



23rd Annual Meeting of the Society of Biological Systematics

21st - 24th March 2022 | virtual meeting

Program and Abstracts

The abstracts are arranged alphabetically by the last name of the presenters. You will also find an index at the end of the abstracts.



Organizers

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Talks marked **S1** to **S17** are student contributions.

Time	Monday, 21.03.	Tuesday, 22.03.	Wednesday, 23.03	Thursday, 24.03.
		Chair: Dominique Zimmermann	Chair: Michael Schmitt	Chair: Gabriele Uhl
09:00	Welcome	Keynote Speaker: Botany	Keynote Speaker: Paleontology	Keynote Speaker: Biodiversity
09:15	Michael Schmitt Biological Systematics at the University of Greifswald	Alexandra Müllner-Riehl Origins of mountain plant biodiversity	Catalina Pimiento Ecological effects of marine extinctions: from the Pliocene to the Anthropocene	Henrik Krehenwinkel From DNA to ecosystems – The promise of biological archives for biodiversity monitoring
	Chair: Peter Michalik			
09:45	Keynote Speaker: Zoology	S8: Incoherencies among morphological and molecular data on the rapidly radiating Gynoxyoid clade (Senecio, Asteraceae) Escobari, B. , Borsch, T. & Kilian, N.	S15: Phylogenetic distribution of traumatic insemination in Strepsiptera (Insecta) Jandausch, K. , van de Kamp, T., Beutel, R.G., Niehuis, O. & Pohl, H.	S16: Using citizen science in the biodiversity research of Nudibranchia Hoffmann, N. , Christa, G. & Bleidißel, S.
10:00	Sergei Tarasov Evolutionary phenomics: emerging tools for semantic species description and ontology-informed phylogenetic methods	S9: NGS based approach to investigating systematics and biogeography of myrmecophytic Macaranga (Euphorbiaceae) Dixit, N. & Guicking, D.	Visual Allometry in Earwigs Pande, A. , Blanke, A., & Rühr, P.	The LifeGate-project - a new weblocation for all living species Freiberg, M.
10:15		S10: Anthropogenic influence shaped the population genetics patterns of the Greater Periwinkle (<i>Vinca major</i> L., Apocynaceae) Raus, H. & Weising, K.	Repeated evolution of extreme locomotor performance independent of changes in extended phenotype use in Austral brown spiders (Amaurobioidea) Wolff, J.O. , Kelly, M.B.J., Khan, K., Wierucka, K., Jones, B., Shofner, R. & Derkarabetian, S.	What is the IceDivA project? Research expeditions and science in the face of Covid-19 Taylor, J. , Kamyab, E., George, K.H., Kieneker, A., Linse, K., Martinez Arbizu, P., Neuhaus, J., Schumacher, M. & Brix, S.
10:30	Breakout rooms			
	Chair: Jörn von Döhren	Chair: Andreas Schmidt-Rhaesa	Chair: Thomas Bartolomaeus	Chair: Jonas Wolff
10:45	S1: First record of the order Polyzoia from the Indian subcontinent with the description of a new genus (Diplopoda, Colobognatha, Siphonotidae) Avinipully Anilkumar, P. , Wesener, T. & Moritz, L.	Processes of evolutionary diversification in Aeonium (Crassulaceae), the most species-rich plant genus of Macaronesian endemics Messerschmid, T.F.E. , Abrahamczyk, S., Bañares Baudet, A., Brilhante, M.A., Egli, U., Hühn, P., Kadereit, J.W., dos Santos, P., de Vos, J. & Kadereit, G.	Status of taxonomic expertise in our society Bartholomaeus, T.	S17: Connectivity of deep-sea basins in the North Atlantic using invertebrate taxa as surrogates – preliminary results Neuhaus, J. , Taylor, J., Linse, K., Martinez Arbizu, P., Dobler, S. & Brix, S.
11:00	S2: Integrative description of three new species of giant pill-millipedes from Thailand Bhansali, S. & Wesener, T.	S11: Don't ask sensis for their age: Evaluating parameter impact on temporal calibration of Macroscelidea phylogenies Hagemann, J. , Hofreiter, M., Bibi, F. & Arnold, P.	CETAF – The Consortium of European Taxonomic Facilities Häffner, E.	Changes in wild bee communities over 100 years in relation to land-use change: A case study in Eastern Austria Zimmermann, D. , Schoder, S., Kratschmer, S., Hainz-Renetzeder, C. & Zettel, H.
11:15	S3: Mitogenomics in <i>Hyles</i> moths: Relationships of Central Asian <i>H. hippophaes</i> and <i>H. chamyla</i> Patzold, F. , Marabuto, E., Daneck, H., O'Neill, M.A., Kitching, I.J. & Hundsdoerfer, A.K.	S12: Genotypic prediction of the phenotype? Testing the concept for the vomeronasal organ of non-model semiaquatic mammalian species. Lächele, U. & Giere, P.	Horizon Europe – Opportunities for Organismic Research Warth, P. , Holstein, J. & Krogmann, L.	Premier assesment of the spider (Araneae) biodiversity found in South America. Dupérré, N

11:30	High quality genomes corroborate 29 chromosomes of the haploid <i>Hyles</i> (Lepidoptera: Sphingidae) karyotype and open wing pattern studies Hundsdoerfer, A.K. , Pippel, M., Patzold, F., Yoshido, A., Marec, F., Daneck, H., Winkler, S., Greve, C., Hiller, M. & Schell, T.	Taxonomy of the Future — Harvesting Universal Metazoan-Level USCO Markers from Genomes for Species Delimitation and Identification Dietz, L. , Mayer, C., Stolle, E., Eberle, J., Misof, B., Podsiadlowski, L., Niehuis, O. & Ahrens, D.	On a mission: biodiversity conservation, natural science collections and global policy-making Buschbom, J. , Carter, J., Ellwood, E.R. & Mayer, P.	Shaping our taxonomic legacy through openly sharing primary biodiversity data in taxonomic revisions Dikow, T.
11:45	Breakout rooms			
	Chair: Manuela Sann	Chair: Saskia Brix	Chair: Thomas Bartolomaeus	
12:15	S4: Discovery of a cryptic species among samples of one of the most common European vespid wasps, <i>Polistes dominula</i> (Hymenoptera: Vespidae) Schweitzer, F. , Bertsch, L. & Niehuis, O.	A comprehensive and systematic revision of the internal anatomy of leather urchins (Echinoidea: Echinothurioida) Ziegler, A. & Anderson, O.F.	FörTax – First Project Year Activities and Preliminary Results of the Inventory Nöske, N. , Miesen, F.W., Stehr, K., Waskow, K.	Student Awards
12:30	S5: How dark of a taxon is Microgastrinae (Braconidae) really? Höcherl, A. & Chimeno, C.	S13: Diversity of Symbiodiniaceae in Cladobranchia and the Microbiome of the aeolid nudibranch <i>Berghia stephanieae</i> Sickinger, C. , Brackwehr, S., Bleidißel, S., Christa, G. & Preisfeld, A.	KennArt - A nationwide initiative for the training of taxonomists Reininghaus, H. , Knauff-Pieper, C., Scherber, C., Linnemann, B. & Göcking, C.	Laudatio of Rensch Prize Winner Gerhard Hazsprunar
12:45	A long-lasting story: To worm out the secret of "the feet" of Desmosomatidae Sars, 1897 Brix, S. , Held, C., Kaiser, S., Jennings, R.M., Driskell, A. & Brandt, A.	S14: The bryozoan genus <i>Reteporella</i> : morphospecies and contrasting population structure inferred from mitochondrial and microsatellite data Baptista, L. , Berning, B., Curto, M., Waeschenbach, A., Meimberg, H., Santos, A.M. & Ávila S.P.	DigiTiB - a teaching tool for the training of taxonomists Michalik, P. and Heethoff, M.	Rensch Prize Presentation Franziska Sophie Bergmeier
13:00	Bizarre morphology in fossil bugs (Insecta: Heteroptera: Pentatomidae) from the Eocene Wedmann, S. , Kment, P., Campos, L. A. & Hörnschemeyer, T.	Biodiversity of free-living nematodes- exploring the tip of the iceberg Herrmann, M.	Provenienzforschung am Zoologischen Forschungsmuseum Alexander Koenig in Bonn Koch, A.	<i>From shallow sands to deep-sea trenches: Towards integrative systematics of Solenogastres (Aplacophora, Mollusca)</i>
13:15	Breakout rooms			Photo session of participants
	Chair: Dagmara Maria Zyla	Chair: Anna K. Hundsdoerfer		
13:30	Morphological disparity of phytophagous scarab beetles in the light of species diversity at different ecochorological scales Ranasinghe, U.G.S.L. , Eberle, J., Benjamin, S.P. & Ahrens, D.	Species delimitation of Hexacorallia and Octocorallia around Iceland using nuclear and mitochondrial DNA and proteome fingerprinting Korfhage, S.A. , Rossel, S., Brix, S., McFadden, C.S., Ólafsdóttir, S.H. & Martínez Arbizu, P.		lunch break
13:45	S6: Diversity and gene flow within the European hermit crab <i>Diogenes pugilator</i> species complex (Crustacea: Anomura: Diogenidae) with description / resurrection of species Erk, C. & Schubart, C.D.	A non-coding gene approach to animal systematics. Fromm, B.		
14:00	S7: Molecular phylogenetic and morphological analyses question current taxonomy of Indo-West Pacific porcelain crabs (Decapoda: Anomura) with emphasis on the genus <i>Petrolisthes</i> Schaubeck, L. & Schubart, C.D.	The evolution of Zoraptera (Insecta) Matsumura, Y. , Beutel, R.G., Rafael, J.A., Yao, I., Câmara, J.T., Lima, S.P. & Yoshizawa, K.		Mitgliederversammlung - General Assembly 14 - 15.30 hs

First record of the order Polyzoniida from the Indian-subcontinent with the description of a new genus (Diplopoda, Colobognatha, Siphonotidae)

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The millipede fauna of the Indian subcontinent is poorly studied with only 270 described species in 90 genera, 25 families and 11 orders being known, of which not a single species belongs to the order Polyzoniida. The >70 species of the species-poor Polyzoniida are generally small, elongate millipedes with conical head, and with the 9th and 10th legs transformed into gonopods in males. Polyzoniida include the three families Polyzoniidae Gervais, 1844, Hirudisomatidae Silvestri, 1896, and Siphonotidae Cook, 1895. The latter family is said to be distinguished from the first two families by the opening of the male gonopore through the coxa of the second leg, a narrow telson, and the presence of a paronychium, but some of these characters are questionable. In the absence of well-developed diagnostic characters for several genera and species, the taxonomy and systematics of the group are poorly known. The Siphonotidae consist of about 12 genera with ca. 30 species distributed in South America, South Africa, Madagascar, SE Asia, Australia and Oceania. Here we propose a new genus with three species of the family Siphonotidae from the southern Western Ghats, the first record for the order Polyzoniida in the Indian subcontinent. The specimens were found inside a decaying piece of bark in a high altitude montane forest and were collected by hand. They are described here in detail using scanning electron microscopy. The new genus belongs to the tribe Rhinotini Hoffman, 1977, alongside the other two genera *Rhinotus* Cook, 1896 and *Siphonoconus* Attems, 1930. The gonopods of the new genus merely resemble two species of the genus *Rhinotus* from New Caledonia and the Seychelles, but differ from the other genera of the tribe Rhinotini in the bifurcation of the second podomere of the anterior telopod into two lamellae like processes. The phylogenetic relationship of the newly described Indian genus with other Siphonotidae remains to be further clarified, but other studies have shown the close biogeographic affinity between the Seychelles and the Indian Western Ghats.

The bryozoan genus *Reteporella*: morphospecies and contrasting population structure inferred from mitochondrial and microsatellite data

Baptista, L.^{1,2,3,4,5}, Berning, B.^{1,6}, Curto, M.^{5,7}, Waeschenbach, A.⁸, Meimberg, H.⁵, Santos, A.M.^{4,9} & Ávila S.P.^{1,2,3,4,10}

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The speciose phidoloporida genus *Reteporella* Busk, 1884, distributed worldwide, displays lace-like, three-dimensional colonies. The morphospecies are notoriously difficult to identify and taxonomic decisions are often hampered by the extreme variation of characters. In the remote Azores Archipelago (central North Atlantic), ten morphospecies have historically been reported, but diversity is thought to be distinctly greater. In this study, we performed phylogenetic reconstructions of Azorean *Reteporella* based on mitochondrial and microsatellite data, including some additional eastern Atlantic and Mediterranean representatives to put their evolution into perspective. The analysis revealed ten mitochondrial lineages, all supported by unique morphological characters. Of these ten lineages, only two – *R. tristis* and *R. atlantica* – match with taxa previously reported in the archipelago, the remaining being identified for the first time in this work. On the other hand, microsatellite data suggest locality-dependent admixture between different lineages, especially in deep waters, and the differentiation of shallow-water individuals of one species, *R. atlantica*. The discordance between mitochondrial and microsatellite results suggests the occurrence of ecologically-driven differentiation of *Reteporella* in the Azores Archipelago, which is a process that needs to be further explored.

Integrative description of three new species of giant pill-millipedes from Thailand

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Millipedes (Class Diplopoda) are one of the most species-rich groups of soil land arthropods and yet remain understudied in many parts of the world. Thailand harbors a species-rich millipede fauna, with over 240 species which have been described. Numerous Thai millipede species are microendemic to small calcareous outcrops. Among the most conspicuous millipedes of the Asian fauna are the giant pill-millipedes, which can roll up, forming a perfect sphere the size of a marble or a Ping-Pong ball. Here we describe three new species of giant pill-millipedes (order Sphaerotheriida), one species of *Sphaerobelum* and two *Zephronia* based on museum samples from Thailand using an integrative approach, combining light microscopy, scanning electron microscopy, CT scans and genetic barcoding. Our dataset includes published sequences of the family Zephroniidae from Thailand, Laos and Malaysia. In addition, we included genetic barcoding data of four recently described Thai *Zephronia* species, *Zephronia lannaensis*, *Z. phrain*, *Z. panhai*, and *Z. golovatchi*, together with new locality records. All new species are found to be genetically distant from other Zephroniidae from Thailand and surrounding countries showing uncorrected interspecific p-distances of >10 %. Both new *Zephronia* species are geographically, morphologically and genetically close to *Z. panhai*, but differ from the latter by >10% p-distance in the COI gene and numerous morphological characters. *S. meridionalis* is genetically and morphologically close to a recently described aberrant *Sphaerobelum*, *S. aesculus*, as well as an undetermined species from Malaysia, and might represent a genus different from *Sphaerobelum*. Virtual 'cybertypes' were created for the two new *Zephronia*. Our study, together with several publications in 2021, show how little we still know about the giant pill-millipede fauna of Thailand and other SE Asian countries.

A long-lasting story: To worm out the secret of "the feet" of Desmosomatidae Sars, 1897

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Our work follows the footsteps of Robert (Bob) Hessler, who was not only the pioneer in desmosomatid phylogeny, but who made a substantial contribution to asellote isopod taxonomy, systematics, and ecology as a whole. His illustrations of the first pereopod as desmosomatid central character (Hessler, 1970) put the first seed toward a desmosomatid phylogeny based on "the feet. There is little doubt about the close relationship of the asellote isopod families Desmosomatidae Sars, 1897 and Nannoniscidae Hansen, 1916, but the taxonomic position of a number of genera is so far unknown (Brix et al. 2021). Meeting Robert Hessler personally during the Deep-Sea Symposium in 2010, the discussion during the poster session changed the view of the first author on "the feet" as a valuable segregating character in desmosomatid systematics. Although more than 200 species in 32 genera have been described from all ocean basins, their phylogenetic relationships are not completely understood. Based on a combined morphological phylogeny using the Hennigian method with a dataset of 107 described species and a molecular phylogeny based on three markers (COI, 16S, and 18S) with 75 species (most new to science), Desmosomatidae and Nannoniscidae came out as separate families, but the concept of the subfamilies Eugerdellatinae Hessler, 1970 and Desmosomatinae Hessler, 1970 was not supported. Within both families, convergent evolution and analogies caused difficulty in defining apomorphies for phylogenetic reconstructions and this is reflected in the results of the concatenated molecular tree. There is no distinct biogeographic pattern in the distribution as the genera occur over the entire Atlantic and Pacific Ocean. Furthermore, poor resolution at deep desmosomatid nodes may reflect the long evolutionary history of the family and rapid evolutionary radiations. And while the data might provide some answers, the story has not yet come to a happy ending, as several genera appear to be para- or even polyphyletic and in need of revision.

References

- Brix, S., Held, C., Kaiser, S., Jennings, R. M., Driskell, A., & Brandt, A. (2021). Evolution and phylogeny of the deep-sea isopod families Desmosomatidae Sars, 1897 and Nannoniscidae Hansen, 1916 (Isopoda: Asellota). *Organisms Diversity & Evolution*, 21(4), 691-717.
- Hessler, R. R. (1970). The Desmosomatidae (Isopoda, Asellota) of the Gay Head-Bermuda Transect. *Bulletin of the Scripps Institution of Oceanography*, 15, 1–185.

On a mission: biodiversity conservation, natural science collections and global policy-making

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Currently, the post-2020 Global Biodiversity Framework (GBF) and its monitoring strategy are under intense development and discussion in preparation for their adoption by the Conference of the Parties (COP15-2) of the UN Convention on Biological Diversity (CBD) later this year.

Expert input submitted by bioDISCOVERY and GeoBon to the Secretariat of the CBD in January 2022 summarizes the conclusions drawn from today's scientific data and knowledge for policy-makers in the title of its report as "Transformative actions on all drivers of biodiversity loss are urgently required to achieve the global goals by 2050" (Leadley et al. 2022).

Policy-makers see a comprehensive, ambitious and actionable post-2020 GBF monitoring framework that is rooted in science as a key tool for guiding, driving and mainstreaming the required transformation. They welcome the contributions of scientists, have identified "very clearly" the importance of data and metadata, and hence the need for investments into monitoring at the local, national and global levels. The goal is a distributed and federated Global Biodiversity Observation System (GBIOS) for the collection of global reference data, similar to the climate reference network.

Starting out from an introduction to the CBD and science-policy advocacy, the presentation will show how the Digital Extended Specimen infrastructure can transform heterogeneous biodiversity information provided by a very diverse community of a multitude of providers with distinct interests and needs into actionable, harmonized digital data. Often mediated by natural science collections, these data then will need to enter in versatile formats and fit-for-use quality the CBD's data pathways via GBIF and additional global partners for transdisciplinary approaches to analyses, assessments and reporting of biodiversity conservation statuses and trends.

References

Leadley P, Krug C, Obura D, et al. (2022) Expert Input to the Post-2020 Global Biodiversity Framework - Transformative actions on all drivers of biodiversity loss are urgently required to achieve the global goals by 2050. 183 pp. Secretariat of the Convention on Biological Diversity, retrieved from <https://www.cbd.int/doc/c/16b6/e126/9d46160048cfcf74cadcf46d/wg2020-03-inf-11-en.pdf> (Feb. 18, 2022).

DNA Taxonomy of the Future — Harvesting Universal Metazoan-Level USCO Markers from Genomes for Species Delimitation and Identification

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Universal single-copy orthologs (USCOs) have recently been proposed and empirically tested as universally applicable markers for species-level taxonomy in animals. Here we report our insights from extensively testing the suitability of these USCOs for species delimitation and identification by screening a large number of metazoan genomes for USCO genes. We are able to show that USCO nucleotide sequences are sufficient for generating robust and reliable phylogenetic relationships ranging from phyla down to the level of closely related species and even populations. Using comparative genomics, we demonstrate that USCO genes are spatially distributed across the entire genome in various metazoan taxa. While the distribution is not completely random, they therefore representatively sample the genetic information. We tested how well USCOs allow delineation of species in three well-studied groups of arthropods and one group of vertebrates for which whole-genome data were available. With few exceptions, the phylogeny based on USCO sequences mirrored the current accepted alpha-taxonomy of the investigated taxa and the published phylogenies based on whole-genome data.

Shaping our taxonomic legacy through openly sharing primary biodiversity data in taxonomic revisions

Dikow, T.

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Taxonomy has a long tradition of describing earth's biodiversity. For the past 25 years or so, taxonomic revisions and monographs have become available in PDF format, which is regarded by most practicing taxonomists to be a good means of digital dissemination. However, a PDF document is nothing more than a text document that can be transferred easily for viewing among researchers and computer platforms. In today's world, traditional taxonomic techniques need to be met with novel tools to make data dissemination a reality, make species hypotheses more robust, and open the field up to rigorous scientific testing. Here, I argue that high-quality taxonomic output is not just the publication of detailed species descriptions and re-descriptions, precise taxon delimitations, easy-to-use identification keys, and comprehensively undertaken and illustrated revisions. Rather, high-quality taxonomic output embraces digital workflows and data standards to disseminate captured and published data in structured, machine-readable formats to data repositories so as to make all data openly accessible. Imagine that a taxonomist today has every original description and every subsequent re-description of a species at her/his fingertips online, has every specimen photograph produced by a previous reviser digitally available in the original resolution, and can take advantage of existing, openly accessible data and resources produced by peers in digital format in the past. When we as taxonomists provide such data, the future of biodiversity discovery will accelerate and our own taxonomic legacy will be enhanced. Cybertaxonomic tools provide methods to accomplish this goal and their use and implementation are here summarized in the context of revisionary taxonomy and monography from the standpoint of a publishing taxonomist. While many of the tools have been around for some time now, very few taxonomists embrace and utilize these tools in their publications. This presentation will provide a summary of the kinds of data that can and should be openly shared (e.g., specimen occurrence data, digital images, taxon names, species descriptions, authors) and outline best practices utilizing globally unique identifiers for specimens and data. A minimum standard for data-sharing is proposed, which, ideally, every taxonomist would follow and the highest data-sharing standard is established in order to make openly accessible every datum collected in revisionary taxonomy and monography.

NGS based approach to investigating systematics and biogeography of myrmecophytic *Macaranga* (Euphorbiaceae)

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Mutualisms and symbiotic associations are considered to be important drivers of biodiversity, especially in the tropics. Here, we take a small step toward unraveling the causes of extreme biodiversity in Sundaland by investigating the evolution of myrmecophytism, a plant-ant mutualistic interaction, in the pioneer plant genus of *Macaranga*. Previous attempts aimed at resolving the evolutionary relationships among myrmecophytic *Macaranga* using ITS sequences were largely fruitless, revealing little to no variation among species. In our study, we go a step further and exploit the technological advancements offered by next generation sequencing (NGS) to reconstruct and evaluate the spatio-temporal evolution of myrmecophytic *Macaranga* and their closest non-myrmecophytic species in order to elucidate how, where and when myrmecophytism originated in this group. Phylogenetic analysis based on genome wide GBS derived SNP data was largely successful in resolving evolutionary relationships at the species level in our study. The analysis revealed myrmecophytic *Macaranga* to be a monophyletic clade within the genus, while also establishing clearly demarcated clade boundaries of the three myrmecophytic taxonomic sections of *Pachystemon*, *Pruinosae*, and *Winklerianae*. Results from our biogeographic analysis unsurprisingly point to the island of Borneo as the birthplace of myrmecophytism in this genus given that this region has played a major role in harboring and preserving rainforests through the cooler and drier conditions of the Pliocene. With these results in hand, we hope to fill in some gaps in the knowledge of the extensive Southeast Asian biodiversity.

Premier assessment of the spider (Araneae) biodiversity found in South America

Dupérré, N.

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South America is the fourth largest continent on the planet; its birds, mammals, and amphibian's biodiversity is relatively well known, but no outright assessment of the continent spider (Araneae) fauna has been done to date. A first assessment revealed that the South American spider fauna comprises 83 families, 1018 genera, and 8302 species, representing 17% of the world spider fauna biodiversity; however, 94% of the spider-specific biodiversity is found nowhere else on earth. A total of 78 species have been introduced in South America, while 30 species were exported from the South American continent to other parts of the world. The South American continent comprises 538 endemic genera, while 315 genera are composed of species that occur strictly in SA and NA. Only 5% of the genera that occur in SA have a worldwide distribution.

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Diversity and gene flow within the European hermit crab *Diogenes pugilator* species complex (Crustacea: Anomura: Diogenidae) with the description / resurrection of species

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An adequate structural knowledge or estimate of regional biodiversity is of high importance when facing environmental risks, such as the loss of a variety of species. Therefore, we analyze phylogeographic structure within the European hermit crab *Diogenes pugilator* (Roux, 1829) (Crustacea: Anomura: Diogenidae), thereby recognizing and naming the comprised evolutionary significant units. The new findings are partly based on a previous study that detected high levels of genetic and morphological variation among populations, revealing the existence of a species complex (Almón et al. 2021). In the present study the foundations are laid for the revalidation of the previously synonymized name *Diogenes ponticus* (Kessler, 1860) for populations from the northeast Mediterranean and the Black Sea. Moreover, this work confirms the genetic separation described for three other distinct morphotypes from western Europe, which until recently were included in the same species. The analyses are based on three different genetic markers, the mitochondrial genes CO1 and 16S rRNA as well as the nuclear 28S rRNA, and resulted in a clear genetic separation of five clades. By combining molecular DNA categorization with subsequent morphological analyses, we were able to detect a concordance of molecular and morphological characters, indicating a longstanding evolutionary independence of the corresponding groups. In addition, we detected a high potential of intraspecific diversity within the here recognized Mediterranean species of *Diogenes*. Since in the marine environment, genetic variability and population genetic structure of a species are shaped by historical and contemporary marine barriers, this work also discusses possible geological and biological processes that may have caused the observed inter- and intraspecific divergence.

Incoherencies among morphological and molecular data on the rapidly radiating Gynoxyoid clade (Senecio, Asteraceae)

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The sunflower subtribe Tussilagineae includes a species-rich lineage of Andean mostly shrubs and trees, the Gynoxyoid clade. This group includes five genera which exhibit not only low genetic distances but also limited morphological differences. Previous morphological studies on this group are entirely based on a set of diagnostic morphological characters excluding any phylogenetic framework. In this study we aim to address hypotheses concerning the evolution of morphological characters previously used on traditional taxonomy studies. For this aim we included a phylogenetic backbone on complete plastid genomes of 21 species of the Gynoxyoid. Moreover, we evaluate the morphological characters on the remaining gynoxyoids to confirm their effectiveness as diagnostic characters. Our results suggest that some conventionally diagnostic characters are highly homoplastic and thus, ineffective for the delimitation of the genera of the Gynoxyoid clade. Based on the results of our analysis and on an extended evaluation of these characters on the remaining 164 species we suggest a delimitation of genera on a set of characters that display stability at supra-specific level and discontinuity at higher levels. An additional taxonomic revision includes a key for all genera, a nomenclatural revision, and a checklist of all species.

The LifeGate-project - a new weblocation for all living species

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The first map of all living organisms has been constructed to show the phylogenetic position and sizes of all major taxonomic levels (domain, phylum, class, order, family, genus and species). The map is available via a zoomable and searchable web application (www.lifegate.idiv.de). The data behind the map, the construction of the map, the content so far and the envisioned content will be explained. All interested researchers in biological sciences and especially those dealing with more than one species are asked to collaborate and complete the map.

CETAF – The Consortium of European Taxonomic Facilities

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CETAF is Europe's network of institutions that hold biological and geological collections. It represents the scientific community of taxonomy and biological systematics at the European level. CETAF was founded by ten European institutions in 1996 and since then has grown to include 71 institutions from 22 countries. Its main objectives are:

- To be the voice for taxonomy and systematics in Europe
- To promote scientific research and access to European collections
- To foster European cooperation and partnerships

In 2009, CETAF became a non-profit association seated in Belgium. It has developed a large number of activities initiated by its members whose experts engage in working groups addressing all major questions about collections, training and research based on taxonomy, and start projects and initiatives. CETAF's work programme is developed by an Executive Committee which is elected by the members. The work of CETAF is supported by the General Secretariat.

Three exemplary high-profile activities developed by the CETAF community shall be highlighted in the presentation:

The Distributed European School of Taxonomy (DEST), that has been founded under the EU-project EDIT (European Distributed Institute of Taxonomy), now under the umbrella of CETAF, offers training in taxonomy, which is urgently needed to face the decline of taxonomic knowledge.

The Distributed System of Scientific Collections (DiSSCo), as a research infrastructure in preparation which was approved as one of the Research Infrastructures of excellence for Europe under the ESFRI Roadmap update 2018, aims to provide unified (digital and physical) access to European Natural Science collections and corresponding data.

The Horizon Europe proposal TETTRIs (Transforming European Taxonomy through Training, Research and Innovations) is CETAF's community response to the call "BIODIV-01-02: Building taxonomic research capacity near biodiversity hotspots and for protected areas by networking natural history museums and other taxonomic facilities", by which the European Commission recognizes the crucial role of taxonomy in protecting biodiversity. In this first CETAF-coordinated proposal, the consortium aims to develop the knowledge and the systems for building taxonomic research capacity. Pilot activities will be funded to implement new concepts in the areas where taxonomic capacity is urgently needed.

Don't ask sengis for their age: Evaluating parameter impact on temporal calibration of Macroscelidea phylogenies

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Macroscelidea or sengis are small mammals endemic to Africa and consists of 20 extant species only. Together with aardvarks, hyraxes, elephants, sea cows and afrosericidans, they form the Afrotheria, the major clade of placental mammals with ancient African origin. Due to mostly cryptic morphological traits, biologist had a hard time disentangling the taxonomic relationships between most but not all currently known 20 species. Molecular evidence led to major systematic revisions of the morphology-based taxonomy. Until now, no sengi phylogeny based on molecular data of all species is available. In addition to this knowledge gap, in terms of time sengis' evolutionary history is still unclear. Two recently published studies come up with highly diverging age estimates and thus evolutionary scenarios of sengis. Both dating approaches are well justified but differ by the kind of data utilized (type of DNA, number of outgroups, number fossil priors).

By using mainly historical specimen and state of the art laboratory techniques like target enrichment and single-stranded DNA libraries, this study provides the first full species Macroscelidea phylogeny, based on concatenated nuclear and mitochondrial data. It further focuses on commonly varied parameters in tree dating approaches (type of DNA, ratio of ingroup to outgroup sampling, included fossil priors) and their impact on temporal calibration of Macroscelidea phylogenies.

Although focusing on a single group our results are of relevance for general application in tree dating. We show that even after correcting for substitution saturation the utilization of mitochondrial DNA results in much older ages than using only nuclear DNA. If outgroups and thus multiple fossil priors are included, the age of the sengi-crown fossil prior has minimal impact. The relative distance of nodes within the sengi phylogeny mainly depends on the type of DNA used. The number of outgroups included has a major effects on the time-calibration.

Biodiversity of free-living nematodes- exploring the tip of the iceberg

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While in many animal taxa the potential number of existing species is not so much higher than the number of described species, we clearly cannot state this in the Phylum Nematoda. Showing the example of one nematode family, Diplogastridae, I will report on the description of new genera and species which is still far from saturation. By exploring new areas and biological niches we have been able to discover diversity in forms and numbers that is mind blowing. Molecular methods for nematode characterisation paired with the possibility to keep nematodes strains alive in the laboratory to perform mating experiments and thus follow the biological species concept is a crucial prerequisite to bring modern taxonomy in nematology to the next level.

How dark of a taxon is Microgastrinae (Braconidae) really?

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Entire families and subfamilies of Diptera and Hymenoptera are referred to as so-called "Dark Taxa": They are hyperdiverse, taxonomically neglected and numerous unseen and undescribed species exist – even in Germany. For these groups, hardly any current identification keys exist, and often there are no taxonomic experts. In order to make these enormously species-rich groups more tangible to science, we use an integrative approach within the project GBOL III: Dark Taxa for the Microgastrinae, a subfamily within the Braconidae (Hymenoptera) and parasitoids of Lepidoptera larvae. Specimens were collected using a large number of malaise trap samples from various habitats in Germany, with a focus on alpine habitats as well as forests, but also urban gardens. Samples are sorted and individuals are selected for DNA-Barcoding by parataxonomists. Using DNA-Barcoding as a way of pre-sorting samples we are able to identify distinct clusters and lineages that putatively represent species. Finally, representative specimens of these clusters (which correlate with BINs) are morphologically verified by experts. Using this workflow allows us to accelerate taxonomic work and glance at results, even with morphological identifications still in the future. In this study, we examine how dark of a taxon Microgastrinae really is and explore ways to tackle this dark diversity.

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Using citizen science in the biodiversity research of Nudibranchia

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Traditional research methods can often provide only limited insight into the biodiversity of marine animals, as extensive habitat analyses require the collection of very large amounts of global-scale data. For instance, biodiversity research on nudibranch sea slugs is often impeded due to time and resource consuming diving trips. To facilitate scientific work by pre-identifying habitats in which target-species occur, citizen science could become a major improvement for the research on nudibranchs.

This exploratory study therefore investigated the extent to which questions about population size, distribution, diet, and adaptive strategies in Nudibranchia can be answered with the help of amateur divers. For this purpose, available photo and video sources from two social media platforms, Instagram and YouTube, were collected and analyzed.

Our results show that there are numerous people around the world who are interested in nudibranchs and share their images on the Internet, particularly on Instagram. When comparing the two platforms, Instagram performs significantly better than YouTube in terms of data quality and quantity. We were able to collect data on 42 species and to provide and confirm results on species distribution. Moreover, to a limited extent, information on the diet and on feeding was obtained. However, an estimation of the population size is not possible based on the collected data. Future studies with an optimized methodological set-up could process data on a larger scale and thus lead to more detailed results.

In summary, with guidance for the implementation of subsequent projects, citizen science has great potential for the study of nudibranchs and their biodiversity.

High quality genomes corroborate 29 chromosomes of the haploid *Hyles* (Lepidoptera: Sphingidae) karyotype and open wing pattern studies

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Taxonomy in the genus *Hyles* still relies largely on the forewing pattern of the adults. However, these patterns are discordant with molecular phylogenetic relationships. Therefore, we focus on understanding the underlying mechanisms, and the current work provides a basis for future studies. Karyotype analyses using FISH techniques revealed $n=29$ chromosomes and the WZ/ZZ sex chromosome system in *Hyles euphorbiae*. The measured genome sizes of *H. vespertilio* and *H. euphorbiae* are estimated with average 1C DNA values of 562 and 472 Mb, respectively. The *H. euphorbiae* genome was PacBio sequenced and amended by Hi-C illumina data yielding a 504 Mb assembly with an N50 of 18.2 Mb and 98% of the data being represented by the 29 largest scaffolds, corroborating the haploid karyotype. Hi-C data were also used for chromosome-level scaffolding of the published *H. vespertilio* genome (Pippel et al., 2020), resulting in a second assembly (651 Mb) with an increased N50 from 7.5 Mb to 22 Mb (again, 98% of the data in the 29 largest scaffolds represent chromosomes). The larger genome size of *H. vespertilio* is accompanied by a proportional increase in repeats from 45% in *H. euphorbiae* to nearly 55% in *H. vespertilio*. The three wing pattern genes, *wingless*, *optix* and *cortex*, are located on three different chromosomes in both species, *H. vespertilio* and *H. euphorbiae*.

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Phylogenetic distribution of traumatic insemination in Strepsiptera (Insecta)

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Traumatic insemination refers the mating practice of some arthropods in which the male pierces the female's integument with its intromittent organ for insemination. Twisted-winged parasites (Strepsiptera) are considered a prime example of an insect order whose species exercise this mode of copulation. However, while traumatic insemination in the Strepsiptera family Mengenillidae with free-living females is undisputed, its occurrence in Stylopodia with permanent endoparasitic females – comprising the majority of species in this insect order – has remained unclear. Rather, observations from a single study on *Xenos vesparum* (Xenidae) that questioned the role of traumatic mating for insemination in this species were generalized to be representative for all Stylopodia. Here we show that integration of data from various imaging methods provides convincing evidence for traumatic insemination being phylogenetically widespread (including extinct families) and the predominant mode of copulation in the insect order Strepsiptera. Specifically, we provide first-time evidence of injury wounds from traumatic insemination in species of Corioxenidae, Elenchidae, Halictophagidae and Xenidae. Using μ CT data to 3D-model the cuticle of copulating pairs of *Stylops ovinae* (Stylopidae) and *X. vesparum*, we additionally visualized the physical piercing of the female's integument by the male's penis in both species. Finally, we show in species of Mengenillidae, Xenidae, and Stylopidae that traumatic mating is associated with the injection of sperm in the female's hemocoel. The results from our study significantly alter our understanding of the reproductive biology of Strepsiptera. They imply that traumatic insemination has been the ancestral mode of copulation in this insect order and has been retained in most, if not all its extant families.

Provenienzforschung am Zoologischen Forschungsmuseum Alexander Koenig in Bonn

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Bisher wird die Provenienzforschung an Naturkundemuseen eher stiefmütterlich behandelt. Doch erst die Kenntnis der genauen Herkunft eines Exemplars, seiner Historie, sowie der damit unmittelbar verbundenen Person/en, die es „gesammelt“, präpariert, erforscht, abgebildet, aufbewahrt und/oder schließlich einem Naturkundemuseum übergeben hat/haben, führt dazu, dass aus einem beliebigen Vertreter einer Art ein Belegexemplar, also ein Unikat mit einer individuellen Geschichte wird. Diese Historie ist wiederum untrennbar mit der Biographie des Sammlers oder der Sammlerin verbunden, deren oder dessen Handeln in das zeitgenössische Geschehen eingeordnet werden muss. Während eines von der Museumspädagogik am Zoologischen Forschungsmuseum Alexander Koenig initiierten und durch die Alexander-Koenig-Gesellschaft finanzierten Projekts konnten im vergangenen Jahr 35 ausgewählte Präparate und Dermoplastiken aus den Ausstellungen auf ihre Provenienz hin untersucht werden. Das Ziel des Projekts ist es, die individuellen Geschichten und Hintergrundinformationen unter Hinzunahme verschiedener Quellen fundiert zu recherchieren und schriftlich festzuhalten, um sie zum Beispiel für (zukünftige) Museumsgruppenbegleiter zur Verfügung zu stellen. Die während des Projekts recherchierten Informationen über elf ausgesuchte Exemplare wurden zudem in Form von zusammenfassenden Texten, teilweise ergänzt durch historische Fotografien, in die Dauerausstellung des Museum Koenig integriert, um die besonderen Geschichten der gezeigten Exemplare für die Besucher verfügbar zu machen. Unter den ausgewählten Präparaten befindet sich etwa die berühmte Bundesgiraffe, welche 1913 vom Museumsgründer Alexander Koenig (1858-1940) aus dem heutigen Südsudan mitgebracht wurde und durch die Eröffnung des Parlamentarischen Rats im Museum Koenig am 1. September 1948 nationale Bekanntheit erlangte. Die kontextualisierte Auseinandersetzung mit sensiblen Sammlungsmaterial aus der Kolonial- und NS-Zeit soll zur öffentlichen Diskussion über die historisch belastete Provenienz naturkundlicher Sammlungen in Deutschland beitragen.

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Species delimitation of Hexacorallia and Octocorallia around Iceland using nuclear and mitochondrial DNA and proteome fingerprinting

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Cold-water corals build up reef structures or coral gardens and play an important role for many organisms in the deep sea. Climate change, deep-sea mining, and bottom trawling are severely compromising these ecosystems, making it all the more important to document the diversity, distribution, and impacts on corals. This goes hand in hand with species identification, which is morphologically and genetically challenging for Hexa- and Octocorallia. Morphological variation and slowly evolving molecular markers both contribute to the difficulty of species identification. In this study, a fast and cheap species delimitation tool for Octocorallia and Scleractinia, and order of the Hexacorallia, of the Northeast Atlantic was tested based on 49 specimens. Two nuclear markers (ITS2 and 28S rDNA) and two mitochondrial markers (COI and mtMutS) were sequenced. The sequences formed the basis of a reference library for comparison to the results of species delimitation based on proteomic fingerprinting using MALDI-TOF MS. The genetic methods were able to distinguish 17 of 18 presumed species. Due to a lack of replicates, using proteome fingerprinting only 7 species were distinguishable. Species that could not be distinguished from one another still achieved good signals of spectra but were not represented by enough specimens for comparison.

Therefore, it is predicted that with an extensive reference library of proteome spectra for Scleractinia and Octocorallia, MALDI-TOF MS may provide a rapid and cost-effective alternative for species discrimination in corals.

From DNA to ecosystems – The promise of biological archives for biodiversity monitoring

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Detecting the imprints of global environmental change on biological communities is a major challenge for current ecological research. The analysis of the effects of environmental change requires standardized and replicated time series data, which is lacking for most ecosystems and taxa. This lack of community level time series data has become particularly evident with recent reports on global insect decline. Natural history collections are currently receiving attention for their potential to document environmental change, but they usually do not provide community level data. Considering this background, new approaches and data sources are urgently needed to understand historical community change in the Anthropocene. Recent developments in high throughput DNA metabarcoding hold great promise to provide the needed data. The analysis of environmental DNA (eDNA), DNA traces left by organisms in their environment, has particularly revolutionized biodiversity research. eDNA is preserved in many biological archives, making it possible to trace taxonomic changes at unprecedented temporal detail. In my presentation, I will give an overview of our work using eDNA analysis in a large biological archive, the German Environmental Specimen Bank (ESB). In the past three decades, the ESB has compiled biotic samples from various ecosystems of Germany, including marine, limnic and terrestrial habitats. The samples are collected according to highly standardized protocols and permanently stored at ultra-low temperatures, which makes them an ideal source of historical eDNA. I will first highlight our recent work on the reconstruction of temporal changes in German forest insect communities from eDNA traces associated with ESB leaf samples. Then I will discuss other sources of community level eDNA in marine, limnic and terrestrial samples of the ESB and show preliminary results on community change in different taxonomic groups across the tree of life in the past 30 years.

Genotypic prediction of the phenotype? Testing the concept for the vomeronasal organ of non-model semiaquatic mammalian species

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The vomeronasal organ (VNO) is the sensory organ of the vomeronasal system, which is involved in the detection of pheromones. The VNO is reduced or absent in some mammalian taxa e.g. some bats and whales. In a previous study the gene *Trpc2*, a marker gene for VNS functionality, was found to be inactivated in the semiaquatic Phocidae and Lutrinae (Hecker *et al.* 2019). In this study we investigated the anatomy of the vomeronasal system of *Lutra lutra* and *Phoca vitulina* to test if this genetic inactivation is reflected in a reduction or absence of the VNO and consequently if the genotype allows a prediction of the phenotype. For the investigation of the specimens we used diceCT, consequently all specimens were stained with iodine solution, μ Ct scans were acquired and 3D models of the VNO were created. We found a reduction of the vomeronasal organ in *Lutra lutra* and absence of the VNO in the specimen of *Phoca vitulina*. To test if this reduction is influenced by the semiaquatic lifestyle or by phylogeny, we included specimens of the coypus (*Myocastor coypus*) and muskrat (*Ondatra zibethicus*) and found the VNO of both species to be present and well developed. Therefore, the reduction of the VNO is possibly more influenced by phylogeny than by the semiaquatic lifestyle. Moreover, the results show that the reduction of the VNO indicated by the genotype, respectively the inactivation of *Trpc2*, is reflected in the anatomy and the genotype allows a prediction of the phenotype. These results might be helpful to gain insights in the anatomy of rare and difficult to study species in the future.

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The evolution of Zoraptera (Insecta)

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Together with Dermaptera, Zoraptera is the first split among the polyneopteran orders. To understand the evolution of Polyneoptera, accumulating more knowledge on zorapteran species is essential. However, in comparison to Phasmatodea and other related groups, there are still large gaps of information. Based on a broad taxon sampling from all continents where the group is known we conducted the first species level phylogeny, using partial sequences of 18S rRNA, Histone 3, 16S rRNA, and 12S rRNA genes. The resulting phylogenetic trees show that Zoraptera is divided into three major clades, and that two of them are composed of species distributed on different continents. The monophyly of these clades is at least partly supported by shared derived morphological features. The divergence age estimation and ancestral distribution area reconstruction unveiled an ancient origin and early radiation initiated in the Permian. The plate tectonics theory suggests that the present distribution of Zoraptera was mainly established by vicariance, rather than dispersal. The three major clades likely originated on the Pangaea supercontinent, or alternatively on the Gondwana and Laurasia supercontinents. Their ancient origin explains previously found conspicuous interspecific divergence variation of the spermatozoa morphology, genital apparatus, sperm structure, and mating behavior, in striking contrast to a highly conserved general body morphology. We also compiled data of available reproductive features and reconstructed the character evolution. Although homologies in the genital character system are not fully established yet, the analyses revealed repeated acquisitions and/or losses of a hyper-elongated intromittent organ, mating hooks, and tergal protuberances. We will discuss desiderates and introduce a part of our latest projects aiming at a better understanding of the evolution of Zoraptera.

Processes of evolutionary diversification in *Aeonium* (Crassulaceae), the most species-rich plant genus of Macaronesian endemics

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Oceanic archipelagos are regarded as natural laboratories for the study of evolution and hold a wealth of examples of endemic plant radiations. The Canary Islands form an archipelago in the Macaronesian floristic region and have a rich history of botanical research. The most species-rich and ecologically diverse plant radiation (largely) endemic to the Canary Islands is the *Aeonium* alliance (Crassulaceae). We studied the biogeographical and ecological setting of diversification processes in *Aeonium* on the basis of a well-sampled and supported phylogeny inferred using a modified ddRADseq approach. Our results show that *Aeonium* is one of few examples of island radiations that successfully re-colonized the continental mainland twice, probably owing to its preference for competition-poor habitats. Founder-event speciation by migration from one island to another and sympatric speciation within single islands were inferred to have taken place in equal parts, underpinning the importance of geographic isolation as well as ecological speciation in island radiations. Furthermore, in lineages that diversified within single islands, morphological and ecological divergence was more pronounced than in lineages with frequent allopatric speciation. Finally, those islands that were found to have the longest continuous history of colonization by *Aeonium* also had the lowest percentages of co-occurring and hybridizing taxon pairs (relative to the number of possible combinations of any two taxa) when compared to islands that received *Aeonium* taxa more recently, indicating a higher degree of ecological differentiation and reproductive isolation between taxa after longer periods of sympatric evolution.

DigiTiB - a teaching tool for the training of taxonomists

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Knowledge of species and species identification are usually taught in the context of practical exercises using collection material or on field trips. However, the availability of material as well as the access to specimens to be identified outside the contact time of such practical exercises can be limiting. We would like to close this gap with DigiTiB.

DigiTiB is designed as a learning and teaching platform that allows virtual and detailed access to numerous species. The platform is divided into different areas including a species lexicon, a training module and a course administration, allowing different approaches to convey and train individuals in the process of species identification. Species are identified using conventional identification literature, such as dichotomous keys, and the result can then be checked in the training module. If the determination is correct, information on the biology of the respective family and/or species appears immediately. Functionally, the extensive image gallery with the so-called superzoom function is of central importance. The images can be greatly enlarged, allowing the recognition of all features relevant to the determination process. For selected groups, additional 3D models created with a photogrammetric method are implemented and interactively linked to the underlying images.

Origins of mountain plant biodiversity

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Comparisons of the plant biodiversity found on mountains have fascinated natural scientists for a long time. Early explorations led to the observation that vegetation and abiotic parameters vary along elevational gradients. Back in the early 19th century, it was already speculated that the biotic and abiotic world would also have possibly shared a common history and could have evolved in concert. The “geobiodiversity” concept appreciates this connection and the increased interest in the union of biological and geological sciences to study the evolution of biodiversity and geodiversity in a common framework. In my talk, I will present insights from recent studies, providing a global comparison of mountain geodiversity and vascular plant diversity, looking both at short-term (ecological) as well as long-term (evolutionary) processes. I will highlight that the complexity of plant evolution in mountain systems is not only determined by contemporary abiotic and biotic factors, but also influenced by historical factors, which need to be better integrated. In addition, the role of mountain topography in affecting species distributions, and the dynamics of speciation and extinction, under climate change need to be considered.

Connectivity of deep-sea basins in the North Atlantic using invertebrate taxa as surrogates – preliminary results

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Estimates of population connectivity are essential to understand the physical and biological processes which shape patterns of genetic variation. The extent to which populations are connected is mainly determined by larval dispersal and post-settlement processes that have a direct effect on the fitness of the recruits (Etter and Bower, 2015). By means of an integrative taxonomic approach, we aim to generate a comprehensive understanding of invertebrate species diversity across adjacent deep-sea basins in the North Atlantic as well as to study their distribution, connectivity, and population dynamics along the Mid-Atlantic Ridge (MAR). The focus will be laid upon species from four taxa which have developed different modes of locomotion and reproduction. These are Cirripedia (sessile spawners), Isopoda (mobile brooders), Bivalvia (sessile brooders and spawners), and Polychaeta (mobile spawners). Material of all taxa, collected on expeditions of the IceAGE (Icelandic Marine Animals: Genetics and Ecology) and IceDivA (Icelandic Marine Animals meets Diversity along latitudinal gradients in the deep sea of the Atlantic Ocean) projects, will be studied by means of an integrative taxonomic approach, combining morphological identification with DNA sequencing, 2bRAD, and proteomics. Assuming that the overall population structures are driven by similar abiotic and biotic factors, we hypothesise that taxa with planktotrophic larvae will show a larger bathymetric range compared to brooding species. Occupying similar habitats across and within deep-sea basins of the MAR, the connectivity and distribution pathways of all four taxa can be investigated comparatively, helping to better understand the patterns of genetic variation in the deep of the North Atlantic Ocean. Here, we present preliminary results on the first taxon of our study, the balanoid cirriped *Bathylasma hirsutum* (Hoek, 1883). The species is distributed along the MAR in the north-east Atlantic, ranging from the Faroe Islands to the Azores with a depth range of 703 to 1635 meters. During the IceAGE_RR research expedition in 2018, *B. hirsutum* was discovered in high densities, in close proximity and downstream to an until then undiscovered hydrothermal vent field on the Reykjanes Ridge. Considering that the species is known to grow in smaller assemblages only, we hypothesise that *B. hirsutum* is opportunistically utilising the downstream nutrition flow generated by hydrothermal venting, enabling the species to grow both larger and in higher numbers.

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FörTax – First Project Year Activities and Preliminary Results of the Inventory

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The main objective of FörTax is to promote taxonomic knowledge as a basis for nature conservation in order to counteract the erosion of taxonomy and species knowledge in various fields of application. FörTax is part of the Federal Biodiversity Programme, funded by the BfN and BMUV over a period of six years.

Since the project was launched in September 2020, numerous measures have been initiated. For example, new training opportunities have been created for future taxonomists and species experts of different ages and levels of expertise, covering different taxonomic groups. The courses are continuously evaluated. In addition, the first FörTax conference (FörTaxCon), took place in November 2020 with an overwhelming response.

Moreover, an inventory is being conducted nationwide. One task is to record and analyse the existing educational offers on taxonomy and species knowledge in order to identify best practice examples. The inventory is currently being deepened with a mini-survey to identify as many taxonomists and species experts as possible who are engaged in training and mentoring. The first results of the mini-survey will be presented.

The formation of a strong network of stakeholders for a long-term strengthening of taxonomy and species knowledge at all levels in Germany is another important goal of these measures.

Visual Allometry in Earwigs

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Vision is the primary sense used by many animals for foraging, mating, hunting, flying, navigation, and detection of predators and conspecifics. Compound eyes are the dominant eye type among arthropods. Due to their design, there is an inherent trade-off between resolution, the ability to resolve spatial detail, sensitivity, the ability to see in the dark, and field of view, the extent of observable area imaged by the eyes. However, how this constraint varies with eye size remains largely unknown. Here, we show that earwigs with bigger eyes have better sensitivity as well as better resolution, with only a slight increase in field of view. We used micro-computed tomography (micro-CT) to calculate ommatidial sizes, interommatidial angles, eye surface areas, and the size and direction of the visual field in 109 species across the phylogeny of earwigs (Dermaptera). An increase in eye surface area, correlates with increased facet sizes, and facet numbers whereas the interommatidial angle decreases, all with slightly negative allometries with respect to head size (measured as centroid size). Additionally, we show that earwigs with larger body lengths have larger heads and larger eyes. Our results demonstrate how earwigs with larger eyes invest primarily in increasing resolution by enlarging the individual facets, decreasing the angles between them, and increasing their number, followed by a slight investment into increasing eye sensitivity. It is likely that this investment into increasing sensitivity as well as resolution helps these mainly nocturnal insects to orient themselves in the dark, whereas their concealed habitats in cracks and crevices likely explain their low investment into increasing the field of view.

Mitogenomics in Hyles moths: Relationships of Central Asian *H. hippophaes* and *H. chamyla*

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The western Palaearctic species of the hawkmoth genus *Hyles* (Lepidoptera: Sphingidae) have long been the subject of molecular phylogenetic research. However, much less attention has been paid to the taxa inhabiting the central and eastern Palaearctic, particularly Central Asia, where almost 50% of the species diversity of the genus occurs. One still unresolved group of species includes *Hyles hippophaes* and *Hyles chamyla*. Despite a largely overlapping morphology and ecology, a plethora of infraspecific taxa display some unique divergent characters over a wide geographical area. We undertook a taxonomic assessment of each population and resolved this species complex using an integrative approach by testing the three main phenotypes—*bienerti*, *chamyla* and *apocyni*—in terms of their morphological, mitochondrial and biogeographical integrity, and to elucidate their evolutionary relationships.

Ecological effects of marine extinctions: from the Pliocene to the Anthropocene

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The fossil record of the marine megafauna, the largest animals in the oceans, has revealed that in the Pliocene (~3Ma), habitat loss caused the extinction of one third of their genera, along with nearly one fifth of their functional diversity. Such a level of ecological loss contrasts with the almost negligible changes after the (mass) extinction of benthic invertebrates around the same time. Unlike the marine megafauna, small invertebrates can share similar ecological traits and thus be highly redundant and ecologically resilient in the face of extinction. The much larger marine megafauna, on the other hand, tends to be functionally unique and therefore highly vulnerable. Given that the Pliocene extinction left the marine megafauna functionally depleted, how will they respond to the current extinction crisis? Forty percent of marine megafaunal species are currently threatened. Simulated extinction scenarios forecast this could result in the loss of up to half of their ecological functions. Sharks, in particular, show greater-than-expected losses of functional diversity. Biogeographic analyses further indicate that megafauna functional richness is globally greatest along the tropical continental shelf and oceanic island environments. Meanwhile, high latitudes harbour the most functionally unique species. The protection of these areas could therefore help safeguard the key ecological functions these organisms play in marine ecosystems.

Morphological disparity of phytophagous scarab beetles in the light of species diversity at different ecochorological scales

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Evolutionary success of lineages becomes visible by species diversity or morphological disparity, but both phenomena appear being not necessarily correlated. High diversity may be linked with low or high morphological disparity, or low diversity combined with low or high morphological disparity. However studies on comparative morphospace disparity in relation to diversity from regional scale to local scale considering different components of landscape and comparing multiple sites are not known to us.

We explore here multiple tropical assemblages of phytophagous scarab beetles (Coleoptera: Scarabaeidae) in Sri Lanka and infer their pattern of morphospace, body size and species diversity along various spatial and ecological scales (i.e., regional to local scale), such as forest types, elevation zones, and collection site. Morphospace disparity was analysed for three different organismal systematic levels, in order to explore the impact of different systematic levels: for 1) all pleurostict chafers (i.e., the entire assemblage), 2) for Sericini only, and 3) for the part of the pleurostict chafers excluding Sericini.

The relation disparity versus species diversity followed two distinctive patterns, one for the entire assemblage (full or partial, i.e., Pleurosticts and Pleurosticts excluding Sericini), and one for the selected narrower lineage, Sericini. For size-corrected (i.e. log-normalized) data we found a significant correlation between diversity and disparity between different forest types and elevation zone, for all pleurostict chafers and also for pleurosticts excluding Sericini, but not for Sericini. The opposite was the case for the different sampling locations in which Sericini showed significance while the entire assemblage not, and neither pleurosticts excl. Sericini. For uncorrected raw data this tendency was similar, but less pronounced. Considering the body size variation of the entire assemblage of herbivore scarabs was observed shrinking towards higher altitudes being linked paralleled by the decrease of species diversity and morphological disparity.

Anthropogenic influence shaped the population genetics patterns of the Greater Periwinkle (*Vinca major* L., Apocynaceae)

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Since the Neolithic period numerous crop plants together with their associated weeds have been spread around the world by humans. In later epochs, exotic ornamental plants were also frequently brought to other, non-resident regions. Some of these species have become naturalized in the wild and are now part of the local flora. A few of the alien newcomers proved to be highly competitive and acquired the ability to displace native plants from their natural habitats. These-so-called ‘invasive’ species can have a fatal impact on biodiversity. Therefore, it is an important question under which circumstances and genetic conditions a non-resident species can switch from a harmless immigrant to a harmful invader.

In the present study, we address this question through a population genetic analysis of the Greater Periwinkle (*Vinca major* L., Apocynaceae). This species is native to the Mediterranean but has been introduced by humans to other areas around the globe. While *V. major* has become established as a “well-behaving” immigrant in many parts of Western and Central Europe, it developed an invasive behavior in the USA, Australia, and New Zealand. For our analyses, we used nine nuclear microsatellite markers to genotype a total of 1901 individuals from 120 *V. major* populations collected from the wild. Plants were sampled from various countries of Southern, Western and Central Europe as well as from parts of the USA, Australia, and New Zealand. The dataset was partitioned for the analysis in three different geographical areas: (1) in the natural distribution range (Western Mediterranean), (2) in areas where this species is considered as harmless immigrant (Central and Western Europe), and (3) in areas where *V. major* has developed an invasive behavior (USA).

In general, the highest levels of genetic diversity were found in the autochthonous distribution range of *V. major*. Diversity indices decreased in the allochthonous area where clonal growth was more commonly observed. In those areas where *V. major* is nowadays classified as invasive, clonal growth even became the predominant mode of propagation, and almost all the sampled localities harbored only one single fixed genotype. Unexpectedly, the genetic diversity of populations from Great Britain is comparatively higher for a region of the allochthonous range. Taken together, our results indicate a strong reduction in the gene pool of *V. major* and a strong tendency to develop a clonal growth pattern especially in populations sampled from the invasive range.

KennArt - A nationwide initiative for the training of taxonomists

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The number of taxonomists has been decreasing for several years. Within the joint project "KennArt - A nationwide initiative for the training of taxonomists", the NABU Nature Conservation Station Münsterland and the Center for Biodiversity Monitoring and Conservation Science (LIB) want to counteract the downward trend. Until 2026, basic, intermediate and advanced courses on 5 groups will be developed. Basic courses on grasses, mosses, hymenoptera and beetles took place in Münster and Bonn in 2021. Advanced courses on dragonflies and all other groups are planned for 2022 and the following years. At the beginning of the project 2020 we conducted an online survey to analyze the need for taxonomy courses. More than 2400 interested people from all federal states in Germany took part in the survey.

We will present the outcomes of the survey and the structure of our first courses. The feedback from the courses and the analysis has shown that the demand for taxonomic courses is high. The goal of the KennArt project is to start at this point and develop courses on species taxonomy and ecology.

Molecular phylogenetic and morphological analyses question current taxonomy of Indo-West Pacific porcelain crabs (Decapoda: Anomura) with emphasis on the genus *Petrolisthes*

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Porcelain crabs are best known for their characteristically easy shedding of limbs, when in danger. This highly diverse family of anomuran crabs (Crustacea: Decapoda) mostly occurs in temperate and tropical oceans worldwide. Nevertheless, the Porcellanidae remain poorly explored until today, including their phylogenetic relationships. This family currently consists of 40 genera, with *Petrolisthes* Stimpson, 1858 being the largest one with 112 valid species. Ortmann (1897) subdivided the genus *Petrolisthes* into five groups based on morphological characters. In the present study, molecular phylogenetic results based on 26 specimens of three taxonomic groups of *Petrolisthes* from the Red Sea and the Indo-West Pacific partly confirm Ortmann's morphological division. Our phylogenetic trees were constructed based on parts of the mitochondrial 16S rRNA-NADH1 gene complex and the nuclear 28S rRNA gene, including several DNA sequences retrieved from GenBank. *Petrolisthes kranjiensis* Johnson, 1970 and *Petrolisthes teres* Melin, 1939 hold a very basal position in the phylogenetic tree, and definitely should not form part of the genus *Petrolisthes*. Most likely, they belong to the genus *Novorostrum* Osawa, 1998 instead. In the case of *Petrolisthes pubescens* Stimpson, 1858, we uncover taxon lumping based on molecular and morphological results, and thus underestimation of real diversity. With this study we contribute to the phylogenetic understanding of porcelain crabs from the Red Sea and other parts of the Indo-West Pacific and relating them to already known data from the Americas. However, further investigation on a much broader level and inclusion of many more species is essential for gaining a better understanding of intergeneric evolutionary relationships and for a more precise estimate of species numbers.

Discovery of a cryptic species among samples of one of the most common European vespid wasps, *Polistes dominula* (Hymenoptera: Vespidae)

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The vespid wasp *Polistes dominula* (Christ, 1791) is an established model in sociobiological research and for understanding neozoic invasions. Previous investigations revealed that its mitochondrial (mt) genomes belong to two distinct haplotype groups that are phylogenetically paraphyletic in respect of *Polistes bucharensis* Erichson, 1849. Whether wasps with mitochondria from the two haplotype groups are reproductively isolated from each other has remained unknown, however. Using a Pool-Seq approach for genome-wide screening of single nucleotide polymorphisms in combination with a comparative analysis of cuticular hydrocarbon (CHC) profiles, we show that *P. dominula* with different mt haplotypes sampled at locations in Southern Germany, where wasps with different mt haplotypes occur syntopically, exhibit fixed differences in more than 17,000 sites of their nuclear genomes and show indications of distinct CHC profiles. However, we also discovered few samples that could represent hybrids, indicating that a reliable group assignment requires a multi-marker approach. Our results indicate that *P. dominula* represents a conglomerate of two biological species. Screen for *Wolbachia* nucleotide sequences in the Pool-Seq data suggests that the two species differ in their infection status, which could contribute to the observed reproductive isolation. The remarkable diversity in ecological, behavioral, and phenotypic traits previously attributed to *P. dominula* could reflect species-specific differences between the two species that may be genetically investigable in the future by means of cross experiments.

Diversity of Symbiodiniaceae in Cladobranchia and the Microbiome of the aeolid nudibranch *Berghia stephanieae*

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With around 1000 described species, Cladobranchia (Heterobranchia, Gastropoda) is a highly diverse taxon of nudibranch gastropods. They are known for their striking colouration and effective defence mechanisms such as the incorporation of nematocysts in special cnidosacs at the tip of their cerata as a result of losing their protective shell. In addition, some cladobranch species established a symbiosis with dinoflagellates of the family Symbiodiniaceae and for some of these photosymbiotic species, such as *Melibe engeli* Risbec, 1937 and *Phyllodesmium briareum* (Bergh, 1896), it was shown that the photobiont can fully support the host during periods of starvation. Although a lot is known about the mechanism of photosymbiosis in cnidarians, marine slugs have been neglected in this regard. Especially the Symbiodiniaceae clades and species involved in this symbiosis are still not characterised. Determining the Symbiodiniaceae found in different cladobranch species can help to improve the understanding of this photosymbiosis. In corals, for example, growth rate, temperature tolerance or disease susceptibility are related to the subclade type of the photobiont. Here we give new insights into cladobranch associations with Symbiodiniaceae by sequencing regions of the Symbiodiniaceae ITS rDNA of a diversity of cladobranch species using Next Generation Sequencing (NGS). Further we investigated the stenophag cladobranch species *Berghia stephanieae* (Valdés, 2005) that feeds exclusively on the sea anemone *Exaiptasia diaphana* (Rapp, 1829) regarding its bacterial community. While the microbiome of Cladobranchia has long been overlooked, studies on other photosynthetically active marine animals such as corals and sponges show the importance of microorganisms, since the host depends on the bacteria for phosphorous fixation, contribution to carbon and sulphur cycling or metal homeostasis, among others. Here we analysed the microbiome by metabarcoding of the bacterial 16S rRNA gene of freshly fed *B. stephanieae* under different one-week starvation conditions (low light, high light and dark).

Evolutionary phenomics: emerging tools for semantic species description and ontology-informed phylogenetic methods

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Analyzing phenotypes is central to much of the research in biology. In biosystematics, phenotypes are used for describing species and characterizing their evolutionary history, as well as reconstructing ancestral organisms that existed on Earth in the past. Although accumulating rapidly through species descriptions and character matrices, phenotypic data derived from different sources, unlike molecular ones, are challenging to compare and analyze, which impedes phenomic-scale research in biology. This happens because organismal anatomies (=phenomes) have complex hierarchical structure (e.g., digits are parts of limbs which, in turn, are parts of body), while anatomical entities have diverse semantic qualities (e.g., shape and coloration of digits and limbs), which are largely neglected by available approaches. Both complex anatomical systems and their semantics can be modeled using ontologies – computer-understandable representation of domain knowledge (e.g., anatomy), with well-defined terms and relationships. The application of ontologies to biosystematics is recent but extremely promising (Yoder et al. 2010; Mungall et al. 2012; Balhoff et al. 2010; Dececchi et al. 2015; Mabee et al. 2018). However, biology is still broadly lacking ontology-driven methods to unlock the hierarchical and semantic information encoded in phenotypes for evolutionary inference.

In this talk, I will explore two emerging tools designed to stimulate the phenomic-scale research in biology. One tool is the new language PhenoScript that aims at providing a user-friendly environment for writing computer-parsable semantic species descriptions and automatic species comparison. Another tool is the R package PARAMO that implements ontology-informed phylogenetic methods for reconstructing dynamics of entire ancestral anatomies. At the end, I will discuss how future developments in ontology-driven approaches can change the way we analyze and represent phenotypic data.

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What is the IceDivA project? Research expeditions and science in the face of Covid-19

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During the Covid-19 pandemic research fleets were docked the World over. To keep their research fleet running, Germany issued emergency “Pandemia calls” for research expeditions to embark and disembark in Emden, Germany. As an answer to these calls the “**Icelandic marine Animals meets Diversity** along latitudinal gradients in the deep sea of the **Atlantic Ocean**” (IceDivA) project was born. This project focuses on abyssal plain communities east and west of the Mid-Atlantic Ridge, as well as planktonic communities throughout the water column. By sampling Northwest and Northeast Atlantic deep-sea basins, IceDivA aims to extend the previous Northeast Atlantic deep-sea program, IceAGE (Icelandic marine Animals: Genetics and Ecology), also linking with the South Atlantic deep-sea programme DIVA (Latitudinal Gradients in BioDiversity in the deep Atlantic), as well as those in the Southern Ocean, providing pan-Atlantic deep-sea samples to investigate topics regarding species richness and evolution. To map the species diversity, and answer questions on the connectivity of deep-sea fauna along latitudinal gradients in the pan-Atlantic Ocean, we sampled in 3,000 m to 5,500 m water depths bridging the Atlantic knowledge gap between prior expeditions. Here we will present an overview of the IceDivA project, including: the narrative of two research cruises; IceDivA1 (08.01-07.02.2021) and IceDivA2 (05.11-09.12.2021), participation in the UN Ocean Decade, ongoing research, preliminary results, and the outlook for the project.

Horizon Europe – Opportunities for Organismic Research

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The Horizon Europe framework program provides funding opportunities for research with a total budget of 95.5 billion euros until 2027. How to find “your” way through the framework, what promising opportunities does it offer within the next two years and where to find support and information will be highlighted in this talk.

The current funding framework is broken down in three pillars and combines excellency in science programmes (pillar 1) through the European Research Council or Marie-Sklodowska- Curie Actions, with a political aspect, addressing global challenges (pillar 2) as well as innovations for Europe (pillar 3). The three pillars are complemented by actions for the development of the research ecosystem by widening participation and spreading excellence. Half of the entire budget under Horizon Europe is directed to pillar 2 and its six clusters. Cluster 6 is of particular interest for ecological and organismic research and broadly addresses “bioeconomy, food, natural resources and environment”. Specific calls are released for two years respectively and follow clear missions and desired outcomes. The role of basic research and taxonomy in particular has been specifically acknowledged in the 2022 call “BIODIV-01-02: Building taxonomic research capacity near biodiversity hotspots and for protected areas by networking natural history museums and other taxonomic facilities”. Further political engagement of the scientific community is necessary, to advise and inform the EC about the crucial role of biological systematics as a foundation for securing biodiversity and healthy ecosystems, so that future funding will be directed appropriately.

References

<https://ec.europa.eu/info/funding-tenders/opportunities/portal/screen/home>

Bizarre morphology in fossil bugs (Insecta: Heteroptera: Pentatomidae) from the Eocene

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Two species of fossil bugs (Insecta: Heteroptera: Pentatomidae) from the Eocene of Messel (Germany) and Green River (North America) exhibit a bizarre and exaggerated morphology with prominent spines at the pronotum and the abdominal margin.

This extreme morphology can serve as defence against small vertebrate predators, such as birds or reptiles, but it also produces a disruptive visual effect and so provides camouflage.

The morphology of these fossil bugs resembles that of bugs belonging to the Triplatygini, which today occur exclusively in Madagascar, as well as that of Discocephalinae or Cyrtocorinae, which today occur in the Neotropics. Due to a lack of conclusive characters, it cannot be excluded that the fossil species may represent a case of remarkable convergence and are not related to either taxon. Phylogenetic analyses confirm that the new genus is a member of Pentatomidae, but its phylogenetic relationships within Pentatomidae remain unsolved.

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Repeated evolution of extreme locomotor performance independent of changes in extended phenotype use in Austral brown spiders (Amaurobioidea)

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Many animals utilize self-built structures – so-called extended phenotypes – to benefit or enhance body functions, such as thermoregulation, prey capture or defence. Yet, it is unclear whether the evolution of animal constructions extends or replaces body functions. Using the diverse clade of Austral brown spiders as a model system, we explored if the evolutionary loss and gain of webs as extended prey capture devices correlated with changes in locomotor performance and leg spination – both functional traits associated with prey capture. For this purpose, we combined the reconstruction of the first phylogenetic tree of the marronoid clade of spiders using UCE target sequence capture, with the assembly of kinematic, morphological and ecological data. We found that in this group extreme locomotor performance with running speeds of over 100 body lengths per second evolved repeatedly – both in web builders and cursorial spiders. Neither running speed nor leg spination was highly correlated with the use of extended phenotypes – each of these traits showed mosaic, independent evolutionary patterns. This indicates that the use of webs does not reduce the selective pressure on body functions involved in prey capture.

A comprehensive and systematic revision of the internal anatomy of leather urchins (Echinoidea: Echinothurioida)

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From other sea urchins (Echinodermata: Echinoidea) the so-called leather urchins (Echinoidea: Echinothurioida) are differentiated by the presence both of a flexible test and hollow spines. The plates are fused into groups of three that overlap with the next set of plates; both are connected via a flexible membrane. In most echinothurioid species, primary or secondary spines carry poison glands that can inflict significant harm when touched without protective equipment - a property that is signified by the colloquial term "fire urchin". Representatives of the Echinothurioida can be found in all oceans of the World, but are composed almost exclusively of inhabitants of deep-sea benthic habitats. Due to the flexibility of their test and the sampling techniques conventionally used for deep-sea organisms, echinothurioid specimens in scientific collections frequently are not in good shape. This aspect - in combination with sea urchin scholars' traditional focus on hard-part anatomy - has resulted in a significant knowledge gap with regard to echinothurioid internal anatomy. Thus, the present study aims to provide the first comprehensive overview of major internal organ systems in this group of enigmatic deep-sea echinoids. Using rare, exceptionally preserved representatives from all eleven extant echinothurioid genera (incl. the elusive *Hemiphormosoma paucispinum* and *Paraphormosoma alternans*) obtained from several collections, a systematic overview of the morphology of the digestive tract, Stewart's organs, water vascular system, Aristotle's lantern as well as further internal structures is given. In addition to standardized dissections and high-resolution photography as well as (contrast-enhanced) micro-computed tomography scans of selected internal organs, stomach contents were screened to provide additional evidence on leather urchin feeding habits. Furthermore, all previously published descriptions and drawings of echinothurioid soft parts were integrated into this study to broaden the range of species analyzed, resulting in the first comprehensive and systematic revision of leather urchin internal anatomy. The implications of this study for echinothurioid and echinoid systematics are discussed and potential avenues for future research on echinothurioid systematics and ecology are proposed.

Changes in wild bee communities over 100 years in relation to land-use change: A case study in Eastern Austria

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The wild bee community of the sand steppe habitat in "Oberweiden", a 120-hectare large protected area in Eastern Austria, was surveyed in the years 2018 and 2019 and complemented with historical bee data from literature and databases from over 100 years. The area is known for its unique fauna and flora since the end of the 19th century. In total, 297 bee species were recorded in the area. During the timespan 1900–1952, 228 species were documented, while only 120 species were detected between 1998 and 2021; forty bee species occurred in both periods. Thirteen species that used to occur in the area, are now considered extinct in Austria (Kratschmer et al. 2021). Thirty-eight species were recorded in the area for the first time in the period 1998–2021. Changes in species composition are analysed in relation to land-use change using historical aerial photographs since the 1960ies. Further, the impact of other possible drivers (e.g., management of the area) will be discussed in the light of the observed changes in bee community.

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