

24th Annual Meeting of the Society of Biological Systematics



28th - 31st March 2023 | Senckenberg Frankfurt a. M. | virtual meeting

Programme and Abstracts



Photo credit: X. Deng, A. Neudecker, H. Knauber, M. Päckert, L. Li, S. Tränkner, S. Wedmann

Organizers:

Angelika Brandt, Michael Hiller, Christian Printzen,
Steffen Pauls, Dieter Uhl, Stefanie Kaiser, Lilian Müller

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Time Schedule of the Conference

Tuesday	
09:00–09:15	Welcome notes by the organizers
09:15–10:00	Main lecture 1 (Zoology) - Christine Ewers-Saucedo: "The reconstruction of anthropogenic change"
	Chair: Angelika Brandt
10:00–10:15	T1: Abdolvahab Maghsoudlou - Distribution and diversity of marine fauna along the Persian Gulf and the Gulf of Oman: Large scale monitoring expeditions
10:15–10:30	T2: Alexandros Vasilikopoulos - Comprehensive whole-genome analyses support the monophyly of Hemirotifera within Syndermata (Gnathifera)
10:30–10:45	T3: Anchita Casaubon* - Integrating the Geometric Morphometrics Toolkit into Deep-Sea Isopod Taxonomy
10:45–11:00	Breakout rooms: Main lecture & T1–3 to meet the speakers
	Chair: Andreas Schmidt Rhaesa
11:00–11:15	T4: Tobias Salden* - Putting ceraphronoid wasps (Insecta: Hymenoptera) back on the map
11:15–11:30	T5: Angelika Brandt - Biodiversity of the North Pacific including new data from the abyss of the Aleutian trench, NE Pacific
11:30–11:45	T6: Carolin Gilgenbach* - Small wasps, big muscles: Front and hind leg modifications in chalcidoid wasps (Hymenoptera: Chalcidoidea)
11:45–12:00	Breakout rooms: T4–6 to meet the speakers
	Chair: Sonja Wedmann
12:00–12:15	T7: Cathrin Manz* - Diversity of the ectomycorrhizal genus <i>Russula</i> (Basidiomycota, Fungi) in the tropics
12:15–12:30	T8: Derya Akdogan* - A new <i>Austroniscus</i> Vanhöffen, 1914 (Isopoda, Asellota, Nannoniscidae) species from the abyss of the Aleutian trench, NE Pacific
12:30–12:45	T9: Dirk Ahrens - A transcriptome-based phylogeny of Scarabaeoidea confirms the sister group relationship of dung beetles and phytophagous pleurostict scarabs (Coleoptera)
12:45–13:00	Breakout rooms: T7–9 to meet the speakers
13:00–14:15	Lunch break
14:15–16:00	Workshop "Conservation Cafe": COP15, a Telescope and We: Developing capacity for empowerment, problem-solving and achieving community goals (Jutta Buschbom, Claus Weiland), no pre-registration required

Wednesday	
29.03.2021	
09:00–09:45	Main lecture 2 (Botany) - Mika Bendiksby: "The potential of fungarium specimens and DNA barcodes in fungal research"
	Chair: Christian Printzen
09:45–10:00	T10: Dorte Janussen - Deep-sea sponges in deep Earth History: Spectacular fossil evidence of the Hexactinellida

10:00–10:15	T11: Ekin Tilic - Postembryonic development of the bone devouring <i>Osedax</i> (Siboglinidae, Annelida)
10:15–10:30	T12: Katja Waskow - FörTax - Promotion of taxonomic knowledge as a basis for nature conservation - Successes, deficits and prospects
10:30–10:45	Breakout rooms: Main lecture & T10–12 to meet the speakers
	Chair: Ekin Tilic
10:45–11:00	T13: Henry Knauber* - Across Trench and Ridge: Differentiation Patterns of the deep-sea <i>Haploniscus belyaevi</i> species Complex (Isopoda: Haploniscidae)
11:00–11:15	T14: Inci Livia Baez* - The Scutellar Plate of the Eucoilina Wasps (Cynipoidea: Figitidae)
11:15–11:30	T15: Jenny Neuhaus* - The deep-sea acorn barnacle <i>Bathylasma hirsutum</i> (Hoek, 1883): first record from a hydrothermal vent field at the Reykjanes Ridge
11:30–11:45	T16: Friedrich Wilhelm Miesen - Fostering species knowledge to counter the biodiversity crisis - the FörTax project
11:45–12:00	Breakout rooms: T13–16 to meet the speakers
12:00–12:15	Laudatio Bernhard-Rensch Prize N.N.
12:15–12:45	Bernhard-Rensch-Prize Presentation: Kevin Karbstein

	Thursday
	30.03.2023
09:00–09:45	Main lecture 3 (Palaeontology) - Fridgeir Grimsson: "The history of European Paleogene flower-insect interactions unraveled using fossil flowers and insects and their associated pollen grains"
	Chair: Dieter Uhl
09:45–10:00	T17: Katharina Kohlenbach* - Diversity and distribution of Ischnomesidae (Crustacea: Isopoda) in the Bering Sea and along the Aleutian trench
10:00–10:15	T18: Harald Letsch - Jumping to new hosts: the diversification of flea beetles (Coleoptera: Chrysomelidae: Alticini) in the context of their host plant associations, with a special focus on crucifers (Brassicales)
10:15–10:30	T19: Miguel Bermúdez-Cova - The enemy of my enemy is my friend: hyperparasitic fungi, hidden fungal diversity in the tropics
10:30–10:45	Breakout rooms: Main Lectures & T17–19 to meet the speakers
	Chair: Heike Wägele
10:45–11:00	T20: Katarzyna Vončina* - Clarification of the taxonomic status of <i>Acanthochitona discrepans</i> Brown, 1827 with the new data for the North-East Atlantic <i>Acanthochitona</i>
11:00–11:15	T21: Martin Päckert - Evolutionary history and circum-Tibetan phylogeographic patterns of Eurasian forest-dwelling passerine birds (Passeriformes)
11:15–11:30	T22: Xiling Deng* -Comparative phylogeography of alpine/subalpine <i>Himalopsyche</i> of the Tibeto-Himalayan region: An assessment of mountain geo-biodiversity hypothesis
11:30–11:45	T23: Laura Spies* - A new species of the isopod family Mesosignidae Schultz, 1969 (Crustacea, Malacostraca) from the Aleutian Trench, North Pacific
11:45–12:00	Breakout rooms: T20–23 to meet the speakers
	Chair: Michael Hiller

12:00–12:15	T24: Oscar Schröder - GloBios – Global Observatory Network for Freshwater Biodiversity in High Mountain Streams
12:15–12:30	T25: Katharina Schienbein* - A new species of the isopod genus <i>Mexicope</i> Hooker, 1985 (Crustacea, Malacostraca) from the Mediterranean Sea off Malta
12:30–12:45	T26: Sonja Wedmann - On the fossil record of social wasps (Hymenoptera: Vespidae: Vespinae)
12:45–13:00	T27: Lars Dietz - Universal single-copy orthologs (USCOs) in population genetics and phylogeography: a case study based on the beetle genus <i>Pachypus</i>
13:00–13:15	Breakout rooms: T24–27 to meet the speakers

Friday	
31.03.2023	
09:00–09:45	Main lecture 4 (Biodiversity) - Martin Irestedt: "The potential of museum collections for studies of biological processes in the era of genomics"
	Chair: Ernesto-Razuri Gonzales
09:45–10:00	T28: Andreas Kelch* - Biodiversity assessment of the isopod family Paramunnidae Vanhöffen, 1914 (Crustacea, Malacostraca) from the Weddell Sea, Southern Ocean
10:00–10:15	T29: Tim Dannenfeld* - Evolution of the hexapod tracheal system
10:15–10:30	T30: Pedro Henrique Dias - In a hole in the ground there lived a tadpole: convergent evolution in fossorial tadpoles
10:30–10:45	Breakout rooms: Main lecture & T28–30 to meet the speakers
	Chair: Anna Hundsdörfer
10:45–11:00	T31: Lijuan Li* -Phylogenetic and taxonomic studies reveal undiscovered diversity in the <i>Lecanora</i> subfusca-group
11:00–11:15	T32: Torben Riehl - Senckenberg Ocean Species Alliance (SOSA) — a project to facilitate discovery, conservation and fascination
11:15–11:30	T33: Zohreh Mirzaee* - More species than ever thought in the enigmatic mantid genus <i>Holaptilon</i> Beier, 1964, (Gonypetidae, Gonypetinae)
11:30–11:45	Breakout rooms: T31–33 to meet the speakers
	Chair: Thomas Bartolomaeus
11:45–12:00	T34: Farzaneh Momtazi - Global distribution and biodiversity of marine Amphipoda (Crustacea: Peracarida)
12:00–12:15	T35: Jörn von Döhren - Identification of nemertean species – what data do we need?
12:15–12:30	T36: Thaynara Lara Pacheco - Dark taxa: large “Little Brown Jobs” - a monographic taxonomy of South American Sericini reveals an enormous hidden diversity in large night active chafer beetles (Coleoptera, Scarabaeidae)
12:30–12:45	Breakout rooms: T34–36 to meet the speakers
12:45–13:00	Student Awards & Closing Ceremony
13:00–14:00	Lunch break
14:00–16:00	Mitgliederversammlung GfBS (General Assembly held in German, GfBS members only)

Talks marked with an asteriks* are student contributions.

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A transcriptome-based phylogeny of Scarabaeoidea confirms the sister group relationship of dung beetles and phytophagous pleurostict scarabs (Coleoptera)

Dietz, L. ^{1#}, Seidel, M. ^{2,3}, Eberle, J. ⁴, Misof, B. ^{1,5}, Pacheco, T.L. ¹, Podsiadlowski, L. ¹, Ranasinghe, S. ¹, Gunter, N.L. ⁷, Niehuis, O. ⁶, Mayer, C. ¹, Ahrens, D.^{1#}

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Scarab beetles (Scarabaeidae) are a diverse and ecologically important group of angiosperm-associated insects. As conventionally understood, scarab beetles comprise two major lineages: dung beetles and the phytophagous Pleurosticti. However, previous phylogenetic analyses have not been able to convincingly answer the question whether or not the two lineages are monophyletic. Here we report our results from phylogenetically analyzing ca. 4,000 genes mined from transcriptomes of more than 50 species of Scarabaeidae and non-scarabaeid Scarabaeoidea. Our results provide convincing support for Scarabaeidae being monophyletic, confirming the debated sister group relationship of dung beetles and phytophagous pleurostict scarabs. Supermatrix-based maximum likelihood and multispecies coalescent phylogenetic analyses strongly imply Melolonthinae being paraphyletic. We consequently suggest various changes in the systematics of Melolonthinae: Sericinae Kirby, 1837 stat. rest. and sensu n. to include the tribes Sericini, Ablaberini and Diphucephalini, and Sericoidinae Erichson, 1847 stat. rest. and sensu n. to include the tribes Automoliini, Heteronychini, Liparetrini, Maechidiini, Scitalini, Sericoidini, and Phyllococini. Both subfamilies appear to consistently form a monophyletic sister group to all remaining subfamilies so far included within pleurostict scarabs. Our results represent a major step towards understanding the diversification history of one of the largest angiosperm-associated radiations of beetles which is discussed in the light of some key innovations.

A new *Austroniscus* Vanhöffen, 1914 (Isopoda, Asellota, Nannoniscidae) species from the abyss of the Aleutian trench, NE Pacific

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The Nannoniscidae Hansen, 1916 are a family of deep-sea isopods with a global distribution. So far, more than 80 species have been described within the family, which could be assigned to 13 genera. The first two species within the nannoniscid genus *Austroniscus* were described by Vanhöffen from East Antarctica in 1914, and to date the genus contains eleven species from nearly all oceans spanning continental shelves to hadal depths. Diagnostic characters of the genus include a broad body form, an unspecialized first antenna, a relatively small branchial chamber and operculum, and a lack of posterolateral spines on the pleotelson. Whilst some of the characters are not very well defined, most the other characters represent plesiomorphies for the family or synapomorphies shared with certain nannoniscid genera. This study aims to improve the diagnosis of *Austroniscus* based on material from the abyss of the eastern Aleutian trench (NE Pacific) collected during the recent AleutBio expedition onboard R/V *Sonne*. The material contained a new *Austroniscus* species and a presumably already described species from the adjacent Kuril Kamchatka trench. The description of the new species is presented here along with a morphological comparison with all other species in the genus to present an amended diagnosis.

The Scutellar Plate of the Eucoilina Wasps (Cynipoidea: Figitidae)

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Throughout their evolution, parasitoid wasps have developed a lot of different striking morphological features. Understanding the form and function of these structures can shine light on the how, when, and why of the parasitoid wasp's megadiversification.

One example of a conspicuous and unique morphological structure is a modification of the mesoscutellum in the Eucoilinae. The cosmopolitan eucoilines are Diptera parasitoids, some genera such as *Leptopilina* are known endoparasitoids of *Drosophila*. Eucoilinae are the most species rich subfamily of the family Figitidae and also the most species rich group within the superfamily Cynipoidea. All known eucoiline species share a distinct modification of the mesoscutellum called the scutellar plate, an autapomorphy of Eucoilinae, which makes them immediately distinguishable from all other parasitoid wasps.

With scanning electron microscopy, micro computed tomography, Synchrotron- μ CT, histology and chemoecology, we investigate the structure, function, and diversity of this remarkable modification in a sample of taxa representing the entire subfamily to learn more about the evolution of this successful group.

The potential of fungarium specimens and DNA barcodes in fungal research

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Natural history collections (NHCs) preserve our natural heritage and biodiversity knowledge by documenting biodiversity through time and in space. The NHCs keep reference material for species, populations, and genetic resources and form the basis for determination literature, red lists, taxonomic research etc. The fungarium is a NHC of dried fungi with associated collection information (as opposed to an herbarium, which is a collection of dried plants). The fungarium represents an important infrastructure and valuable source for fungal research and biodiversity management. The fungarium is the sole source of material from the past and for fungal type specimens, the latter essential in taxonomy. Use of fungarium specimens in research will reduce cost and potential risk with fieldwork. In the fungarium, you will find material that are no longer available for collection due to red listing or extinction. You may also find the material that you didn't find during fieldwork as well as the material you didn't know you would be needing. The fungarium is full of expert validated fungal specimens. Such specimens form an efficient source for building the fungal DNA barcode reference library, which in turn enables DNA barcoding (the use of a standardized DNA sequence for species identification). Apart from making species identification possible for others than the fungal specialist, DNA barcoding also enables tracing biodiversity in mixed samples. Since 2014, Fungarium O has routinely sequenced the fungal DNA barcode for interesting fungarium specimens, both for species identification and for contributing to the fungal barcode reference library. Apart from speeding up the identification process, DNA barcoding standardizes studies, reveals cryptic species, and links different stages of ontogenesis, sexual and asexual morphs, or different sexes. As such, one may say that DNA rescued mycology from the confusing dual nomenclature.

The enemy of my enemy is my friend: hyperparasitic fungi, hidden fungal diversity in the tropics

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The term “hyperparasite” refers to an organism that parasitizes another parasitic organism. Hyperparasitism caused by fungi growing on plant parasitic fungi is widespread in nature, but hyperparasitic fungi have rarely been investigated. Most species were briefly described in the past, when molecular sequence data could not yet be obtained for systematic investigation. Therefore, molecular sequence data are lacking for many species of hyperparasitic fungi and there are few systematic studies available. Sampling events in Panama and Benin were performed for the past few years as part of an exploratory survey to study the diversity of hyperparasitic fungi in the tropics. As an example, we show findings of our ongoing project about hyperparasites on colonies of Black Mildews (Melolales, Ascomycota), a species rich group of plant-parasitic fungi commonly found in the tropics. A species checklist, morphological analyses of new and poorly documented species, tritrophic networks, DNA extraction experiments and preliminary phylogenetic analyses have been made. Hyperparasites may significantly impact ecosystems, and therefore it is necessary to increase our understanding about these understudied and diverse organisms. We need further morphological, molecular and ecological studies on these fungi in order to understand their diversity, evolution and biology.

Biodiversity of the North Pacific including new data from the abyss of the Aleutian trench, NE Pacific

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The AleutBio (Aleutian Trench Biodiversity Studies) expedition was conducted from 24.7.-6.9.2022 with RV Sonne to the Northeast (NE) Pacific into the Bering Sea as well as the Aleutian Trench (SO-293). This expedition follows four previous expeditions to the Northwest Pacific (NWP) conducted in collaboration with Russian scientists over the past decade, providing an excellent baseline for the AleutBio expedition. These comparative expeditions were the Russian-German SoJaBio (Sea of Japan Biodiversity Studies) expedition to the Sea of Japan in 2010, the Russian-German KuramBio I (Kuril-Kamchatka Biodiversity Studies) expedition to the NWP abyssal near the Kuril-Kamchatka Trench (KKT) in 2012, and the Russian-German SokhoBio (Sea of Okhotsk Biodiversity Studies) expedition in 2015, and finally the KuramBio II expedition in 2016 to the abyssal and hadal of the KKT. The objectives of these expeditions were to survey organismic biodiversity and biogeography, conduct environmental DNA analyses to identify biodiversity hotspots, and also to conduct trophic characterization of benthic organisms. We will provide an outline of our work in the North Pacific including the benchmark studies of the Beneficial (Biogeography of the northwest Pacific fauna. A benchmark study for estimations of alien invasions into the Arctic Ocean in times of rapid climate change) project.

COP15, a Telescope and We: Developing capacity for empowerment, problem-solving and achieving community goals

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In December 2022 the [Conference of the Parties \(COP15\)](#) to the [UN Convention on Biological Diversity](#) (CBD) adopted the [Kunming-Montreal Global Biodiversity Framework](#) (GBF) as well as complementary decisions for its implementation, including an extensive monitoring framework. The GBF is a significant achievement and will guide biodiversity conservation world-wide for the next 30 years.

The adoption of the GBF is testimony to the capacity of countries in very different circumstances and with divergent value systems and socio-cultural backgrounds to find consensus and achieve a joint goal. Despite strong concerns, incompatible positions and a global political context of rising conflict, parties found acceptable solutions and joint ways forward for highly contested topics, as for example resource mobilization, utilization of digital sequence information, and gender.

In this overall context it stands out that the negotiations for the [knowledge management](#) components in support of the GBF and its monitoring were stalled by an apparently irreconcilable clash that led to the removal of knowledge management from its [dedicated decision](#) and the postponement of its adoption by another two years, i.e. until COP16.

Knowledge management with its associated ecosystem of analog and digital infrastructures, social interactions and human resources lies at the heart of scientific collections. With the development of the [Digital Extended Specimen](#) concept, the global collection, biodiversity sciences and informatics communities have laid the foundation for a global infrastructure of [open](#), [FAIR](#) and [CARE](#) biodiversity data and their integration into [emerging wider global data spaces](#). Realized, such a vast and complex infrastructure certainly would be the James Webb telescope of planetary biodiversity monitoring.

In the proposed session, we would like to explore ways for talking about “the things that don’t work that well”. Small as they might seem, eventually they might have contributed to and eventually led to the removal of knowledge management from the GBF and thereby limited societal will, political support and hindered progress. We propose a [conservation café](#) setting for sharing experiences, observations, and ideas for potential solutions.

This [United Nations Academic Impact](#) (UNAI) definition for [Capacity Building](#) can provide inspiration for finding a joint way for the now and towards the future..

Integrating the Geometric Morphometrics Toolkit into Deep-Sea Isopod Taxonomy

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Macrostylidae Hansen, 1916 is a family of deep-sea isopods with a worldwide distribution at depths ranging from relatively shallow (4 m) to hadal (11,000 m). While current taxonomic organization recognizes only one nominal genus, *Macrostylis* Sars, 1864, research indicates complex phylogeographic patterns that justify splitting this taxon into multiple genera. The current estimate of 90 described species is a likely an underestimate as recent deep-sea expeditions studying benthic fauna have led to the discovery of several new species, with the majority still pending description. Additionally, approximately 50% of macrostylid species descriptions are based on one sex, and frequently on a single specimen, likely due to extreme sexual dimorphism. Historically, species diagnoses of macrostylid isopods have consisted of traditional morphometrics, i.e., comparisons of external and internal characters using linear measurements. However, the discovery that several different species are male and female conspecifics instead, coupled with a morphologically uniform genus, suggests a need for updated taxonomic methods. Geometric morphometrics has emerged as a powerful technique for species delimitation. This technique combines Cartesian coordinates and multivariate statistics and has been used successfully for quantifying morphological variation in various taxa. Here, we propose the use of an integrated approach combining molecular genetics, traditional morphometrics and geometric morphometrics to study macrostylid isopods and to find taxonomically informative traits.

Evolution of the hexapod tracheal system

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Tracheae are (in terms of species that use them) the most common breathing organs in terrestrial animals. Next to hexapods, they also occur in Myriapoda, oniscoidean isopods, Onychophora, and in various groups of arachnids. In all of these groups, the tracheae comprise a system of fine tubes with chitinous lining, created by ectodermal invaginations that branch through parts or the whole body and transport oxygen and CO₂ to and from tissues. They are connected to the exterior via openings in the body wall, the stigmata or spiracles.

These structural similarities led to the assumption that the tracheal system of different groups of arthropods is homologous (e.g. the “Tracheata-Hypothesis”). On the other hand, an independent origin of the tracheal system in Hexapoda and Myriapoda is suggested by molecular data and even the homology of the hexapod tracheal system was questioned. These independent origins are supported by the hypothesis that arthropods became at least seven times independently terrestrial.

In the talk, we show that our knowledge of the hexapod tracheal system, especially for the apterygote groups that are most crucial for the ancestral condition of Hexapoda, is only rudimentary and in many cases contradictory. As a result, three possible scenarios can be drafted for the hexapod ground plan: 1) The tracheal system was not present in ancestral hexapods but evolved independently in different extant lineages. 2) The last common ancestor of Hexapoda had a comparatively uncomplex tracheal system that became independently more complex in various lineages. 3) The last common ancestor of Hexapoda had a comparatively complex tracheal system that was independently reduced in some lineages. We currently have no evidence or line of argumentation for any of the three proposed hypotheses, as the available data is simply insufficient. Thus, any potential relationship hypotheses for Hexapoda based on the tracheal system should be treated with high caution.

The major reason for our lack of information about the tracheal system are the difficulties to study and compare this highly complex 3-dimensional system with traditional morphological methods such as dissection, histology and line drawings. In the last part of the talk, we present modern analytical approaches based on 3D models generated by μ -computed tomography and highlight which results and analyses they allow to compare and understand tracheal systems.

Comparative phylogeography of alpine/subalpine *Himalopsyche* of the Tibeto-Himalayan region: An assessment of mountain geo-biodiversity hypothesis

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As one of the most extraordinary mountain systems on Earth, the Tibeto-Himalayan Region (THR), is not only famous for its geographic and climatic influence at a global scale, but also prominent for harbouring high levels of biodiversity at present day. To explain the evolution of mountain biodiversity, a theory named “the mountain-geobiodiversity hypothesis” explores the interaction of topography, climate and biology. In this study, we tested this hypothesis in the Himalayas and the Hengduan Mountains on a group of caddisflies that is endemic to this area. In each mountain range, we investigated a species inhabiting high elevation and a species inhabiting low elevation. We incorporated genomic and ecological evidence to reveal the population structure, demographic history, and species potential habitat range dating back to the last glacial maximum (LGM) of the four target species. The results indicated that in both mountain regions, the high-elevation species showed a strong local differentiation, which may be a consequence of longstanding population isolation and only in-situ displacement along the elevational gradient during climate change. In comparison, populations of the low-elevation species were shaped by river basins, which indicates greater regional dispersal activity in the past and/or present. Results of demographic history and species distribution modelling

supported a demographic expansion for most of the species during the LGM linked to an increase of potential habitat. Our results indicate that climate fluctuations during the LGM promoted the species pump effect for caddisflies in the region, thus leading to a local or regional movement along the elevational gradient. Species in the Himalayas generally exhibited an east-west oriented dispersal. Species from the Hengduan Mountains showed greater north-south connectivity on the north-south orientation to a wider extent, suggesting that species or populations have a higher chance to survive in the Hengduan Mountains by in-situ displacement (along the altitudinal gradients) and long-distance dispersal (along the latitudinal gradients) during glaciation. Overall, our study demonstrated that historical geodiversity and climate fluctuations interact and influenced the diversification process of caddisflies in the THR, thus providing empirical evidence for the MGH.

In a hole in the ground there lived a tadpole: convergent evolution in fossorial tadpoles

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Convergent evolution is the independent evolution of homoplastic character-states in different lineages, often associated with similar selective pressures. Although this phenomenon is widespread in the tree of life and well documented for many groups of animals and plants it is understudied and poorly understood. For instance, there is still intense debated regarding several theoretical aspects of convergent evolution; one of the central issues in convergent evolution is the question of contingency. For some researchers, the evolutionary process is highly contingent, and the outcomes of evolution are a product of historical connectivity. To others, the evolutionary process is predictable and deterministic. I investigated convergent evolution. Tadpoles have been historically grouped in ecomorphological guilds based on overall external morphology similarity, ecology, and putative feeding mechanism. Members of the same guilds very often evolved convergent phenotypes, and therefore are excellent models to study the phenomena of convergent evolution. In this study I investigated convergent evolution in fossorial tadpoles; I examined external morphology, musculo-skeletal system, buccopharyngeal cavity, and visceral components of the unrelated larvae of Centrolenidae (South American), *Cardioglossa* (Arthroleptidae; Africa), and *Staurois* (Ranidae, Asia) larvae. The three taxa exhibit a strong pattern of convergency in all examined phenotypic system, suggesting adaptive value in these traits. Based on empirical data and theoretical considerations, I discuss the idea of contingency vs determinism in convergent evolution.

Universal single-copy orthologs (USCOs) in population genetics and phylogeography: a case study based on the beetle genus *Pachypus*

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The scarab beetle genus *Pachypus* (Coleoptera: Scarabaeidae) from the central Mediterranean region is a phylogenetically isolated lineage (Pachypodini) and notable for exhibiting extreme male-biased dispersal. Females have both pairs of wings completely reduced and consequently are flightless, living almost exclusively underground. Previous molecular analyses of the genus based on four mitochondrial and nuclear genes and morphometric data have shown the presence of several unrecognized species within the genus, but also an enormous amount of oversplitting in species delimitation with mtDNA. Here we investigate the phylogeny and population genetics of *Pachypus* using targeted enrichment to generate a large dataset of metazoan universal single-copy orthologs (USCOs), including 978 genes that have recently been proposed as a universal marker set for species delimitation in animals (i.e., Metazoa). We obtained a well-supported phylogeny of *Pachypus*, which agrees in many respects with previously published results from the 4-marker set, but it also shows some significant differences. Our results show strong geographic differentiation even between spatially close localities, consistent with the poor dispersal abilities especially of females, which apparently affects the entire genetic structure within species. Despite this, our results suggest gene flow between different populations, including hybridization between species. The data show Sardinia as a hotspot of diversity within *Pachypus* and allow us to suggest some scenarios on the biogeographic history of the genus, especially connected with the drying of the Mediterranean during the Messinian Salinity Crisis which appears to have been crucial for the currently observed distribution of the species and lineages. While genomic markers were able to detect these ancient signals from the phylogeny, mtDNA results were influenced by more recent hybridizations that probably occurred within the current distribution ranges. The results further demonstrate the resolving power of metazoan USCOs as a marker set for population genetics, species delimitation, and phylogeny.

The reconstruction of anthropogenic change

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Human actions have changed the global ecosystem irrevocably. To understand the consequences of these changes, we need to reconstruct the past. This base line allows us to evaluate which species are changing in abundance or distribution, genetically or ecologically. Reconstructing the past is an inherently difficult endeavour, as we cannot actually go back in time and sample past populations. However, natural history museums contain many "Zeitzeugen" that we can interrogate with novel molecular, morphological and statistical approaches. I will talk about my work on historical collections to reconstruct species extinctions and anthropogenically driven range expansions in molluscs and crustaceans.

Small wasps, big muscles: Front and hind leg modifications in chalcidoid wasps (Hymenoptera: Chalcidoidea)

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Parasitoid wasps are distinguished not only by their high species numbers but also by amazing morphological features. A lot of structures have undergone modifications and transformations in the course of parasitoid wasp evolution. In particular, members of the superfamily Chalcidoidea exhibit a lot of fascinatingly different structures. Understanding these structures might lead us to an answer of the questions on their possible functions, and hence their role in the parasitoid wasps' biology. A particularly conspicuous morphological feature are strikingly enlarged femora in combination with curved tibiae in both males and females. This feature evolved within Chalcidoidea two times independently on fore legs and at least five times independently on hindlegs, with legs of all groups being superficially similar in external appearance. In this study, the genera *Oodera* (Ooderidae), *Heydenia* (Heydeniidae), *Dirhinus* (Chalcididae) and *Leucospis* (Leucospidae) were analysed. While *Leucospis* and *Dirhinus* evolved modified hind legs, the rare *Heydenia* and *Oodera* evolved enlarged femora on their front legs. The multiple convergent evolution implies strong evolutionary pressure and a prominent function in the wasps' life history. Using a combination of scanning electron microscopy, μ CT, and 3D modeling, we examined the leg modifications and gained first insights into the internal leg morphology of these taxa.

The history of European Paleogene flower-insect interactions unraveled using fossil flowers and insects and their associated pollen grains

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The interaction between flowers and visiting insects is evident on every continent except Antarctica. Despite the current close relationship between angiosperms and insects, little is known about flower-insect interactions through the geological record. While some exceptional findings have been reported that spotlight individual insect taxa and their potential pollen source, large-scale investigations comprising complete fossil faunas and floras from the same sedimentary units are missing. Even more, investigations on successive assemblages of different ages comprising fossil flowers and insects have until now not been conducted in relation to flower-insect interactions. Here we report some preliminary results from ongoing studies on Paleogene flower-insect interactions using in-situ/adhered pollen from fossil flowers and insects. So far, we have studied flowers and insects from four Paleogene localities in

France and Germany, including Menat (middle-late Paleocene, Selandian-Thantian, 61–56 Ma), Messel (middle Eocene, early Lutetian, c. 48 Ma), Eckfeld (middle Eocene, middle Lutetian, c. 44 Ma), and Enspel (late Oligocene, late Chattian, c. 24 Ma). As representatives for the manifold discoveries we have made so far, three examples are presented herein. 1) Our study revealed a close relationship between bees (Apoidea) and the plant subfamily Tilioideae (comprising the genera *Craigia*, *Mortoniendron*, and *Tilia*) spanning over 30 million years. We have identified Apoidea bees with adhering Tilioideae pollen from all four localities. In addition, we have discovered several fossil flowers from Enspel with in-situ Tilioideae pollen enabling a morphological/anatomical comparison with extant flowers of the subfamily. 2) During our work, *Parthenocissus* (Vitaceae) pollen keeps surfacing in various samples. Pollen from this genus has now been discovered inside the guts of several fossil insects and/or adhering to their exterior. *Parthenocissus* pollen has been found in association with various Coleoptera, Diptera, and Hymenoptera, and it is currently one of the most frequently occurring pollen types found in association with fossil Paleogene insects from Europe. 3) By extracting in-situ pollen from anthers of fossil compressed flowers, we have identified several rare plant taxa, one of them a unique Onagraceae flower bud. This middle Eocene fossil from Eckfeld, Germany, represents the first and only pre-historic *Ludwigia* flower record ever discovered. We also found *Ludwigia* pollen adhering to the exterior of two different fossil beetles, one belonging to Buprestidae and the other to Scarabaeidae, from the same sediments/locality. These fossils provide the first-ever direct evidence for paleo-flower-insect visitation in *Ludwigia*/Onagraceae. Interestingly, we did not discover any *Ludwigia* pollen on the several hymenopteran fossils investigated, although hymenopterans being the main flower visitors and pollinators of living *Ludwigia*. These findings might suggest that beetles were the main flower visitors and potential pollinators of European *Ludwigia* during the Eocene and that there has been a shift in primary pollinators for *Ludwigia* over time.

The potential of museum collections for studies of biological processes in the era of genomics

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Natural history collections constitute an important repository of genetic information. Many specimens have been collected in geographic areas where they no longer exist or where collecting is no longer possible, others represent populations or species that have gone extinct. Furthermore, species and populations have often been sampled throughout an extensive time period, which is particularly valuable for studies of genetic change through time. With the advent of High-Throughput sequencing, these specimens have become accessible for large-scale genomic research. Here, I summarize our experiences of re-sequencing hundreds of bird genomes from historical museum specimens and give examples of how these resources may be utilized in research focusing on, e.g., phylogenetic relationships, biogeography and speciation processes. I also discuss the benefits and limitations with genomic data obtained from historical museum specimens, and how crowd-sourcing may expand the utilization of these resources to projects that may not be in the front-line of biological research but have a major interest for lay citizens such as birdwatchers.

Deep-sea sponges in deep Earth History: Spectacular fossil evidence of the Hexactinellida

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The fossil sponge record is variable. Whereas skeletal elements (spicules) of sponges are commonly found in marine and occasionally also in limnic sediments, these isolated remains are mostly of limited taxonomic and stratigraphic value. However, siliceous sponges with rigid skeletons, Hexactinellida (glass sponges) and “Lithistida” (class Demospongiae), are mostly well-preserved and abundant, or even rock-forming, especially in the Upper Mesozoic. Hexactinellida are a well-defined monophyletic sponge class, known in the fossil record since Early Cambrian with its time of prosperity in the Late Cretaceous. Special Lagerstätten “fossil windows” provide a unique view into the evolution and Paleocology of rarely preserved glass sponges, which are generally poorly known and today live in deep-water environments. The Upper Cretaceous Arnager Limestone of Bornholm (Denmark) is representative of such rare deposits of extraordinarily preserved lyssacinosan (non-rigid) hexactinellids. Especially informative Early Paleozoic fossil sponges are found in various Lagerstätten of South China (e.g. Dohrmann et al 2022), including the first definitely articulated sponge fossils from Yangtze Platform (Yunnan) and Anhui (e. g. Wen Wu et al. 2005). Fossils evidence combined with molecular clock results (Dohrmann et al. 2013) demonstrates the eminently conservative evolutionary morphology of the Hexactinellida.

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Biodiversity assessment of the isopod family Paramunnidae Vanhöffen, 1914 (Crustacea, Malacostraca) from the Weddell Sea, Southern Ocean

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The long evolutionary history and isolation through geologic and climatic events over the last 30 Ma resulted in a unique and high benthic biodiversity in the Southern Ocean. Much of this biodiversity is still unknown and many species undescribed. The present study aims to improve the knowledge on isopod diversity of the family Paramunnidae Vanhöffen, 1914 and investigates the influence of environmental variables of this environment on their species composition and richness. Paramunnids are asellote isopods and due to their size between 0.4-3 mm, their inability to swim and reduced gene flow (as peracarids are brooders), they are interesting to study regarding their occurrences and range sizes. Samples were collected during four expeditions in various areas of the Atlantic sector of the Southern Ocean. Sampling areas were characterised by different regimes of ice coverage including the seasonally ice-covered Filchner Trough (JR275) and Eastern Antarctic Peninsula (PS118), as well as the Prince Gustav Channel (JR17003a) which was formerly covered by an ice shelf and the South Orkney Islands (JR15005) with very low sea-ice concentrations or ice free.

With about 2494 out of 17293 isopod individuals the Paramunnidae are the second most abundant isopod family of the sampled material. The family is characterised by a high diversity, with 30 species from 11 genera. Approximately 23 species are unknown. Abundances and number of paramunnid species varied between sampling areas. Statistical analyses revealed that ice coverage was the main environmental variable driving paramunnid assemblage structure and species richness. Our results showed that the knowledge on Southern Ocean isopod diversity is still far from understood and investigated as many species are still discovered. Climate change is rapidly changing the Southern Ocean environment, it is therefore very likely that the consequent loss of sea ice will highly threaten future Southern Ocean isopod diversity.

Across Trench and Ridge: Differentiation Patterns of the deep-sea *Haploniscus belyaevi* Species Complex (Isopoda: Haploniscidae)

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The role of geomorphological features as drivers for benthic deep-sea biodiversity remains poorly understood. By disentangling the putative *Haploniscus belyaevi* Birstein, 1963 species complex from the abysso-hadal Kuril-Kamchatka Trench (KKT) region in the North-west Pacific Ocean, we aim to shed light on deep-sea differentiation and how it is related to potential bathymetric barriers such as the KKT and the Kuril-Island Ridge (KIR). Our integrative taxonomic approach featured morphological and molecular delimitation methods, also considering the post-marsupial development due to pronounced sexual dimorphism. Mitochondrial 16S and COI markers were sequenced and several molecular species delimitation methods were applied. By combining the different results we were able to delineate six distinct species within the *belyaevi* complex, including several morphologically cryptic species, and found hints of three additional species groups in the complex. Even though several of these species were distributed across the KKT and/or KIR, limited gene flow and depth-differentiation were indicated supporting previous notions that these geomorphological features play a role in deep-sea benthos speciation.

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Diversity and distribution of Ischnomesidae (Crustacea: Isopoda) in the Bering Sea and along the Aleutian trench

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Studying the distribution of species across spatial and bathymetric scales supports our understanding of the ecological and environmental factors and processes that shape biogeographical patterns in the deep sea. Especially against the background of climate change, it is crucial to decode the environmental forces that shape species distribution in order to be able to identify changes in the future. The aim of this study is to investigate the distribution and diversity of the deep-sea isopod family Ischnomesidae in the Northeast Pacific (NEP), and how it links to environmental drivers. The material comes from the recent AleutBio expedition (SO293), which conducted sampling in the Bering Sea and along the eastern Aleutian Trench and where the Ischnomesidae represented one of the most dominant isopod families. Species were initially differentiated morphologically, with the results later to be supplemented by molecular analysis as part of an integrative taxonomic approach. Our initial findings revealed high diversity in this family, with almost 30 morpho-species identified, most of which were putatively new to science. Since Ischnomesidae, like all isopods, are brooders and due to their non-swimming lifestyle they have limited dispersal capabilities. The high biodiversity over large bathymetric and geographical distances was consistent with our expectations and also with the results of previous studies of Ischnomesidae from trench regions in the NW Pacific. The great diversity of species presented in this study underlines the importance of taxonomic work and the necessity to know more about the environmental factors underlying their dispersal. In times of anthropogenic climate change and the associated loss of biodiversity, it is important to know what is living there, because only known species can be studied and protected.

Jumping to new hosts: the diversification of flea beetles (Coleoptera: Chrysomelidae: Alticini) in the context of their host plant associations, with a special focus on crucifers (Brassicales).

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Within leaf beetles (Chrysomelidae), the flea beetle tribe (Alticini) forms by far the largest group. It comprises about 8.000 species in about 500 genera and is nowadays distributed on every continent except Antarctica, being most diverse in Central and South America. Given these enormous species number, flea beetles are associated with probably up to 100 different plant families. Conspicuously, a quarter of flea beetle diversity is displayed by only ten species-rich genera, whereas about 380 genera comprise less than ten species. This indicates differential modes of host plant adaptations and subsequent diversification in this tribe. Two species-rich alticine genera are associated with plants of the order Brassicales as host plants. *Phyllotreta* comprises about 300 species, which almost exclusively feed on Brassicales. In contrast, only about 50 of the about 240 species of *Psylliodes* are specialized on Brassicales, whereas the remaining species are associated with at least 20 different host plant families including species specialized on Solanaceae, Poaceae or Fagaceae, as well as polyphagous species. We investigated the history of crucifer feeding among flea beetles and its potential impact on the diversification of *Psylliodes* and *Phyllotreta*. To test for differential diversification patterns among alticine groups in the context of their host plant associations, we constructed the phylogenetic relationships of 608 alticine species and applied several frameworks of clade-specific diversification rate analyses. We found that diversification significantly differs between alticine groups. However, this pattern is only partly associated with crucifer host use.

Phylogenetic and taxonomic studies reveal undiscovered diversity in the *Lecanora subfusca* group

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Lecanora Ach. is one of the largest and most widespread genera of lichens, which is traditionally considered to include species with lecanorine apothecia, simple, hyaline ascospores produced in *Lecanora*-type asci. Species in *Lecanora* are currently assigned to several different genera or species groups, but many phylogenetic and taxonomic issues remain unresolved. The core group, the *L. subfusca*-group, was characterized by the content of atranorin in the thallus and the presence of oxalate crystals in the apothecial margin. However, anatomy and chemistry are not strictly correlated and the systematic rank and phylogenetic positions of many species are still unsettled. Our study focuses on the *L. subfusca*-group in China, as part of ongoing project 'Lecanomics', aims to clarify the phylogenetic relationships of the *L. subfusca* group in China and species delimitations within this group, to provide a more natural taxonomic system. Specimens were examined from China and surrounding areas, investigated with morphological and chemical methods, a preliminary phylogenetic framework of *Lecanora* is reconstructed based on multiple gene loci, species diversity and potentially new taxa are presented

Distribution and diversity of marine fauna along the Persian Gulf and the Gulf of Oman: Large scale monitoring expeditions

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Abstract

Large Scale oceanographic expeditions, jointly funded by INIOAS, Iran's National Environment Fund (INEF) and Department of Environment of Iran (DOE), collected new inshore and offshore biodiversity data of the macrobenthose along the Persian Gulf and the Gulf of Oman during COVID-19 outbreak (2019-2021). Distribution and diversity of macrobenthos, plankton, sensitive coastal ecosystems (i.e., coral reefs, mangrove forests, seagrass and seaweed beds), sea turtles, and marine mammals excluding fish and sea birds was monitored during those expeditions. We will combine the data of these expeditions with available open data to analyse the biodiversity and community composition of the marine fauna. We aim to identify hotspots and key environmental parameters which affect the community composition, diversity, and endemism of studied taxa in the Persian Gulf and the Gulf of Oman. We will use Hill biodiversity analyses and Redundancy analyses to estimate the taxa richness and identify the knowledge gaps in the Persian Gulf. This will help scientists in Iran or elsewhere to plan their future expeditions to those underdamped areas. The results of this study also provide necessary information particularly on definition of new Ecologically or Biologically Significant Areas (EBSA) for DOE of Iran to manage better Iran marine environments. Until now we identified new solitary coral habitats (*Truncatoflabellum mortenseni* Cairns and Zibrowius, 1997) lied near to Abu-Musa and Sirri Islands in the Persian Gulf.

Diversity of the ectomycorrhizal genus *Russula* (Basidiomycota, Fungi) in the tropics

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Species of the genus *Russula* (Basidiomycota, Fungi) are key components of ectomycorrhizal ecosystems worldwide. Nevertheless, their diversity in the tropics is largely underexplored. We aim to document the species diversity in this genus in Panama (Central America) and Benin (West Africa) based on morphological characteristics and the analysis of the ITS nrDNA region of specimens obtained during several field forages. Long term research in Panama revealed a diversity of 90 *Russula* species present in the country, mostly in montane *Quercus* dominated tropical forests. Of a large number of presumably new species in Panama, six were formally described as new for science so far. For Benin, the analysis of 283 collections revealed a diversity of 50 species from savannah woodlands and gallery forest habitats. *Russula* subsect. *Inflatinae* is identified as a predominantly African lineage sister to *Russula* subsection *Virescentinae*. Species in this group are characterised by densely reticulated spore ornamentation and small single-celled pileocystidia with a terminal knob. Within our material from Benin, we identified ten species in subsect. *Inflatinae* based on multigene phylogenetic analysis, of which, at least four are new to science.

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Fostering species knowledge to counter the biodiversity crisis - the FörTax project

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The erosion of biodiversity is one of the largest crises we are facing today and an erosion of species expertise accompanies it. To overcome this loss of expertise, the FörTax-project aims to spread species knowledge widely into the society to arouse interest for the nature surrounding us as a basis for its protection. The 6-year term project, funded by the BMUV and BfN within the Federal Biological Diversity Programme, already fulfilled some of its goals: among others, a user-oriented online database providing information about projects, trainings, and institutions offering opportunities of species knowledge mediation, some of which are also designed by the FörTax team itself, has been established. While the LIB-Museum Koenig is offering the FörTax club, a participatory weekly course for teenagers (age 14+), the DELATTINIA is creating an academy for species knowledge in the Saarland. Additionally the entomological society in Krefeld is preparing entomological educational films for self-learning. All courses and educational materials are designed together with the department for biology education of the University of Bonn, who concomitantly evaluate the educational offers of the project. A second main task of FörTax is the founding of a nationwide network of people focusing on species knowledge, including experts, citizen scientists, and students. The first FörTaxCon in 2021 - held online with already 500 participants - marked the start of this network and began connecting all different kinds of species experts and interested people. FörTaxCon2, which will be held in November 2023, will be aimed at finding solutions for the problems the community is facing. Once again as a sustainable online-only event, FörTaxCon2 will be open to a wide range of participants: to interested scientists and educators from the field of biodiversity research and other experts (e. g., from authorities, nature conservation consultancies and the educational sector), who are active in mediation or have a need of species knowledge, but also to interested people from all walks of life and all ages. The conference will not only include talks, workshops, and digital booths, but also new formats and innovative platforms to discuss needs and possibilities in the field of species knowledge.

More species than ever thought in the enigmatic mantid genus *Holaptilon* Beier, 1964, (Gonypetidae, Gonypetinae)

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The mantid genus *Holaptilon* (Gonypetidae, Gonypetinae) is composed of small, runner mantids. Both sexes are apterous, which is rare in the order Mantodea. Due to their clandestine lifestyle, comparatively little is known about this genus, and studies concerning its distribution and taxonomy are scarce. Furthermore, only a few specimens of this genus are available in museum collections. The genus was once established for a single species, *Holaptilon pusillum*, by Beier (1964) based on material collected in Jerusalem. Later, *Holaptilon brevipugilis* Kolnegari, 2018 was described with material from Iran. The systematic placement of this genus was recently changed by moving it from Mantidae to Gonypetidae, and its subfamily changed from Amelinae to Gonypetinae (Schwarz and Roy 2019). Here, we present new data on this genus based on more than 70 *Holaptilon* specimens collected from various provinces of Iran. We conducted extensive morphological analyses, including examination of male and female genitalia and morphological hypervolume PCA. As many of the morphological characters appear to be homoplastic, they cannot be used to define the species within this genus. In addition, we used four molecular markers (mitochondrial and nuclear DNA) to gain a better understanding of species delimitation and phylogenetic relationships. We discovered an important inter- and intra-specific variation. Based on our data, we add four new species to this genus, each of which exhibits a unique distribution within Iran. We provide an identification key plus data regarding this enigmatic genus's distribution, ecology, and biology.

Global distribution and biodiversity of marine Amphipoda (Crustacea: Peracarida)

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Due to high number of species (more than 10500 species), high biomass, and occupying different ecological niche, the order Amphipoda are known as a dominant crustacean group in marine ecosystems. The taxonomy and biodiversity of amphipods is dynamic and many new species are being introduced every year. In this study, the global distribution and diversity patterns of marine amphipod is being investigated worldwide, and also the main environmental driving factors which delimit those patterns will be identified. The occurrence data was extracted from the Ocean Biodiversity Information System (OBIS) and Global Biodiversity Information Facility (GBIF), in addition to our own sampling efforts in the Persian Gulf. More than 1,500 unique occurrence records from the Persian Gulf were standardise based on Darwin core and will be submitted to OBIS, and finally will be merged with the available open-access data for the biodiversity analyses. The environmental data including depth, temperature, salinity, sediment type, current velocity, oxygen, iron, nitrate, silicate, and phosphate were extracted from BIOORACLE for Generalized Additive Model (GAM) and Generalized linear model (GLM) analyses to investigate the correlation between species richness and environmental variables. We will plot the global alpha, gamma, and beta species richness of amphipods and reveal the hot spot of the species richness and data knowledge gaps of the amphipods. The species richness, sampling effort, and expected species richness (ES50) will be calculated per area. The outputs of this research could be identified as the baseline study for implementing management strategies and ecosystem restorations for Amphipods, regionally (Persian Gulf and the Gulf of Oman) and globally.

The deep-sea acorn barnacle *Bathylasma hirsutum* (Hoek, 1883): first record from a hydrothermal vent field at the Reykjanes Ridge

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To fathom shifts in biological communities of the Atlantic Ocean, it is crucial to understand their present ecological state. The research project “Icelandic marine Animals meets **Diversity** along latitudinal gradients in the deep sea of the **A**tlantic Ocean” (IceDivA) focuses on abyssal plain communities along the Mid-Atlantic Ridge (MAR). By sampling 3000 – 5500 m deep basins east and west of the MAR, IceDivA extends the previous Northeast Atlantic deep-sea programme IceAGE (**I**celandic marine **A**nimals: **G**enetics and **E**cology) and bridges knowledge gaps of previous deep-sea expeditions. Within the framework of the recent IceDivA2 expedition, connectivity and population dynamics of benthic invertebrates representing different reproductive traits are compared across adjacent deep-sea basins. Combining morphological studies with phylogenetic and next-generation sequencing methods, the results will be overlaid with ecological and functional trait factors to investigate drivers in speciation patterns and population structure. Here, we present results on the population dynamics and connectivity of *B. hirsutum*, as well as provide *in situ* footage on their growth patterns and association with other deep-sea fauna. As the species is able to sustain large populations in non-venting deep-sea habitats, we hypothesise the barnacle to opportunistically utilise nutrient flows supplied by the vent field ecosystem to extend its habitat range along the Reykjanes Ridge.

Dark taxa: large “Little Brown Jobs” - a monographic taxonomy of South American Sericini reveals an enormous hidden diversity in large night active chafer beetles (Coleoptera, Scarabaeidae)

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The South American Sericini is the sister clade of all other Old World/Nearctic Sericini but they represent only 5% of the tribe's total species richness. Sericini is a monophyletic megadiverse polyphagous herbivorous chafer beetle tribe of Scarabaeidae (Coleoptera). With a cosmopolitan distribution, the tribe includes ca 4500 described species. This lets us to believe the South American Sericini lineage either represents an entirely understudied taxon, or we find confirmation for this asymmetry of species diversity between the continents' lineages which then would require a plausible hypothesis for explanation.

For this objective we performed an exhaustive taxonomic revision of all South American species of the tribe and studied unidentified specimens. In total, we examined around 4000 specimens from many collections from South America, the USA, and Europe. Based on morphology-informed phylogenetic analyses, we also revised the generic classification.

Resulting from so far concluded works, one new genus and 18 species were described (including the first two species of Sericini with no feeding at the imago stage), and around 80 new species are currently in process of description. The absolute majority of new species (ca 80) we found for the night active genus *Astaena* Erichson, 1847, of which all representatives are characterized by an almost uniform appearance, a coffee-bean-like, brown, oval body lacking striking and clear colour, shape, or surface structure patterns. Interestingly these *Astaena* species are by far larger than the diurnal species, which are much smaller in body size, and which have generally striking colour patters. Based on routinely taken morphometric measurements in process of the taxonomic revision, we also explored patterns of morphospace and were able to discover two distinct morphospace patterns in relation to activity patterns.

Evolutionary history and circum-Tibetan phylogeographic patterns of Eurasian forest-dwelling passerine birds (Passeriformes)

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In the Northern Hemisphere, the Qinghai-Tibet Plateau (QTP) is the largest geographic barrier for dispersal of montane organisms. Accordingly, montane species of the forested plateau margins in the East, South and West are characterized by distinct phylogeographic patterns and phylogenetic relationships to their counterparts north of the QTP. In Eurasian passerine birds, one major pattern is remarkably congruent across different bird taxa: One Himalayan-Chinese sister phylogroup (clades 1 and 2) is opposed to another Northern Palearctic phylogroup (clade 3). In most passerine taxa studied to date divergence times among the three vicariant phylogroups (clades 1-3) have been dated back to the early Pleistocene. To date, the number of currently recognized species-level taxa in clades 1, 2 and 3 largely depended on phenotypical distinctiveness, rather than on genetic divergence or behavioral differences, such as vocalizations. Furthermore, repeated range contractions and expansions during glacial cycles and in the Holocene have shaped current parapatric distributions including narrow zones of range overlap at the southern and eastern QTP margins, for example in Central/Western Nepal or in the Chinese Qingling Mountains. Patterns of divergence and admixture in these contact zones large correlate with divergence of phenotypical and bioacoustic traits among locally sympatric taxa. We compare these circum-Tibetan phylogeographic patterns among species of nutcrackers (Corvidae), tits (Paridae) and other passerine families.

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Senckenberg Ocean Species Alliance (SOSA) — a project to facilitate discovery, conservation and fascination

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Invertebrates are the dominant components of marine biodiversity. However, most of these species are unknown, unprotected and utterly underappreciated by science and society. The Senckenberg Ocean Species Alliance (SOSA) is a 10-year project dedicated to breaking down barriers in species-based marine research and conservation. The core activities of SOSA are:

- (1) speeding up species descriptions of marine invertebrates without sacrificing quality by providing technical taxonomic services;
- (2) supporting conservation through the Marine Invertebrate Red-List Authority (MIRLA) within the IUCN global Red List of Threatened species;
- (3) stimulating societal engagement with and appreciation of marine biodiversity through a wide range of creative public outreach.

We first aim to devise new approaches to describe species and make names available quicker than is done at present. Our first goal is to provide the necessary organizational backbone and staff support to build a global network of volunteer contributors for species-based conservation. The aim in 10 years is to bring both taxonomy and global Red List assessments to places where they are most urgently needed by franchising out this new work model to regions with high marine biodiversity.

Caught your interest? Approach us to become part of the rapidly growing international SOSA networks: we want to support colleagues to integrate Red List assessments including providing assessor training. And you can support SOSA in fighting the “taxonomic bottleneck”, as a client or as a taxonomic expert collaborator. Stay tuned through our project website and social media!

Putting ceraphronoid wasps (Insecta: Hymenoptera) back on the map

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Parasitoid wasps are a megadiverse group of Hymenoptera with ecological and economical importance. The number of currently described species does not reflect the true species diversity. One of the most severely understudied parasitoid wasp groups is Ceraphronoidea. Our studies on ceraphronoid wasps from the biodiversity hotspots in the central-eastern Afrotropical regions (Kenya, Tanzania) and the Caucasus (Armenia, Georgia) support this hypothesis. So far, we already described 88 new species, more than doubling the number of Ceraphronoidea species from the Afrotropical mainland (65 vs. 153 Ceraphronoidea). Recently, we made the first ever targeted efforts to collect Ceraphronoidea from the Caucasus, a hotspot virtually unstudied for the superfamily. The collected specimens will be treated in a first integrative species diversity exploration approach, combining morphological examination and DNA-Barcoding. Preliminary results indicate a high diversity in both Ceraphronidae and Megaspilidae, with many species new to science to be expected. In summary, our results highlight that it is necessary and also possible to illuminate the grotesquely understudied parasitoid wasp fauna. We hope that our studies will bring the necessary momentum for the exploration of the diversity of small-bodied and megadiverse insect groups by providing the basic taxonomic knowledge that is much needed for protecting biodiversity and understanding evolution and the networks of life on earth.

A new species of the isopod genus *Mexicope* Hooker, 1985 (Crustacea, Malacostraca) from the Mediterranean Sea off Malta

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The marine isopod family Acanthaspidiidae Menzies, 1962 of the superfamily Janiroidea has a global distribution, with species described from shelf to hadal depth. However, the majority of species has been thus far recorded from deep waters and the Southern hemisphere. To date 36 species have been described in the family belonging to three accepted genera: *Ianthopsis* Beddard, 1886; *Iolanthe* Beddard, 1886; and *Mexicope* Hooker, 1985. In this study, a new species in the genus *Mexicope* is described from the Maltese continental shelf (Mediterranean Sea). The genus *Mexicope* consists of three accepted species, *Mexicope kensleyi* Hooker, 1985 from a shallow-water coral reef habitat in the Florida Middlegrounds, Gulf of Mexico, *Mexicope westralia* Just, 2001 from coastal waters off southwestern Australia, and *Mexicope sushara* Bruce, 2004 from coastal waters off New Zealand. In this study, a new species of *Mexicope* is described from the Maltese continental shelf (Mediterranean Sea). The new species presented here is the first member of the whole family from the Mediterranean Sea. It is represented by a single male specimen collected in Maltese waters off Ġnejna Bay at a depth of 120 m. The new *Mexicope* species was analyzed and compared to the other species in the genus based on morphology. An identification key to the species of *Mexicope* is presented. The new species can be differentiated from its known congeners by the unique combination of the following characters: cephalothorax with preocular spine large and pointed anterolaterally, rostral projection blunt, eyes reduced; pereonal sternites with ventral spine-like processes; pereonite 2 lateral margins with single projection; pleotelson lateral margin with spine-like setae, posterior apex long, projecting to approximately half of the length of the uropod protopod; pleopods 1 lateral lobes projecting beyond medial lobes, apices pointed laterally; uropod exopod approximately 0.5 endopod length.

GloBios – Global Observatory Network for Freshwater Biodiversity in High Mountain Streams

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While global climate change is affecting all environments, the effects are especially pronounced in high-altitude mountain streams. The disappearance of alpine glaciers and the shifting of ecosystems to higher altitudes is projected to disturb and fragment benthic invertebrate communities in this vulnerable environment. GloBios is an international project aiming to assess taxonomy and biodiversity of trichopterans, plecopterans and chironomids in high-altitude streams of South American, Central American and European mountain ranges. Using barcoding, metabarcoding and species distribution modelling approaches, we aim to identify species that are especially vulnerable to climate change due to low genetic diversity, habitat specificity and small distribution ranges. Here we present benthic macroinvertebrate biogeography and community data for the European Alps.

A new species of the isopod family Mesosignidae Schultz, 1969 (Crustacea, Malacostraca) from the Aleutian Trench, North Pacific

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The Mesosignidae Schultz, 1969 are a relatively small family of marine isopods with so far 17 species described in five genera. The family is known to be globally distributed and regarded as a typical deep-sea family. Here, we present a new species in the genus *Mesosignum* Menzies, 1962 collected from the abyssal and hadal of the Aleutian Trench (AT, NE Pacific) at depths between 4842 and 6503 m. The material was collected as part of the recent AleutBio expedition (SO293) onboard R/V *Sonne* that aimed to characterize deep-sea communities along the eastern AT. In total, two species were discriminated by morphological means, which could be identified to be a new and an already known species (*M. elegantulum* Birstein, 1963). The new species is most similar to *M. truncatum* Menzies & George, 1972 and *Kurilosignum latum* (Birstein, 1970), which were described from the Peru-Chile trench in the South-eastern Pacific, and the Kuril-Kamchatka trench in the North-western Pacific respectively. However, differences can be observed, for instance, in the dorsal ornamentation and overall body shape. In addition to the description of the new species and a morphological comparison with known species in the genus, the taxonomic validity of genera within the family is here discussed, since not all appear to be unambiguously defined and may require a revision.

Postembryonic development of the bone devouring *Osedax* (Siboglinidae, Annelida)

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Osedax (Latin os, 'bone'; edax, 'to devour') is a bizarre annelid known for its unusual life-history, relying on the bones of dead sunken vertebrates. These peculiar bone-worms have a marked sexual dimorphism, with macroscopic females and microscopic dwarf males. The females depend on a unique heterotrophic symbiosis that allows utilising bones as a source of nutrition, whereas dwarf males solely rely on a finite amount of maternally deposited yolk resources. Herein, we describe the postembryonic development of *Osedax japonicus*, using traditional immunohistochemistry labelling and CLSM and introduce a staging system for this organism. We describe several morphogenetic processes; like neurogenesis, myogenesis and ciliary patterning in both males and females and show that the sexual dimorphism in *Osedax* is the outcome of a metamorphic arrest in male development (=progenesis). Furthermore, we focus specifically on the development of *Osedax*'s hook-like bristles (chaetae). Chaetae are chitinous, extracellular structures and one of the most characteristic features of all Annelida. Chaetogenesis occurs within epidermal invaginations, where the intricate interplay of several cells and the controlled modulation of dynamic microvilli, coupled with chitin secretion forms the bristle in a process that resembles a biological 3D printer. *Osedax* only bears a fixed set of chaetae, and unlike other annelids chaetal development is restricted to a very short time period during the postembryonic development. In addition to a morphological characterisation of chaetogenesis using serial TEM, we also present initial results on the differential expression of genes involved in this process, and their expression patterns (in-situ HCR).

Comprehensive whole-genome analyses support the monophyly of Hemirotifera within Syndermata (Gnathifera)

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The spiralian clade Syndermata comprises four subclades: the endoparasitic Acanthocephala, the epizoic Seisonidea, and the free-living Bdelloidea and Monogononta. Bdelloidea, Monogononta and Seisonidea have traditionally been the members of the Rotifera Phylum that was later expanded to include the Acanthocephala (Rotifera s.l.). Resolving the evolutionary relationships among these four syndermatan subclades is essential for understanding the evolution of endoparasitism in Acanthocephala. However, the phylogenetic relationships among syndermatan groups are highly debated. Some phylogenomic studies of spiralian relationships suggest Seisonidea as the sister group to all other Syndermata. On the other hand, studies focusing exclusively on the relationships of Syndermata support Pararotatoria (Seisonidea+Acanthocephala) within monophyletic Hemirotifera (Syndermata excl. Monogononta). Additionally, phylogenetic studies of Syndermata have so far mostly relied on genome subsampling approaches and only a few have included the most closely related animal Phylum of Syndermata in the analyses (i.e., Micrognathozoa). Here, we use publicly available whole-genome sequencing data from all syndermatan subclades to reevaluate their phylogenetic relationships. To this end, we apply a novel combination of methods namely: 1) concatenation-based phylogenomic analyses using site-heterogeneous models, 2) whole-genome microsynteny analyses and 3) species-tree methods that utilize multi-copy orthogroups. Our results show that datasets that are less likely affected by systematic error in concatenation-based analyses support the Hemirotifera hypothesis in agreement with the results of the other two phylogenetic approaches. The scenario of acanthocephalan endoparasitism emerging via an ancestral epizoic stage is also supported by the herewith inferred monophyly of Pararotatoria, albeit not from all approaches. Our study underlines the importance of integrating several sources of evidence for resolving difficult phylogenetic questions.

Identification of nemertean species – what data do we need?

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DNA-barcoding for the identification of species holds great promise for fast and easy assessment of biodiversity, especially in taxonomically challenging groups such as Nemertea (ribbon worms). Their predatory lifestyle bears a currently underestimated ecological relevance by presumably drastically impacting their respective prey communities. Nemertea are unsegmented, spiralian worms with only few distinct external morphological characters to be used for identification. Furthermore, it becomes more and more evident that species complexes are rampant in this group of worms, the reasons for that, however still being unclear. In the past, species identification and taxonomy had been based on characters of internal anatomy, that recently have been assumed as being too variable to be used for reliable identification to species level. The talk reports on the usefulness and practicability of molecular barcoding for species identification in Nemertea and points out potential shortcomings and pitfalls of this method, most problematic being the absence of reference data. To provide useful species identification based on molecular barcodes in the future, current scientific practice has to combine molecular data with ecological and traditional morphological methodology in an integrative taxonomic approach.

Clarification of the taxonomic status of *Acanthochitona discrepans* Brown, 1827 with the new data for the North-East Atlantic *Acanthochitona*

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Chitons, also known as polyplacophorans, comprise one of the eight extant classes of molluscs. These entirely marine animals are found worldwide, from the intertidal to the deep-sea habitats. Their characteristic features are eight overlapping and articulating plates, but they are famous for a number of features, such as iron-infused teeth, and unique sensory adaptations such as the elaborate aesthete system that penetrates their shells. Among around 1000 known living species, one of the most widespread and species-rich genera (ca. 90 species) is *Acanthochitona*. This genus is very distinctive and easily recognised by large tufts of bristles on the girdle between the valves. Some *Acanthochitona* species in the North Atlantic were described in the 18th century, namely *A. fascicularis* Linnaeus, 1767 from Algeria and *A. crinita* Pennant, 1777 from Scotland. Soon after, Brown introduced the third European species, *A. discrepans* from Wales, without giving a description (the description was provided in the second edition of his book). As a result, for almost 200 years these three *Acanthochitona* species have been confused, resulting in numerous erroneous records, and their geographic ranges and potential co-occurrence remained unclear. A 1985 review of Mediterranean species designated neotypes for *A. fascicularis* and *A. crinita*, and a lectotype for *A. discrepans*. However, that publication provided a rather historic review of the history of nomenclature confusion of NE Atlantic *Acanthochitona* species and lacked their detailed descriptions. In this work we provide a new integrative assessment of these three species including morphological and molecular data. *Acanthochitona discrepans* is closely related to both *A. crinita* and *A. fascicularis*, but constitutes a separate lineage and a valid species. This work clarifies the taxonomic composition of *Acanthochitona* in the NE Atlantic, and also the specific characters that effectively diagnose species in this diverse genus that no doubt includes many additional undiscovered species in other regions.

FörTax - Promotion of taxonomic knowledge as a basis for nature conservation - Successes, deficits and prospects

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Knowledge of all different kinds of species and taxonomic expertise is not only essential for science and all efforts to protect nature; moreover, it also touches very different fields of interest including both, private and professional clientele. However, the number of educational supply of appropriate courses declined over the past 20 years. Thus, we were very pleased that in 2020 the BMU and BfN funded the 6-year-term FörTax project for the nationwide promotion and dissemination of taxonomic knowledge in Central-European flora and fauna. The project including three Institutions (Zoological Research Museum Alexander Koenig-Leibniz Institute for Biodiversity of Animals, the didactics of biology at the University of Bonn and the Natural Research Society of the Saarland (Delattinia)) aims to analyze record and develop educational offers on taxonomy for various ages and levels of education knowledge. The resulting network of facilities and institutions that train species experts is to be consolidated and expanded in three conferences (every two years, starting in November 2021). A final guideline is intended to support the educational institutions in being able to offer appropriate educational programs beyond the duration of the project in order to increase taxonomic knowledge in science and society and thus ultimately to significantly promote nature and species conservation in the long term.

On the fossil record of social wasps (Hymenoptera: Vespidae: Vespinae)

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The oldest fossil records of solitary vespine wasps are from the Early Cretaceous. Social wasps, belonging to either Vespinae or Polistinae, probably were present by the Late Cretaceous, because a fossil nest was recorded from the Late Cretaceous of Utah (USA).

The fossil record of body fossils of vespine wasps comprises currently 16 fossil species (Abels & Wedmann 2022). The extinct genus *Palaeovespa* occurred with eight species in the Paleocene and Eocene of Europe and North America. The oldest species was found in the Paleocene of Menat (France), two additional species are known from Eocene Baltic amber, and five more species from the late Eocene of Florissant (USA). This extinct genus represents the oldest eusocial Vespinae.

Until recently, Oligocene fossils of the genus *Vespa* were the oldest representatives of extant vespine wasps. Six species of *Vespa*, the hornets, were reported from three localities of Oligocene and Miocene age in Europe and Asia, namely from Rott in Germany, Radoboj in Croatia and Shanwang in China. Together with two species of hornets, a nocturnal hornet species of the extant genus *Provespa* was described from the Middle Miocene of Shanwang in China.

Currently, the genus *Vespula* is the oldest fossil record of an extant vespine genus (Abels & Wedmann 2022). It was recorded from the Eocene fossil site Messel, Germany, and indicates that in the Eocene the evolution of wasps was more advanced than previously known. Divergence time estimations within Vespidae based on analyses of mitochondrial genomes fit well with this new fossil clue.

References

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