimens, enabling reconstructions of genetic diversity, adaptations, and evolutionary processes in unprecedented detail across time and space. For a long time, such molecular approaches were largely restricted to dry collections, while wet-preserved material—particularly ethanol- and formalin-preserved specimens—remained inaccessible due to chemically induced DNA fragmentation and cross-linking. Over the past decade, however, dedicated protocols have transformed the field, making it possible to recover DNA even from specimens heavily exposed to formalin and opening new avenues for genomic studies in groups predominantly preserved in fluid, such as amphibians. Applying a museomics approach allowed us to generate the first molecular data for name-bearing anuran type specimens housed in European museum collections, providing the foundation for robust assessments of genetic diversity and distribution for West African *Werneria* toads and clarifying taxonomic boundaries within the Tanzanian *Nectophrynoides viviparus* complex. Establishing a recent protocol dedicated to overcoming formalin-induced DNA damage in our historical laboratory at University Potsdam has further unlocked specimens once considered unusable, enabling the generation of molecular data for the supposedly extinct northern Darwin's frog (*Rhinoderma rufum*) from Chile. These case studies underscore the indispensable role of museum specimens as irreplaceable genetic archives essential for documenting biodiversity, informing conservation management, and understanding evolutionary histories.

**Corresponding author:** Alice Petzold (petzoldalice@gmail.com)

## HOW COFFEE CONQUERED THE WORLD: TRACING THE HISTORICAL SPREAD OF ARABICA COFFEE TREES USING HERBARIUM GENOMICS

**Authors:** Bawin, Y. [1,2,3,4,5], Salojärvi, J. [6,7,8], Rombauts, S. [2,9], Kelchtermans, M. [1,3], Stoffelen, P. [2], Smets, E. [1,10,11], Taylor, C.M. [12], Honnay, O. [1], Roldán-Ruiz, I. [2,3], Janssens, S.B.[1,4], Ruttink, T. [2,3]

**Affiliations:** [1] Department of biology, KU Leuven, Leuven, Belgium; [2] Department of Plant Biotechnology and Bioinformatics, Ghent University, Zwijnaarde, Belgium; [3] Plant Sciences Unit, Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Melle, Belgium; [4] Meise Botanic Garden, Meise, Belgium; [5] Hasselt University, Hasselt, Belgium; [6] School of Biological Sciences, Nanyang Technological University, Singapore, Singapore; [7] Organismal and Evolutionary Biology Research Programme, University of Helsinki, Helsinki, Finland; [8] Singapore Centre for Environmental Life Sciences Engineering, Nanyang Technological University, Singapore, Singapore; [9] Center for Plant Systems Biology, VIB, Ghent, Belgium; [10] Naturalis Biodiversity Centre, Leiden, The Netherlands; [11] Plant Sciences, Institute of Biology Leiden, Leiden University, Leiden, The Netherlands; [12] Missouri Botanical Garden, St. Louis, Missouri, USA

**Abstract:**

Arabica coffee (*Coffea arabica*) is one of the most popular beverages in the world. It is produced in over fifty tropical countries from trees that predominantly belong to two lineages of coffee varieties: Typica and Bourbon. The species *C. arabica* is endemic to the Afromontane rainforest of southwest Ethiopia. From there, humans spread coffee plants from one country to the next via consecutive introductions that started in the 15th century. Although historical records describe several of these introductions, they are often ambiguous and difficult to verify. To clarify relationships between coffee plants from different coffee growing zones, we genetically profiled 351 wild and cultivated *C. arabica* individuals from living collections and herbaria through genotyping-by-sequencing, whole-genome sequencing, and HiPlex amplicon sequencing. A phylogenetic tree based on 691 polymorphic loci confirmed multiple introduction events as described in historical literature. We found distinct origins for Typica and Bourbon coffee plants that could be traced back to East Ethiopian and Yemeni accessions. Our results provide a powerful molecular toolkit for cultivar authentication and a phylogenetic backbone for coffee breeding programs and conservation strategies. This study demonstrates how herbarium genomics can resolve historical dispersal patterns of crops and facilitate the conservation of crop genetic resources.

**Corresponding author:** Yves Bawin (yves.bawin@meisebotanicgarden.be)

# 19TH CENTURY SYMBIODINIACEAE BASELINES RETRIEVED FROM MUSEUM COLLECTIONS INDICATE AN INCREASED PREVALENCE OF THERMOTOLERANT SYMBIONTS IN PRESENT DAY RED SEA CORALS

**Authors:** Frade, P.R. [1], Roch, C. [1,2], Hume, B. [3], Sattmann, H. [1], Herndl, G. [4], & Haring, E. [1]

**Affiliations:** [1] Natural History Museum Vienna, Vienna, Austria; [2] IMBRSea, International Master of Science in Marine Biological Resources, Ghent, Belgium; [3] University of Konstanz, Konstanz, Germany; [4] University of Vienna, Vienna, Austria

**Abstract:**

Elevated sea surface temperatures have driven coral reef degradation to unprecedented levels on a global scale. The resilience of coral reefs is highly dependent on the mechanisms underpinning adaptation and acclimatisation at the level of symbiosis between the coral animal and its Symbiodiniaceae endosymbionts. However, baseline data on coral-symbiont associations from before the onset of major anthropogenic influences on coral reefs are lacking, thus preventing us from understanding coral holobiont adaptation on multi-decadal to century time scales. Here, we demonstrate that the Symbiodiniaceae community of ~150-year-old ethanol-conserved museum specimens can be characterized by analysing the ITS2 subregion of the nuclear ribosomal RNA gene cluster. Using the wet coral collection of the Natural History Museum in Vienna (Austria), amplicon-based metagenomics and the SymPortal analytical framework, we characterized coral-Symbiodiniaceae associations in eight genera of scleractinian corals (*Acropora*, *Echinopora*, *Madrepora*, *Platygyra*, *Pocillopora*, *Porites*, *Stylophora*, *Seriatopora*) and three genera of octocorals (*Sarcophyton*, *Sinularia*, *Tubipora*) collected from the Red Sea between 1878-1896 to generate a coral symbiont early industrial baseline. Through comparisons with published results of modern symbiont communities, we show that historical Red Sea corals predominantly associated with *Cladocopium* symbionts and that there is an increase in relative abundance of *Durusdinium* symbionts in modern samples. Historical associations, similar to modern associations, demonstrate a high symbiont host-specificity. Our findings provide an invaluable first insight into the community composition prior to the onset of anthropogenic climate change and thus, serve as guideline and starting point for future studies. The present study also demonstrates the importance of protecting and preserving specimens and the invaluable insights that can be obtained from studying historical scientific collections.

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# SPECIES-SPECIFIC LOSS OF GENETIC DIVERSITY AND INBREEDING FOLLOWING AGRICULTURAL INTENSIFICATION

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**Abstract:**

Land-use change driven by agricultural intensification is a major contributor to insect declines globally. As a result of population decline and subdivision, species lose genetic diversity, reducing adaptive potential and increasing genetic load. We examine how genetic diversity has changed over the past century in three focal and five additional Polyommatinae butterfly species in Sweden by sequencing specimens from museum collections. As reference bias from fragmented DNA made comparing these samples to modern sequences unreliable even under alignment protocols optimized for historical samples, we constructed variation graphs for sequence alignment that include genetic variation identified in modern samples. We found that this approach reduced reference bias and sample type biases in downstream results, improving comparability. Based on 59 historical and 90 contemporary genomes, we document a 6% decline in genetic diversity in the grassland specialist *Cyaniris semiargus*, driven by increased isolation. In contrast, generalist *Polyommatus icarus* and heathland specialist *Plebejus argus* have maintained genetic diversity and connectivity. Reduced heterozygosity in *Cy. semiargus* reflects increases in runs of homozygosity, increasing the homozygosity of derived mutations at missense and conserved positions. While genomic erosion is currently mild, it lags demographic change. We infer demographic declines in *Cy. semiargus* that are considerably larger than declines in genetic diversity. We use simulations to show that only mild losses of genetic diversity are expected at the early stages of demographic decline, leaving populations with substantial genetic extinction debt. Two of five additional species have suffered similar reductions in genetic diversity, underscoring that restoration of grassland habitat is necessary to restore gene flow and halt further genomic erosion in specialist grassland insects.

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# THE EXTENDED SPECIMEN APPROACH TO SPECIATION RESEARCH: INTEGRATING GENOMIC, MORPHOLOGICAL, AND DISTRIBUTIONAL DATA TO REVEAL THE ACTION OF SEXUAL SELECTION IN A BIRD HYBRID ZONE

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**Abstract:**

Sexual traits are widely recognized to evolve early in the speciation process and have been considered by taxonomists as primary contributors to reproductive isolation. However, it remains unclear whether sexual selection alone can maintain species boundaries over time, particularly when demographic shifts driven by climate change increase opportunities for hybridization between nascent species. Using the extended specimen framework, we integrated genomic, morphological, and distributional data to investigate speciation processes in a moving avian hybrid zone between black-headed and red-headed buntings. Employing collectomics, distributional analyses uncovered previously unrecognized ecological divergence between the species and supported a demographic scenario of asymmetric range expansion during the current interglacial period. Whole-genome data corroborated this hypothesis and revealed that approximately 1.5% of the genome exhibits elevated differentiation consistent with selection against gene flow. Morphological analyses demonstrated that selection acting on male plumage traits imposes stronger reproductive barriers than on morphometric characters. Collectively, these findings highlight sexual selection as the dominant force maintaining species boundaries despite extensive range shifts. This study exemplifies how combining museomics, extended specimen data, and collectomics provides a powerful integrative approach to understanding early speciation mechanisms and the resilience of species boundaries in spite of dynamic distributional changes driven by climate change.

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# HOW MANY BABIES IN THE BUSH? REEVALUATING SPECIES DIVERSITY AND EVOLUTIONARY HISTORY OF WESTERN DWARF GALAGOS (GALAGOIDES) IN AFRICA'S GUINEO-CONGOLIAN FORESTS.

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**Abstract:**

Understanding evolutionary processes in biodiversity-rich regions, like Africa's Guineo-Congolian forests, is crucial to explain patterns of species richness and endemism. We conducted population genetics and phylogenetic analyses to clarify species boundaries in the western dwarf galagos (genus *Galagoides*), a clade with unclear morphological diagnoses. Genotypic clustering analysis based on genomic data from 130 museum specimens reveals two broadly co-distributed groups with minimal genetic admixture and similar substructure patterns across sub-Saharan rainforests. Transitions between these lineages align with the Sanaga River Basin, suggesting that shared historical landscape shifts have shaped similar patterns of population structure across species. Cranial trait differentiation further supports evolutionary divergence. Our findings underscore the value of historical DNA to clarify species boundaries, aiding IUCN data-deficient species in understudied Africa's lowland rainforests.

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# ANCIENT DNA OF THE TORONTO SUBWAY DEER ADDS TO THE EXTINCTION LIST OF ICE AGE MEGAFAUNA

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**Abstract:**

The Late Pleistocene was a time of global megafaunal extinctions that were particularly severe in North America. The continent lost many mammal taxa, but the validity of several remains ambiguous, including a high proportion of Cervidae taxa. *Torontoceros hypogaeus* is represented by a single specimen (ROMM75974) discovered in 1976 during excavation work for the Toronto subway in Canada. The species was described based on its unique antler morphology, but the variable nature of that trait and the species near absence in the fossil record leads to uncertainty concerning its systematic relationships. We used ancient DNA to clarify the taxonomic relationship and evolutionary history of *T. hypogaeus*. We performed mitochondrial and whole genome analyses with related cervids and showed that ROMM75974 has a close affinity, but relatively high divergence from *Odocoileus* sister species. While some ambiguity remains, ROMM75974 could represent a distinct *Odocoileus* species to be included in the list of extinct North American taxa. This unique population was likely adapted to open landscape, which was rapidly replaced with dense woodland in this region at the end of the Pleistocene, highlighting the role of climate change in the extinction of megafauna biodiversity at the end of the ice age.

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# ANCIENT DNA DOCUMENTS THE PRESENCE OF AN EXTINCT LINEAGE OF EUROPEAN BISON IN WESTERN EUROPE

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**Abstract:**

Among the bovids occurring in Europe during the Late Pleistocene, the aurochs (*Bos primigenius*), the steppe bison (*Bison priscus*) and the European bison (*Bison bonasus*) went extinct in the wild. To trace and understand their population decline, species identification of archaeological bones is essential, but, when these show too few morphological characters, ancient DNA can be a powerful tool to document past biodiversity.

To document the population decline of bovids during the transition between the Late Pleistocene and the Holocene, we analysed the ancient DNA of two bovid bone fragments (a metatarsus and a first phalanx), dating from 14.93–14.31 ka cal. BP and 11.97–11.76 ka cal. BP (calibrated thousand years before present), respectively, and collected in a small rock-shelter named Grotte Genvier, Belgium. Shotgun sequencing produced 25.49 and 0.10% of endogenous DNA, with average lengths of 53 and 50 bp and covering more than 90 and 15% of the mitochondrial genome, respectively. DNA data of both samples matched one lineage of European Bison (called Bb1) that showed a more northern distribution and went extinct in the early Holocene (ca. 9 ka). It diverged ca. 97 ka from the other lineage (called Bb2), which showed a more southern distribution and survived the Late Pleistocene megafaunal extinctions (but ended up as 54 captive individuals during the 20th century). These results are informative about the southern distribution of lineage Bb1 during its decline because after 15 ka, all records available for this lineage are from Scandinavia.

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# REVISITING MUSEUM ARCHIVES TO REVISE FAUNAL BIOGEOGRAPHY - THE PALEOGENOMIC HISTORY OF COMMON VOLES IN THE BRITISH ISLES

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**Abstract:**

Museum collections across the United Kingdom preserve an underused record of small mammal fauna from early excavations. The common vole (*Microtus arvalis*), long considered absent from mainland Britain and restricted to the Orkney archipelago, provides a valuable case study for re-evaluating British faunal history. Early 20th-century excavations recovered Microtus remains from several British sites, but ambiguous morphology and the assumption of local absence meant these specimens received little attention. Using ancient DNA methods on archival material excavated between the 1910s and recent decades, we identify *M. arvalis* among faunal assemblages from mainland Britain. Material from over four museums representing sixteen sites across the British Isles spanning the Late Pleistocene to Early Holocene provides data to reconstruct the species' history. Low-coverage nuclear genomes confirm the taxonomic assignment of 22 specimens from six sites as *M. arvalis*. Mitochondrial phylogenies placed them within the Western North clade of western mainland Europe, suggesting colonisation from continental Europe via southern Britain towards Orkney. Affinity between ancient southern samples and modern Orkney specimens indicates population continuity before the isolation of the archipelago. Orkney voles, including ancient Birsay Bay and Links of Noltland, form a distinct sublineage diverging ~9.6 ka BP, predating Neolithic settlement and consistent with natural colonisation before postglacial sea-level rise. These findings indicate that *M. arvalis* was formerly present on mainland Britain and later became locally extirpated, and the Orkney population could be a remnant. This study demonstrates the value of museum collections and palaeogenomics for re-assessing long-standing biogeographic assumptions.

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# DNA OF TYPE AND HISTORICAL SPECIMENS AS THE WAY OF BACK UP OF VALUBLE INFORMATION ABOUT COLLECTIONS AT RISK

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**Abstract:**

The Russian war of aggression against Ukraine and the ongoing threat of shelling in Kharkiv since 2022 pose an imminent risk of losing valuable scientific collections, including type specimens of more than one hundred animal taxa, housed in the Museum of Nature at V. N. Karazin Kharkiv National University.

We argue that, in addition to traditional digitization methods (such as scanning and imaging), DNA skimming and genome sequencing of total DNA extracts from tissue samples of type and historical biological specimens represent the most comprehensive approach to preserving biologically relevant information—including potential ecological context—associated with each specimen.

Here, we present the results of a collaborative effort aimed at sequencing the collections of the Museum of Nature.

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# INTEGRATING (IMMUNE)GENOMIC INFORMATION FROM HISTORIC SAMPLES IN CONSERVATION RECOMMENDATIONS FOR ENDANGERED SPECIES.

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**Abstract:**

Museum collections harbour an immense treasure of past and sometimes lost biodiversity. Harvesting genomic data from ancient or historic material for comparative analyses with modern data from endangered populations provides valuable information of the demography of a species including potential bottlenecks, hybridisation, and population fragmentation. In this talk, we will present (immune) genomic diversity of historic versus modern wild felids, namely jaguar and cheetah. We will show how the inclusion of historic samples can inform management recommendations for the conservation of modern endangered populations.

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# MUSEOMICS REVEALS WHETHER HUMANS TRIGGERED WIDESPREAD GENOME INVASIONS ACROSS SPECIES

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**Abstract:**

When we compared the genomes of 200-year-old fruit flies (*Drosophila melanogaster*) from museum collections and recently captured wild flies we were surprised to find that large parts of the fruit fly genome were missing from the old specimens. About 1 million base pairs, roughly 1% of the genome, were absent from the old flies. These missing parts largely consist of transposable elements (TEs)—parasitic DNA sequences that replicate in genomes. TEs can occasionally be horizontally transferred (HT) between species by an unknown mechanism. Traditional approaches, such as comparing the genomes of different species, suggest that HT is a rare event. However, these approaches suffer from several limitations and thus underestimate the true extent of HT. Museomics enables an alternative approach: by comparing the genomes of old and extant specimens we can for the very first time obtain an unbiased estimate of the true extent of HT. Our work showed that in total 12 different TEs have invaded the fruit fly genome over the last 200 years, suggesting that the extent of HT in insects may be massive. This finding raises a lot of questions, such as whether human activity led to an increase in rate of genome invasions and whether other species show a similarly high rate of genomic invasions.

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## WHAT WAS OLD IS NEW AGAIN: RECENT ADVANCE AND PERSPECTIVE OF MUSEOMICS IN COLEOPTERA

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**Abstract:**

Natural history collections (NHC), most often kept in research institutions such as museums or universities, are spatio-temporal testimonies to biological diversity. Indeed, they provide information about the presence of species in a given place, during a given period. They therefore represent what we currently know about this biodiversity. A significant challenge hindering the examination of these historical processes lies in the difficulty of obtaining biological material from all regions where species are distributed. The significant biodiversity in collections makes it possible to bypass this obstacle by taking into account not only present biodiversity, but past biodiversity as well. NHCs are therefore remarkable tools for understanding the origin and evolution of biodiversity. Despite their inherent richness, these collections are often underutilized, particularly concerning their genetic resources. Recent advancements in methods now facilitate the sequencing of highly fragmented DNA, unlocking the potential of often-aged collection specimens. While specimens within NHCs are conventionally employed in a traditional taxonomic context, they also contain genetic information waiting to be explored. For example, museomics has been used to resolve phylogenies, for accurate species designation using DNA from type specimens, to reveal cryptic species, to assess the phylogenetic relationship of extinct lineages, and to investigate genetic changes in populations over time. Moreover, molecular analysis of museum specimens can also accelerate the process of species discovery. This presentation aims to highlight recent advances and perspectives of museomics in Coleoptera. We investigate the advantages and disadvantages of this approach, demonstrating how collections are now considered as indispensable sources of molecular data and offering a deeper understanding of evolutionary processes.

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## MUSEOMICS IN UNDERSTANDING GREAT APE EVOLUTION

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**Abstract:**

Museomics—the genomic study of museum specimens—is transforming research on great apes by allowing us to recover and analyze historical DNA and RNA from preserved specimens over centuries. As many great ape populations have declined drastically over the last century, museum collections provide irreplaceable snapshots of past genetic diversity, population structure, and evolutionary change. We have sampled valuable great ape museum collections from diverse museums in Europe, including the Museum of Natural History Vienna, of various types, such as teeth, skin and wet specimens. Upon preparing the DNA and RNA libraries using the samples, we screened the data and assessed the features of each specimen type, screened against potential pathogens, and finally, tried to recover authentic genomes and transcriptomes.

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# A MOLECULAR REFERENCE DATABASE OF MITOCHONDRIAL GENOMES FOR FRESHWATER FISH IN FRANCE

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**Abstract:**

In the last decade, non-invasive approaches to studying biodiversity, such as eDNA or metabarcoding are being employed extensively and with efficacy in aquatic environments for investigative purposes. Nevertheless, the effectiveness of these approaches hinges upon the availability of a reliable molecular reference database. Voucher specimens stored in museum collections are the cornerstone of establishing a reliable reference dataset. However, the majority of sequences currently accessible in public databases are insufficiently reliable. This is due to several factors, including the absence of vouchers specimens, the lack of available sequences for some taxa, and identification inaccuracies or errors.

Despite significant advances in the taxonomic understanding of the fish fauna of France over the past two decades, there remains a dearth of comprehensive molecular data. These precludes the full identification and interpretation of sequence data obtained by eDNA and metabarcoding. The decision was therefore taken to established a molecular reference database, in close collaboration with taxonomic experts, comprising the complete mitochondrial genomes of all freshwater fish species occurring in France.

This database will be accessible and searchable by all relevant parties (researches, institutions, NGOs…), with the aim of strengthening molecular expertise and use. Specimens from recent surveys will be combined with those from museum collections in order to ensure the reliability of the sequences. The aim is also to enhance the value of museum collections by including sequences of type specimens within a comprehensive dataset. Finally, the database of complete mitochondrial genomes enables interoperability with the markers commonly used in various ichthyological studies (12S, 16S, COI or Cytb), ranging from taxonomic reviews and eDNA studies to phylogenetics analyses and population genetics studies.

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