GeoBio-Center LMU
Report 2022 - 2024

GeoBio-Center^{LMU} Report 2022 - 2024

Editor: Dirk Erpenbeck

Contents: Elena Cuesta, Gonzalo Gomez-Saez, Sebastian Höhna, Gerrit Nanninga, Paul Schmidt, Gert Wörheide

Layout: Martine Focke, Dirk Erpenbeck

GeoBio-Center ^{LMU}, Richard-Wagner-Str. 10, 80333 München - http://www.geobio-center.uni-muenchen.de

Contents

Welcoming note

Dear Ladies and Gentlemen, dear Colleagues,

Prof. Dr. Gert Wörheide
Spokesperson of the GeoBio-Center [LMU]

It is with great pleasure that I present the Biannual Report of the GeoBio-Center LMU for the years 2022–2024. This report documents the scientific achievements and ongoing activities of our member groups and provides an impressive overview of the breadth and depth of research undertaken within our network. The GeoBio-Center continues to serve as a central platform for interdisciplinary collaboration at the interface of the earth- and biological sciences, fostering integrative research that addresses fundamental questions about the evolution of life and Earth through time.

The research groups represented in this report reflect the full spectrum of geobiological investigation — from paleontology and sedimentology to geochemistry, molecular systematics, evolutionary biology, geomicrobiology, and biogeochemistry. Together, they exemplify the diversity and strength of our community, combining field-based, experimental, and molecular approaches to explore biological processes in their earth science context. The collaborative spirit among these groups remains one of the defining qualities of the GeoBio-Center, enabling innovative perspectives on both ancient and modern biosphere–geosphere interactions.

During the past two years, our members have advanced numerous national and international research initiatives, contributed to high-impact publications, and successfully acquired third-party funding to support new projects and infrastructure. The dedication of our early-career researchers, doctoral candidates, and students continues to play a vital role in shaping the future of our field. Their enthusiasm and creativity, together with the commitment of our senior scientists, ensure the continued excellence and visibility of the GeoBio-Center within LMU and the wider research community.

I would like to express my sincere appreciation to all members for their contributions to research, teaching, and outreach, and to those who have been instrumental in preparing this report. It provides not only a record of our achievements but also a reflection of the collegial and interdisciplinary culture that defines our center.

I invite you to explore the following pages as a testament to the vitality and success of the GeoBio-Center and to the shared commitment of its members to advancing geobiological science.

Gert Wörheide

Spokesperson, GeoBio-Center LMU

Members of the GeoBio-Center[LMU]

Prof. Dr. emer. Reinhard Agerer	LMU, Systematics, Biodiversity and Evolution of Plants
Prof. Dr. emer. Wladyslaw Altermann	University of Johannesburg, Dept. of Geology, South Africa
Prof. Dr. Michael Amler	University of Cologne
Dr. Thodoris Argyriou	American College of Greece, Greece
Dr. Michael Balke	SNSB, Bavarian State Collection for Zoology
PD Dr. Ehrentraud Bayer	SNSB, Botanical Garden Munich-Nymphenburg
Prof. Dr. Julia Bechteler	LMU, Systematics, Biodiversity and Evolution of Plants
PD Dr. Andreas Beck	SNSB, Bavarian State Collection for Botany
Prof. Dr. Madelaine Böhme	University of Tübingen, Senckenberg Center for Human Evolution and Paleoecology
Prof. Dr. Richard Butler	University of Birmingham, UK
Dr. Diego Castanera	University of Zaragoza, Spain
Dr. Ana Catalán	LMU, Evolutionary Biology
Dr. John Clarke	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Alessio Capobianco	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Elena Cuesta	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Julia Brenda Desojo	Consejo Nacional de Investigaciones Científicas y Técnicas: La Plata, Argentina
Prof. Dr. Dirk Erpenbeck	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Eva Facher	LMU, Systematics, Biodiversity and Evolution of Plants
PD Dr. Andreas Fleischmann	SNSB, Bavarian State Collection for Botany & LMU, Faculty of Biology
Dr. Günter Försterra	Pontifical Catholic University of Valparaíso, Chile
Prof. Dr. Anke Friedrich	LMU, Dept. of Earth and Environmental Sciences, Geology
Dr. Maren Gaulke	Philippine Endemic Species Conservation Project (PESCP)
Dr. Juan Carlos Gaviria	Centro Jardin Botánico, Fac. Ciencias, ULA, Venezuela
Prof. Dr. Stuart Gilder	LMU, Dept. of Earth and Environmental Sciences, Geophysics
Dr. Frank Glaw	SNSB, Bavarian State Collection for Zoology
PD Dr. Ursula Göhlich	Natural History Museum Vienna, Austria
Dr. Gonzalo Gomez-Saez	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Prof. Dr. Marc Gottschling	LMU, Systematics, Biodiversity and Evolution of Plants
Dr. Erika Griesshaber-Schmahl	LMU, Dept. of Earth and Environmental Sciences, Crystallography
Prof. Dr. emer. Gerhard Haszprunar	LMU, Faculty of Biology, Systematic Zoology

Prof. Dr. Joachim Haug	LMU, Zoomorphology
PD Dr. Carolin Haug	LMU, Graduate School Life Science Munich
Dr. Axel Hausmann	SNSB, Bavarian State Collection for Zoology
Prof. Dr. Verena Häussermann	San Sebastián University, Chile
Prof. Dr. emer. Wolfgang Heckl	TUM
Prof. Dr. emer. Ernst Hegner	LMU, Dept. of Earth and Environmental Sciences, Mineralogy, Petrology and Geochemistry
Prof. Dr. Martin Heß	LMU, Systematic Zoology
Prof. Dr. emer. Günter Heubl	LMU, Systematics, Biodiversity and Evolution of Plants
Prof. Dr. Sebastian Höhna	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Prof. Dr. Stefan Hölzl	SNSB, Riescrater-Museum, Nördlingen & LMU, Faculty of Geosciences
Prof. Dr. Gudrun Kadereit	LMU, Systematics, Biodiversity and Evolution of Plants & SNSB, Botanical Garden Munich-Nymphenburg
Dr. Baran Karapunar	University of Leeds, UK
Dr. A. Kempe	München
Prof. Dr. Manfred Krautter	Plüderhausen
Dr. Barbara Kremer	Institute of Paleobiology, Biogeology Department, Polish Academy of Sciences
Prof. Dr. Michael Krings	SNSB, Bavarian State Collection for Palaeontology and Geology & LMU, Faculty of Geosciences
Prof. Dr. Christian Laforsch	University of Bayreuth
Dr. Helmut Lehnert	Oberottmarshausen
Prof. Dr. emer. Reinhold Leinfelder	Holzkirchen
Prof. Dr. Dario Leister	Faculty of Biology, LMU
Prof. Dr. Yu Liu	Yunnan University, Kunming, China
Dr. Adriana Lopez Arabello	München
PD Dr. Renate Matzke-Karasz	LMU, Faculty of Geosciences
PD Dr. Christoph Mayr	FAU Erlangen-Nürnberg & LMU Faculty of Geosciences
Prof. Dr. Roland Melzer	SNSB, Bavarian State Collection for Zoology & LMU Faculty of Biology
Dr. Gerrit Nanninga	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
PD Dr. Michael Nickel	Stuttgart
Dr. Martin Nose	SNSB, Bavarian State Collection for Palaeontology and Geology
Prof. Dr. Alexander Nützel	SNSB, Bavarian State Collection for Palaeontology and Geology & LMU, Faculty of Geosciences
Prof. Dr. William Orsi	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Prof. Dr. Jörg Overmann	SNSB, Bavarian State Collections of Natural History

Prof. Dr. Joris Peters	LMU, Faculty of Veterinary Medicine & Bavarian State Collection for Anthropology and Palaeoanatomy
Prof. Dr. emer. Nikolai Petersen	LMU, Department of Earth and Environmental Sciences, Geophysics
Dr. Stefan Raidl	München
Prof. Dr. Oliver Rauhut	SNSB, Bavarian State Collection for Palaeontology and Geology & LMU, Faculty of Geosciences
PD Dr. Mike Reich	Staatliches Naturhistorisches Museum, Braunschweig
Prof. Dr. Bettina Reichenbacher	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Nicola Reiff	SNSB, Bavarian State Collection for Zoology
Dr. Bernhard Ruthensteiner	SNSB, Bavarian State Collection for Zoology
Dr. Ulrich Schliewen	SNSB, Bavarian State Collection for Zoology
Prof. Dr. emer. Wolfgang Schmahl	LMU, Dept. of Earth and Environmental Sciences, Crystallography
Prof. Dr. Michael Schrödl	SNSB, Bavarian State Collection for Zoology & LMU, Faculty of Biology
Prof. Dr. emer. Florian Siegert	München
Prof. Dr. Herwig Stibor	Faculty of Biology, LMU
Prof Dr. Elena Sturm	LMU, Dept. of Earth and Environmental Sciences, Crystallography
Prof. Dr. Ralph Tollrian	Ruhr-University, Bochum
PD Dr. Anneke van Heteren	SNSB, Bavarian State Collection for Zoology & LMU, Faculty of Biology
Dr. Winfried Werner	SNSB, Bavarian State Collection for Palaeontology and Geology
Prof. Dr. Christian Wild	University of Bremen
Prof. Dr. Gert Wörheide	LMU, Dept. of Earth and Environmental Sciences, Palaeontology & Geobiology
Dr. Shinnosuke Yamada	International University of Health and Welfare, Narita, Japan
Dr. Anže Žerdoner Čalasan	LMU, Systematics, Biodiversity and Evolution of Plants
Prof Dr. Albert Zink	SNSB, Bavarian State Collection of Anthropology

SYMPOSIUM
20 Years GeoBio-Center[LMU]
21.10.2022

The GeoBio-Center LMU marked its twentieth anniversary with a symposium entitled “Past, Present, and Future”, held on 21 October 2022 at the Botanical Institute in Munich. Following the annual General Meeting, the event opened with welcoming remarks from Prof. Dr. Gert Wörheide (Speaker, GeoBio-Center LMU), Prof. Dr. Oliver Jahraus (Vice President for Teaching and Studies, LMU), Prof. Dr. Joris Peters (General Director, Bavarian Natural History Collections – SNSB), Prof. Dr. Dario Leister (Dean, Faculty of Biology, LMU), and Prof. Dr. Claudia Trepmann (Dean, Faculty of Geosciences, LMU). Their addresses highlighted the center’s achievements over two decades and its pivotal role in promoting interdisciplinary research across the life and earth sciences.

Figure: Welcoming remarks from Prof. Dr. Oliver Jahraus (Vice President for Teaching and Studies, LMU)

The scientific programme reflected the breadth of geobiological research at LMU and beyond. New member Prof. Dr. Gudrun Kadereit (Chair of Systematics, Biodiversity and Evolution of Plants, LMU) opened the academic program with a talk on plant evolutionary dynamics in arid environments, followed by a series of contributions from past members. Prof. Dr. Christian Wild (University of Bremen; Emmy Noether Group Leader 2006–2010) examined the responses of reef-building organisms to rapid environmental change. Prof. Dr. Richard Butler (University of Birmingham; Emmy Noether Group Leader 2011–2013) presented new insights into the Triassic emergence of dinosaurs and their close relatives. After a coffee break, Prof. Dr. Christine Böhmer (University of Kiel; Marie Skłodowska-Curie Postdoctoral Fellow 2020–2021) provided an evolutionary perspective on organismal form and function. Dr. Sebastian Höhna (LMU; Emmy Noether Group Leader since 2019; ERC Starting Grantee 2022) addressed the causes of historical biodiversity fluctuations, and Dr. Gonzalo Gomez (LMU; Emmy Noether Group Leader since 2022) explored the impact of ocean deoxygenation on dissolved organic matter sequestration. Finally, Natalie Barbosa (Project AlpSenseRely) reported on the development of early-warning systems for climate-driven alpine hazards.

Together, these presentations showcased the breadth and diversity of interdisciplinary research pursued within the GeoBio-Center and demonstrated how the center has supported the scientific and career advancement of many of its members. A convivial evening reception concluded the event, fostering exchange among attendees and underscoring the continued relevance of the GeoBio-Center as an integrative hub shaping the future of geobiology and biodiversity research at LMU and beyond.

Figure: Programme SYMPOSIUM 20 Years GeoBio-CenterLMU

Marie S. Curie ITN "IGNITE" - Illuminating Biodiversity Genomics Across the Tree of Life

(Coordinator: Prof. Dr. Gert Wörheide)

Scope and Objectives

The European Innovative Training Network (ITN) IGNITE (2018–2022) was a Marie Skłodowska-Curie Action coordinated at the GeoBio-Center, LMU Munich. It brought together 15 doctoral researchers and 12 European partner institutions to advance biodiversity genomics of non-model invertebrates and to train a new generation of scientists in integrative genomics, bioinformatics, and evolutionary biology. IGNITE addressed major gaps in our understanding of animal genome evolution and biodiversity by combining cutting-edge sequencing technologies with innovative computational tools. The program aimed to: (1) produce high-quality genome and transcriptome resources for diverse, underrepresented invertebrate taxa; (2) develop and optimise analytical software for genome assembly and phylogenomic inference; (3) resolve key evolutionary relationships among major animal lineages; and (4) identify novel bioactive compounds with potential biomedical applications.

Key Achievements and Research Highlights:

Expanding Genomic Resources for Non-Model Invertebrates

IGNITE significantly broadened the genomic representation of early-diverging animal groups by generating chromosome-level assemblies and transcriptomes from sponges (Porifera), molluscs (Mollusca), rotifers (Rotifera), chaetognaths (Chaetognatha), and other understudied phyla. New protocols for in situ chromosome conformation capture (Hi-C) were developed and optimized for soft-bodied marine invertebrates, enabling high-contiguity assemblies even from challenging tissues. This work produced the first chromosome-scale genomes for several species, including the freshwater sponge *Ephydatia muelleri*, which remains a reference model for sponge biology and early animal evolution, and the first single-cell RNAseq dataset of another freshwater sponge, *Spongilla lacustris*.

Methodological Innovations in Genome Assembly and Annotation

IGNITE early-stage researchers (ESRs) developed and benchmarked several open-source tools that are now widely used in genome assembly and scaffolding. These include instaGRAAL and GraphUnzip for high-quality scaffolding and haplotype phasing, MTG-Link for targeted local assembly, and the TransPi pipeline for de novo transcriptome assembly of non-model organisms. Collectively, these tools improved genome completeness and accuracy, particularly for species with high heterozygosity or complex repeat landscapes. The program also advanced the use of energy-efficient algorithms in phylogenetic inference, resulting in faster and more sustainable computation across bioinformatics workflows.

Reconstructing Animal Evolutionary History

A major focus of IGNITE was the reconstruction of the animal tree of life using genome-scale datasets. ESRs applied innovative models to resolve difficult phylogenetic questions, such as the rooting of the animal tree (Porifera vs. Ctenophora) and relationships within the Ecdysozoa. Using novel amino acid recoding approaches and improved fossil calibrations, IGNITE researchers produced some of the most comprehensive evolutionary timetrees for metazoans to date. Their work has provided new insights into the early diversification of animals and the evolution of key developmental genes.

*Figure: Textile cone snail (*Conus textile*) - 2005 Richard Ling; "Dragon eye" coral,* Zoanthus *sp. - 2013 Kazvorpal;* Catostylus *sp. (stingless jellyfish) - 2007 Profberger; Stomatopod crustacean (mantis shrimp) - 2008 Silke Baron; Chambered Nautilus - 2008 Hans Hillewaert; Nudibranch* Berghia coerulescens *- 2009 Parent Géry; Purple* Polycarpa aurata *(Sea squirt) - 2006 Nhobgood.. Composition by A. Antunes*

Bioactive Compounds and Sponge Holobionts

Beyond phylogenomics, IGNITE explored the biomedical potential of marine invertebrates and their symbionts. High-quality host-symbiont (holobiont) genomes revealed novel biosynthetic pathways responsible for secondary metabolites. Notably, the project identified a candidate antibiotic compound and a conserved hybrid NRPS-PKS enzyme family involved in the biosynthesis of 3-alkylpyridine alkaloids (3-APs), bioactive molecules with potential anticancer and antimicrobial properties. These findings strengthen the role of sponges as promising sources for natural product discovery.

Novel Insights into Development and Physiology

Other ESRs investigated fundamental biological processes, including early embryonic gene regulation, cellular coordination in sponges, and the evolution of maternal gene expression. Functional proteomics and high-resolution imaging revealed new details of contractile behaviour and cell signalling in *Spongilla lacustris*, providing clues to the origins of muscle-like and nervous functions in early animals. These studies combined cell biology, proteomics, and genomics, integrating molecular and organismal perspectives across disciplines.

Advancing Open Biodiversity Data and FAIR Principles

IGNITE also contributed to the digital transformation of biodiversity research. Through the OpenBiodiv knowledge graph and related software, researchers improved the accessibility, interoperability, and reusability of biodiversity data in line with FAIR principles. Tools such as the Pensoft Annotator and Omics Data Paper workflow now enable seamless integration of genomic and taxonomic information into open knowledge networks.

Software Development and Computational Advances

A distinctive outcome of IGNITE was its emphasis on reproducible and sustainable bioinformatics. Several ESR projects enhanced computational tools such as RootDigger, a program for rooting phylogenetic trees using non-reversible models, and Lagrange-NG, a new-generation biogeographic inference tool optimised for parallel computing. These developments have broad applications across evolutionary biology, epidemiology, and even beyond biology – one IGNITE tool (Phylourny) creatively applied phylogenetic algorithms to predict tournament outcomes.

Training, Collaboration, and Impact

IGNITE was the first international training program focused specifically on invertebrate biodiversity genomics. Its 15 doctoral fellows received comprehensive interdisciplinary training combining molecular biology, bioinformatics, evolutionary theory, and science communication. Network-wide training events included specialised workshops, software development bootcamps, and internships at partner institutions and industry hosts across Europe. Despite the disruptions caused by the COVID-19 pandemic, most ESRs successfully completed their research projects and many already defended their PhD theses.

The program fostered strong collaborations between universities, research institutes, and private-sector partners, bridging academic excellence with applied innovation. Several IGNITE graduates have since taken up research and data science positions in academia and industry, underscoring the network's success in preparing scientists for the rapidly expanding field of biodiversity genomics.

IGNITE's socio-economic impact lies in its legacy of high-quality genomic data, open-source tools, and human capacity building. The project substantially enhanced Europe's expertise in genome-based biodiversity science and established LMU Munich and the GeoBio-Center as leading hubs for invertebrate genomics research.

Figure: Early Stage Researcher of ITN IGNITE

Outlook and Legacy

IGNITE concluded in 2022 with an outstanding scientific and training record. It generated foundational genomic resources for underrepresented animal groups, developed widely adopted analytical tools, and inspired a new generation of researchers fluent in both biological and computational sciences. The knowledge and infrastructure created by IGNITE continue to support ongoing European initiatives in biodiversity genomics, including the Aquatic Symbiosis Genomics (ASG) project and future doctoral networks building upon its model. The program exemplifies how integrative, collaborative, and open approaches can illuminate the complexity of life's evolution and unlock nature's molecular potential for innovation.

Selected Key Publications from IGNITE

Baudry L, Guiglielmoni N, Marie-Nelly H, Cormier A, Marbouty M, Avia K, Mie YL, Godfroy O, Sterck L, Cock JM, Zimmer C, Coelho SM, Koszul R (2020) instaGRAAL: chromosome-level quality scaffolding of genomes using a proximity ligation-based scaffolder. Genome Biol 21:148. doi: 10.1186/s13059-020-02041-z

Bettisworth B, Stamatakis A (2021) Root Digger: a root placement program for phylogenetic trees. BMC Bioinformatics 22:225. doi: 10.1186/s12859-021-03956-5

Dimitrova M, Meyer R, Buttigieg PL, Georgiev T, Zhelezov G, Demirov S, Smith V, Penev L (2021) A streamlined workflow for conversion, peer review, and publication of genomics metadata as omics data papers. Gigascience. doi: 10.1093/gigascience/giab034

Farhat S, Bonnivard E, Pales Espinosa E, Tanguy A, Boutet I, Guiglielmoni N, Flot J-F, Allam B (2022) Comparative analysis of the *Mercenaria mercenaria* genome provides insights into the diversity of transposable elements and immune molecules in bivalve mollusks. BMC Genomics 23:192. doi: 10.1186/s12864-021-08262-1

Guiglielmoni N, Houtain A, Derzelle A, Van Doninck K, Flot J-F (2021) Overcoming uncollapsed haplotypes in long-read assemblies of non-model organisms. BMC Bioinformatics 22:303. doi: 10.1186/s12859-021-04118-3

Howard RJ, Giacomelli M, Lozano-Fernandez J, Edgecombe GD, Fleming JF, Kristensen RM, Ma X, Olesen J, Sørensen MV, Thomsen PF, Wills MA, Donoghue PCJ, Pisani D (2022) The Ediacaran origin of Ecdysozoa: integrating fossil and phylogenomic data. J Geol Soc London 179:jgs2021–107. doi: 10.1144/jgs2021-107

Kenny NJ, Francis WR, Rivera-Vicéns RE, Juravel K, de Mendoza A, Díez-Vives C, Lister R, Bezares-Calderón LA, Grombacher L, Roller M, Barlow LD, Camilli S, Ryan JF, Wörheide G, Hill AL, Riesgo A, Leys SP (2020) Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge *Ephydatia muelleri.* Nat Commun 11:3676. doi: 10.1038/s41467-020-17397-w

Musser JM, Schippers KJ, Nickel M, Mizzon G, Kohn AB, Pape C, Ronchi P, Papadopoulos N, Tarashansky AJ, Hammel JU, Wolf F, Liang C, Hernández-Plaza A, Cantalapiedra CP, Achim K, Schieber NL, Pan L, Ruperti F, Francis WR, Vargas S, Kling S, Renkert M, Polikarpov M, Bourenkov G, Feuda R, Gaspar I, Burkhardt P, Wang B, Bork P, Beck M, Schneider TR, Kreshuk A, Wörheide G, Huerta-Cepas J, Schwab Y, Moroz LL, Arendt D (2021) Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. Science 374:717–723. doi: 10.1126/science.abj2949

Ruperti F, Becher I, Stokkermans A, Wang L, Marschlich N, Potel C, Maus E, Stein F, Drotleff B, Schippers KJ, Nickel M, Prevedel R, Musser JM, Savitski MM, Arendt D (2024) Molecular profiling of sponge deflation reveals an ancient relaxant-inflammatory response. Curr Biol 34:361–375.e9. doi: 10.1016/j.cub.2023.12.021

Simion P, Narayan J, Houtain A, Derzelle A, Baudry L, Nicolas E, Arora R, Cariou M, Cruaud C, Gaudray FR, Gilbert C, Guiglielmoni N, Hespeels B, Kozlowski DKL, Labadie K, Limasset A, Llirós M, Marbouty M, Terwagne M, Virgo J, Cordaux R, Danchin EGJ, Hallet B, Koszul R, Lenormand T, Flot J-F, Van Doninck K (2021) Chromosome-level genome assembly reveals homologous chromosomes and recombination in asexual rotifer *Adineta vaga*. Sci Adv 7:eabg4216. doi: 10.1126/sciadv.abg4216

Zhao Y, Antunes A (2022) Biomedical potential of the neglected molluscivorous and vermivorous *Conus* species. Mar Drugs 20:105. doi: 10.3390/md20020105

Figure: Participants of the first Summer School organized by IGNITE in Split, Croatia.

Coordinator: Prof. Gert Wörheide, Chair of Paleontology & Geobiology, LMU Munich / GeoBio-Center LMU

Funding: Marie Skłodowska-Curie Innovative Training Network IGNITE (H2020-MSCA-ITN-2017; Grant No. 764840)

Duration: 2018–2022

Website: https://ignite-itn.eu

Contact: woerheide@lmu.de

ERC and DFG Emmy-Noether Group “Statistical Methods in Phylogenetics and Macroevolution”

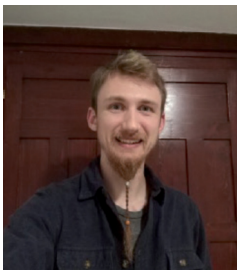
(Prof. Dr. Sebastian Höhna)

Dr. Alessio Capobianco
Postdoctoral researcher

Dr. Gustavo Darlim
Postdoctoral researcher

Dr. Nicolas Lichilin
Postdoctoral researcher

Dr. David Cerny
Postdoctoral researcher



Killian Smith
Doctoral candidate

Bjørn T. Kopperud
Doctoral candidate

Wenjie Zhu
Doctoral candidate

Basanta Khakurel
Doctoral candidate

Haoqing Du
Doctoral candidate

Priscilla Lau
Research assistant

Prof. Dr. Sebastian Höhna
Group leader

Our research group works on a wide range of statistical methods, ranging from evolutionary biology, population genetics and phylogenetics to paleo-phylogenetics. Our primary aim is to develop new statistical models and computational methods to answer one of the major questions in evolutionary biology and paleobiology: what are the causes and processes that have shaped biodiversity over time and space? We want to understand why some groups of organisms, like cichlid fishes, contain thousands of species, while others, like crocodiles, have very few.

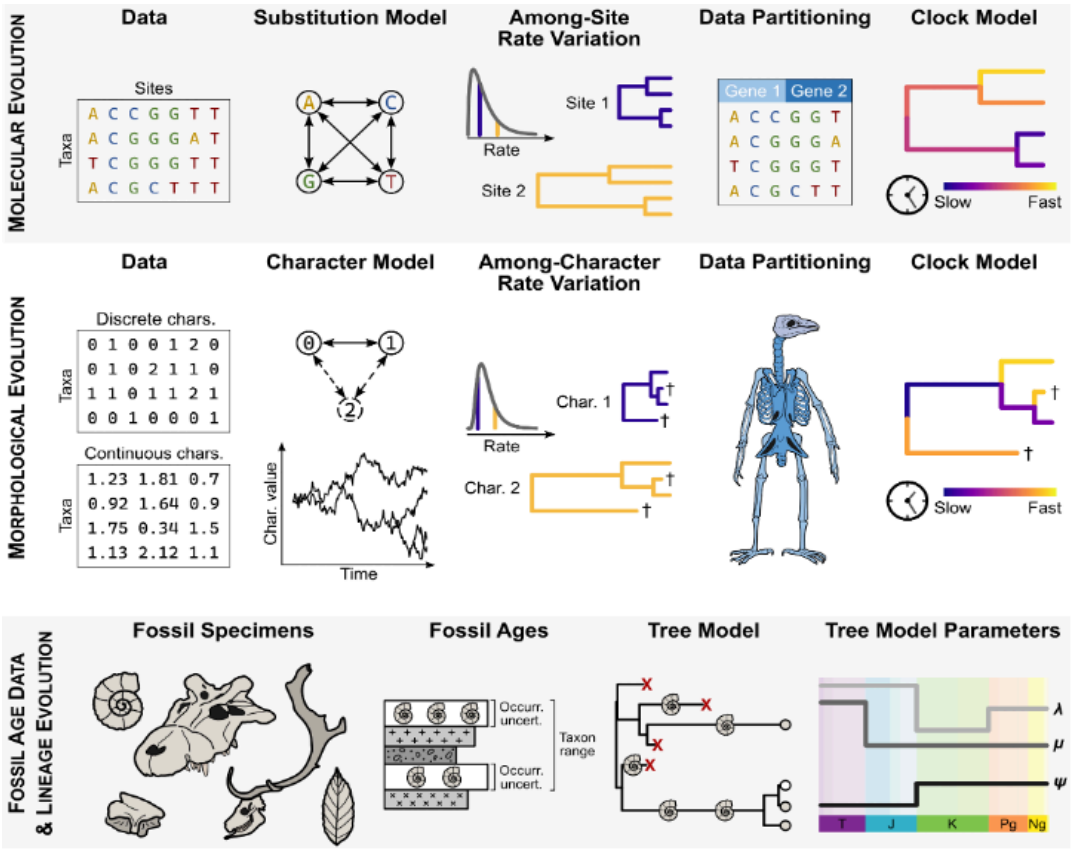
The group is primarily funded by an ERC Starting Grant (2023-2027), a DFG Emmy-Noether Project (2019-2026) and some specific DFG research grants (e.g., within the two priority programs TaxonOMICS and G-Evol). Our main goal is to develop statistical methods to study the biological processes that produce and impact current-day biodiversity. We are taking a phylogenetic approach to describe the relationship among species (both extant and extinct) with a specific focus on the divergence time between species. Ultimately, we want to study what processes drive historical biodiversity and are responsible for the fluctuations, such as major increases and decreases, of biodiversity over geological timescales. To answer these questions, we will take a multidisciplinary approach combining statistics, computer science, paleobiology, and evolutionary biology.

MacDrive (ERC-ERC Starting Grant-funded project):

The MacDrive project pursues a holistic approach to understanding the drivers of diversification by integrating fossil taxa into phylogenies of extant taxa. The project aims to address five key questions:

- Are diversification rate estimates from phylogenies without fossils reliable?
- What patterns of diversification rates can be inferred from phylogenies?
- How have diversification rates changed over time and among lineages for major groups such as Artiodactyla, Carnivora, Crocodyliformes and Squaliformes?
- Are diversification rates correlated with environmental factors and/or species-specific factors?
- Are species-specific factors correlated with survival probabilities of mass extinction events?

To answer these questions, the project involves developing new statistical models, implementing them in open-source software with efficient algorithms, producing new morphological datasets and phylogenies, and performing large-scale statistical analyses about macroevolutionary diversification. A key component of this project involves how to place extinct taxa represented by fossils into evolutionary trees, from modeling how morphological characters evolve to using the FBD (Fossilized-Birth-Death) class of models to reconstruct how lineages have speciated, gone extinct, and have been sampled in the fossil record.



Picture: Schematic workflow of a total-evidence fossil tip-dating analysis.

To test for lineage-specific shifts in diversification rates, we developed the PESTO program (Phylogenetic Estimation of Shifts in the Tempo of Origination). PESTO can estimate branch-specific diversification rates and branch-specific rate shift events efficiently even for species-rich phylogenies (> 20,000 taxa). PESTO uses an existing model, the birth-death-shift model, but uses a novel algorithm based on belief propagation techniques to calculate branch rates.

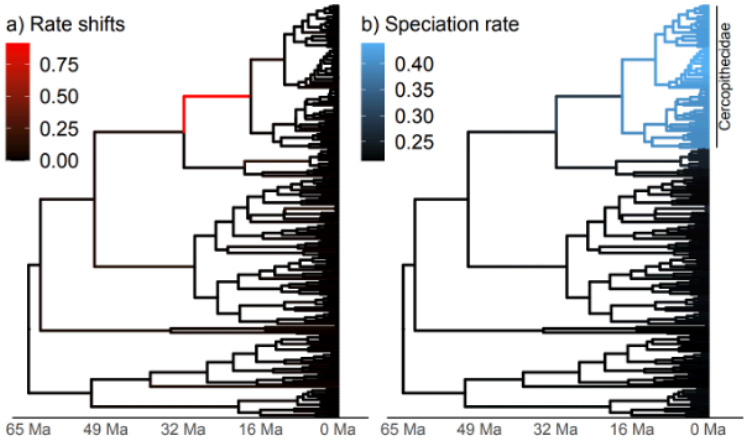


Figure: Example of a lineage-specific diversification rate analysis for primates. On the left we show the branches with supported rate shift events, and on the right we show the lineage-specific speciation rate (Kopperud & Höhna 2025).

MacDrive-Trait: Studying macroevolutionary drivers of trait evolution

On a macroevolutionary scale, i.e., over millions of years and across hundreds of closely related species, we can study adaptation by how the mean trait value per species evolves around a trait optimum. Over macroevolutionary timescales, this trait optimum will not be stable but instead vary over time, e.g., due to changes in the global environment, and across species, e.g., specialization on different diets. The currently most sophisticated approach uses the Ornstein-Uhlenbeck process, which contains three parameters: the rate of adaptation, the rate of drift, and the trait optimum. In this project we develop a novel approach to study trait adaptation over macroevolutionary timescales by extending the basic theory of Ornstein-Uhlenbeck processes. Specifically, we will develop a state-dependent Ornstein-Uhlenbeck model where all three parameters (the rate of adaptation, the rate of drift, and the trait optimum) can vary among species and/or vary over time.

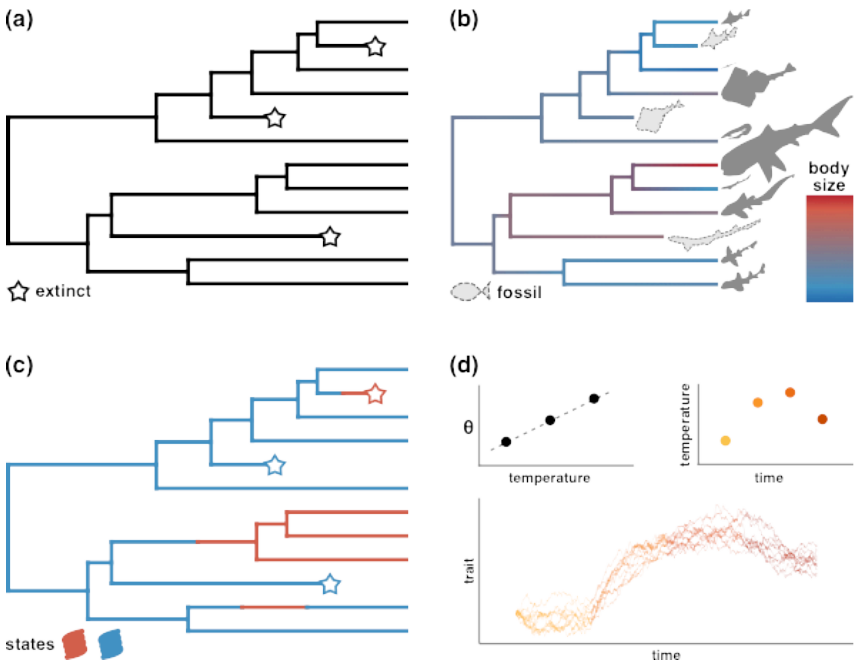


Figure: Schematic of a discrete-trait dependent continuous trait evolution. The different sub-figures depict how the body size depends on some underlying binary state.

GEvol project: Modeling gene expression evolution in fireflies

Gene expression is a key driver of trait variation, particularly among closely related species. This project aims to develop innovative methods to study gene expression evolution using phylogenetic models such as Brownian motion and Ornstein-Uhlenbeck processes, which correspond to different evolutionary scenarios. Specifically, we extend the models to allow for within-species variance, a critical yet underexplored aspect of gene expression.

In this project, we use the firefly family (Lampyridae) as a novel study system to investigate gene expression evolution. Fireflies exhibit recurrent sexual dimorphism across the phylogeny. As sexual dimorphism is inherently linked to sex-biased gene expression, this makes fireflies an ideal model for sex-biased gene expression evolution. We collect over 20 firefly species from Europe and Neotropics, with varying levels of sex dimorphism, and obtain gene expression data from both sexes. Using our newly extended phylogenetic models, we aim to uncover how sex-biased gene expression evolves and its relationship with sexual dimorphism across the firefly phylogeny.

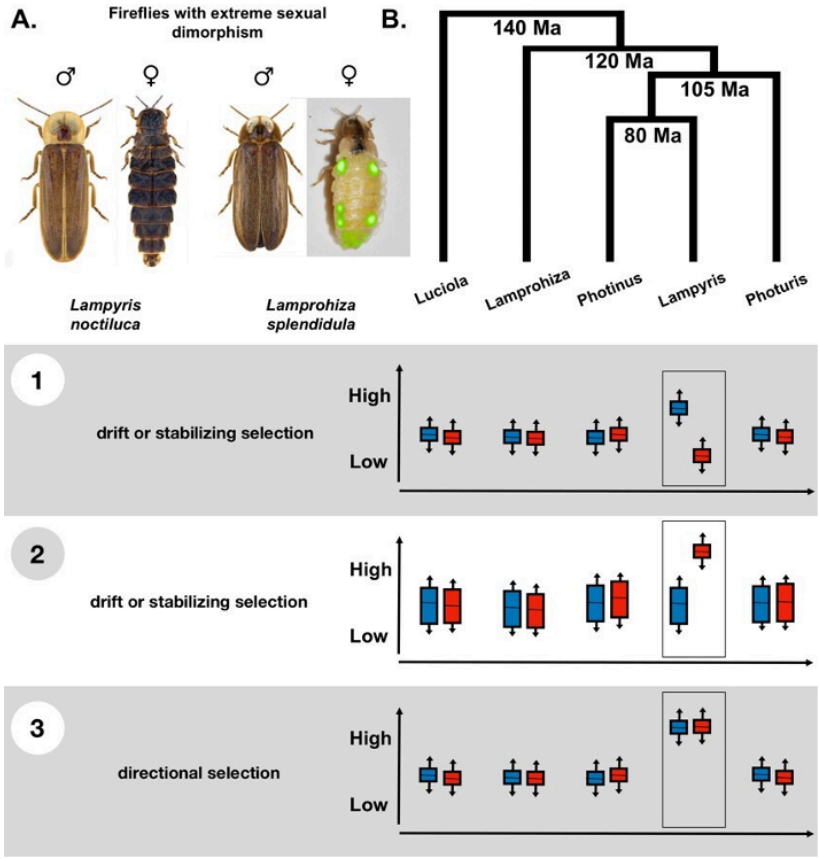


Figure: Schematic of different gene expression evolution scenarios with specific focus on sex-biased gene expression evolution. Our work here focuses on fireflies and is part of the DFG-SPP 2349.

Contact: hoehna@lmu.de

Website: https://hoehnalab.github.io

DFG Emmy-Noether project “OXYGEDOM”

(Dr. Gonzalo V. Gómez Sáez)

Seawater stores as much carbon in the form of dissolved organic matter (DOM) as there is carbon dioxide (CO_2) in the atmosphere. Due to its great size, shifts in reactivity of the marine DOM pool strongly impact global biogeochemical cycles. Microbial metabolisms in the oceans are directly responsible for the production, degradation and recycling of DOM, but little is known about how the complex pool of DOM shapes microbial communities and vice versa.

At the "Biogeochemistry & Climate Change" group of Dr. Gómez-Sáez, a combination of state-of-art techniques in analytical chemistry and microbial ecology are used to experimentally investigate biogeochemical interactions between microbes and DOM in the context of deoxygenation and warming, two of the major side effects of climate change in the ocean.

Group picture of the DFG Emmy-Noether research group in Biogeochemistry & Climate Change, after scientific expedition onboard RV Aurora in August 2025. From left to right: Gonzalo Gómez-Sáez, Ömer Coskun, Marit Renken, Laurin Lidl. Copyright: Gonzalo Gómez-Sáez

Deoxygenation effects on DOM sequestration in a changing ocean

Over a period of just 50 years (from 1960 to 2010) global oceanic oxygen reserves have been reduced by 2% and the anoxic waters have quadrupled, mainly due to anthropogenic global warming and eutrophication. Ocean deoxygenation leads to an expansion of oxygen minimum zones (OMZs), which contain higher concentrations of DOM (carbon and sulfur) than the oxygenated ocean. Recent advances in analytical chemistry characterize the DOM at the molecular level in unprecedented detail, revealing new insights into its source and history by Fourier transform ion-cyclotron resonance mass spectrometry (FT-ICR-MS). Current progress in sequencing technology can predict specific functions contributing to the molecular activity of microbial communities in environmental samples by metatranscriptomics. The synergistic coupling of FT-ICR-MS and metatranscriptomics is therefore of great importance to connect DOM cycling with microbial activities in OMZs. Our aim in this research topic, funded by the German Research Foundation (DFG) as an Emmy-Noether Research Group (2022-2028), is to identify the effects of ocean deoxygenation on DOM sequestration due to interactions with microbial communities and the marine carbon and sulfur cycles.

Organosulfur cycling by active uncultivated microbes

In marine sediment, organosulfur compounds represent a significant fraction of organic matter with a key role in carbon sequestration. In coastal and marine OMZs, microbial communities play a key role in the production, degradation and transformation of dissolved organic sulfur (DOS) compounds. While the cycling of inorganic sulfur has been widely studied, the microbial diversity involved in the cycling of DOS remains largely unknown. We investigate the cycling and microbial reactivity of key organosulfur compounds - such as taurine and methionine - in marine sediments and OMZs. Using quantitative DNA stable isotope probing (qSIP) with labeled DOS substrates (e.g. ^{13}C-taurine), we aim to target the main active microbes driving organosulfur cycling in the ocean. This research is conducted as part of the DFG Emmy-Noether research group, in collaboration with the Geomicrobiology group of Prof. William Orsi at LMU and GeoBio-Center.

Deoxygenation effects on microbial element cycling in the Mariager Fjord

Deoxygenation in Danish waters is an increasing problem with 2023 experiencing the most severe anoxia in 20 years. Mariager Fjord is the longest fjord in Jutland and the second longest fjord in Denmark. Due to nutrient loading from land combined with its topography, Mariager Fjord has anoxic bottom waters between spring and late fall, but is typically flushed with oxygen-rich seawater from the Kattegat during winter. This research topic was part of the DeoxyMar scientific expedition supported by DCH (Denmark). It involved a ship transit from Aarhus Bay to Mariager Fjord and the Kattegat open waters in August 2025, onboard the research vessel RV Aurora with Dr. Gómez-Sáez as Chief Scientist. Our aim is to provide a mechanistic and quantitative understanding for microbial element cycling interactions under varying levels of deoxygenation. Together with LMU, cooperation partners in the DeoxyMar project include universities and research centers from Denmark (Center for Electromicrobiology from Aarhus University, University of Southern Denmark SDU from Odense) and Sweden (University of Goteborg).

Photo: CTD cast during oceanographic expedition to collect water column samples from specific depths within the oxygen minimum zone.
Copyright: Gonzalo Gomez-Saez

Warming effects on Antarctic microbes and organic matter cycling

Last report of IPCC clearly stated that nowhere is climate change more visible than in the polar regions, making them the most critical reference regions for the detection and understanding of global change and its effects on biodiversity and ecosystem functioning. The polar biome is a highly connected ecosystem with linkages all over its components and beyond. However, can we consider the Antarctic region an early warning site? With atmospheric CO_2 concentrations and global temperature rising in the next few decades, the ocean will become warmer, less oxygenated and more stratified. The lack of knowledge about environmental drivers behind microorganisms and DOM pool functioning in response to these changes, especially in polar regions, limits our capacity to understand and predict the consequences of human activities and its associated global effects. This research topic includes samples obtained from the NEIGE project, with field and experimental work in Antarctica performed in December 2023 onboard the National Geographic Explorer by Dr. Gómez-Sáez and the other Co-PI of the project, Dr. David Velázquez (UAM, Madrid, Spain). Both researchers were "Visiting Scientists" with funds from Lindblad Expeditions and National Geographic.

Photo: Heading into the Lemaire Channel at 65° South, Antarctica. Copyright: Gonzalo Gómez-Sáez

Key publications:

Gomez-Saez GV, Dittmar T, Holtappels M, Pohlabeln AM, Lichtschlag A, Schnetger B, Boetius A, Niggemann J (2021). Sulfurization of dissolved organic matter in the anoxic water column of the Black Sea. Science Advances 7 (25), eabf6199. DOI: 10.1126/sciadv.abf6199

Coskun ÖK, Orsi WD, D´Hondt S, Gomez-Saez GV (2025). Identifying the active microbes driving organosulfur cycling from taurine and methionine in marine sediment. ISME communications, ycaf033. DOI: 10.1093/ismeco/ycaf033.

Press release: https://www.lmu.de/en/newsroom/news-overview/news/polar-research-warming-in-the-cooler.html

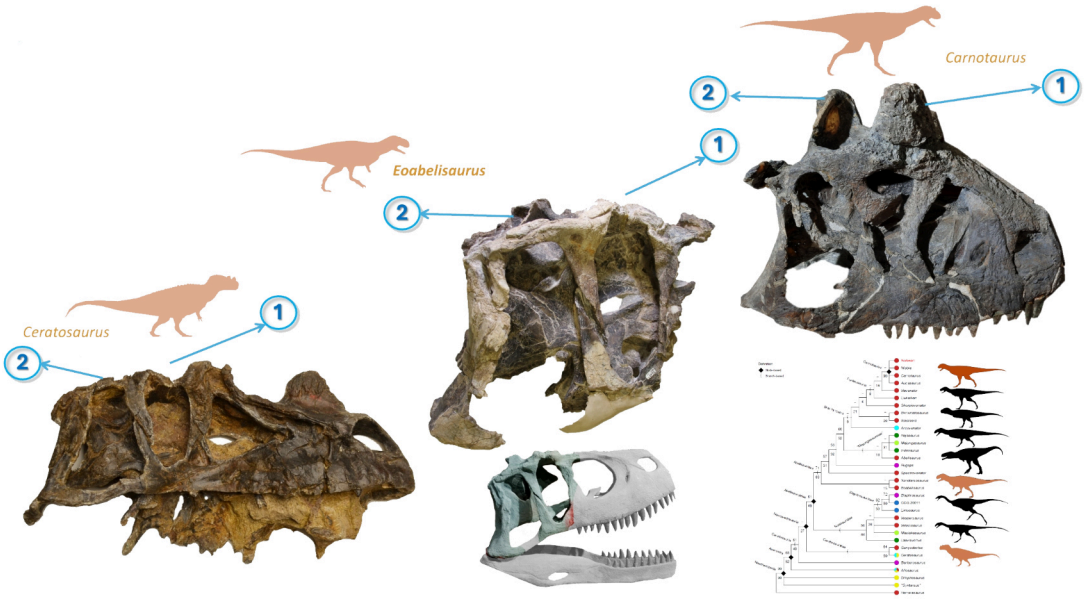
Contact: g.gomez@lmu.de

Marie S. Curie Actions Project "JurRad" - Unravelling the jurassic radiation of Averostra (Dinosauria, Theropoda)

(Dr. Elena Cuesta)

Non-avian theropods, one of the principal lineages of Dinosauria and the lineage leading to extant birds, represent the majority (more than 40%) of all named dinosaur species, more than any other major clade. Therefore, their evolutionary history is significant to understand dinosaur diversity, Mesozoic terrestrial ecosystems, and the evolutionary origin of modern birds.

The Marie S. Curie Actions Project “JurRad” (2023-2025) focuses on the evolution of the major group of theropod dinosaurs: Averostra. However, despite being one of the most studied groups, it is also one of the most debated within theropods due to the unclear phylogenetic interrelationship of its ‘basal’ members and the relationships between their major clades. Averostra radiated explosively from the Early to Late Jurassic (from 182.7-145 million years), with the Pliensbachian-Toarcian extinction event (182 million years ago) probably being one of the major causes for this explosive evolution. The increase in the rate of morphological change that followed the extinction, together with the fragmentary nature of the fossil record of the ‘basal’ members could be the cause of the difficulties in unraveling the interrelationships among Averostra. The main goal of this research is to obtain a robust and synthetic view of the evolutionary drivers of this radiation of Averostra during the Jurassic, to explore when averostrans originated at the latest and unravel the impact of the previous extinction on their radiation and how the different lineages were established in the aftermath.



Skull of Ceratosaurus*,* Eoabelisaurus *and* Carnotaurus*, three ceratosaurian taxa, showing distinct features, such as: 1. absence or presence of frontal horns; 2. height of nuchal crest. Phylogenetic tree after Pol et al., 2024*

Averostran theropods, either ceratosaurs or tetanurans, seem to have been very rare in the Early Jurassic, and all Early Jurassic representatives are based on such fragmentary material that it is difficult to firmly establish their averostran affinities (as opposed to being on the stem-line towards averostrans). The record in Laurasia is poorly represented by the ceratosaur *Saltriovenator* from the Sinemurian of Italy, the largest predatory dinosaur known from the Early Jurassic. This temporal range has a better record of averostran in Gondwana landmasses with the discoveries of the ceratosaur *Berberosaurus* from the Pliensbachian-Toarcian of Morocco, and the rich fossil record

from the Cañadon Asfalto Formation (Toarcian-Bajocian; Chubut province, Argentina). The latter Formation represents, so far, the most important vertebrate-bearing unit of the latest Early-early Middle Jurassic in Gondwana, if not globally. Recent radiometric dating has shown that the age of the Cañadón Asfalto Formation from the south of Cerro Cóndor is 179.17 ± 0.12 Ma (Toarcian; Early Jurassic). This formation has yielded several averostran taxa, such as the early branching tetanuran theropods *Piatnitzkysaurus* and *Condorraptor*, the ceratosaurian *Eoabelisaurus* and a probable early allosauroid, *Asfaltovenator*. These specimens, especially the most recently described, are the most complete pre-Late Jurassic representatives of their respective clades, and show very interesting character combinations that will certainly have a bearing on our understanding of averostran evolution.

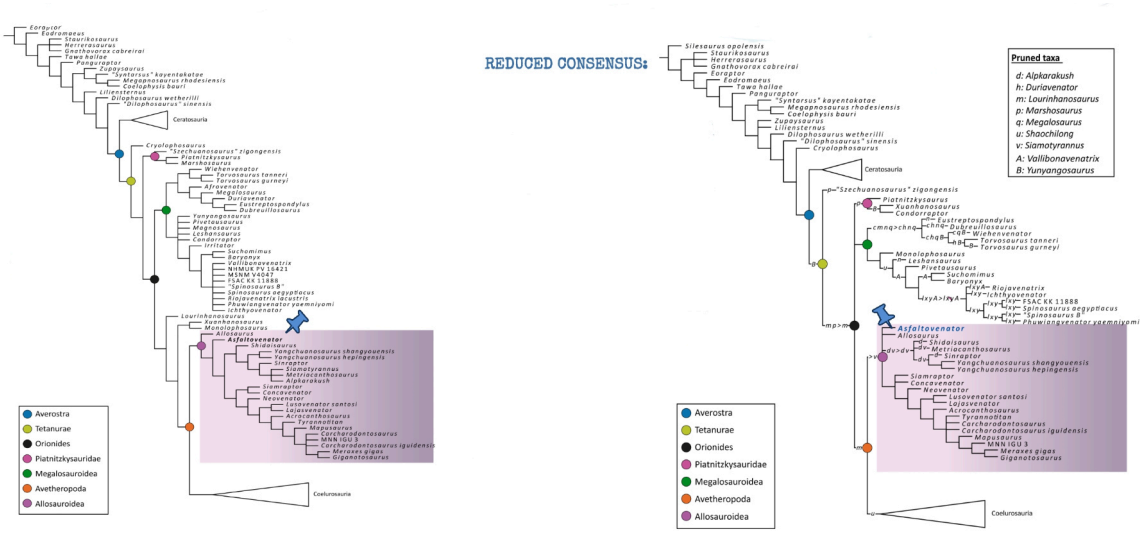
The main objective of this project is to study in detail these most complete early members of the two main averostran lineages from the Cañadón Asfalto Formation, *Eoabelisaurus mefi* and *Asfaltovenator vialidadi*, and carrying out phylogenetic analyses of this group. Subsequently, it will assess the morphological changes within a phylogenetic context in the early evolution of Averostra, and evaluate its connection with the Pliensbachian-Toarcian extinction event and consequent radiation of theropods.

“Jurassic Argentinean Park”: Averostran taxa from Cañadón Asfalto Formation

Eoabelisaurus mefi Pol and Rauhut, 2012, is represented by the type specimen that consists of an almost complete skeleton, lacking only the premaxilla, maxilla, lower jaw and the most distal caudal vertebrae. *Eoabelisaurus* was originally recovered as an abelisaurid, but its phylogenetic position within Ceratosauria is still debated. Posterior studies showed different results, such as *Eoabelisaurus* falls out as an abelisauroid outside the abelisaurid-noasaurid dichotomy, within Abelisauridae or within Ceratosauridae. *Eoabelisaurus* has few modifications of the skull relative to other abelisauroids and has a unique combination of plesiomorphic and apomorphic features in the forelimbs, such as the plesiomorphic unreduced humerus or the derived morphology of robust and short metacarpals in the manus). Given furthermore the completeness of the specimen, *Eoabelisaurus* thus has the potential to provide essential information to unravel the evolutionary scenario for abelisauroids, ceratosaurs and averostran theropods in general.

The holotype of *Asfaltovenator vialidadi* Rauhut and Pol, 2019 is an almost complete skeleton with a complete skull, presacral vertebrate column, complete both forelimbs and partial hindlimbs. *Asfaltovenator* is one of the oldest known and most complete pre-Late Jurassic tetanuran and it is a probably early-branching allosauroid. *Asfaltovenator* has several implications in early tetanuran phylogenetic relationships due to the unusual character combination of features that were previously considered synapomorphies of Megalosauroidea, such as a pronounced kink in the anterodorsal margin of the maxillary ascending process or an anterior expansion of the dentary, with synapomorphies of Allosauroidea, such as a pronounced supranarial fossa or the presence of pneumatic foramina in the nasal; and characters that are plesiomorphic in tetanurans, such as the absence of a medial pneumatic recess in the maxilla. Unravelling the evolutionary scenario of these mosaic-like occurrences of characters in both taxa will improve the inferences about the relationships of the major clades in Averostra (Ceratosauria and Tetanurae) and their subordinate lineages.

The previous studies of these taxa allowed to shed light on the hypothesis of a rapid radiation of Averostra because: (1) they show a mosaic-like morphological data and interesting character combinations that provide information on macroevolutionary processes in this lineage; (2) they are branching at the base of major clades of Averostra, which have common difficulties to unravel their phylogenetic relationship; and (3) both holotypes represent the most complete Early-Middle Jurassic representatives of averostran theropods that have been found so far for their respective lineages.



Preliminary phylogenetic results of Asfaltovenator *using equally weighting and implied weighting in parsimonious analysis. The recovered position of this taxon is in Allosauroidea in both analysis, but the group* Piatnitzkysaurus*, formed by jurassic taxa, changes the position in the topology of the tree.*

Novelties in the study of Eoabelisaurus and Asfaltovenator

The anatomical description of *Eoabelisaurus* and *Asfaltovenator* and preliminary phylogenetic analyses demonstrate:

1) *Eoabelisaurus* possesses a mosaic of features between *Ceratosaurus*, an early branching taxon in Ceratosauria, and Abelisaurids, even with the most derived members. For example, it has lower nuchal crest than derived abelisaurids and lacks strong ornamentation, but it has a supraorbital brow in the postorbital, the bone situated posterior to the orbit as in derived abelisaurids. The specialization of its skull and forelimb follow a trend typical of this group towards the gigantism of its most derived members.

2) The stable position of *Asfaltovenator* in allosauroids and its influence on the changes in the topology of the trees, related to other groups as the position of Piatnitzkysaurids, are related to its completeness and its potential to provide pivotal information about the evolution of the clade.

Both taxa from Cañadón Asfalto formation have provided information to understand the phylogenetic characters of their groups, improving the morphological matrices used in previous studies regarding Averostra. Further research using macroevolutionary analysis with phylogenies will be necessary to unravel the evolutionary history of this group and improve the phylogenies of Averostra.

Contact: cuesta@snsb.de

DFG-Project "ChemTrail" – Sensory enrichment to augment fish community development on degraded coral reefs

(Dr. Gerrit Nanninga)

This project is funded by the German Research Foundation (Deutsche Forschungsgemeinschaft – DFG; duration 2024-2026) and seeks to harness natural processes in sensory ecology to supplement recovery and resilience in coral reef ecosystems.

Picture: Coral reef fish larvae. Photo: G. Nanninga

Coral reefs worldwide are being degraded at unprecedented rates through anthropogenic impacts. To save these important ecosystems, decision makers are increasingly turning towards coral restoration. However, current restoration approaches are costly and limited in scale. This project aims to use chemosensory enrichment to enhance the development of coral reef fish communities at degraded reefs. Fishes perform a range of functional roles on the reef that are vital for habitat recovery and resilience. Local abundance of fishes is governed by recruitment of pelagic larvae that use olfactory cues emitted by the reef community to navigate towards settlement habitat. However, degraded reefs smell less favorable than healthy reefs and therefore receive less recruitment. This feedback-loop hampers reef recovery. By mimicking the chemosensory signal of a healthy reef habitat, we can attract fish (and potentially coral) larvae to degraded reefs or restoration sites, thereby enhancing natural reef recovery. Specifically, we aim to:

(1) **Assess the chemosensory signature of natural reef communities**
Water from coral reefs in different health states (from healthy to degraded) will be analyzed for Biogenic Volatile Organic Compounds (BVOCs) and Dissolved Organic Matter (DOM) using in situ sorptive extraction and water sample analyses. In collaboration with Dr. Gonzalo Gomez-Saez from LMU and Prof. Sergio Rasmann from the University of Neuchâtel, Switzerland.

(2) **Test, which (mixes of) natural reef compounds are most attractive to fish larvae**
We will use behavioral observations in choice flumes to assess the potential of specific target compounds, identified on step one, to attract fish and invertebrate larvae. During these experiments, individual larvae can freely choose between two non-overlapping streams of water carrying different chemosensory signals.

(3) **Develop a method to achieve sustained release of the relevant compounds in situ**
We will test a hybrid biomaterial that releases the focal settlement cues via a nanoparticle–biopolymer delivery system. The material is called SNAP-X and was developed by the Coral Reef Ecophysiology and Engineering Lab at Scripps Institution of Oceanography in California to enhance coral settlement. We aim to adapt the approach for reef fishes. In collaboration with Dr. Daniel Wangpraseurt from Scripps, USA.

(4) **Test & refine chemosensory enrichment to enhance fish recruitment in field experiments**
The final step will be to test the developed approach in the field. Fish recruitment will be monitored over four weeks on small artificial patch reefs, some of which are treated with the newly developed SNAP-X (treatment) and some of which are not (control).

Steps 1 (water sampling), 2 (behavioral experiments), and 4 (field experiments) are implemented in the Maldives in collaboration with the Anantara Dhigu Resort. In the long run, we aim to establish this approach as a cheap and effective new tool to support coral reef restoration worldwide.

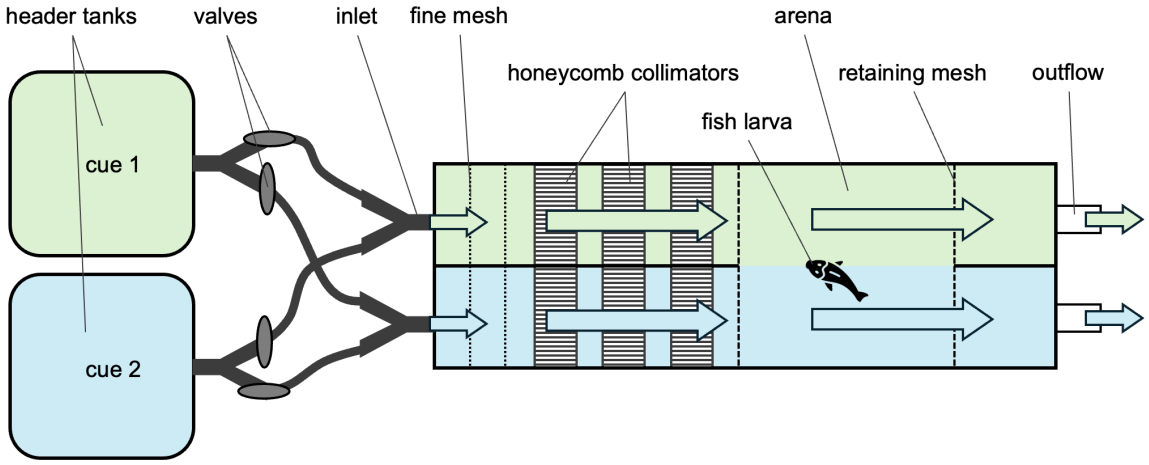


Figure: ChemTrail experimental workflow

Contact: g.nanninga@lmu.de

Publications in ISI-Indexed Journals 2022 - 2024 (260)

Agne S, Ekins M, Galitz A, Hofreiter M, Preick M, Straube N, Wörheide G, Erpenbeck D (2022) Keratose sponge MuseOMICS: setting reference points in dictyoceratid demosponge phylogeny. Zootaxa 5195(3):296-300.

Albani Rocchetti G, Carta A, Mondoni A, Godefroid S, Davis CC, Caneva G, Albrecht MA, Alvarado K, Bijmoer R, Borosova R, Bräuchler C, Breman E, Briggs M, Buord S, Cave LH, Da Silva NG, Davey AH, Davies RM, Dickie JB, Fabillo M, Fleischmann A, Franks A, Hall G, Kantvilas G, Klak C, Liu U, Medina L, Reinhammar LG, Sebola RJ, Schönberger I, Sweeney P, Voglmayr H, White A, Wieringa JJ, Zippel E, Abeli T (2022) Selecting the best candidates for resurrecting extinct-in-the-wild plants from herbaria. Nat Plants 8:1385-1393.

Amaral AP, Gombos D, Haug GT, Haug C, Gauweiler J, Hörnig MK, Haug JT (2023) Expanding the fossil record of soldier fly larvae—an important component of the Cretaceous Amber forest. Diversity (Basel) 15(2):247.

Amaral AP, Haug JT, Haug C, Linhart S, Müller P, Hammel JU, Baranov V (2024) Expanding the Mesozoic record of early brachyceran fly larvae, including new larval forms with chimera-type morphologies. Insects 15(4):270.

Arce SI, Haug C, Haug JT, Amaral AP (2024) Driven apart: fossil parasitic long-legged velvet mite larvae on gall midges represent a long lost parasitic association between mites and dipterans. Palaeoentomology 7(2):254-264.

Arce SI, Haug C, Müller P, Haug JT, Fu Y-Z (2024) Oldest record of a larva of long-legged velvet mite (Erythraeoidea) parasitising an immature planthopper. Palaeoentomology 7(4):461-464.

Argyriou T, Alexopoulos A, Carrillo-Briceño JD, Cavin L (2022) A fossil assemblage from the mid-late Maastrichtian of Gavdos Island, Greece, provides insights into the pre-extinction pelagic ichthyofaunas of the Tethys. PLoS One 17(4):e0265780.

Argyriou T, Giles S, Friedman M (2022) A Permian fish reveals widespread distribution of neopterygian-like jaw suspension. eLife 11:e58433.

Bakayeva S, Nützel A, Kaim A (2024) An elusive ancestry of Neogastropoda: a potential of Maturifusidae, Pseudotritoniidae, and Purpurinidae as the stem groups. C R Palevol 23(31):481-509.

Balke M, Bilton DT, García M, Viloria ÁL, Villastrigo A, Hendrich L (2022) Two new high Andean species of *Liodessus* diving beetles from Venezuela (Coleoptera, Dytiscidae, Bidessini). Alp Entomol 6:7-12.

Balke M, Mainda T, Neven K, Hendrich L, Basantes MS, Prieto C, Villastrigo A (2024) Recent range expansion and lineage idiosyncratic population structure of *Liodessus* diving beetles in the high Andes (Coleoptera: Dytiscidae, Bidessini). PLoS One 19:e0308683.

Balke M, Neven K, Villastrigo A, Ospina-Torres R, Prieto C, Gutierrez Rubiano N, Lotta I, Dueñas LF, Hendrich L (2023) Eastern Colombian Páramo *Liodessus* Guignot, 1939 diving beetles are genetically structured, but show signs of hybridization, with description of new species and subspecies (Coleoptera, Dytiscidae). Zookeys 1143(1):165-187.

Balke M, Panjaitan R, Surbakti S, Shaverdo H, Hendrich L, van Dam MH, Lam A (2022) NextRAD phylogenomics, sanger sequencing and morphological data to establish three new species of New Guinea stream beetles. Alp Entomol 6:51-64.

Baranov V, Haug C, Fowler M, Kaulfuss U, Müller P, Haug JT (2022) Summary of the fossil record of megalopteran and megalopteran-like larvae, with a report of new specimens. Bull Geosci 97(1):89-108.

Baranov V, la Fuente RP, Engel M, Hammel J, Kiesmüller C, Hörnig M, Pazinato P, Stahlecker C, Haug C, Haug J (2022) The first adult mantis lacewing from Baltic amber, with an evaluation of the post-Cretaceous loss of morphological diversity of raptorial appendages in Mantispidae. Fossil Record 25(1):11-24.

Baranov VA, Haug JT, Greenwalt DE, Harbach R (2022) Diversity of culicomorphan dipterans in the Eocene Kishenehn Konservat-Lagerstätte (Montana, USA) and its palaeoecological implications. Palaeontologia Electronica, 25(1):a4.

Baranov VO, Haug JT, Kaulfuss U (2024) New records of immature aquatic Diptera from the Foulden Maar Fossil-Lagerstätte, New Zealand, and their biogeographic implications. PeerJ 12:e17014.

Barbosa N, Leinauer J, Jubanski J, Dietze M, Münzer U, Siegert F, Krautblatter M (2024) Massive sediment pulses triggered by a multi-stage 130 000 m3 alpine cliff fall (Hochvogel, DE-AT). Earth Surf Dyn 12:249-269.

Bartoszek K, Tredgett Clarke J, Fuentes-González J, Mitov V, Pienaar J, Piwczyński M, Puchałka R, Spalik K, Voje KL (2024) Fast mvSLOUCH: Multivariate Ornstein-Uhlenbeck-based models of trait evolution on large phylogenies. Methods Ecol Evol 15:1507-1515.

Bauersachs T, Schubert CJ, Mayr C, Gilli A, Schwark L (2024) Branched GDGT-based temperature calibrations from Central European lakes. Sci Total Environ 906:167724.

Becerra MG, Pol D, Porro LB, Paulina-Carabajal A, Rauhut OWM (2022) Craniomandibular osteology of *Manidens condorensis* (Ornithischia: Heterodontosauridae) from the upper Lower Jurassic of Argentina. J Vertebr Paleontol 42(3):e2181087.

Beck A, Casanova-Katny A, Gerasimova J (2023) Metabarcoding of Antarctic lichens from areas with different deglaciation times reveals a high diversity of lichen-associated communities. Genes (Basel) 14(5):1019.

Belojević J, Mortier MS, Oberweiser MM, Braig F, Haug JT, Haug C (2024) The history of short-tailed whip scorpions: changes in body size and flagellum shape in Schizomida. Swiss J. Palaeontol 143:24.

Belojević J, Wess V, Jaklin A, Pfannkuchen M, Melzer RR (2022) Decapods on Adriatic gas platforms - benthic climbers and planktonic drifters? (Crustacea, Decapoda). Spixiana 45:27-33.

Bicknell RDC, Kimmig J, Budd GE, Legg DA, Bader KS, Haug C, Kaiser D, Laibl L, Tashman JN, Campione NE (2022) Habitat and developmental constraints drove 330 million years of horseshoe crab evolution. Biol J Linn Soc Lond 136:155-172.

Bicknell RDC, Melzer RR, Schmidt M (2022) Three-dimensional kinematics of euchelicerate limbs uncover functional specialization in eurypterid appendages. Biol J Linn Soc Lond 135:174-183.

Bicknell RDC, Schmidt M, Rahman IA, Edgecombe GD, Gutarra S, Daley AC, Melzer RR, Wroe S, Paterson JR (2023) Raptorial appendages of the Cambrian apex predator *Anomalocaris canadensis* are built for soft prey and speed. Proc Biol Sci 290:20230638.

Bidaye RG, Al-Jufaili SM, Charmpila EA, Jawad L, Vukić J, Reichenbacher B (2022) Possible links between phenotypic variability, habitats and connectivity in the killifish *Aphaniops stoliczkanus* in Northeast Oman. Acta Zool 104:262-278.

Billenstein RJ, Höhna S (2024) Comparison of Bayesian coalescent skyline plot models for inferring demographic histories. Mol Biol Evol 51(5):msae073.

Borges R, Boussau B, Höhna S, Pereira RJ, Kosiol C (2022) Polymorphism-aware estimation of species trees and evolutionary forces from genomic sequences with RevBayes. Methods Ecol Evol 13:2339-2346.

Braig F, Haug C, Haug JT (2023) Diversification events of the shield morphology in shore crabs and their relatives through development and time. Palaeontologia Electronica 26:1-23.

Braig F, Haug C, Haug JT (2023) Phenotypic variability in the shield morphology of wild- vs. lab-reared eumalacostracan larvae. Nauplius 31:e2023004.

Braig F, Haug C, Haug JT (2024) Morphological diversity in true and false crabs reveals the plesiomorphy of the megalopa phase. Sci Rep 14:8682.

Braig F, Haug JT, Ahyong ST, Garassino A, Schaedel M, Haug C (2023) Another piece in the puzzle of mantis shrimp evolution-fossils from the Early Jurassic Osteno Lagerstätte of Northern Italy. Comptes Rendus Palevol 22:17-31.

Braig F, Popp T, Zippel A, Haug GT, Linhart S, Müller P, Weiterschan T, Haug JT, Haug C (2023) The diversity of larvae with multi-toothed stylets from about 100 million years ago illuminates the early diversification of antlion-like lacewings. Diversity (Basel) 15(12):1219.

Braig F, Torres G, Giménez L, Haug JT (2024) Outline analysis as a new method for investigating development in fossil crabs. Palaeontologia Electronica 27:1-13.

Buchner L, Linhart S, Kalmar G, Arce S, Haug GT, Haug JT, Haug C (2024) New fossil lacewing larvae with trumpet-shaped elongate empodia provide insight into the evolution of this attachment structure. Riv Ital Paleontol Stratigr 130(1):67-80.

Capobianco A, Friedman M (2024) Fossils indicate marine dispersal in osteoglossid fishes, a classic example of continental vicariance. Proc Biol Sci 291:20241293.

Capobianco A, Zouhri S, Friedman M (2024) A long-snouted marine bonytongue (Teleostei: Osteoglossidae) from the early Eocene of Morocco and the phylogenetic affinities of marine osteoglossids. Zool J Linn Soc 203(1):zlae015.

Catalan A, Höhna S, Lower SE, Duchen P (2022) Inferring the demographic history of the North American firefly Photinus pyralis. J Evol Biol 35:1488-1499.

Cavin L, Argyriou T, Romano C, Grădinaru E (2024) Large durophagous fish from the Spathian (late Early Triassic) of Romania hints at earlier onset of the Triassic actinopterygian revolution. Pap Palaeontol 10(2):e1553.

Charqueño-Celis F, Dubois N, Zolitschka B, Pérez L, Mayr C, Massaferro J (2024) Climate and environmental history of Laguna Polo, Santa Cruz, Southern Patagonia (49°S) since 1300 CE. J Paleolimnol 72:163-178.

Charqueño-Celis F, Sigala I, Zolitschka B, Pérez L, Mayr C, Massaferro J (2022) Responses of testate amoebae assemblages (Amoebozoa: Arcellinida) to recent volcanic eruptions, inferred from the sediment record in Laguna Verde, southern Patagonia, Argentina. J Paleolimnol 67:115-129.

Chen A, Porras L, Ma H, Hou X, Wörheide G (2023) A new sponge genus from the Chengjiang biota with an intriguing combination of skeletal characters. Palaontol Z 97:443-450.

Chen Z, Doğan Ö, Guiglielmoni N, Guichard A, Schrödl M (2022) Pulmonate slug evolution is reflected in the de novo genome of *Arion vulgaris* Moquin-Tandon, 1855. Sci Rep 12:14226.

Chen Z, Schrödl M (2022) How many single-copy orthologous genes from whole genomes reveal deep gastropod relationships? PeerJ 10:e13285.

Clarke JT, Davis RB (2024) Salinity plays a limited role in determining rates of size evolution in fishes globally across multiple scales. Glob Ecol Biogeogr 33(9): e13883.

Conci N, Griesshaber E, Rivera-Vicéns RE, Schmahl WW, Vargas S, Wörheide G (2024) Molecular and mineral responses of corals grown under artificial Calcite Sea conditions. Geobiology 22:e12586.

Cooper SL, López-Arbarello A, Maxwell EE (2024) First occurrence of a† coccolepidid fish (? Chondrostei:† Coccolepididae) from the Upper Lias (Toarcian, Early Jurassic) of southern Germany. Palaeontologia Electronica 27:1-25.

Coskun ÖK, Gomez-Saez GV, Beren M, Özcan D, Günay SD, Elkin V, Hoşgörmez H, Einsiedl F, Eisenreich W, Orsi WD (2024) Quantifying genome-specific carbon fixation in a 750-meter deep subsurface hydrothermal microbial community. FEMS Microbiol Ecol 100(5):fiae062.

Coskun ÖK, Gomez-Saez GV, Beren M, Ozcan D, Hosgormez H, Einsiedl F, Orsi WD (2023) Carbon metabolism and biogeography of candidate phylum "Candidatus Bipolaricaulota" in geothermal environments of Biga Peninsula, Turkey. Front Microbiol 14:1063139.

Coskun ÖK, Vuillemin A, Schubotz F, Klein F, Sichel SE, Eisenreich W, Orsi WD (2022) Correction to: Quantifying the effects of hydrogen on carbon assimilation in a seafloor microbial community associated with ultramafic rocks. ISME J 16(3):900.

Desojo JB, Rauhut OWM (2024) Reassessment of the enigmatic *"Prestosuchus" loricatus* (Archosauria: Pseudosuchia) from the Middle-Late Triassic of southern Brazil. Anat Rec (Hoboken) 307:974-1000.

Dirnberger M, Bauer E, Reichenbacher B (2024) A new freshwater gobioid from the Lower Miocene of Turkey in a significantly amended total evidence phylogenetic framework. J Syst Palaeontol 22(1):2340498.

Dohrmann M, Reiswig HM, Kelly M, Mills S, Schätzle S, Reverter M, Niesse N, Rohde S, Schupp P, Wörheide G (2023) Expanded sampling of New Zealand glass sponges (Porifera: Hexactinellida) provides new insights into biodiversity, chemodiversity, and phylogeny of the class. PeerJ 11:e15017.

Ebert M, Ekrt B, Lam C, Kölbl-Ebert M, López-Arbarello A (2022) Drawings intended for Agassiz (1833-1843): taxonomic implications for fishes from the Solnhofen Archipelago curated in Prague. Neues Jahrb Geol Palaontol Abh 306:227-263.

Ebert M, López-Arbarello A (2024) The problematic genus Liodesmus Wagner and a new genus of Caturoidea (Halecomorphi, Neopterygii) from the upper Jurassic solnhofen-archipelago. Diversity (Basel) 16:568.

Eitel M, Osigus H-J, Brenzinger B, Wörheide G (2024) Beauty in the beast - Placozoan biodiversity explored through molluscan predator genomics. Ecol Evol 14(4):e11220.

Ekins M, Erpenbeck D, Debitus C, Petek S, Mai T, Wörheide G, Hooper JNA (2023) Revision of the genus Fascaplysinopsis, the type species *Fascaplysinopsis reticulata* (Hentschel, 1912) (Porifera, Dictyoceratida, Thorectidae) and descriptions of two new genera and seven new species. Zootaxa 5346:201-241.

Ekins M, Erpenbeck D, Wörheide G, Hooper JNA (2023) Deep Water Polymastiidae (Porifera, Polymastiida) from the south west pacific. Zootaxa 5369:57-88.

Elbrächter M, Gottschling M, Hoppenrath M, Keupp H, Kusber W-H, Streng M, Tillmann U, Versteegh GJM, Zonneveld KAF (2023) (258-260) Proposals to eliminate contradiction between Articles 11.7 and 11.8 and to equate non-fossil with fossil names of dinophytes for purposes of priority. Taxon 72(3):684-686.

Erpenbeck D, van Soest RWM, Wörheide G, Kelly M (2023) Genetic data confirms the enigmatic demosponge *Janulum* as haplosclerid. Zootaxa 5254:147-150.

Fabreti LG, Coghill LM, Thomson RC, Höhna S, Brown JM (2024) The expected behaviors of posterior predictive tests and their unexpected interpretation. Mol Biol Evol 41(3):msae051.

Fabreti LG, Höhna S (2022) Convergence assessment for Bayesian phylogenetic analysis using MCMC simulation. Methods Ecol Evol 13:77-90.

Fernandes AE, Pol D, Rauhut OWM (2024) The oldest monofenestratan pterosaur from the Queso Rallado locality (Cañadón Asfalto Formation, Toarcian) of Chubut Province, Patagonia, Argentina. R Soc Open Sci 11:241238.

Fleischmann A, Gonella PM, Rojo S, Mengual X (2022) Attracted to feed, not to be fed upon - on the biology of *Toxomerus basalis* (Walker, 1836), the kleptoparasitic "sundew flower fly" (Diptera: Syrphidae). J Trop Ecol 38:241-253.

Foerster SÍA, Clarke JT, Õunap E, Teder T, Tammaru T (2024) A comparative study of body size evolution in moths: evidence of correlated evolution with feeding and phenology-related traits. J Evol Biol 37:891-904.

Francis WR, Eitel M, Vargas S, Garcia-Escudero CA, Conci N, Deister F, Mah JL, Guiglielmoni N, Krebs S, Blum H, Leys SP, Wörheide G (2023) The genome of the reef-building glass sponge *Aphrocallistes vastus* provides insights into silica biomineralization. R Soc Open Sci 10:230423.

Freund M, Graus D, Fleischmann A, Gilbert KJ, Lin Q, Renner T, Stigloher C, Albert VA, Hedrich R, Fukushima K (2022) The digestive systems of carnivorous plants. Plant Physiol 190:44-59.

Fürsich FT, Schneider S, Werner W, Lopez-Mir B, Pierce CS (2022) Life at the continental-marine interface: palaeoenvironments and biota of the Alcobaça Formation (Late Jurassic, Central Portugal), with a formal definition of the unit appended. Paleobiodivers Paleoenviron 102:265-329.

Galitz A, Ekins M, Folcher E, Büttner G, Hall K, Hooper JNA, Reddy MM, Schätzle S, Thomas OP, Wörheide G, Petek S, Debitus C, Erpenbeck D (2023) Poriferans rift apart: molecular demosponge biodiversity in Central and French Polynesia and comparison with adjacent marine provinces of the Central Indo-Pacific. Biodivers Conserv 32:2469-2494.

Galitz A, Ekins M, Reddy MM, Folcher E, Dumas M, Butscher J, Thomas OP, Voigt O, Wörheide G, Petek S, Erpenbeck D (2024) Molecular genetic biodiversity assessment of the Wallis Island sponge fauna in the Tropical Pacific. J Mar Biol Assoc U K 104:e56.

Galitz A, Vargas S, Thomas OP, Reddy MM, Wörheide G, Erpenbeck D (2024) Genomics of terpene biosynthesis in dictyoceratid sponges (Porifera) - what do we (not) know? Chem Biodivers 21:e202400549.

García Chapori N, Laprida C, Lo Prete D, Chiessi CM, Mayr C, Violante RA (2022) Holocene palaeoceanographic history of the western South Atlantic. J South Am Earth Sci 117:103896.

Gauweiler J, Amaral AP, Haug C, Haug JT (2024) Armoured Lepidopteran caterpillars preserved in non-fossil resins and what they tell us about the fossil preservation of caterpillars. Insects 15:380.

Gerasimova JV, Beck A, Scheunert A, Kulkarni O (2024) De Novo genome assembly of *Toniniopsis dissimilis* (Ramalinaceae, Lecanoromycetes) from long reads shows a comparatively high composition of biosynthetic genes putatively involved in melanin synthesis. Genes (Basel) 15:1029.

Gerasimova JV, Otte V, Urbanavichene IN, Urbanavichus GP, Beck A (2023) High diversity of *Bacidia* (Ramalinaceae, Lecanorales) species in the Caucasus as revealed by molecular and morphological analyses. Lichenologist 55:275-296.

Gierl C, Dohrmann M, Keith P, Humphreys W, Esmaeili HR, Vukić J, Šanda R, Reichenbacher B (2022) An integrative phylogenetic approach for inferring relationships of fossil gobioids (Teleostei: Gobiiformes). PLoS One 17:e0271121.

Göhring A, Hölzl S, Mayr C, Strauss H (2023) Identification and quantification of the sea spray effect on isotopic systems in α-cellulose (δ13C, δ18O), total sulfur (δ34S), and 87Sr/86Sr of European beach grass (*Ammophila arenaria*, L.) in a greenhouse experiment. Sci Total Environ 856:158840.

Göhring A, Hölzl S, Mayr C, Strauss H (2023) Multi-isotope fingerprints of recent environmental samples from the Baltic coast and their implications for bioarchaeological studies. Sci Total Environ 874:162513.

Gonella PM, Sano PT, Rivadavia F, Fleischmann A (2022) A synopsis of the genus *Drosera* (Droseraceae) in Brazil. Phytotaxa 553:1-76.

Gottschling M, Elbrächter M, Tillmann U (2022) Comments on Mertens et al. (2022): the taxonomic identity of *Micracanthodinium setiferum* (Lohmann) Deflandre (Dinophyceae incertae sedis) remains elusive, and its epitypification is not achieved. Palynology 46:1-3.

Gottschling M, Wietkamp S, Bantle A, Tillmann U (2024) Oxytoxaceae are prorocentralean rather than peridinialean dinophytes and taxonomic clarification of heterotrophic Oxytoxum lohmannii (≡ "*Amphidinium*" *crassum*) by epitypification. Sci Rep 14:6689.

Grabowski M, Kopperud BT, Tsuboi M, Hansen TF (2023) Both diet and sociality affect primate brain-size evolution. Syst Biol 72:404-418.

Grabowski M, Pienaar J, Voje KL, Andersson S, Fuentes-González J, Kopperud BT, Moen DS, Tsuboi M, Uyeda J, Hansen TF (2023) A cautionary note on "A cautionary note on the use of Ornstein Uhlenbeck models in macroevolutionary studies." Syst Biol 72:955-963.

Gruber D, Ruiz-Agudo C, Rao A, Pasler S, Cölfen H, Sturm EV (2024) Complex coacervates: From polyelectrolyte solutions to multifunctional hydrogels for bioinspired crystallization. Crystals (Basel) 14:959.

Guimarães Fabreti L, Höhna S (2023) Nucleotide substitution model selection is not necessary for Bayesian inference of phylogeny with well-behaved priors. Syst Biol 72:1418-1432.

Gürkan S, Stemplinger B, Rockinger A, Knechtel J, Gottschling M (2024) Bumps on the back: An unusual morphology in phylogenetically distinct *Peridinium* aff. *cinctum* (= *Peridinium tuberosum*; Peridiniales, Dinophyceae). Org Divers Evol 24:1-15.

Hagdorn H, Reich M, Gaitzsch B, Schneider J (2023) Ein Vierteljahrtausend verschollen: Der Lange'sche Encrinit aus dem Muschelkalk der Querfurter Mulde (Sachsen-Anhalt)--Syntypus von *Encrinus liliiformis* Lamarck, 1801. Z Dtsch Ges Geowiss 174:143-166.

Hagg W, Mayer C, Münzer U, Barbosa N, Schuler H-M, Staudacher M (2023) Estimating local surface glacier mass balance from migration of the 1918 Katla eruption tephra layer on Sléttjökull, southern Iceland. Ann Glaciol 64:147-155.

Hájek J, Alarie Y, Benetti CJ, Hamada N, Springer M, Hendrich L, Villastrigo A, Ospina Torres R, Basantes MS, Balke M (2024) Underestimated diversity and range size of diving beetles in tank bromeliads—Coleoptera of "hygrofloric" lifestyle (Dytiscidae). Zool J Linn Soc 200:720-735.

Hájek J, Šťastný J, Hendrich L, Balke M (2023) A review of the genus *Platynectes* from the Solomon Islands (Coleoptera: Dytiscidae: Agabinae). Acta Entomol Mus Natl Pragae 63(1):57-74.

Hájek J, Zippel A, Müller P, Pankowski MG, Hendrich L, Balke M (2024) *Copelatus* diving beetles (Coleoptera, Dytiscidae) from early Miocene Mexican amber, with description of a new species displaying distinct sexual dimorphism. J Paleontol 98:830-837.

Hassenbach C, Buchner L, Haug GT, Haug C, Haug JT (2023) An expanded view on the morphological diversity of long-nosed antlion larvae further supports a decline of silky lacewings in the past 100 million years. Insects 14(2):170.

Haszprunar G (2022) An update to the 2014 nomenclator of Valvatidae. Zookeys 1092:147-194.

Haug C, Baranov VA, Hörnig MK, Gauweiler J, Hammel JU, Perkovsky EE, Haug JT (2022) 35 million-year-old solid-wood-borer beetle larvae support the idea of stressed Eocene amber forests. Paleobiodivers Paleoenviron 103:521-530.

Haug C, Braig F, Haug JT (2023) Quantitative analysis of lacewing larvae over more than 100 million years reveals a complex pattern of loss of morphological diversity. Sci Rep 13:6127.

Haug C, Haug GT, Haug JT (2024) The first record of disruptive colouration in holometabolan larvae from about 100 million-year-old Kachin amber is a lacewing larva with dark stripes on the legs. Palaeoentomology 7:719-722.

Haug C, Haug GT, Kiesmüller C, Haug JT (2023) Convergent evolution and convergent loss in the grasping structures of immature earwigs and aphidlion-like larvae as demonstrated by about 100-million-year-old fossils. Swiss J. Palaeontol 142:21.

Haug C, Haug JT, Haug GT, Müller P, Zippel A, Kiesmüller C, Gauweiler J, Hörnig MK (2024) Fossils in Myanmar amber demonstrate the diversity of anti-predator strategies of Cretaceous holometabolan insect larvae. iScience 27:108621.

Haug C, la Fuente RP, Baranov V, Haug G, Kiesmüller C, Zippel A, Hörnig M, Haug J (2023) The first fossil record of a mantis lacewing pupa, and a review of pupae in Mantispidae and their evolutionary significance. Riv Ital Paleontol Stratigr 129(1):185-205.

Haug C, Posada Zuluaga V, Zippel A, Braig F, Müller P, Gröhn C, Weiterschan T, Wunderlich J, Haug GT, Haug JT (2022) The morphological diversity of antlion larvae and their closest relatives over 100 million years. Insects 13:587.

Haug C, Tun KL, Lay Mon T, Hnin WW, Haug JT (2023) The strange holometabolan beak larva from about 100 million years old Kachin amber was physogastric and possibly wood-associated. Palaeoentomology 6(4):372-384.

Haug C, Zippel A, Hassenbach C, Haug GT, Haug JT (2022) A split-footed lacewing larva from about 100-million-year-old amber indicates a now extinct hunting strategy for neuropterans. Bull Geosci 97(4):453-464.

Haug C, Zippel A, Müller P, Haug JT (2022) A modern type of ant-like stone beetle larva preserved in 99-million-year-old Kachin amber (Coleoptera: Staphylinidae, Scydmaeninae). Fragm Entomol 54:193-200.

Haug C, Zippel A, Müller P, Haug JT (2023) Unusual larviform beetles in 100-million-year-old Kachin amber resemble immatures of trilobite beetles and fireflies. Palaontol Z 97(3):485-496.

Haug GT, Haug C, van der Wal S, Müller P, Haug JT (2022) Split-footed lacewings declined over time: indications from the morphological diversity of their antlion-like larvae. Palaontol Z 96:29-50.

Haug GT, Haug JT, Haug C (2024) Convergent evolution of defensive appendages - a lithobiomorph-like centipede with a scolopendromorph-type ultimate leg from about 100 million-year-old amber. Paleobiodivers Paleoenviron 104:131-140.

Haug JT, van der Wal S, Gröhn C, Hoffeins C, Hoffeins H-W, Haug C (2022) Diversity and fossil record of larvae of three groups of lacewings with unusual ecology and functional morphology: Ithonidae, Coniopterygidae and Sisyridae. Palaeontol Electronica 25.2.a14.

Haug JT, Baranov V, Braig F, Haug C (2024) Morpho-ecospaces, or how to measure biodiversity in a different way. Acta Zool 105:496-513.

Haug JT, Engel MS, Mendes dos Santos P, Haug GT, Müller P, Haug C (2022) Declining morphological diversity in snakefly larvae during last 100 million years. Palaontol Z 96:749-780.

Haug JT, Fraaije RH, Haug C (2023) A new species of possible archipolypodan millipede from the Carboniferous of the Netherlands with unusually long tergites. Comptes Rendus Palevol 22:595-604.

Haug JT, Fu Y, Müller P, Haug GT, Haug C (2024) Quantitative morphology of fossil adephagan beetle larvae including a first record from the Jehol biota does not indicate major diversity losses over time. Zootaxa 5562:76-93.

Haug JT, Haug C (2022) 100 Million-year-old straight-jawed lacewing larvae with enormously inflated trunks represent the oldest cases of extreme physogastry in insects. Sci Rep 12:12760.

Haug JT, Haug C (2022) Another strange holometabolan larva from Kachin amber—the enigma of the beak larva (Neuropteriformia). Palaeoentomology 5:276-284.

Haug JT, Haug C (2023) New details of the enigmatic 100 million years old antlion-like larvae of *Ankyloleon* (Myrmeleontiformia, Neuroptera). Eur J Taxon 908(1):135-154.

Haug JT, Haug C, Wang Y, Baranov VA (2022) The fossil record of lepidopteran caterpillars in Dominican and Mexican amber. Lethaia 55:1-14.

Haug JT, Haug GT, Haug C (2023) Reconstructing the history of lacewing diversification: shape heterochrony and core tree as tools for reconstructing evolutionary processes. Neues Jahrb Geol Palaontol Abh 308:1-21.

Haug JT, Hörnig MK, Kiesmüller C, Pazinato PG, Baranov V, Haug C (2022) A 100-million-year-old ensiferan with unusual mouthparts and comments on the evolution of raptorial appendages within Polyneoptera. Geodiversitas 44(4):57-73.

Haug JT, Kiesmüller C, Haug GT, Haug C, Hörnig MK (2022) A fossil aphidlion preserved together with its prey in 40 million-year-old Baltic amber. Paleobiodivers Paleoenviron 103(1):155-163.

Haug JT, Linhart S, Haug GT, Gröhn C, Hoffeins C, Hoffeins H-W, Müller P, Weiterschan T, Wunderlich J, Haug C (2022) The diversity of aphidlion-like larvae over the last 130 million years. Insects 13:336.

Haug JT, Tun KL, Haug GT, Than KN, Haug C, Hörnig MK (2023) A hatching aphidlion-like lacewing larva in 100 million years old Kachin amber. Insect Sci 30:880-886.

Haug JT, Zippel A, Linhart S, Müller P, Haug C (2024) Unusual snakefly larvae in about 100 million-year-old amber and the evolution of the larva-pupa transition. Palaeoentomology 7:104-111.

Hegner E, Alexeiev DV, Messling N, Tolmacheva TY, Willbold M (2022) Cambrian-Ordovician mid-ocean ridge magmatism in the Kyrgyz Middle Tianshan and origin of the Karaterek ophiolite. Lithos 410-411:106576.

Helmbrecht V, Weingart M, Klein F, Braun D, Orsi WD (2023) White and green rust chimneys accumulate RNA in a ferruginous chemical garden. Geobiology 21:758-769.

Herbert Mainero A, Al-Jufaili SM, Jawad L, Reichenbacher B (2023) Sex dimorphism and evidence of sexually selected traits: A case study on the killifish *Aphaniops stoliczkanus* (Day, 1872). Acta Zool 104:473-487.

Herbert Mainero A, Vasilyan D, Reichenbacher B (2024) Two new genera of killifish (Cyprinodontiformes) from the Middle Miocene of the Bugojno Basin, Bosnia and Herzegovina: insights into the lost diversity of Valenciidae. J Syst Palaeontol 22(1): 2412539.

Heß M, Haacke C (2023) 2000 feet under the sea - visiting deep sea habitats off Roatan (Honduras). Spixiana 45(2):151-158

Höhna S, Hsiang AY (2024) Sequential Bayesian phylogenetic inference. Syst Biol 73:704-721.

Höhna S, Kopperud BT, Magee AF (2022) CRABS: Congruent rate analyses in birth-death scenarios. Methods Ecol Evol 13:2709-2718.

Holzer VJC, Kretschmann J, Knechtel J, Owsianny PM, Gottschling M (2022) Morphological and molecular variability of *Peridinium volzii* Lemmerm. (Peridiniaceae, Dinophyceae) and its relevance for infraspecific taxonomy. Org Divers Evol 22:1-15.

Hörnig MK, Haug C, Müller P, Haug JT (2022) Not quite social - possible cases of gregarious behaviour of immatures of various lineages of Insecta in 100-million-year-old amber. Bull Geosci 97(1):69-87.

Juravel K, Porras L, Höhna S, Pisani D, Wörheide G (2023) Exploring genome gene content and morphological analysis to test recalcitrant nodes in the animal phylogeny. PLoS One 18:e0282444.

Karapunar B, Höhna S, Nützel A (2024) Phylogeny of the longest existing gastropod clade (Pleurotomariida) reconstructed with Bayesian and parsimony methods and its implications on gastropod shell characters. J Syst Palaeontol 22(1):2384141.

Karapunar B, Nützel A, Ketwetsuriya C (2022) A low-diversity Peruvispira-dominated gastropod assemblage from the Permian Ratburi Group of Central Thailand. Alcheringa Australas J Palaeontol 46:147-155.

Karapunar B, Nützel A, Seuss B, Royal H. Mapes (2022) Taxonomy and diversity of slit-band gastropods (Order Pleurotomariida) and some slit bearing Caenogastropoda from the Pennsylvanian of the USA. Pap Palaeontol 8(2):e1417.

Karapunar B, Todd JA, Nützel A (2024) Slit-bearing gastropods in the Jane Longstaff collection at the natural history museum, London from the Visean (Carboniferous) of Dalry, Ayrshire, Scotland. J Paleontol 98:79-101.

Karapunar B, Werner W, Simonsen S, Bade M, Lücke M, Rebbe T, Schubert S, Rojas A (2023) Drilling predation on Early Jurassic bivalves and behavioral patterns of the presumed gastropod predator—evidence from Pliensbachian soft-bottom deposits of northern Germany. Paleobiology 49:642-664.

Kevrekidis C, Moritz T, Cerwenka AF, Bauer E, Reichenbacher B (2024) Uncovering the relationships among herring-like fossils (Clupei: Teleostei): a phylogenetic analysis. Zool J Linn Soc 202(3):zlae115.

Khakurel B, Grigsby C, Tran TD, Zariwala J, Höhna S, Wright AM (2024) The fundamental role of character coding in Bayesian morphological phylogenetics. Syst Biol 73:861-871.

Kiesmüller C, Haug GT, Haug C, Müller P, Hörnig MK, Haug JT (2024) New indications for the life habits of long-legged aphidlion-like larvae in about 100-million-year-old amber. Palaontol Z 98:429-441.

Kiesmüller C, Haug JT, Müller P, Hörnig MK (2022) A case of frozen behaviour: A flat wasp female with a beetle larva in its grasp in 100-million-year-old amber. Mitt Mus Nat Berl Foss Rec 25:287-305.

Kiesmüller C, Haug JT, Müller P, Hörnig MK (2022) Debris-carrying behaviour of bark lice immatures preserved in 100 million years old amber. Palaontol Z 96:231-258.

Kopperud BT, Lidgard S, Liow LH (2022) Enhancing georeferenced biodiversity inventories: automated information extraction from literature records reveal the gaps. PeerJ 10:e13921.

Kopperud BT, Magee AF, Höhna S (2023) Rapidly changing speciation and extinction rates can be inferred in spite of nonidentifiability. Proc Natl Acad Sci U S A 120: e2208851120.

Kretschmann J, Žerdoner Čalasan A, Knechtel J, Owsianny PM, Facher E, Gottschling M (2022) Evolution of Thoracosphaeroideae (Peridiniales, Dinophyceae) and a case of atavism in taxonomically clarified *Chimonodinium lomnickii var. wierzejskii* from the Polish Tatra Mountains. Eur J Phycol 57:406-421.

Kroh A, Gaudin J, Reich M (2022) *Oloughlinia*, a replacement name for *Clarkiella* Heding in Heding & Panning, 1954 (Echinodermata: Holothuroidea: Sclerodactylidae). Zootaxa 5178:397-399.

Krueger T, Bateman PW, Fleischmann A, Cross AT (2023) Better to risk limb than life: some insects use autotomy to escape passive predation by carnivorous plants. Arthropod Plant Interact 17:593-599.

Krueger T, Cross AT, Hübner J, Morinière J, Hausmann A, Fleischmann A (2022) A novel approach for reliable qualitative and quantitative prey spectra identification of carnivorous plants combining DNA metabarcoding and macro photography. Sci Rep 12:4778.

Krueger T, Cross AT, Rangers D, Fleischmann A (2023) *Drosera maanyaa-gooljoo*, a new species of *Drosera* section *Arachnopus* (Droseraceae) from the Buccaneer Archipelago and Yampi Peninsula, northwest Kimberley region, Western Australia. Phytotaxa 618:31-46.

Krueger T, Robinson A, Bourke G, Fleischmann A (2023) Small leaves, big diversity: Citizen science and taxonomic revision triples species number in the carnivorous *Drosera microphylla* complex (*D. section ergaleium*, Droseraceae). Biology (Basel) 12:141.

Laibl CF, Currado JLC, Morinière J, Schrödl M (2023) Barcoding coffee grounds - Exploring pteropod gastropod biodiversity with dregs in collection jars. Sci Mar 87(2): e061.

Lindberg DR, Haszprunar G (2022) Laudatio for Dr. Winston F. Ponder - a life of malacology. Molluscan Res 42:261-270.

Linhart SJ, Müller P, Haug GT, Haug C, Haug JT (2023) An overview of crawling water beetle larvae and a first possible record from 100-million-years-old Myanmar amber. Palaeontologia Electronica, 26(3):a42.

López-Arbarello A, Brocke R (2024) New generic name for a small Triassic ray-finned fish from Perledo (Italy). Swiss J. Palaeontol 143:30.

López-Arbarello A, Concheyro A, Palma RM, Aguirre-Urreta B (2023) The early fossil record of Caturoidea (Halecomorphi: Amiiformes): biogeographic implications. Swiss J. Palaeontol 142:33.

López-Arbarello A, D'Emic MD (2022) New fossils, new ideas: selected contributions of vertebrate paleontology to scientific knowledge. J Vertebr Paleontol 42(6): e2267264.

López-Arbarello A, Ebert M (2023) Assignment of nomen protectum status to *Eugnathus* [= Furo] orthostomus Agassiz, 1842. J Vertebr Paleontol 43(6):e2357331.

López-Arbarello A, Ebert M (2023) Taxonomic status of the caturid genera (Halecomorphi, Caturidae) and their Late Jurassic species. R Soc Open Sci 10:221318.

López-Romero FA, Stumpf S, Kamminga P, Böhmer C, Pradel A, Brazeau MD, Kriwet J (2023) Shark mandible evolution reveals patterns of trophic and habitat-mediated diversification. Commun Biol 6:496.

Lustri L, Antcliffe JB, Saleh F, Haug C, Laibl L, Garwood RJ, Haug JT, Daley AC (2023) New perspectives on the evolutionary history of xiphosuran development through comparison with other fossil euchelicerates. Front Ecol Evol 11:1270429.

Manconi R, Erpenbeck D, Fromont J, Wörheide G, Pronzato R (2022) Discovery of the freshwater sponge genus *Corvospongilla* Annandale (Porifera: Spongillida) in Australia with the description of a new species and phylogeographic implications. Limnology (Tokyo) 23:73-87.

Martínez-Gómez J, Song MJ, Tribble CM, Kopperud BT, Freyman WA, Höhna S, Specht CD, Rothfels CJ (2024) Commonly used Bayesian diversification methods lead to biologically meaningful differences in branch-specific rates on empirical phylogenies. Evol Lett 8:189-199.

McDonald PJ, Brown RM, Kraus F, Bowles P, Arifin U, Eliades SJ, Fisher RN, Gaulke M, Grismer LL, Ineich I, Karin BR, Meneses CG, Richards SJ, Sanguila MB, Siler CD, Oliver PM (2022) Cryptic extinction risk in a western Pacific lizard radiation. Biodivers Conserv 31:2045-2062.

Meng Y, Davison J, Clarke JT, Zobel M, Gerz M, Moora M, Öpik M, Bueno CG (2023) Environmental modulation of plant mycorrhizal traits in the global flora. Ecol Lett 26:1862-1876.

Mengel L, Linhart S, Haug GT, Weiterschan T, Müller P, Hoffeins C, Hoffeins H-W, Baranov V, Haug C, Haug JT (2023) The morphological diversity of dragon lacewing larvae (Nevrorthidae, Neuroptera) changed more over geological time scales than anticipated. Insects 14:749.

Messling N, Jodder J, Hegner E, Hofmann A, Wemmer K, Willbold M (2023) Mobilization of tungsten in Greenstone belts of the Archean kaapvaal and singhbhum cratons. Geochem Geophys Geosyst 24(12): e2023GC011161.

Michaelis T, Wunderlich A, Coskun ÖK, Orsi W, Baumann T, Einsiedl F (2022) High-resolution vertical biogeochemical profiles in the hyporheic zone reveal insights into microbial methane cycling. Biogeosciences 19:4551-4569.

Michat MC, Alarie Y, Balke M (2023) *Bunites distigma* (Brull, 1837): discovery of the second- and third-instar larvae and phylogenetic relationships within the Colymbetinae (Coleoptera: Dytiscidae). Zootaxa 5353:551-566.

Mohn RA, Zenil-Ferguson R, Krueger TA, Fleischmann A, Cross AT, Yang Y (2023) Dramatic difference in rate of chromosome number evolution among sundew (*Drosera* L., Droseraceae) lineages. Evolution 77:2314-2325.

Moles J, Brenzinger B, Berning MI, Martynov A, Korshunova T, Schrödl M (2024) Systematic rearrangements in an all-genus phylogeny of side-gilled slugs (Heterobranchia: Pleurobranchida). Zool J Linn Soc 202:zlad162.

Müller A, Stark M, Schottenhammel S, John U, Chacón J, Klingl A, Holzer VJC, Schöffer M, Gottschling M (2024) The second most abundant dinophyte in the ponds of a botanical garden is a species new to science. J Eukaryot Microbiol 71:e13015.

Nikonova E, DeCata J, Canela M, Barz C, Esser A, Bouterwek J, Roy A, Gensler H, Heß M, Straub T, Forne I, Spletter ML (2024) Bruno 1/CELF regulates splicing and cytoskeleton dynamics to ensure correct sarcomere assembly in *Drosophila* flight muscles. PLoS Biol 22:e3002575.

Nützel A, Karapunar B (2023) On Triassic *Murchisonia*-like gastropods - surviving the end-Permian extinction to become extinct in the Late Triassic. Acta Palaeontol Pol 68:539-559.

Nützel A, Nose M, Hautmann M, Hochleitner R (2023) Latest Triassic (Sevatian-Rhaetian) reef carbonates from the Northern Calcareous Alps (Austria), their mollusc dwellers, and their fate at the end-Triassic extinction event. Palaontol Z 97:265-309.

Nützel A, Schweigert G, Karapunar B (2022) The earliest gastropod with varices from the Mesozoic and the first record of decapod crustaceans from the St. Cassian Formation, Dolomites, Italy - a possible example of Triassic predator-prey interaction. Neues Jahrb Geol Palaontol Abh 305:153-160.

Orsi WD (2023) A rapid method for measuring ATP + ADP + AMP in marine sediment. Environ Microbiol 25:1549-1558.

Orsi WD (2023) Quantitative microbial ecology: Future challenges and opportunities. Environ Microbiol 25:91-96.

Orsi WD, Inagaki F (2023) Decoding geobiological evolution from microbiomes. Sci Adv 9:eadg5448.

Orsi WD, Vuillemin A, Coskun ÖK, Rodriguez P, Oertel Y, Niggemann J, Mohrholz V, Gomez-Saez GV (2022) Carbon assimilating fungi from surface ocean to subseafloor revealed by coupled phylogenetic and stable isotope analysis. ISME J 16:1245-1261.

Palazzesi L, Hidalgo O, Barreda VD, Forest F, Höhna S (2022) The rise of grasslands is linked to atmospheric CO_2 decline in the late Palaeogene. Nat Commun 13:293.

Pätzold J, Feyrer B, Saumweber J, Hilger HH, Gottschling M (2023) Observations on flower and fruit anatomy in dioecious species of *Cordia* (Cordiaceae, Boraginales) with evolutionary interpretations. Org Divers Evol 23:77-90.

Pazinato PG, Müller P, Haug JT (2023) New species of Tanaidacea from Cretaceous Kachin amber, with a brief review of the fossil record of tanaidacean crustaceans. Fossil Record 26:39-50.

Popovic I, Bergeron LA, Bozec Y-M, Waldvogel A-M, Howitt SM, Damjanovic K, Patel F, Cabrera MG, Wörheide G, Uthicke S, Riginos C (2024) High germline mutation rates, but not extreme population outbreaks, influence genetic diversity in a keystone coral predator. PLoS Genet 20:e1011129.

Qu Y, Yin Z, Kustatscher E, Nützel A, Peckmann J, Vajda V, Ivarsson M (2023) Traces of ancient life in oceanic basalt preserved as iron-mineralized ultrastructures: Implications for detecting extraterrestrial biosignatures. Astrobiology 23:769-785.

Rauhut OWM, Bakirov AA, Wings O, Fernandes AE, Hübner TR (2024) A new theropod dinosaur from the Callovian Balabansai Formation of Kyrgyzstan. Zool J Linn Soc 201(4):zlae090.

Reich M (2023) Where are all the Ordovician sea cucumbers (Echinodermata)? Estonian J Earth Sci 72:157.

Reich M, Kutscher M (2023) A new alcyonacean octocoral (Anthozoa) from the Late Silurian of Gotland, Sweden. Palaontol Z 97:729-739.

Reichenbacher B, Bannikov AF (2022) Diversity of gobioid fishes in the late middle Miocene of northern Moldova, Eastern Paratethys - part I: an extinct clade of Lesueurigobius look-alikes. Palaontol Z 96:67-112.

Reichenbacher B, Bannikov AF (2023) Diversity of gobioid fishes in the late middle Miocene of northern Moldova, Eastern Paratethys—Part II: description of *†Moldavigobius helenae* gen. et sp. nov. Palaontol Z 97:365-381.

Reichenbacher B, Přikryl T (2024) Revision and phylogenetic placement of one of the earliest freshwater gobies from the Lower Oligocene of Central Europe. Hist Biol 37(9): 2071-2089.

Reichenbacher B, Vukić J, Šanda R, Schliewen UK, Esmaeili HR, Kassar A (2023) Skeletal traits and otoliths can unravel the relationships within European Gobiidae (*Gobius* lineage sensu lato). Zool J Linn Soc 199:656-687.

Reimer JD, Peixoto RS, Davies SW, Traylor-Knowles N, Short ML, Cabral-Tena RA, Burt JA, Pessoa I, Banaszak AT, Winters RS, Moore T, Schoepf V, Kaullysing D, Calderon-Aguilera LE, Wörheide G, Harding S, Munbodhe V, Mayfield A, Ainsworth T, Vardi T, Eakin CM, Pratchett MS, Voolstra CR (2024) The Fourth Global Coral Bleaching Event: Where do we go from here? Coral Reefs 43:1121-1125.

Reiss L, Mayr C, Pasda K, Einwögerer T, Händel M, Lücke A, Maier A, Wissel H (2023) Changing food webs before and during the Last Glacial Maximum based on stable isotopes of animal bone collagen from Lower Austria. J Quat Sci 38:1337-1356.

Reiss L, Mayr C, Pasda K, Joachimski MM, Einwögerer T, Händel M, Maier A (2024) Seasonal climate variations during Marine Isotope Stages 3 and 2 inferred from high-resolution oxygen isotope ratios in horse tooth enamel from Lower Austria. J Quat Sci 39:531-546.

Reiss L, Stüwe C, Einwögerer T, Händel M, Maier A, Meng S, Pasda K, Simon U, Zolitschka B, Mayr C (2022) Evaluation of geochemical proxies and radiocarbon data from a loess record of the Upper Palaeolithic site Kammern-Grubgraben, Lower Austria. E& G Quat Sci J 71:23-43.

Renner SS, Scherz MD, Schoch CL, Gottschling M, Vences M (2024) Improving the gold standard in NCBI GenBank and related databases: DNA sequences from type specimens and type strains. Syst Biol 73:486-494.

Rivera-Vicéns RE, Garcia-Escudero CA, Conci N, Eitel M, Wörheide G (2022) TransPi-a comprehensive TRanscriptome ANalysiS PIpeline for de novo transcriptome assembly. Mol Ecol Resour 22:2070-2086.

Schächinger PM, Schrödl M, Wilson NG, Moles J (2022) Crossing the polar front—Antarctic species discovery in the nudibranch genus *Tritoniella* (Gastropoda). Org Divers Evol 22:431-456.

Schlauer J, Fleischmann A, Hartmeyer SRH, Hartmeyer I, Rischer H (2024) Distribution of acetogenic naphthoquinones in Droseraceae and their chemotaxonomic utility. Biology (Basel) 13:97.

Schmidt M, Achterhold K, Pfeiffer F, Melzer RR (2024) Kinematics of elongate harvestmen chelicerae: Comparative range of motion analyses in extant *Ischyropsalis* (Dyspnoi, Opiliones). Zoology (Jena) 167:126219.

Schmidt M, Hou X, Mai H, Zhou G, Melzer RR, Zhang X, Liu Y (2024) Unveiling the ventral morphology of a rare early Cambrian great appendage arthropod from the Chengjiang biota of China. BMC Biol 22:96.

Schmidt M, Hou X, Zhai D, Mai H, Belojević J, Chen X, Melzer RR, Ortega-Hernández J, Liu Y (2022) Before trilobite legs: *Pygmaclypeatus daziensis* reconsidered and the ancestral appendicular organization of Cambrian artiopods. Philos Trans R Soc Lond B Biol Sci 377:20210030.

Schmidt M, Martin I, Melzer RR (2024) Just a matter of size? Evaluating allometry and intersexual heterometry in *Pagurus bernhardus* using ratios and indices (Decapoda, Anomura). Integr Zool 19:807-823.

Schmidt M, Melzer RR (2024) The “elongate chelicera problem”: A virtual approach in an extinct pterygotid sea scorpion from a 3D kinematic point of view. Ecol Evol 14:e11303.

Schmidt M, Melzer RR, Bicknell RDC (2022) Kinematics of whip spider pedipalps: a 3D comparative morphofunctional approach. Integr Zool 17:156-167.

Schmidt M, Melzer RR, Plotnick RE, Bicknell RDC (2022) Spines and baskets in apex predatory sea scorpions uncover unique feeding strategies using 3D-kinematics. iScience 25:103662.

Schneider S, Fürsich FT, Werner W, Pierce CS (2023) Comment on: Magalhães et al., Middle Jurassic multi-scale transgressive-regressive cycles: An example from the Lusitanian Basin Depositional Rec 9:1161-1166.

Sepp T, Baines C, Kreitsberg R, Scharsack JP, Nogueira P, Lang T, Fort J, Sild E, Clarke JT, Tuvikene A, Meitern R (2024) Differences on the level of hepatic transcriptome between two flatfish species in response to liver cancer and environmental pollution levels. Comp Biochem Physiol C Toxicol Pharmacol 275:109781.

Shaverdo H, Balke M (2022) A species-group key and notes on phylogeny and character evolution in New Guinean *Exocelina* Broun, 1886 diving beetles (Coleoptera, Dytiscidae, Copelatinae). Zookeys 1131:31-58.

Shaverdo H, Hájek J, Hendrich L, Surbakti S, Panjaitan R, Balke M (2023) Austrelatus gen. nov., a new genus of Australasian diving beetles (Coleoptera, Dytiscidae, Copelatinae), with the discovery of 31 new species from New Guinea. Zookeys 1170:1-164.

Shaverdo H, Hendrich L, Surbakti S, Panjaitan R, Balke M (2024) Revision of the *Austrelatuspapuensis* group with descriptions of 42 new species from New Guinea (Coleoptera, Dytiscidae, Copelatinae). Zookeys 1201:1-165.

Shimpi GG, Vargas S, Bentlage B, Wörheide G (2024) Mitochondrial DNA damage, repair and copy number dynamics of *Sclerophytum* sp. (Anthozoa: Octocorallia) in response to short-term abiotic oxidative stress. J Exp Mar Bio Ecol 580:152051.

Sikora B, Unsoeld M, Melzer RR, Friedrich S, Skoracki M (2023) First records of picobiine mites associated with birds-of-paradise: Can interspecific sexual behaviour of hosts play a role in the distribution of quill mite parasites? Animals (Basel) 13(9):1509.

Skoracki M, Unsoeld M, Kosicki JZ, Melzer RR, Friedrich S, Sikora B (2024) Enigmatic host-mite relationships: Unraveling the distribution of quill mites on Birds-of-Paradise. Int J Parasitol 54:415-427.

Smith K, Ayres D, Neumaier R, Wörheide G, Höhna S (2024) Bayesian phylogenetic analysis on multi-core compute architectures: Implementation and evaluation of BEAGLE in RevBayes with MPI. Syst Biol 73:455-469.

Solà E, Leria L, Stocchino GA, Bagherzadeh R, Balke M, Daniels SR, Harrath AH, Khang TF, Krailas D, Kumar B, Li M-H, Maghsoudlou A, Matsumoto M, Naser N, Oben B, Segev O, Thielicke M, Tong X, Zivanovic G, Manconi R, Baguñà J, Riutort M (2022) Three dispersal routes out of Africa: A puzzling biogeographical history in freshwater planarians. J Biogeogr 49:1219-1233.

Stojakowits P, Mayr C (2022) Quaternary Palynostratigraphy of Germany with special emphasis on the Late Pleistocene. Stratigraphy & Timescales 7:81-136.

Szöllősi GJ, Höhna S, Williams TA, Schrempf D, Daubin V, Boussau B (2022) Relative time constraints improve molecular dating. Syst Biol 71:797-809.

Teimori A, Esmaeili HR, Zarei F, Reichenbacher B (2022) COI gene sequences confirm the taxonomic validity of the tooth-carp *Aphaniops hormuzensis* (Teleostei: Aphaniidae) from southern Iran. Zool Middle East 68:34-40.

Tillmann U, Beran A, Gottschling M, Wietkamp S, Hoppenrath M (2022) Clarifying confusion - *Prorocentrum triestinum* J.Schiller and *Prorocentrum redfieldii* Bursa (Prorocentrales, Dinophyceae) are two different species. Eur J Phycol 57:207-226.

Tillmann U, Gottschling M, Sunesen I, Wietkamp S, Dzhembekova N, Rodriguez Hernández F, Tardivo Kubis J, Sar E, Kaufmann M, Hoppenrath M (2024) Morphological and molecular characterization of *Prorocentrum bidens* (formerly known as *P. compressum*) and description of the closely related *Prorocentrum bisaeptum* sp. nov. (Prorocentrales, Dinophyceae). Phycologia 63(5):431-452.

Tillmann U, Gottschling M, Wietkamp S, Hoppenrath M (2023) Morphological and phylogenetic characterisation of *Prorocentrum spinulentum*, sp. nov. (Prorocentrales, Dinophyceae), a small spiny species from the North Atlantic. Microorganisms 11:271.

Tillmann U, Wietkamp S, Gottschling M, Hoppenrath M (2023) *Prorocentrum pervagatum* sp. nov. (Prorocentrales, Dinophyceae): A new, small, planktonic species with a global distribution. Phycological Res 71:56-71.

Tillmann U, Wietkamp S, Kretschmann J, Chacón J, Gottschling M (2023) Spatial fragmentation in the distribution of diatom endosymbionts from the taxonomically clarified dinophyte *Kryptoperidinium triquetrum* (= *Kryptoperidinium foliaceum*, Peridiniales). Sci Rep 13:8593.

Toledo M, Bilton DT, Balke M, Schizzerotto A, Villastrigo A (2023) A new, putatively semisubterranean, *Rhithrodytes* diving beetle from southwestern Sardinia (Coleoptera: Dytiscidae). Acta Entomol Mus Natl Pragae 63(1):125-133.

Trejos-Espeleta JC, Marin-Jaramillo JP, Schmidt SK, Sommers P, Bradley JA, Orsi WD (2024) Principal role of fungi in soil carbon stabilization during early pedogenesis in the high Arctic. Proc Natl Acad Sci U S A 121: e2402689121.

Tribble CM, Freyman WA, Landis MJ, Lim JY, Barido-Sottani J, Kopperud BT, Höhna S, May MR (2022) RevGadgets: An R package for visualizing Bayesian phylogenetic analyses from RevBayes. Methods Ecol Evol 13:314-323.

Tsuboi M, Kopperud BT, Matschiner M, Grabowski M, Syrowatka C, Pélabon C, Hansen TF (2024) Antler allometry, the Irish elk and Gould revisited. Evol Biol 51:149-165.

Uthicke S, Pratchett MS, Bronstein O, Alvarado JJ, Wörheide G (2024) The crown-of-thorns seastar species complex: knowledge on the biology and ecology of five corallivorous *Acanthaster* species. Mar Biol 171:32.

van der Sprong J, de Voogd NJ, McCormack GP, Sandoval K, Schätzle S, Voigt O, Erpenbeck D, Wörheide G, Vargas S (2024) A novel target-enriched multilocus assay for sponges (Porifera): Red Sea Haplosclerida (Demospongiae) as a test case. Mol Ecol Resour 24:e13891.

van der Wal S, Haug JT (2023) Reconstructing the life cycle of the isopodan group Aegidae with morphological descriptions and the importance of immature stages. Nauplius 31:e2023007.

van Heteren AH, Friess M, Détroit F, Balzeau A (2022) Covariation of proximal finger and toe phalanges in *Homo sapiens*: A novel approach to assess covariation of serially corresponding structures. Am J Biol Anthropol 177:471-488.

van Heteren AH, Germonpré M (2023) Geometric morphometric assessment of the fossil bears of Namur, Belgium: Allometry and ecomorphology. Boreas 52:498-506.

van Wassenbergh S, Ortlieb EJ, Mielke M, Böhmer C, Shadwick RE, Abourachid A (2022) Woodpeckers minimize cranial absorption of shocks. Curr Biol 32:3189-3194.e4.

Vargas S, Leiva L, Eitel M, Curdt F, Rohde S, Arnold C, Nickel M, Schupp P, Orsi WD, Adamska M, Wörheide G (2023) Body-plan reorganization in a sponge correlates with microbiome change. Mol Biol Evol 40(6):msad138.

Vargas S, Zimmer T, Conci N, Lehmann M, Wörheide G (2022) Transcriptional response of the calcification and stress response toolkits in an octocoral under heat and pH stress. Mol Ecol 31:798-810.

Vidal-Miralles J, Kohnert P, Monte M, Salvador X, Schrödl M, Moles J (2024) Between sea angels and butterflies: A global phylogeny of pelagic pteropod molluscs. Mol Phylogenet Evol 201:108183.

Villa A, Reichenbacher B (2022) Reinterpretation of girdled lizard remains from Switzerland documents the first occurrence of the lacertid *Janosikia* outside of Germany. Palaontol Z 96:129-134.

Villalba de Alvarado M, Collado Giraldo H, Arsuaga JL, Bello Rodrigo JR, van Heteren AH, Gómez-Olivencia A (2022) Looking for the earliest evidence of *Ursus arctos* LINNAEUS, 1758 in the Iberian Peninsula: the Middle Pleistocene site of Postes cave. Boreas 51:159-184.

Villastrigo A, Cooper SJB, Langille B, Fagan-Jeffries EP, Humphreys WF, Hendrich L, Balke M (2024) Aridification and major geotectonic landscape change shaped an extraordinary species radiation across a world's extreme elevational gradient. Commun Biol 7:1500.

Villastrigo A, Deharveng L, Balke M (2023) New Caledonia's enigmatic terrestrial diving beetle *Typhlodessus monteithi* is a derived species of Paroster. Zool Scr 52(2):176-183.

Vuillemin A, Coskun ÖK, Orsi WD (2022) Microbial activities and selection from surface ocean to subseafloor on the Namibian continental shelf. Appl Environ Microbiol 88:e0021622.

Wang Q, Purrafee Dizaj L, Huang J, Kumar Sarker K, Kevrekidis C, Reichenbacher B, Reza Esmaeili H, Straube N, Moritz T, Li C (2022) Molecular phylogenetics of the Clupeiformes based on exon-capture data and a new classification of the order. Mol Phylogenet Evol 175:107590.

Watts CHS, Villastrigo A, Langille BL, Stringer DN, Bradford TM, Humphreys WF, Austin AD, Balke M, Cooper SJB (2023) Phylogenetic placement and description of *Ngaliadessus humphreysi* gen. et sp. nov., Watts & Villastrigo (Coleoptera: Dytiscidae), a subterranean diving beetle from the Ngalia Basin in central Australia. Aust Entomol 62:300-309.

Weingart M, Chen S, Donat C, Helmbrecht V, Orsi WD, Braun D, Alim K (2023) Alkaline vents recreated in two dimensions to study pH gradients, precipitation morphology, and molecule accumulation. Sci Adv 9:eadi1884.

Windholz GJ, Carballido JL, Coria RA, Zurriaguz VL, Rauhut OWM (2023) How pneumatic were the presacral vertebrae of dicraeosaurid (Sauropoda: Diplodocoidea) dinosaurs? Biol J Linn Soc Lond 138:103-120.

Windholz GJ, Cerda IA, Carballido JL, Rauhut OWM (2023) Palaeobiological inferences for the South American dicraeosaurid *Brachytrachelopan mesai* (Dinosauria; Sauropoda) based on bone histology of the holotype. Hist Biol 35:1871-1880.

Wolf L, Melzer RR, Lehmann T (2022) Rediscovery after 25 years - first photographic documentation and DNA barcoding of the deep-sea pycnogonid species *Ascorhynchus hippos* Turpaeva, 1994 (Chelicerata, Pycnogonida, Ascorhynchidae) from the Kuril-Kamchatka Trench. Zoosystematics and Evolution 98:257-262.

Wörheide G, Kaltenbacher E, Cowan Z-L, Haszprunar G (2022) A new species of crown-of-thorns sea star, *Acanthaster benziei* sp. nov. (Valvatida: Acanthasteridae), from the Red Sea. Zootaxa 5209:379-393.

Xu Y, Jubanski J, Bittner K, Siegert F (2024) Roof plane parsing towards LoD-2.2 building reconstruction based on joint learning using remote sensing images. Int J Appl Earth Obs Geoinf 133:104096.

Zhang M, Liu Y, Hou X, Ortega-Hernández J, Mai H, Schmidt M, Melzer RR, Guo J (2022) Ventral morphology of the non-trilobite artiopod Retifacies abnormalis Hou, Chen & Lu, 1989, from the early Cambrian Chengjiang Biota, China. Biology (Basel) 11:1235.

Zhu B, Stark M, Kretschmann J, Gottschling M (2024) Intercalary plate dynamics in Peridiniopsidaceae (Peridiniales) observed in the tiny dinophyte *Parvodinium* cf. *inconspicuum*. System Biodivers 22(1):2379859.

Zippel A, Baranov VA, Hammel JU, Hörnig MK, Haug C, Haug JT (2022) The first fossil immature of Elmidae: an unusual riffle beetle larva preserved in Baltic amber. PeerJ 10:e13025.

Zippel A, Haug C, Elverdi Z, Müller P, Haug JT (2023) Possible fungus-eating cucujiformian beetle larvae with setiferous processes from Cretaceous and Miocene ambers. Fossil Record 26:191-207.

Zippel A, Haug C, Gauweiler J, Hörnig MK, Haug GT, Haug JT (2022) A small beetle larva preserved in 23-million-year-old Mexican amber: possible first fossil record of an immature variegated mud-loving beetle. Bol Soc Geol Mex 74:A150322.

Zippel A, Haug C, Hoffeins C, Hoffeins H-W, Haug JT (2022) Expanding the record of larvae of false flower beetles with prominent terminal ends. Riv Ital Paleontol Stratigr 128(1):81-104.

Zippel A, Haug C, Müller P, Haug JT (2022) First fossil tumbling flower beetle-type larva from 99 million-year-old amber. Palaontol Z 96:219-229.

Zippel A, Haug C, Müller P, Haug JT (2022) The first fossil false click beetle larva preserved in amber. Palaontol Z 97:209-215.

Zippel A, Haug C, Müller P, Haug JT (2024) Elateriform beetle larvae preserved in about 100-million-year-old Kachin amber. Palaontol Z 98:245-262.

Annex: Reports and Press Releases

Low CO2 concentrations

The team led by LMU researcher Sebastian Höhna reports in Nature Communications.

12.01.2022

Ecosystems on our planet have changed from dense forests to open-habitat ecosystems such as grasslands which provide resources for large grass-feeding mammals (e.g., horses). A team led by Sebastian Höhna, head of an Emmy Noether research group at the GeoBio-Center at LMU, now have analyzed the timing of the radiation of grasslands' most important plant families (grasses and daisies) using information provided by time-calibrated molecular phylogenies and a novel Bayesian statistical model.

© RF-Foto - stock.adobe.com

The scientists found that the most important diversification of grasses and daisies occurred about 20 million years ago. Interestingly, the onset of the diversification of grasslands appears to have occurred just after a significant global drop of atmospheric CO_2. Plants absorb carbon dioxide and release oxygen and water vapour through stomata in their leaves. Low CO_2 concentrations trigger opening of stomatal pores which increases the loss of water. The scientists assume that carbon limitation and water stress due to lower atmospheric CO_2 favored grasslands at the expense of forests.

Luis Palazzesi, Oriane Hidalgo, Viviana D. Barreda, Félix Forest, Sebastian Höhna: The rise of grasslands is linked to atmospheric CO2 decline in the late Palaeogene. Nature Communications 2022

Paleobiology: complex family relationships

An international team of researchers led by LMU paleontologist Bettina Reichenbacher has managed to classify fossils of one of the most species-rich fish groups into a family tree for the first time.

11.07.2022

Gobies are one of the most species-rich groups of ocean and freshwater fish. Found throughout the world in around 2,300 species divided between eight families, the Gobioidei suborder is highly diverse. Understanding how, why, and when this diversity came about is very complicated.

Ancestral but specialized: *Rhyacichthys guilberti* Dingerkus & Séret 1992 from Solomon. Its body shape is an adaptation to strong water flow conditions.

In helping to answer these questions, goby fossils can make a definite contribution. After all, they are direct evidence of goby diversity many millions of years ago. First, however, scientists had to find out whether the fossil gobies belong to one of today's families – and if so, which one. And this problem could not be solved – at least sufficiently – before now, as the individual goby families have acquired only few new traits, so-called apomorphies, in the course of their evolution. And few of these important traits generally survive in fossil gobies. For this reason, most fossil gobies could not be assigned to a family before now, or only with a high degree of uncertainty.

Rare ancestral beauty in its native habitat: *Protogobius attiti* Watson & Pöllabauer 1998 from New Caledonia.

To solve this problem, an international team of researchers led by LMU paleontologist Bettina Reichenbacher took the existing molecular family tree of the gobies and for the first time supplemented the molecular data with morphological data.

Through this technique, the researchers were able to then "add" fossil goby species to the established family tree of today's gobies. Or, to put it another way, the fossils were "placed" in the family tree of their current descendants. Some of the fossils ended up in a place in the family tree where previous studies had indicated they might belong; others ended up in entirely new, sometimes surprising family surroundings. "We see our approach as groundbreaking for all further phylogenetic investigations into fossil gobies," says Reichenbacher. The researchers hope that this will yield a better understanding of the evolutionary history of these fascinating fish.

Citation: Gierl C, Dohrmann M, Keith P, Humphreys W, Esmaeili HR, Vukić J, et al. (2022) An integrative phylogenetic approach for inferring relationships of fossil gobioids (Teleostei: Gobiiformes). PLoS ONE 17(7): e0271121. https://doi.org/10.1371/journal.pone.0271121

Environmental Medal of Bavaria for Andreas Fleischmann

GeoBio-Center LMU member PD Dr. Andreas Fleischmann received the Environmental Medal of Bavaria.

23.09.2022

LMU GeoBio-Center member PD Dr. Andreas Fleischmann received the Environmental State Medal of Bavaria yesterday afternoon. During an honorary ceremony in the former Dominican Church in Bamberg, Minister of State Thorsten Glauber presented the award.

Minister of State Thorsten Glauber (left) and Dr. Andreas Fleischmann

As curator for flowering plants at the Botanical State Collection Munich (SNSB-BSM), as lecturer for systematic botany at the LMU and honorary member of the Bavarian Botanical Society, Andreas Fleischmann contributes his broad expertise to environmental protection.

"You provide society with the facts needed to advance environmental protection in Bavaria," said State Minister Thorsten Glauber, explaining the award. "I would particularly like to highlight your successful scientific communication on the environmental topics of biotope destruction and flower strip management and your expert commitment to the environmental policy discussion on species loss, effective species protection and the establishment of biotope bridges."

The Bavarian State Medal for Special Services to the Environment is the highest award that the Bavarian state has to bestow in this field. It is awarded annually by the Bavarian State Minister for the Environment and Consumer Protection to individuals or associations who have rendered outstanding services to nature conservation and environmental protection. This year, eleven people received the medal.

How Scientists Used Lasers, Satellites and Planes to Map One of Indonesia's Biggest Sources of Emissions

07.11.2022

blog authored by Katie Fletcher for globalforestwatch.org

Drainage canals in peatland, Central Kalimantan, Indonesia. Photo: Flickr/World Resources Institute

Twenty years ago, GeoBio-Center member Prof. Dr. Florian Siegert, was conducting ecology research in Borneo when a series of fires blazed across Indonesia. The Asian Forest Fires of 1997-1998 burned thousands of miles of rainforest, creating a haze and air quality disaster that caused $5-6 billion in economic losses and endangered the long-term health of 70 million people.

Siegert is also managing director of RSS - Remote Sensing Solutions GmbH, which has been one of the leading companies for earth observation in Germany for more than 20 years. The company specializes in the processing and analysis of satellite data in the fields of environmental monitoring, nature conservation, climate change and natural hazards.

The rampant spread of the fires through the vast tropical rainforest struck Siegert. Why were these fires happening, and why were they so aggressive?

Seeking answers to those questions led Siegert to where he is today, the winner of a $1 million prize for mapping Indonesia's peat, boggy lands composed of decaying organic matter. It's just the latest achievement in a long career exploring peat, an often overlooked yet vitally important ecosystem in the global battle to fight climate change.

As Siegert and his team studied the 1997-1998 fires, it became clear that rainforests in places like Borneo and Sumatra grow on peat, and there were still vast layers of peatland had not yet been burned

"Peatlands at that time were basically uninhabited – strange ecosystems with acidic water and many endemic plants," Siegert recalled. "We wanted to find out more about the ecology of this ecosystem and how it was formed."

Peat, Long Buried, Starts to Burn

In 2002, Siegert and team published a landmark paper exposing a dire problem: When tropical peat burns, it releases massive carbon emissions.

Knowing just how thick these unburned layers of peat were was now critical to understanding how much carbon remained within the peat—and how much damage it would cause if it were to burn.

Peat Swamp, Central Kalimatan, Indonesia. Photo: Flickr/World Resources Institute

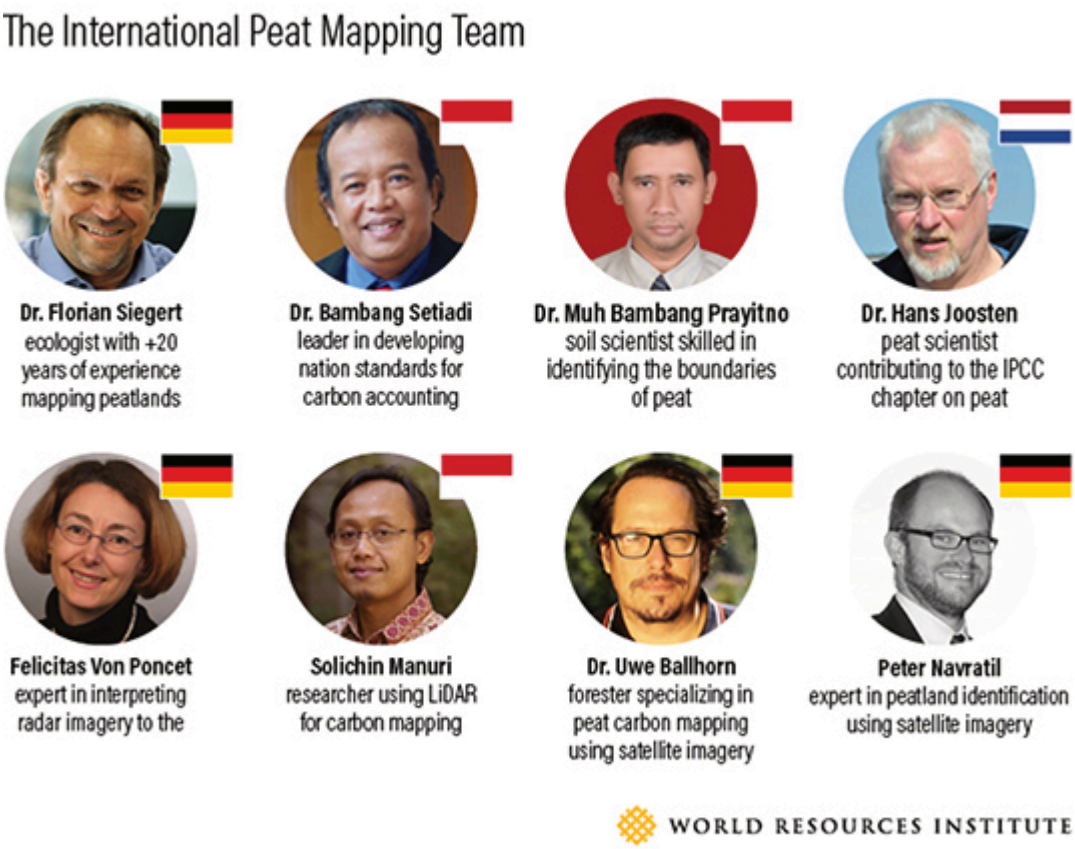
Siegert and researchers began collecting field data in collaboration with Indonesian and European universities, resulting in more than 10 years of concerted research on the specific properties of peat swamps and why exactly they burn. "We started to drill holes in peat swamps to see how thick the layer was and did analysis of the biomass materials to get an understanding of how exactly it was formed," Siegert explained.

Indonesia's record-breaking 2015 fire season demonstrated how important this research continues to be today. Half of the fires burned on peatland, igniting a carbon bomb that catapulted the country from the world's sixth-largest emitter to its fourth-largest. Global pressure for Indonesia to protect and restore its peatlands increased.

Without a precise understanding of the location, type, extent and depth of Indonesia's peat, though, this task would be nearly impossible. In response, the Indonesian Geospatial Information Agency (BIG) opened the Indonesian Peat Prize contest. The team that came up with the best way to map peat would be awarded a $1 million prize—and their contribution would form the basis for Indonesia's national action on peat.

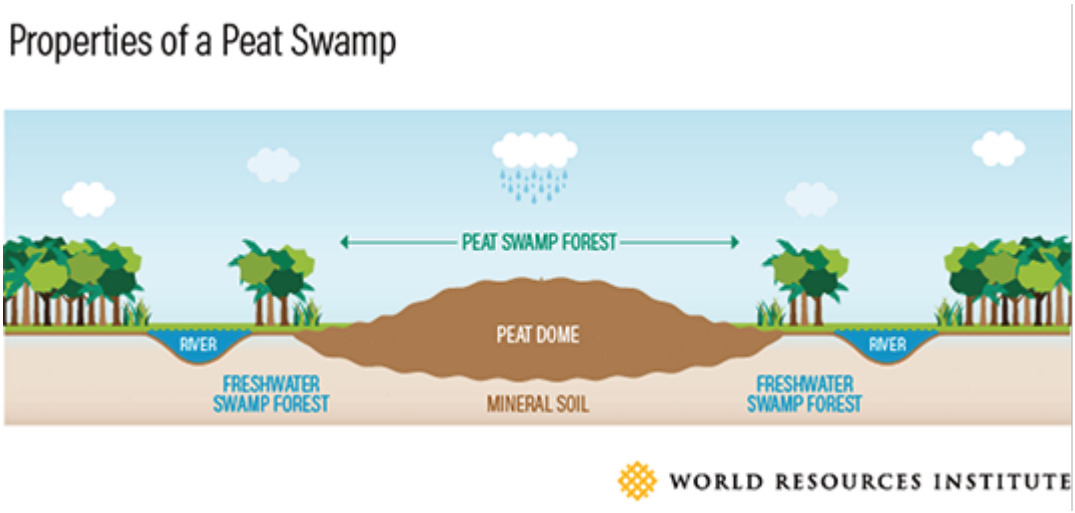
The Perfect Peat Map: Lasers, Planes and Satellites

When Siegert heard about the Peat Prize, he began hand-selecting a team of partners he'd worked with over the last 15 years.



The team's diverse experts would have to address both parts of mapping peatlands: distribution and topography.

The first step towards assessing peat distribution was to identify already burned or degraded peat no longer recognizable as peat swamp in recent satellite imagery. To do this, the team used historic Landsat satellite imagery dating back to the 1970s, which enabled them to view peat swamp forest distribution and how it changed over time. Using more recent, higher-resolution Sentinel-2 satellite imagery, the team could identify additional characteristics typical for peatland such as drainage canals and double-check information gathered from Landsat.



With a better understanding of the peat's distribution, they moved on to determine the thickness of peat locations—a process also accomplished in two steps. Peat is characteristically formed in dome-like structures; you can guess how much peat there is by mapping the topography of the domes in the landscape. Satellite images taken from the Airbus WorldDEM provided a first look at how tall each peat dome might be. The team then innovatively used LiDAR—which works as sonar does with sound, but with lasers—to create a very detailed

topography (up to 1m resolution in xy and 10 cm resolution in elevation) and digital 3D representation of selected areas. (Flying LiDAR light beam instruments from airplanes cost more than any other part of the peat mapping process, but the team maximized its efficiency by only using this method to cross-check select areas of the topography map produced by WorldDEM.)

Finally, the team hired locals who lived nearby these peat areas to drill several dozens of holes into the soil. They examined each hole to see how deep the peat went—a kind of fact-check for the satellite-based work that could be efficiently replicated by Indonesians across the country.

This combination proved to be the most accurate, efficient and affordable submission in the Indonesian Peat Prize content, and the International Peat Mapping team won the $1 million prize. The Indonesian government will now use the team's methodology—as well as select elements of other submissions, including a helicopter-based frame for measuring peat thickness with electromagnetic waves—as the standard for mapping the entire country's peatlands.

The Potential for Peat Restoration

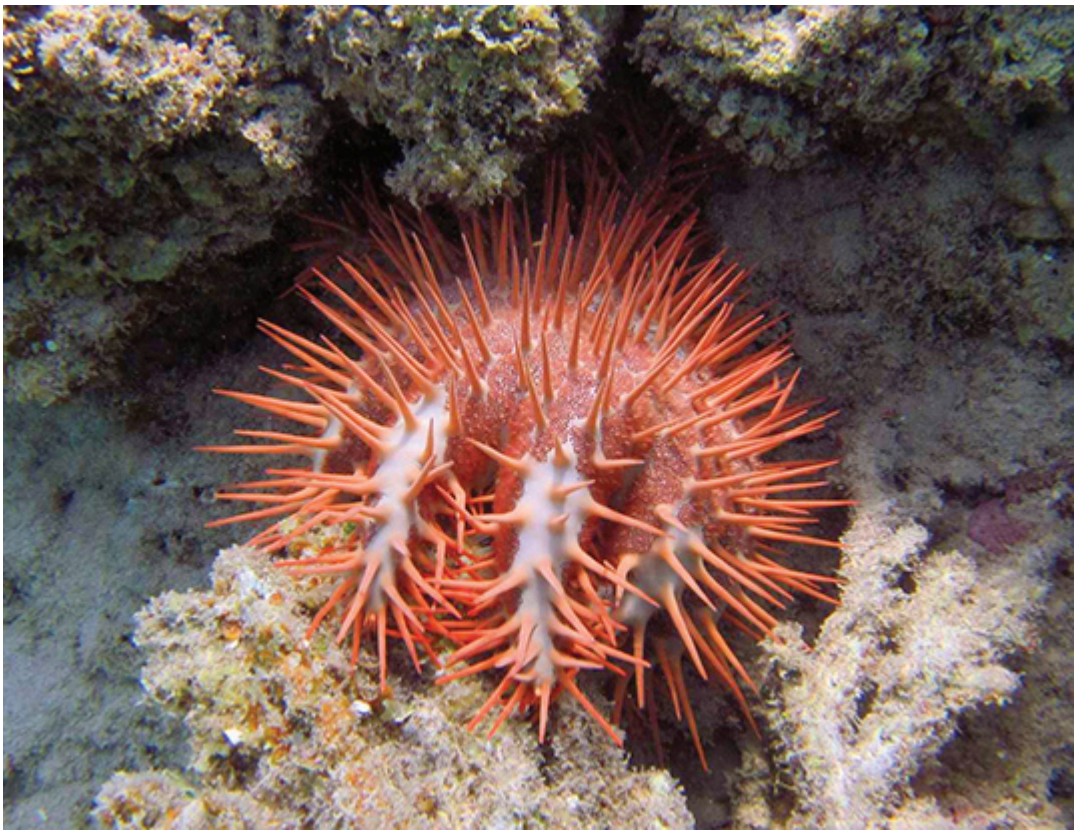
After paying back the investment made by Remote Sensing Solutions, his 15-person company that funded the initiative, Siegert plans to apply the winnings to do research on peat restoration. He also intends to enhance academic cooperation among universities to develop a "peat thesis" program that deals specifically with restoration of peat. Finally, Siegert says he'll also work to expand this effort beyond Indonesia to explore the completely unknown—and luckily, undisturbed—peatlands in Africa.

Crown-of-thorns seastar from Red Sea

LMU and SNSB researchers have identified coral-eating crown-of-thorns seastars in the Red Sea as distinct species that occurs only in this location.

11.11.2022

Tropical coral reefs are among the most endangered ecosystems on Earth. In addition to climate change, coral-eating crown-of-thorns seastars (Acanthaster spp.) pose one of the biggest threats in parts of the Indo-Pacific region. Up to 40 cm in length, these creatures feed mainly on the polyps of fast-growing stony corals. Mass outbreaks are not uncommon, whereby the seastars propagate at a rapid rate and many thousands of individuals can destroy large areas of coral reef. Such mass outbreaks have become increasingly frequent over recent decades, partly because the natural enemies of the seastars have been decimated by overfishing.



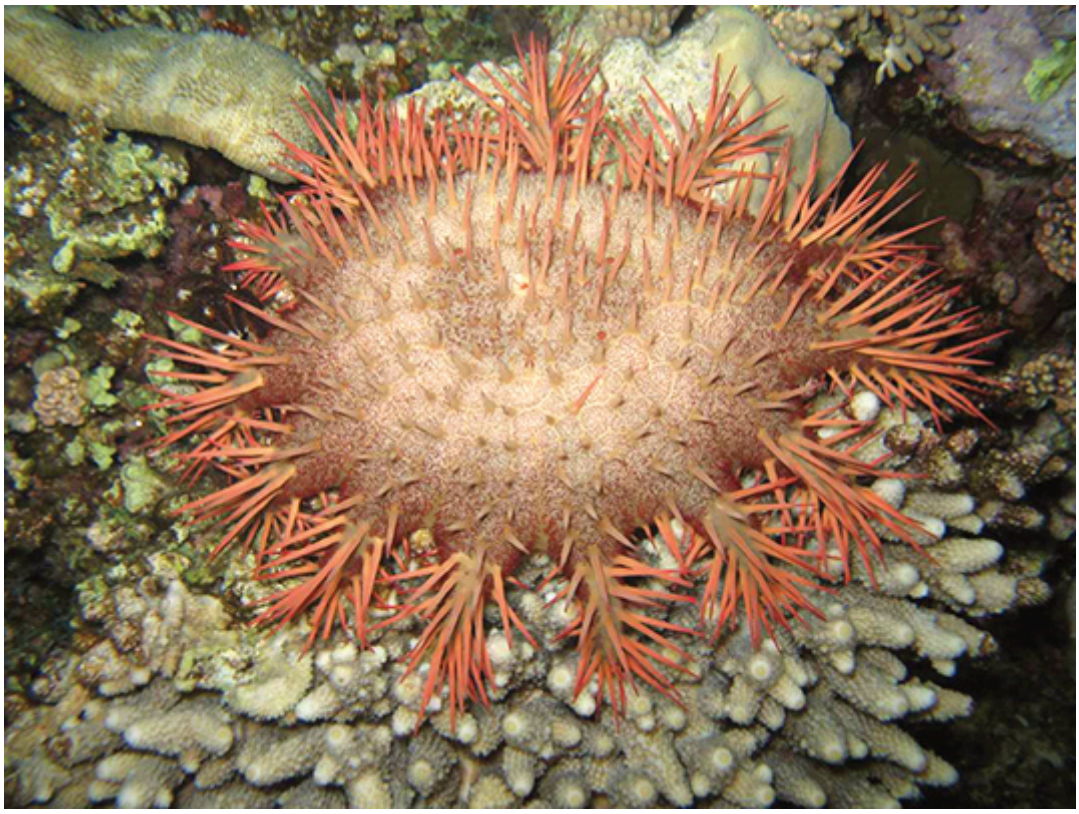
Crown-of-thorns seastar from Red Sea; Foto: PD Dr. Oliver Voigt

Crown-of-thorns seastars are widely distributed throughout the Indo-Pacific region. They get their name from the large venomous spines that protrude from their arms. Based on regional morphological differences, various species had been described in the past. However, the relationships between them remained somewhat hazy. "It was long assumed that the first species in the genus described, Acanthaster planci, was distributed from the Red Sea and the Indian Ocean over the entire Pacific," says Gert Wörheide, Professor of Paleontology and Geobiology at LMU. However, DNA barcoding data from a doctoral thesis supervised by Wörheide showed more than 10 years ago that A. planci can be subdivided into four strongly diverging genetic lineages, which presumably represent different species. A team led by Wörheide and Gerhard Haszprunar, Professor of Systematic Zoology at LMU, has now demonstrated with the aid of morphological investigations and genetic analyses that the crown-of-thorns seastar native to the Red Sea form a distinct species, which has been given the name Acanthaster benziei. "This underlines once again the importance of the Red Sea as an ecosystem with unique fauna and numerous endemic species," emphasizes Wörheide. The new species name honors John Benzie, Professor at University College Cork, who has done pioneering work with his groundbreaking genetic studies on crown-of-

thorns seastars in the 1990s and his comprehensive collection.

Fewer arms, thinner spines

With A. benziei, the scientists managed to describe a new species of crown-of-thorns seastar for the first time in several decades. "Although isolated particular features had already been observed in crown-of-thorns seastars from the Red Sea, such as a tendency to a more nocturnal lifestyle and probable lower toxicity of the spines, we didn't know yet that it was actually a distinct species," says Wörheide. The research confirmed clear differences between A. benziei and the other species of the "A. planci" species complex. In addition to characteristic sequences in the mitochondrial DNA, this included morphological features such as a lower number of arms and thinner, differently shaped spines.



Crown-of-thorns seastar from Red Sea; Foto: PD Dr. Oliver Voigt

"Now that we know it's a distinct species, we can direct our attention to the biology, ecology, and toxicology of A. benziei and the other Acanthaster species," says Wörheide. In the past, scientists had also observed a lower tendency for mass outbreaks in Red Sea crown-of-thorns seastars. "Such outbreaks are known primarily from Acanthaster cf. solaris in the western Pacific and regularly cause major damage to the Great Barrier Reef, whereas the phenomenon appears to be less severe in the Red Sea – whether species-specific characteristics are a contributing factor could be the object of future investigations," says Wörheide. Most data that have been gathered to date on the biology and ecology of crown-of-thorns seastars comes from Acanthaster cf. solaris from the western Pacific. "By clearly distinguishing the various species of coral-eating crown-of-thorns seastars, we can carry out more detailed research into the dynamics of mass outbreaks, one of the multiple stressors that affect tropical reefs. Ultimately, this is a step in the direction of better management of reef ecosystems."

Original publication

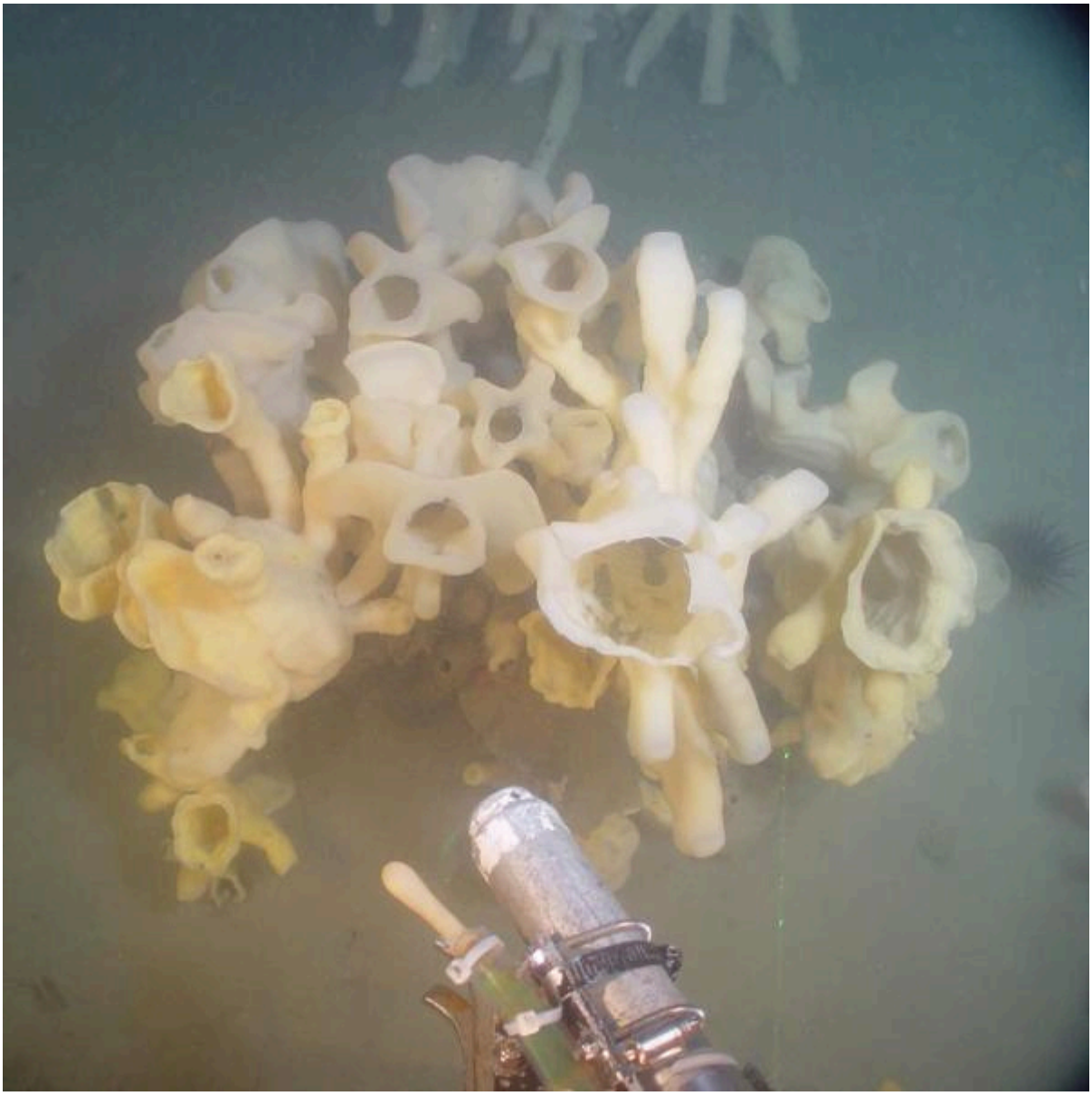
Gert Wörheide, Emilie Kaltenbacher, Zara-Louise Cowan, Gerhard Haszprunar. A new species of crown-of-thorns sea star, Acanthaster benziei sp. nov. (Valvatida: Acanthasteridae), from the Red Sea. ZOOTAXA, 2022. 5209 (3), 379–393

Glass sponge genome furnishes insights into evolution of biomineralization

The genome of a glass sponge species suggests that silica skeletons evolved independently in several groups of sponges.

27.06.2023

Researchers led by geobiologist Professor Gert Wörheide have decoded the genome of *Aphrocallistes vastus*, a reef-building glass sponge found off the coast of British Columbia. The sponge possesses a unique skeletal structure of amorphous silicon dioxide, from which the class of glass sponges gets its technical name – Hexactinellida. Well-annotated and contiguous genomes are an indispensable resource for understanding the evolution, development, and metabolic capacities of organisms. However, the ecologically important sponges are underrepresented with respect to available genome resources.



The reef-building glass sponge *Aphrocallistes vastus* is found off the coast of British Columbia in Canada. | © Sally Leys and CSSF ROPOS

As the researchers report in the journal *Royal Society Open Science,* the sponge species possesses a compact genome with numerous nested genes. The study identified several genes connected with the growth of the animals, and in particular with the formation of their mineral skeleton. Its results suggest that the biomineralization of silicon dioxide developed independently in different sponge classes. "Our investigations shed a new light on the biology of glass sponges, provide valuable insights into their evolutionary history, and highlight their ecological significance, deepening our understanding of these mysterious organisms and their important role in marine ecosystems," says Wörheide.

Original publication

Warren R. Francis, Michael Eitel, Sergio Vargas, Catalina A. Garcia-Escudero, Nicola Conci, Fabian Deister, Jasmine L. Mah, Nadège Guiglielmoni, Stefan Krebs, Helmut Blum, Sally P. Leys, Gert Wörheide: The genome of the reefbuilding glass sponge *Aphrocallistes vastus* provides insights into silica biomineralization. Royal Society Open Science, 2023

New source of information on evolution of European gobies

A team led by LMU paleontologist Bettina Reichenbacher has demonstrated for the first time that 'earstones' and skeletal traits permit to recognize familial relationships of the fish.

25.07.2023

Unravelling the evolution of European gobies. This pictures shows a specimen of Gobius cruentatus | © Uli Schliewen / SNSB-ZSM

Gobiidae (gobies) is one of the most species-rich families of marine and freshwater fish in Europe. They are generally quite small (maximum 10 cm), spend the vast majority of their lives on the floors of waterbodies, and make substantial contributions to the functioning of various ecosystems by virtue of their abundance and variety. An important strand of research into today's gobies seeks to understand their evolutionary history through molecular analyses and with the help of fossils. Fossils are vitally important because they are the only direct evidence we have to know which gobies existed many millions of years ago.

It is a scientific challenge, however, to precisely classify fossil gobies – that is to say, determining to which present-day gobies they are most closely related. Molecular methods are of course not available for fossils, but we do have their hard parts, namely the bones of their skeletons, their teeth, scales, and 'earstones' – or otoliths to give them their scientific name. Otoliths are biomineralizations in the inner ear of gobies (and indeed all bony fish). Primarily, they help the fish with balance, orientation, and acoustic communication. But whether hard parts such as skeletal traits or otoliths permit precise classification of a goby fossil could not be established with certainty before now.

An international team of scientists led by Professor Bettina Reichenbacher from the Department of Earth and Environmental Sciences at LMU and the GeoBio-Center at LMU has now presented a comprehensive dataset on the skeletal traits and otoliths of present-day European gobies in the Zoological Journal of the Linnean Society. The researchers document that the morphology of otoliths allows classification at the levels of genus and species and even between closely related dwarf gobies, and that skeletal traits and morphometric otolith variables can be diagnostic for a goby lineage. They conclude that the new data are a valuable reference tool for evaluating the phylogenetic relationships of fossil gobies. "Our results pave the way for future research into goby fossils in the context of their familial relationships with the gobies of today, thus making a significant contribution to our knowledge of the evolutionary history of this highly interesting family," says Reichenbacher.

Original publication

Reichenbacher, B., Vukić, J., Šanda, R., Schliewen, U. K., Esmaeili, H. R., & Kassar, A.: Skeletal traits and otoliths can unravel the relationships within European Gobiidae (Gobius lineage sensu lato). Zoological Journal of the Linnean Society, 2023

Geobiology: new placozoan habitat discovered

Traces of DNA in the stomachs of predatory snails give a team led by LMU geobiologist Gert Wörheide new insights into the ecology of placozoans.

11.04.2024

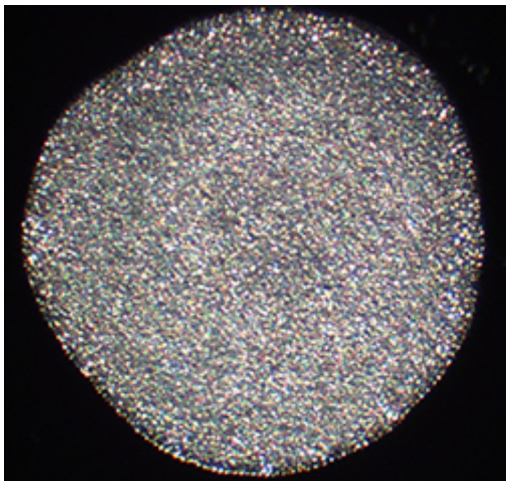


Foto: Placozoan species *Hoilungia hongkongensis*, © Hans-Jürgen Osigus, Stiftung Tierärztliche Hochschule Hannover

Placozoans are among the simplest animals and occur worldwide in coastal waters. It was previously assumed that the tiny creatures, which measure just a few millimeters, live either on hard surfaces – such as rocks, corals, and mangrove roots – or float in open coastal waters as so-called "swarmer" stages. Through analysis of DNA traces in the stomachs of predatory sea slugs, a team led by LMU geobiologist Professor Gert Wörheide has demonstrated that the animals also live in the seabed sediment, a habitat they were previously thought not to colonize. In addition, they are more genetically diverse than had been known, as the researchers report in the journal Ecology and Evolution.

With their flat, disk-shaped bodies, all placozoans worldwide look strikingly similar. Nevertheless, Wörheide and his team were already able to demonstrate in previous studies that there are huge genetic differences between them. "These differences are comparable with those between humans and mice," emphasizes the geobiologist.

Due to their diminutive size and inconspicuousness, placozoans are challenging to study in their natural environments. To gain a better insight into the ecology of the animals, the researchers exploited the fact that small shell-less sea slugs from the Rhodopidae family feed on placozoans.

Among the undigested meals of sea snails

"We hoped we could find undigested remains of placozoans in the stomach contents of the snails, which we could then perform molecular analyses on," recounts Dr. Michael Eitel, lead author of the study. "To this end, we bioinformatically investigated publicly accessible genetic data for the snails for traces of placozoan DNA." To the researchers' surprise, they also identified the DNA of placozoans in the stomachs of snails that live exclusively in seabed sediments – a habitat that all experts had previously ruled out for the very fragile placozoans. "Clearly, however, their presence in sediments is a normal occurrence and could even play a key role in their biology, particularly in their sexual reproduction, about which we have only rudimentary knowledge," says Eitel.

Furthermore, the scientists discovered an unexpectedly large genetic diversity. In the stomach contents of just two snails, they found five genetically different lineages, of which three had never been described before. In the view of the researchers, this indicates that the diversity of placozoans is much greater than previously assumed. "Our results will have a big impact on our picture of the developmental history of one of the oldest phyla on Earth," says Wörheide. "At the same time, the major new habitat discovery literally adds another dimension to the ecology of placozoans."

Info: Michael Eitel, Hans-Jürgen Osigus, Bastian Brenzinger, Gert Wörheide: Beauty in the beast - Placozoan biodiversity explored through molluscan predator genomics. Ecology and Evolution 2024

Paleontology: new fossil fish genus discovered

LMU paleontologists have identified a new genus of fossil goby, revealing evolutionary secrets of a lineage that stretches back millions of years.

10.06.2024

Gobies or Gobioidei are one of the most species-rich groups of marine and freshwater fish in Europe. Spending most of their lives on the bottom of shallow waterbodies, they make substantial contributions to the functioning of many ecosystems. With the identification of a new genus of a fossil freshwater goby, students of the international master program Geobiology and Paleobiology at LMU and paleontologist Bettina Reichenbacher, professor at the Department of Earth- and Environmental Sciences and the GeoBio-Center at LMU, have made a discovery that provides critical insights into the evolutionary history of these fish.

Measuring up to 34 mm, the small fish of the new genus †*Simpsonigobius* were discovered in 18-million-year-old rocks in Turkey and are marked by a distinct combination of morphological features, including otoliths (hearing stones) with a unique shape.

Fossil fish of the new genus †*Simpsonigobius*. | Photo: Moritz Dirnberger

To determine the relationships of †*Simpsonigobius* within the gobioid phylogenetic tree, the researchers utilized a "total-evidence" phylogenetic dataset, which they enhanced in order to combine a total of 48 morphological characters and genetic data from five genes for 48 living and 10 fossil species. In addition, the team employed "tip-dating" for fossil gobioid species for the first time. This is a phylogenetic method in which the age of the fossils (= tips) included in the phylogenetic tree is used to infer the timing of the evolutionary history of the entire group.

The results show that the new genus is the oldest skeleton-based member of the family Oxudercidae – which is classified among the "modern" gobies (families Gobiidae and Oxudercidae) – and the oldest freshwater goby within this modern group. The tip-dating analysis estimated the emergence of the Gobiidae at 34.1 million years ago and that of the Oxudercidae at 34.8 million years ago, which is consistent with previous dating studies using other methods. Moreover, stochastic habitat mapping, in which the researchers incorporated fossil gobies for the first time, revealed that the gobies probably possessed broad salinity tolerance at the beginning of their evolutionary history, which challenges previous assumptions.

"The discovery of †*Simpsonigobius* not only adds a new genus to the Gobioidei, but also provides vital clues about the evolutionary timeline and habitat adaptations of these diverse fishes. Our research highlights the importance of analyzing fossil records using modern methods to achieve a more accurate picture of evolutionary processes," says Reichenbacher. First author Moritz Dirnberger, currently a doctoral candidate at the University of Montpellier, adds: "The findings are expected to pave the way for further studies on gobioid evolution and the role of environmental factors in shaping their diversity."

Original Publication

Dirnberger M., Bauer E., Reichenbacher B. (2024): A new freshwater gobioid from the Lower Miocene of Turkey in a significantly amended total evidence phylogenetic framework. Journal of Systematic Paleontology 2024. https://doi.org/10.1080/14772019.2024.2340498

Warming in the cooler

The Antarctic is a key region for the global climate – and here, too, the greenhouse effect is leaving its mark. From the research magazine EINSICHTEN

19.06.2024

Expedition Antarctica

The Southern Ocean plays a major role in the global heat and carbon cycle. How is climate change altering ocean currents, ice fields and the activity of microorganisms?
© Gonzalo Gomez

Huge fields of sea ice, kilometer-thick ice sheets, and enormous glaciers: A few weeks after returning from Antarctica, Gonzalo Gomez-Saez is still overwhelmed. “You’re really alone there, in the middle of nowhere, surrounded by untouched beauty,” raves the Biogeochemist. Far away from civilization, humans are just guests in that extreme environment. But as remote as this world seems, far-reaching changes are taking place: The dramatic shrinking of sea ice, rising temperatures, and disappearing glaciers attest to the impact of climate change even here. How microbial communities respond to temperature changes, is one of the questions that Gomez-Saez investigates.

Meanwhile, Alexander Haumann, Professor of Physical Geography with Focus on Oceanography at the Department of Geography, mostly studies the physical world: “Many people probably don’t realize that the Southern Ocean stores vast amounts of anthropogenic CO2 and heat,” says Haumann. “The ocean as a whole absorbs around 90 percent of the heat that is additionally absorbed by the climate system through fossil emissions. Three-quarters of this amount end up in the Southern Ocean. And it’s a similar story with carbon dioxide. Also there a relatively large share is taken up by the Southern Ocean.” As such, the Southern Ocean has been one of the most important brakes on global warming

Read more about highlights of research in the current issue of our LMU magazine EINSICHTEN at www.lmu.de/einsichten.

"Of course, changes in the Southern Ocean don’t influence our weather of tomorrow, but in the long term the influence on our local climate and the people in Europe is massive."

Alexander Haumann

Gathering samples by motorboat

As a guest scientist from Lindblad Expeditions - National Geographic, Gomez-Saez had the opportunity to travel to Antarctica.

© Emily Mall

Polar regions release CO2 from the deep ocean

As the planet's "cooler," the Antarctic powers winds and ocean currents. Consequently, it also drives global cycles such as heat and carbon cycles. But what happens if climate change alters ocean circulation and the properties of the Southern Ocean? That is one of the questions that Haumann seeks to answer. In contrast to the tropics and subtropics, where the temperature differences between warm surface water and cold deep water create such robust stratification that hardly any exchange takes place, the water layers mix more easily in the cold Antarctic. "Around 80 percent of global deep water masses from the Pacific and Atlantic only resurface in the Southern Ocean," says Haumann. Because the deep ocean contains about 40 times more carbon dioxide than the atmosphere, there is a natural release of CO2 in the polar regions when deep waters return to the surface, whereas CO2 is absorbed by the ocean in other regions. If the circulation and mixing of water layers change, this can alter the balance of these and many other processes in turn.

Gonzalo Gomez-Saez | © David Velazquez

The influence of biological processes on the carbon stored in the oceans is a subject being investigated by Gonzalo Gomez-Saez, leader of an interdisciplinary Emmy Noether research group at LMU's Department of Earth and Environmental Sciences. A sizable portion of organic carbon is contained in dissolved organic material, which radiocarbon analyses indicate has been accumulating in the ocean for over 6,000 years in some cases.

Why these substances are not metabolized remains a puzzle to marine scientists. In the Antarctic, as visiting scientists on the Lindblad Expeditions-National Geographic 'Journey to Antarctica' voyage (funded from LEX-NG funds), Gomez-Saez and his Spanish colleague David Velázquez, National Geographic Explorer from Universidad Autónoma de Madrid collected water, ice, and soil samples. "It was especially challenging to conserve our samples without the microbes growing or incurring cell damage," recalls Gomez-Saez. "But I am confident we will obtain some novel and exciting results on the interplay between microbes and dissolved organic matter in this vulnerable ecosystem."

"You're really alone there, in the middle of nowhere, surrounded by untouched beauty."

Gonzalo Gomez-Saez

© Gonzalo Gomez

The Antarctic as early warning system for climate change

Currently, the samples are still being stored at minus 20 degrees in the town of Ushuaia in Tierra del Fuego. As soon as they arrive at his laboratory in Munich, Gomez-Saez will investigate the ability of the microbes to process various kinds of dissolved organic substances. To this end, he will use carbon compounds labeled with stable isotopes to track their development and undertake genetic studies to analyze which microbes are active when. “Colder temperatures could lead to higher carbon contents,” explains Gomez-Saez. Through his experiments, he wants to ascertain, among other things, what influence temperature has on microbial activity and whether certain forms of dissolved organic matter are more enticing for microbes than others.

Which molecules make up the dissolved organic material in his samples? Where do they come from? How are they metabolized? Gomez-Saez investigates these questions in cooperation with research groups at the GeoBio-Center of LMU, at the Max Planck Institute in Bremen and at the University of Oldenburg. This is where one of the most powerful mass spectrometers in Germany is located, capable of determining the mass of thousands of molecules simultaneously with extremely high precision.

Gomez-Saez hopes his results will help bring about a better understanding of the effects of climate change on ocean ecosystems. “The rise in temperature predicted for the coming decades will impose new conditions on all living creatures on the planet. The Antarctic could be a very sensitive and valuable early warning system for understanding global warming,” says Gomez-Saez, who also researches another effect of climate change in the ocean with his group, one that chiefly affects the mid-latitudes: the enlargement of ocean zones lacking in oxygen. As with the exchange of CO_2 between ocean and atmosphere, the stratification of water masses also plays a role here, as it can prevent water circulation and therefore ventilation.

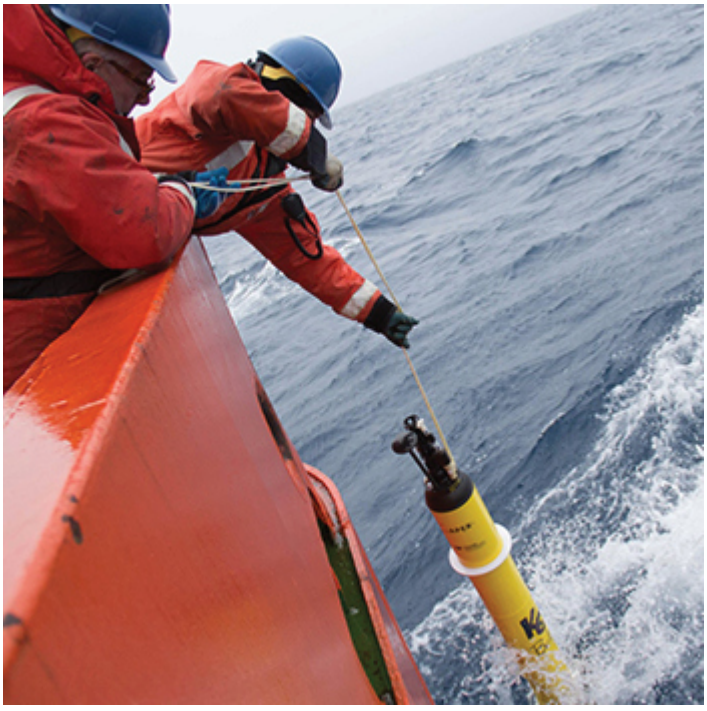
Gonzalo Gomez-Saez examines the freshly collected samples on board the ship.
| © David Wright & Elizabeth Elliott

"The Antarctic could be a very sensitive and valuable early warning system for understanding global warming."

Gonzalo Gomez-Saez

Gonzalo Gomez-Saez sampled water, ice and soil in the Antarctic - to protect the penguins, sometimes wearing a full-body suit.
© David Velazquez

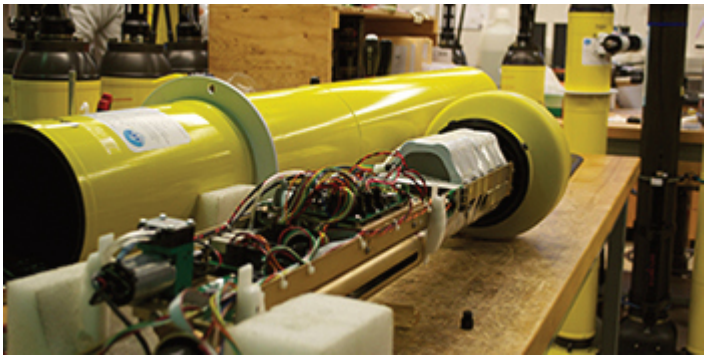
More precise measurements from the Southern Ocean



An Argo float is lowered into the water. | © Isa Rosso, SOCCOM Project, Princeton University

New measurements indicate that the natural cycle of the Southern Ocean probably releases more CO2 than previously assumed. As Haumann explains, however, it is currently difficult to say how much CO2 actually comes from the ocean, and whether this is influenced by climate change. These uncertainties are bound up with the difficulties climate models currently have in correctly representing the system in the Southern Ocean – partly owing to the dearth of measurements from this region.

"The Antarctic region is unlike many other regions on Earth, and many of the global models were developed with data from other regions," says Haumann. In a new project, for which – in collaboration with the Alfred Wegener Institute and LMU – he received a Starting Grant from the European Research Council (ERC) and a Helmholtz Young Investigator Group, the climate scientist plans to collect new insights to improve climate models in this region. One of the goals of the project is to better understand the exchange between surface and deep water in the Southern Ocean and assess its effect on changes in the global climate.

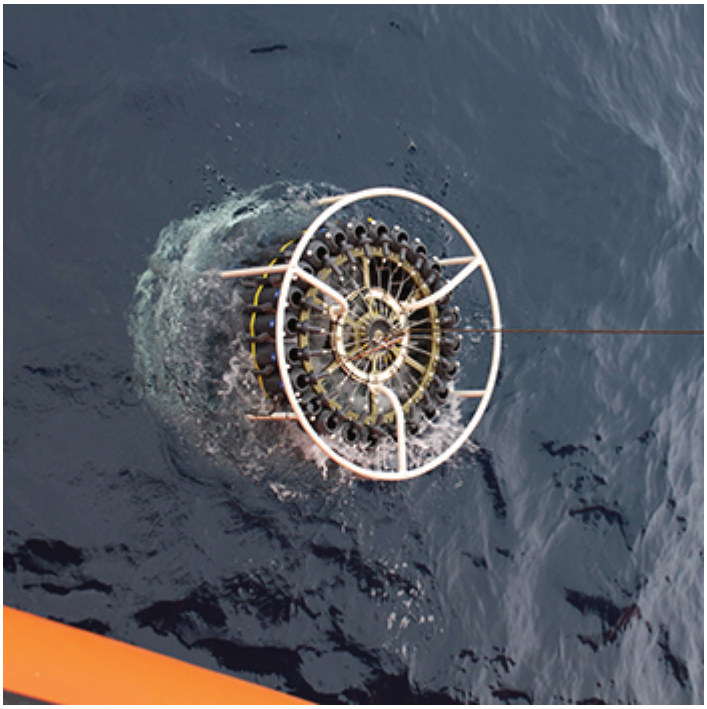


Collecting data for climate models

Argo floats move through the oceans with the current, sinking into the depths of the sea and rising again every ten days. © Isa Rosso, SOCCOM Project, Princeton University

"Many people probably don't realize that the Southern Ocean stores such vast amounts of anthropogenic CO2 and heat."

Alexander Haumann



A standard oceanographic device: the CTD rosette | © Alexander Haumann

Much of his data comes from so-called Argo floats: Some 3,500 of these automated floats currently drift with the ocean currents, sink every ten days to a depth of up to 2,000 meters, and then rise again to the surface. During the entire time, they assiduously measure temperature, salinity, and pressure. Further sensors can also be fitted to measure things like the pH value and nitrate concentration. "This data is very helpful, as the floats even survive under the ice and continue to record data there. When spring comes around, it's always exciting to see if they come back."

A standard measuring instrument that is used in oceanography frequently and for many decades is the so called CTD rosette: a cylindrical metal frame, which the researchers fit with numerous sensors. In addition, bottles are attached around the frame to collect water samples at various depths – high-tech messages in a bottle, as it were. This way, the Alfred Wegener Institute collected important measurement time series in the Southern Ocean for many decades. They are critical for Haumann and his team to better understand the long-term climatic changes and the associated changes in the heat, carbon, and water cycle of this region.

Untouched solitude?

Completely alone, in the midst of supposedly untouched nature, is what Antarctica feels like. But despite this isolation, nature there is also changing due to human influences.
© David Velazquez

The system tips

Current results from Haumann's research concern the dramatic disappearance of sea ice, which reached record levels in 2023. Unlike in the Arctic, almost the entire sea ice in the Antarctic forms every year, when the uppermost layer of the ocean freezes in winter. Most of the ice is produced in the coastal regions of the Ross Sea and the Weddell Sea, sometimes dubbed "ice factories of Antarctica". Up until 2015, these areas of ice actually expanded, to the surprise of many scientists. "The cause was presumably stronger winds, which carried the sea ice further out from the ice factories. This created an open area of ocean that could then freeze again," explains Haumann. "But from 2015, the system suddenly tipped." Within two years, some four million square kilometers of ice disappeared – a trend that has continued to this day after a brief interlude of recovery.

Haumann. According to his results, several factors are converging. Firstly, there are natural decadal fluctuations of salinity, which determines the stability of the water column stratification in the Southern Ocean. In the polar regions, cold water lies on top of warmer water. They would actually mix, as cold water is denser than warmer water and should sink. "But that doesn't happen because the water above is generally less salty than the water below," explains Haumann. If this distribution changes, the stratification can become unstable and more heat can reach the surface, causing more ice to melt. Early satellite images from the 1970s show that the sea ice also vanished back then, which the climate scientist attributes to this effect.

"The big question is whether this is a natural process or should be interpreted as a climate change signal."
Alexander Haumann

Today, however, the menace is coming from the deep: Compared to the 1970s, the deep waters bring considerably more heat close to the surface. "We're seeing that the water at a depth of 150 meters has warmed up a lot," explains Haumann. "If the stratification now becomes more unstable due to a higher salinity – and that is what is currently happening – then this warm water entrains into the surface layer more easily." As part of the global overturning circulation – a gigantic water conveyor belt that connects the Atlantic, Pacific, and Indian Oceans with the Southern Ocean – water flows from the tropics and subtropics toward the South Pole. Scientists expect that more and more heat will reach Antarctica in this way due to global warming.

© Isa Rosso, SOCCOM Project, Princeton University

Tipping points in the past as well

Oceanographers have been observing for years how glaciers, which of course extend deep into the water, are melting from below. "But the sea ice at the surface was shielded for a long time by low salinities in the upper 100 meters," notes Haumann. But now the consequences of warming are becoming visible here, too, and Haumann thinks it is possible that a tipping point is being reached through a combination of global warming and decadal fluctuations. If the sea ice cover remains smaller in the long term, there would be consequences for numerous organisms that critically depend on this environment. Moreover, with less sea ice more heat could get into the ocean, which would further impede ice formation and disrupt the ocean circulation – a vicious cycle.

as to whether the tipping point is natural or related to climate change, as such tipping points have probably also occurred in the past – in connection with ice ages, for instance.

"The rise in temperature predicted for the coming decades will impose new conditions on all living creatures on the planet."

Gonzalo Gomez-Saez

Whether these effects can reverse again remains unclear. Ice and ocean mutually affect each other and there are many feedback effects that are not yet well understood. What is certain is that the polar regions are particularly susceptible to climate change. Through the study of ocean dynamics, water properties, and biological processes, Haumann and Gomez-Saez are investigating different facets of this complex system and contributing to our understanding of the changes that will shape the future of the planet. “People always think it’s so far away,” observes Haumann. “Of course, changes in the Southern Ocean don’t influence our weather of tomorrow, but in the long term the influence on our local climate and the people in Europe is massive.”

Text: Monika Gödde

Gert Wörheide elected to the Leibniz-Sozietät

20.06.2024

Marine geobiologist and palaeontologist Professor Gert Wörheide has been elected to the Leibniz-Sozietät der Wissenschaften zu Berlin, one of the oldest scientific societies in the world. Wörheide holds the Chair of Paleontology and Geobiology at the Department of Earth and Environmental Sciences at LMU and is the spokesperson for its GeoBio-Center. He is also Director of the Bavarian State Collection of Paleontology and Geology and the Munich Paleontological Museum. One focus of his research is on the biodiversity and evolution of marine organisms, in particular sponges (Porifera). He investigates these using modern molecular biological methods.

Professor Gert Wörheide | © LMU

The Leibniz-Sozietät der Wissenschaften zu Berlin, to which Gert Wörheide was elected in May, follows in the tradition of the Churfürstliche Brandenburgische Societät der Wissenschaften founded by Gottfried Wilhelm Leibniz in 1700. Today, the Society works as an interdisciplinary association of scientists and aims to promote the humane use of science. The aim is for the natural, technical, social and human sciences to work together and for theory and practice to be combined. The non-partisan association currently has more than 300 members.

Retreating glaciers: fungi enhance carbon storage in young Arctic soils

Melting Arctic glaciers are in rapid recession, and microscopic pioneers colonize the new exposed landscapes. LMU researchers have revealed that yeasts play an important role in soil formation in the Arctic.

03.07.2024

Roughly a tenth of the land surface of the Earth is covered by glacial ice. However, glaciers are retreating ever further and ever faster as a consequence of global warming. As they do so, they expose new landscapes which for millennia have been covered in ice, with extremely limited contact with air, light, and nutrients: conditions that are very challenging for life to survive. After glacial ice melts and retreats, various microbial lifeforms colonize the now accessible bedrock, accumulating nutrients and forming new soils and ecosystems. As soil can be a significant carbon store under the right circumstances, how exactly new soils form after the melting of glaciers is a question of great scientific and societal relevance.

Svalbard's climate is warming seven times faster than the rest of the world, causing its glaciers to rapidly retreat.
© James A. Bradley

The very first pioneers of the inhospitable terrain are microorganisms such as bacteria and fungi. "Microbes determine how much carbon and nitrogen can be stored in the young soils," explains Professor William Orsi from the Department of Earth and Environmental Sciences at LMU. "But little is known about the exact processes behind this nutrient stabilization through microbial activity." To better understand them, Orsi and his team studied soils in the Arctic that have recently been exposed. Their investigations were part of the dissertation of Orsi's doctoral student Juan Carlos Trejos-Espeleta and were carried out in close cooperation with Arctic biogeochemist and CNRS researcher Dr. James Bradley from the Mediterranean Institute of Oceanography in France. The study was funded by the German National Science Foundation (DFG), the Natural Environment Research Council (NERC), and the National Science Foundation (NSF). The results of the study, in which other researchers from the United States, the United Kingdom, and Switzerland were involved, have now been published in the journal Proceedings of the National Academy of Sciences (PNAS).

"In the high Arctic, the melting of glaciers is particularly dramatic. Ice-free terrestrial environments are expanding there at an extraordinarily fast rate."

William Orsi

Timeline of colonization

The object of their analyses was the glacier foreland of Midtre Lovénbreen, a retreating valley glacier in the northwest of Spitsbergen. "In the high Arctic, the melting of glaciers is particularly dramatic," says Orsi. "Ice-free terrestrial environments are expanding there at an extraordinarily fast rate." James Bradley, who first worked at the site in 2013, said: "A decade ago I was drilling ice cores into the glacier. When we returned in 2021, the glacier had shrunk and instead of ice there were barren, seemingly lifeless soils". But upon laboratory-based analyses of these soils, the researchers found that they contain incredibly diverse communities of microbes.

The newly exposed areas are ideal for researching incremental changes in the soil. The closer soil is to the glacier margin, the younger it is; whereas the further away soil is, the more time life has had to colonize the terrain. Immediately beyond the ice, there is a zone of glacial rocky debris where no visible plant life exists, followed by moraines with isolated mosses and lichens, and after this only then do flowering plants and soil begin to form in an advanced stage of development. As such, receding glacier edges are ideal natural laboratories for observing the various stages of soil development. The ecosystems are some of the most pristine, delicate, and vulnerable habitats on the planet, and they are rapidly colonised by specialised microbes, even though they are subject to extremes in temperature, light, water and nutrient availability.

Dr. James Bradley collects soil samples from the Midtre Lovénbreen glacier forefield.

Orsi's team investigated the microbial composition of the various areas by means of DNA analysis while also measuring the cycling and flow of carbon and nitrogen. Through experiments involving isotope labeled amino acids, they were able to precisely follow the microbial assimilation and metabolism of organic carbon. "We were especially interested in what proportion of carbon microorganisms lock in the soil as biomass and how much they release back into the atmosphere as carbon dioxide," says Juan Carlos Trejos-Espeleta.

Pioneer fungi sequester carbon in the soil

Their main focus was on fungi – a class of organism that is much better than bacteria at storing a lot of carbon in the soil and keeping it there. The ratio of fungi to bacteria is an important indicator of carbon storage: More fungi mean more carbon in the soil, while more bacteria generally lead to the soil emitting more CO2. "In high Arctic ecosystems, the variety of fungi is particularly high compared to that of plants, which increases the likelihood that fungal communities could play a key role there as ecosystem engineers," reckons Orsi. Discovering more about the carbon assimilation processes of fungal and bacterial populations and carbon flow processes in the ecosystem is crucial for making accurate predictions about how terrestrial ecosystems in the Arctic will respond to future warming.

"Our results demonstrate that fungi will play a critical role in future carbon storage in Arctic soils as glaciers shrink further and more of Earth's surface area is covered by soil."

William Orsi

And indeed, the researchers were able to show that fungi – or more precisely, specific basidiomycete yeasts – play a decisive role in the early stabilization of the assimilated carbon. According to the study, they are the fungal pioneers in the young postglacial soils and make a decisive contribution to the enrichment of organic carbon. The research team found that these specialized fungi are not only able to colonise the harsh Arctic landscapes before any other more complex life, but that they also provide a foothold for soil to develop by building up a base of organic carbon which other life can use. In soils in medium and late stages, bacteria increasingly dominate amino acid assimilation, leading to a significant reduction in the formation of biomass and an increase in CO2 from respiration. "Our results demonstrate that fungi will play a critical role in future carbon storage in Arctic soils as glaciers shrink further and more of Earth's surface area is covered by soil" summarizes Orsi.

Neue „Flora von Bayern“ – 50 Jahre Teamwork von Ehrenamt, Wissenschaft und Naturschutz

17.10.2024

Botanische Staatssammlung München

110 Jahre nachdem Franz Vollmann von der Bayerischen Botanischen Gesellschaft mit seiner „Flora von Bayern 1914“ die letzte Übersicht zur Pflanzenwelt Bayerns veröffentlicht hat, erscheint nun eine neue, umfassende „Flora von Bayern“. Dem vierbändigen Mammutwerk geht eine mehr als 50 Jahre andauernde intensive floristische Erfassung, Kartierung und Dokumentation der Pflanzenwelt in ganz Bayern voraus. Mehr als 200 ehrenamtliche Citizen Scientists haben an dem Projekt mitgearbeitet. Koordiniert wurde das Projekt an der Botanischen Staatssammlung München.

Die neue Flora von Bayern enthält die gesamte botanische Artenübersicht sowie den aktuellen Zustand der Pflanzenwelt Bayerns von der Rhön bis ins Allgäu. Dabei blickten die Botaniker auch in die Vergangenheit: Die Beobachtungsdaten umfassen Pflanzenvorkommen aus Bayern im Zeitraum der letzten 250 Jahre. In jahrelanger Arbeit wurden von der Botanischen Staatssammlung München (SNSB-BSM), der Bayerischen Botanischen Gesellschaft, dem Landesamt für Umwelt und der für das Projekt gegründeten Arbeitsgemeinschaft Flora von Bayern auch Angaben aus älterer Literatur sowie alle bayerischen Herbarien mit ihren zum Teil historischen Herbarbelegen ausgewertet. Gesammelt wurden insgesamt fast 16 Millionen Beobachtungsdaten – kuratiert und ausgewertet vom Landesamt für Umwelt sowie den Staatlichen Naturwissenschaftlichen Sammlungen Bayerns (SNSB), insbesondere mit Unterstützung der Expertinnen und Experten für wissenschaftliche Daten am SNSB IT Zentrum. An der Initiative Flora von Bayern waren neben den beteiligten Wissenschaftlerin-nen und Wissenschaftlern auch mehr als 200 ehrenamtliche Kartiererinnen und Kartierer beteiligt – ein herausragendes Citizen Science Projekt für die bayerische Botanik.

Überblick über den Zustand der bayerischen Pflanzenwelt

Die Erfassung von Bayerns Flora über einen so langen Zeitraum ermöglicht einen genauen Überblick zum Zustand der Pflanzenwelt Bayerns: Welche Pflanzen sind gefährdet und verschwinden? Welche Arten breiten sich aus? Betrachtet wird dabei nicht nur das gesamte Landesgebiet, sondern auch einzelne Regierungsbezirke und Naturräume im Detail. Von den im Projekt insgesamt 5.886 nachgewiesenen Pflanzensippen sind 3.065 einheimisch. 1.955 Arten sind sogenannte Neophyten, Pflanzen, die nach der Entdeckung Amerikas 1492 in Bayern eingewandert sind oder eingeschleppt wurden. Von diesen Neophyten sind 380 mittlerweile fest in Bayern etabliert, sprich heimisch geworden, 208 mit Tendenz zur Einbürgerung, 1.367 kommen nur spontan

oder unbeständig verwildert vor. Von den 3.065 ein-heimischen Pflanzenarten sind 82 ausgestorben (2,5 %). 88 Pflanzenarten (2,7 %) sind endemisch für Bayern, das heißt, sie kommen weltweit nur dort vor.

Fast 6.000 bayerische Pflanzensippen in einem Buch

Das nun gedruckte Werk umfasst vier Bände mit insgesamt fast 3.000 Seiten. Unter den 5.886 Pflanzensippen, die in Bayern nachgewiesen wurden, sind 4.778 Arten, 1.313 Unterarten, 109 Varietäten und 708 Hybride. Im Buch finden sich tausende farbige Verbreitungskarten, Fotos sowie ausführliche Artentexte, verfasst von über 60 Autorinnen und Autoren. Für Bayern besonders typische oder seltene Arten werden in ihrem natürlichen Lebensraum gezeigt.

Die neue Flora von Bayern wird herausgegeben von der Bayerischen Botanischen Gesellschaft, den Autoren Prof. Dr. Lenz Meierott, PD Dr. Andreas Fleischmann von der Botanischen Staatssammlung München (SNSB-BSM), Marcel Ruff vom Bayerischen Landesamt für Umwelt (LfU), Jürgen Klotz und – posthum – Dr. Wolfgang Lippert (ehemals Kurator an der Bot-anischen Staatssammlung München). Alle Beteiligten freuen sich, das Werk nun endlich der Öffentlichkeit präsentieren zu können. Die festliche Buchvorstellung findet im Rahmen eines „Tages der Bayernflora" am Samstag den 26. Oktober 2024 im Großen Hörsaal der Botanischen Staatssammlung München statt.

Publikation:
Meierott, L., Fleischmann, A., Klotz, J., Ruff, M., & Lippert, W. (2024): Flora von Bayern. – Haupt-Verlag, Bern, 2880 Seiten

Kontakt:
PD Dr. Andreas Fleischmann, Kurator für Blütenpflanzen
SNSB – Botanische Staatssammlung München
Menzinger Straße 67, 80638 München
Tel: 089 17861240, E-Mail: fleischmann@snsb.de

Foto: Das Brandknabenkraut Neotinea ustulata ist eine von insgesamt 72 Orchideenarten, die wild in Bayern vorkommen. (Foto: Andreas Fleischmann, SNSB-BSM)

Foto: Die Silberwurz Dryas octopetala ist eine typische Pflanze der bayerischen Alpen. Ihre Vor-kommen entlang der Alpenflüsse sind bereits stark zurückgegangen, wie anhand der Verbrei-tungskarten in der Flora von Bayern ersichtlich ist. Früher kam die Pflanze an der Isar bis München vor. (Foto: Andreas Fleischmann, SNSB-BSM)

Foto: Das Augsburger Steppengreiskraut Tephroseris integrifolium subsp. vindelicorum ist ein En-demit Bayerns. Diese Pflanzenart kommt weltweit nur auf dem Lechfeld vor, nirgendwo sonst. (Foto: Andreas Fleischmann, SNSB-BSM)

Fossil killifish: new findings reveal unforeseen diversity

LMU paleontologists have investigated 15 million year old fossils and obtained new insights into the species diversity and lifestyle of killifish.

23.12.2024

Killifish, or egg-laying toothcarps, are known for their ecological adaptability and species diversity. Two families of killifish exist in Europe today: the highly species-rich Aphaniidae and the relatively species-poor Valenciidae, which has just three species. How these differences in species diversity originated is one of the questions that the group of Professor Bettina Reichenbacher investigates. With an international team, the LMU paleontologists have now demonstrated through their study of fossil killifish that the Valenciidae were once much richer in species. Moreover, they have discovered possible causes for their disappearance.

The researchers analyzed fossil killifish from a new site in the Dinaric Alps in Bosnia and Herzegovina. In this region, where fossil killifish were previously almost unknown, a freshwater lake existed for around 250,000 years during the Middle Miocene, roughly 14.8 million years ago. This lake offered an ideal habitat for the 3-4 cm large fish. In total, the research team managed to excavate the skeletons of 179 fish, 94 of which even had preserved otoliths in their skulls. “It’s extremely rare to find skeletons with preserved otoliths; these fossils are key discoveries,” says Reichenbacher.

Recovery of the fossils at the new site in Bosnia and Herzegovina.
| © Davit Vasilyan, Jurassica Museum, Porrentruy, Schweiz

Two new fossil genera

By studying the typical shape of otoliths, scientists can determine the species. Meanwhile, the skeletal features allow them, for example, to reconstruct the family relationships of the fish. The researchers were able to assign the new discoveries from Bosnia and Herzegovina to the family Valenciidae and identify two new fossil genera:

Miovalencia and Wilsonilebias, both of which were represented with two species. Three of these species were previously unknown, while the fourth was already identified from earlier otolith finds but not recognized as Valenciidae.

Fossil skeleton of *Wilsonilebias langhianus*, one of the newly discovered species.
© Andrea Herbert Mainero

To the surprise of the researchers, moreover, the skeleton of Wilsonilebias had a specialized structure supporting the anal fin. This suggests that Wilsonilebias reproduced through internal fertilization, as today's 'live-bearing' toothcarps do. "Yet this does not necessarily mean that Wilsonilebias gave birth to live young, as some fish today lay eggs even after fertilization has occurred internally," says Reichenbacher. "Nevertheless, our results show that some Valenciidae used different reproduction methods in the past as compared to their current descendants, which reproduce exclusively by means of external fertilization. It may even have been one of the secrets of their success at that time."

Four killifish species in a single lake would seem to be quite a lot. Andrea Herbert Mainero, doctoral student and lead author of the study, hypothesizes that the species divided up their habitat and thus their food sources. The two Wilsonilebias species probably lived in deeper water, where they may have fed on plankton. The rounded otoliths of Wilsonilebias support this conjecture, as many fish species that live in deeper water today are characterized by rounded otoliths. By contrast, the two species of Miovalencia might have lived in shallow areas near the shore, where they would have benefited from a rich array of algae and ground-dwelling microorganisms.

Relics of a greater diversity

Furthermore, the discoveries demonstrate that there were 6 genera and 17 species of Valenciidae in the Miocene, whereas just one genus with three species is extant today. Some 14.8 million years ago, at the end of the so-called Middle Miocene Climatic Optimum, the climate was mainly warm and humid, such that there were sufficient lakes, large and small, for killifish to develop. In the further course of the Miocene, the climate became drier and many of these lakes disappeared. "We conjecture that Valenciidae couldn't adapt to this climatic change, with a consequent decline in diversity," says Herbert Mainero. "As such, the three species today are relics of a once much greater diversity," adds Reichenbacher. The new research findings offer valuable insights into the historical development of Eurasian fauna and highlight the importance of protecting the three extant Valencia species, of which one is endangered and the two others are threatened with extinction.

Andrea Herbert Mainero, Davit Vasilyan, Bettina Reichenbacher: Two new genera of killifish (Cyprinodontiformes) from the Middle Miocene of the Bugojno Basin, Bosnia and Herzegovina: insights into the lost diversity of Valenciidae. Journal of Systematic Palaeontology 2024