

**Program and Abstracts of the
22nd Meeting of the GfBS
(Gesellschaft für Biologische Systematik)**

**Online Conference of the Society for Biological Systematics 2021
at the worldwide web from 1st to 4th of March 2021**

jointly organized by

Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn

and

Institut für Evolutionsbiologie und Zooökologie, University of Bonn

Conference homepage: <https://www.gfbs-home.de/tagungen/gfbs-jahrestagung>

The inviting Organizers are:

Prof. H. Wägele: ZFMK, email: h.waegele@leibniz-zfmk.de

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Introduction and Welcome Address

Dear Participants of the 22st Conference of the Gesellschaft für Biologische Systematik,

due to the Covid-19 pandemic, this conference is held for the first time as a virtual meeting. When deciding to organize this conference via the Zoom software, the reaction of participants, the number of submissions, and also technical details were obscure. The board of the society therefore decided to provide at least a stage for young researchers to present their studies in the form of talks. But we decided against poster session to keep the conference manageable for our small team.

This is the fourth time that the meeting is housed in Bonn after 1998, 2001, and 2015. It was meant to be a joint meeting with the International Society of Systematics in 2021, UK. Unfortunately, first the Brexit and finally the Covid-19 pandemic led to the virtual format of a national conference. However, this is a good chance to include international colleagues and also students to participate not only from German speaking countries, but worldwide. We also did not choose a specific theme with main speakers invited to a specific topic, but chose the speakers as representatives of the organism groups – present and past –, the Society stands for. The various talks also reflect the broadness of our society, but will also address the political topics that nowadays influence our studies on organismal biology.

We will neither have an icebreaker nor have joint breaks with canapés, unfortunately. Also, there won't be a conference dinner in a noisy restaurant with consolidating collaborations while drinking nice beverages. We will all miss these social side events that make a conference unforgettable. But we do hope that with this virtual meeting, we provide at least a platform for our young researchers to participate, share their research and stay connected. As in earlier years, the student talks will be evaluated and the best student contributions will be awarded. In addition, the **Bernhard Rensch-Preis** will be awarded and there will be a **Mitgliederversammlung** (General Assembly) at the end of the conference with many interesting topics with regard to the development of our Society for Biological Systematics.

With this welcome in English we would also like to take care of our increasingly international members, some of whom started their careers here in Germany and who are still associated to our Society, irrespective whether they are now in Australia, Indonesia or Colombia.

Below, we provide detailed information about how you can access the conference, and how you stay connected with us or with other participants. We provide the overall time schedule with talks and further activities and will guide you through the day with the daily scheduled talks and the respective abstracts to the talks. We, the organizers, would like to thank the JuSys for organizing the student evaluation again this year, and we would like to thank the Museum Alexander Koenig for providing financial support to keep the conference free of charges.

We are looking forward to this exciting GfBS conference in a completely new form and with unforeseen challenges, but with many interesting topics provided by you.

The organizers:

Heike Wägele, André Koch and Thomas Bartolomaeus

Technical Information about how to join the meeting

- **How to access the meeting as audience?**

All registered participants will get a zoom link provided three days before the congress starts. This link will be valid during the whole congress, so you can use it every day at any time to join the meeting.

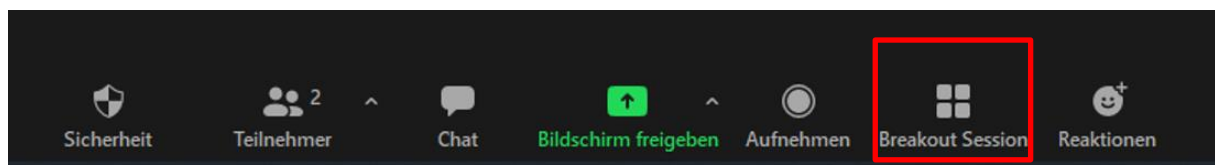
By opening Zoom via this link, you will be automatically directed to a waiting room. You will be allowed to enter the conference shortly before the daily sessions start. In case your name does not appear properly, you can change this by clicking on the name that appears on your screen with the right mouse button and choose **“rename/umbenennen”**.

Your microphone will be muted by default, when entering the conference. During the talks, you might also switch off your video for a better connection.

You can ask questions to the speakers after the talk, as long as the presentation window of 15 minutes is not exceeded. Please raise your blue hand or write your question in the chat. It would also help, if you switch on your video, in case you want to ask questions.

For addressing your questions, you may also use the respective breakout room *after* the session, where speakers will be available again (see below).

We will have specific **breakout sessions/rooms for all speakers (called Talk 1, Talk 2, Talk 3)** throughout the meeting that can be chosen after each session for further discussions with all speakers of the previous session. The speakers are invited to stay there for at least the break time of 15 minutes. There will also be additional **breakout rooms (called Café A, Café B, Café C, ...)**, that will invite you to visit in case you want to continue chatting in a more private environment. You are free to choose any of these rooms, which will be available during all sessions and also thereafter. These “coffee-table” breakout rooms are open to everybody. Attendees are visible by their names, similar to a coffee break in a larger room with groups of people forming around the tables. Just make sure, to bring your own catering at home! To enter the breakout rooms, please press the button **“breakout session”** (see red square in the screen shot below). **Press the button “Raum Verlassen” (= exit room) to return to the main session and the talks.**



- **How to access the meeting as a speaker?**

Please check the computer that you will use for the Zoom conference before the session starts, in which your talk is scheduled. You need to make sure that your microphone is working. You should also be familiar with handling the screen sharing option (**green button: “Bildschirm freigeben”**).

If you feel unsure about the process, please participate in the training sessions on Wednesday 24th of February between 10:00 and 12:00 am, or on Thursday 25th of February between 2:00 and 4:00 pm. Please contact the organizers (organizers@gfbs-home.de) or (h.waegele@leibniz-zfmk.de) for a time slot.

During the conference, please join the session in which you are giving your talk at least 10 minutes before your presentation starts. You will have access to the session as outlined above and at any time.

The chair person will introduce you shortly with your name and affiliation, when your talk starts. This is the time to share your screen with the audience. Then you can start giving your presentation.

After your talk, you will have the possibility to answer questions from the audience, if there is time left within your 15 minutes time slot. In addition, we kindly ask you speakers to **enter a breakout room via the breakout session button** (see red square in the screen shot above) to answer further questions during the break following your session. The breakout rooms will be numbered according to the order of your talks in the respective session (i.e., the first speaker shall wait in breakout room “talk 1” and so on). We also kindly ask the main speakers to be available in the breakout room called “Main lecture” after the first session. We will help you to enter the breakout rooms, in case you have problems.

You need to **press the button “Raum verlassen” (= exit room), to return to the main session** and the talks.

- **Further Information on special virtual Events**

There will be a **photo session** on Thursday 4th of March right before the General Assembly. Please join this session at 1pm with your video and your full name on. We will make screenshots of all participants. The pictures will be made public as a group photo of the conference in the Newsletter and on the website of the GfBS at: <https://www.gfbs-home.de/tagungen/gfbs-jahrestagung>. If you object to the publication please switch off your video.

The **Mitgliederversammlung/General Assembly** will take place as the final meeting during the conference. The schedule of the meeting is at the end of this Abstract volume. It would be nice if you could stay and participate. There will be a Umfrage/survey during the Mitgliederversammlung (General Assembly) held in German. We will guide you through the process.

- **Confirmation of Participation**

If you need a confirmation letter that you participated in this conference with a talk, please let us know: organizers@gfbs-home.de

We wish you a pleasant conference!

Time Schedule of Conference: Please see end of schedule for [information](#) on [colour codes](#). Talks marked **S1 to S15** are student contributions.

	Monday 1/3/2021	Tuesday 2/3/2021	Wednesday 3/3/2021	Thursday 4/3/2021
09:00–09:15	Welcome note by the organizers	-	-	-
09:15–10:00	Main lecture 1: Zoology Renske Onstein: Co-evolutionary dynamics between fruits and frugivores: insights from two keystone tropical plant families (Arecaceae and Annonaceae) Chair: Alex Zizka	Main lecture 2: Botany Dirk Albach: Using collections efficiently, non- to minimal destructively Chair: Marc Appelhans	Main lecture 3: Palaeontology David Grossnickle: Jaw shapes of extant and extinct mammals provide insight on the origins of mammalian diversity Chair: Julia Schultz	Main lecture 4: Biodiversity Pedro Frade: Codiversification and biodiversity loss in reef-building corals Chair: Dominique Zimmermann
10:15–10:30	Excluding spatial sampling bias does not eliminate over-splitting in DNA-based species delimitation analyses <u>Lukic, D.</u> , Eberle, J., Thormann, J., Holzschuh, C. & Ahrens, D.	S3: How often do they do it? An in-depth analysis of the hybrid zone of two grass snake species (<i>Natrix astreptophora</i> , <i>N. helvetica</i>) <u>Asztalos, M.</u> , Schultze, N., Ihlow, F., Geniez, P., Berroneau, M., Delmas, C., Guiller, G., Legentilhomme, J., Kindler, C. & Fritz, U.	S8: Morphological and molecular variability in <i>Peridinium volzii</i> (Peridiniaceae, Dinophyceae) and its relevance for infraspecific taxonomy <u>Holzer, V.</u> , Kretschmann, J., Owsiany, P.M. & Gottschling, M.	A change in paradigm: From publications to publishing building blocks of digital accessible biodiversity knowledge <u>Agosti, D.</u> , Bénichou, L. & Penev, L.
10:30–10:45	Whole genome-wide analysis to target the cause of sex ratio skew in <i>Altica lythri</i> <u>Zeng, C.</u> , Rohlfing, K. & Dobler, S.	S4: Adaptive introgression or parallel evolution – tracing the origin of a novel reproductive strategy in Sulawesi ricefishes <u>Flury, J.M.</u> , Meusemann, K., Nolte, A.W., Hilgers, L., Herder, F., Spanke, T., Misof, B. & Schwarzer, J.	S9: Carnassial shape variation in Carnivora, Hyaenodonta and Dasyuomorphia compared by geometric morphometrics <u>Lang, A.J.</u> & Martin, T.	The Biodiversity Crisis Response Committee of SPNHC: Mitigating biodiversity loss and advocating for the collections community's contributions to conservation efforts Ellwood, L., Bentley, A., <u>Buschbom, J.</u> , Karim, T., Mast, T., Nelson, G., Wheeler, E.
10:45–11:00	S1: Reproductive anomalies in a flea beetle – Why does one mitochondrial haplotype of <i>Altica lythri</i> produce only female progeny? <u>Sanken, A.</u> , Zeng, C. & Dobler, S.	S5: Quantitative analysis of spore shapes improves identification of fungi <u>Ordynets, A.</u> & Kessler, S.	S10: Suctorial feeding in millipedes (Myriapoda: Diplopoda): The head morphology of the Colobognatha <u>Moritz, L.</u> , Blanke, A. & Wesener, T.	The Nagoya Protocol – what does it mean for you? <u>Karger, E.</u>

11:00–11:15	Breakout rooms: Main lecture Talk 1-3 to meet the speakers Café A, Café B, Café C, ...	Breakout rooms: Main lecture Talk 1-3 to meet the speakers Café A, Café B, Café C, ...	Breakout rooms: Main lecture Talk 1-3 to meet the speakers Café A, Café B, Café C, ...	Breakout rooms: Main lecture Talk 1-3 to meet the speakers Café A, Café B, Café C, ...
11:15–11:30	The Leipzig Catalogue of Vascular Plants (LCVP) – A new online catalogue of all extant vascular plant species names <u>Freiberg</u> , M., Winter, M., Gentile, A., Zizka, A., Muellner-Riehl, A.N., Weigelt, A. & Wirth, C.	Adding leaves to the Lepidoptera tree: Capturing hundreds of nuclear genes from old museum specimens Mayer, C., Dietz, L., Call, E., Kukowka, S., Martin, S. & <u>Espeland</u> , M.	S11: Comparative skull morphology in typhlopoid blindsnakes of the genus <i>Letheobia</i> via Micro-CT <u>Rech</u> , I. & Koch, C.	National Research Data Infrastructure – how the NFDI4BioDiversity mobilizes and presents valuable community data <u>Ebert</u> , B. & Glöckner, F.O.
11:30–11:45	Molecular data, supported by morphology, prove polyphyly and allow generic recircumscription of <i>Dysoxylum</i> (Meliaceae), a species-rich tropical rainforest tree genus <u>Holzmeier</u> , L., Hauenschild, F., Mabberley, D.J. & Muellner-Riehl, A.N.	S6: Plastid phylogenomics of the Gynoxoid group (Senecioneae, Asteraceae) highlights the importance of motif-based sequence alignment amid low genetic distances <u>Escobari</u> , B., Borsch, T., Quedensley, T.S. & Gruenstaeudl, M.	Morphological boundaries among the species of the Caucasian rock lizards (Genus <i>Darevskia</i>) <u>Gabelaia</u> , M., Misof, B., Tarkhnishvili, D. & Wipfler, B.	Introducing GBOL III: Dark Taxa, targeting Central Europe's unknown insect biodiversity <u>Rdusch</u> , V. & Peters, R.S. – on behalf of the GBOL III: Dark Taxa consortium
11:45–12:00	Phylogenetics of the Neotropical montane tree genus <i>Ruagea</i> (Meliaceae) <u>Rojas-Andrés</u> , B.M., Lihanova, Y., Pennington, T. & Muellner-Riehl, A.N.	Why all Codes of Nomenclature, not just the Zoological Code, should allow DNA sequences (or assembled genomes) as sole or additional type material of species names Renner, S.S.	Dragons in Neglect: Taxonomic Revision of Sulawesi Sailfin Lizards (<i>Hydrosaurus</i> Kaup, 1828) Denzer, W., Campbell, P., Manthey, U., Glässer-Trobisch, A. & <u>Koch</u> , A.	FörTax – Promotion of taxonomic knowledge as a basis for nature conservation: Successes, deficits and prospects <u>Waskow</u> , K., Nöske, N., Stehr, K. & Miesen F.W.
12:00–12:15	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,
12:15–12:30	S2: Symbiont recognition and establishment in the nudibranch <i>Berghia stephanieae</i> Melo Clavijo, J., Bleidißel, S., Preisfeld, A. & Christa, G.	S7: Biodiversity patterns of herbivore scarab chafers (Coleoptera: Scarabaeidae) in Sri Lanka <u>Ranasinghe</u> , U.G.S.L., Eberle, J., Bohacz, C., Benjamin, S.P. & Ahrens, D.	S13: How to stay attached – Morphological adaptations in the reproductive system of the female pelvic brooder <i>Oryzias eversi</i> <u>Schüller</u> , A., Herder, F., Spanke, T., Schwarzer, J., Vehof, J. & Wipfler, B.	Presentation of Student Awards by Fabian Deister & Laudatio of Rensch Prize Winner by Mark Gottschling

12:30–12:45	Tracing sponge (palaeo)eco-evolutionary drivers through deep time <u>Schuster</u> , A. & Canfield, D.E.	Evolutionary trends of antennal surface structures in scarab beetles Bohacz, C., Pacheco, T.L. & <u>Ahrens</u> , D.	S14: Pelvic brooding in Sulawesi ricefishes (Belontiiformes; Adrianichthyidae): Parallel evolution in a specialized reproductive strategy <u>Spanke</u> , T., Flury, J.M., Hilgers, L., Nolte, A. W., Utama, I. V., Herder, F., Wipfler, B., Misof, B. & Schwarzer, J.	Rensch Prize Presentation: Diversity, morphology, and taxonomy of selected dinophytes <u>Kretschmann</u> , J.	
12:45–13:00	Holistic description of new deep sea macrofauna (Cephalopoda: Cirrata) using a minimally invasive approach <u>Ziegler</u> , A. & Sagorny, C.	Insights into the mechanisms of sex bias in the hybridogenetic flea beetle, <i>Altica lythri</i> <u>Rohlfing</u> , K., You, L., Franke, S. & Dobler, S.	S15: Sexual dimorphism in an adaptive radiation: Does intersexual niche differentiation result in ecological character displacement? <u>Wasiljew</u> , B., Pfaender, J., Wipfler, B., Gabelaia, M., Utama, I.V., Wantania, L.L. & Herder, F.		
13:00–13:15	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Breakout rooms: Talk 1-3 to meet the speakers Café A, Café B, Café C,	Photo session of participants and short break	
13:15–14:00	-	-	-	Mitgliederversammlung (General Assembly held in German) & Closing ceremony	
	Colour codes for sessions:	Arthropods	Fishes	Plants & Fungi	General Topics
		Squamates	Marine Organisms	Mammals	Others

Daily Schedules and Abstracts sorted by daily order:

Monday	
1/3/2021	
09:00–09:15	Welcome Note by the Organizers
09:15–10:00	Main lecture 1: Zoology Renske Onstein: Co-evolutionary dynamics between fruits and frugivores: insights from two keystone tropical plant families (Arecaceae and Annonaceae) (Chair: Alex Zizka)
10:15–10:30	Excluding spatial sampling bias does not eliminate over-splitting in DNA-based species delimitation analyses <u>Lukic, D., Eberle, J., Thormann, J., Holzschuh, C. & Ahrens, D.</u>
10:30–10:45	Whole genome-wide analysis to target the cause of sex ratio skew in <i>Altica lythri</i> <u>Zeng, C., Rohlfing, K. & Dobler, S.</u>
10:45–11:00	S1: Reproductive anomalies in a flea beetle – Why does one mitochondrial haplotype of <i>Altica lythri</i> produce only female progeny? <u>Sanken, A., Zeng, C. & Dobler, S.</u>
11:00–11:15	Breakout rooms: Main lecture / Talk 1-3 to meet the speakers / Café A, Café B, Café C
11:15–11:30	The Leipzig Catalogue of Vascular Plants (LCVP) – A new online catalogue of all extant vascular plant species names <u>Freiberg, M., Winter, M., Gentile, A., Zizka, A., Muellner-Riehl, A.N., Weigelt, A. & Wirth, C.</u>
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12:30–12:45	Tracing sponge (palaeo)eco-evolutionary drivers through deep time <u>Schuster, A. & Canfield, D.E.</u>
12:45–13:00	Holistic description of new deep sea macrofauna (Cephalopoda: Cirrata) using a minimally invasive approach <u>Ziegler, A. & Sagorny, C.</u>
13:00–13:15	Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C

Main lecture 1:

Co-evolutionary dynamics between fruits and frugivores: insights from two keystone tropical plant families (Arecaceae and Annonaceae)

Onstein, R.E.¹

¹ Evolution & Adaptation group, German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany, e-mail: renske.onstein@idiv.de

The interaction between fruits and frugivores (i.e. fruit-eating and seed-dispersing animals) is prominent in tropical rainforests. Seeds can be moved across long distances, while frugivores obtain important nutrients. Both fruits and frugivores have evolved adaptive traits to facilitate their interactions, which may explain the evolution of plant 'trait syndromes' in relation to particular frugivore guilds (e.g., birds, mammals), or the matching between frugivore and plant traits, such as body size / fruit size and colour vision / fruit colour. I will discuss the consequences of trait evolution for the co-evolutionary dynamics between fruits and frugivores, particularly focusing on the role of seed dispersal in (1) the disjunct tropical distribution of rainforest lineages, and (2) co-diversification between plant lineages with conspicuous (reddish) fruit colours and frugivore lineages with trichromatic vision (those that can distinguish red from green). To illustrate this, I will use examples from two keystone tropical plant families: palms (Arecaceae) and custard apples (Annonaceae).

Excluding spatial sampling bias does not eliminate over-splitting in DNA-based species delimitation analyses

Lukic, D.¹, Eberle, J.², Thormann, J.¹, Holzschuh, C.³ & Ahrens, D.¹

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³ Spitzeckweg 11, 9500 Villach, Austria

DNA-barcoding and DNA-based species delimitation are major tools in DNA taxonomy. Sampling schemes have been a central debate in in this context, because the geographical composition of samples affect the accuracy of DNA-barcoding. The investigation of the performance of DNA-barcoding in absence of geographic sampling bias would be adequate to test the accuracy of data and species delimitation approaches under simpler conditions. Here, we present an empirical data set sampled from a single locality in a Southeast-Asian biodiversity hotspot (Laos: Phou Pan mountain). We investigate the performance of various species delimitation approaches on a megadiverse assemblage of herbivore chafer beetles (Coleoptera: Scarabaeidae: Sericini) to infer whether species delimitation suffers in the same way from exaggerate infraspecific variation despite the lack of geographic genetic variation that led to inconsistencies between entities from DNA-based and morphology-based species inference in previous studies. For this purpose, a 658 bp fragment of the mitochondrial cytochrome c oxidase subunit 1 (*cox1*) was analysed for a total of 186 individuals of 56 morphospecies. Tree based and distance based species delimitation methods were used. All approaches showed a rather limited match ratio (max. 77%) with morphospecies. PTP and TCS prevailingly over-splitting morphospecies, while 3% clustering and ABGD also lumped several species into one entity. ABGD revealed the highest congruence between molecular operational taxonomic units (MOTUs) and morphospecies. Disagreements between morphospecies and MOTUs were discussed in the context of historically acquired geographic genetic differentiation, incomplete lineage sorting, and hybridization. The study once again highlights how important morphology still is in order to correctly interpret the results of molecular species delimitation.

Whole genome-wide analysis to target the cause of sex ratio skew in *Altica lythri*

Zeng, C.¹, Rohlfing, K.² & Dobler, S.³

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² Molecular Evolutionary Biology, Institute of Zoology, Martin-Luther-King Platz 3, 20146 Hamburg, Germany, e-mail: kim.rohlfing@uni-hamburg.de

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The flea beetle *Altica lythri* has undergone two rounds of hybridization with closely related species that resulted in three coexisting mitochondrial haplotypes. Each mtDNA haplotype is widely associated with a particular *Wolbachia* strain which apparently drove the haplotypes to widespread occurrence. One of the haplotype/*Wolbachia* combinations (HT1/wA1) exhibits pronounced reproductive anomalies: only females can be found and will exclusively produce female offspring but need to copulate with males of the other haplotypes to lay fertile eggs. So far, the genetic basis responsible for the lack of males in one haplotype but not in the others is still unclear.

Using Pool-Seq and ddRAD sequencing, we apply whole genome-wide analysis of SNPs, to decide between two possible explanations for the lack of males among HT1 beetles. Firstly, sex- or haplotype-specific alleles which only occur in the other haplotypes and cannot be found in HT1 individuals could suggest genomic conflicts between introgressed mtDNA genes and nuclear genes that consequently lead to the lack of heterogametic males with HT1. Alternatively, alleles from parasitic cytoplasmic elements found in seemingly uninfected HT1 females would hint to reproduction manipulating genes of the parasitic bacteria that have been transferred to the nucleus and thereby persist in uninfected females. A currently constructed genomic map and transcriptomic analyses further help to identify the robust differences between the three haplotypes of *A. lythri*.

References

Jäckel, R., Mora, D., & Dobler, S. (2013). Evidence for selective sweeps by *Wolbachia* infections: phylogeny of *Altica* leaf beetles and their reproductive parasites. *Molecular Ecology*, **22**(16), 4241-4255.

S1: Reproductive anomalies in a flea beetle – Why does one mitochondrial haplotype of *Altica lythri* produce only female progeny?

Sanken, A.¹, Zeng, C.¹ & Dobler, S.¹

¹ Molekulare Evolutionsbiologie, Universität Hamburg, Hamburg, Germany, e-mail: alina.sanken@uni-hamburg.de

The flea beetle *Altica lythri* exhibits complex population genetic structures with conspicuous reproductive anomalies. One of its three mitochondrial haplotypes (HT1) is known to produce only female offspring. Additionally, copulation with a male possessing a different haplotype (HT2 and HT3) is necessary to produce fertile eggs. Current evidence indicates that the production of fertile eggs occurs through gynogenesis, a form of parthenogenetic reproduction, in which the sperm is merely needed to trigger development of the eggs. In this case, even with successful mating, males would not pass their genomes to the next generation.

To establish whether paternal genomes are completely excluded or whether some fraction of paternal gene leakage is happening, we use ddRAD markers to analyse paternity. This technique allows us to monitor several thousand markers throughout the genome simultaneously, and ultimately reveal whether parts of the male genome appear in the offspring. We also use histological analyses to investigate whether normal meiosis takes place in the ovaria of HT1 females. Finally, by using fluorescent antibodies that bind to the centromere of chromosomes as well as a fluorescent DNA stain, we validate the chromosome numbers at different stages of egg development. Our preliminary results indicate that there is paternal leakage in the all-female HT.

The Leipzig Catalogue of Vascular Plants (LCVP) – A new online catalogue of all extant vascular plant species names

Freiberg, M.^{1,2}, Winter, M.², Gentile, A.², Zizka, A.^{2,3}, Muellner-Riehl, A.N.^{2,4}, Weigelt, A.^{1,2} & Wirth, C.^{1,2,4,5}

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³ Naturalis Biodiversity Center, Darwinweg 2, 2333 CR Leiden, The Netherlands

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We present a new and improved list of all known extant vascular plant species names, the Leipzig Catalogue of Vascular Plants (LCVP - Freiberg et al. 2020), now available for download (<https://idata.idiv.de/ddm/Data/ShowData/1806>; DOI:10.25829/idiv.1806-40-3009). The catalogue consists of a simple text list of more than 1,3 million records of all published names of vascular plants, including 351,180 accepted species names, 48,257 infraspecific taxon names, and 846,279 synonyms. Large-scale online databases and several thousand published papers were consulted to guarantee the consideration of the most recent phylogenetic and evolutionary evidence for the position of the genera in families and orders, and for providing sound arguments for acceptance or rejection of a species or genus name. This allowed a substantial reduction of unresolved species names and a significant increase in the number of accepted names. The LCVP is implemented in a user-friendly R-package (<https://github.com/idiv-biodiversity/lcvplants>) to facilitate accessibility to the data and its application. The LCVP constitutes a useful reference taxonomic backbone for systematists, biogeographers, macroecologists, and plant conservationists.

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Molecular data, supported by morphology, prove polyphyly and allow generic recircumscription of *Dysoxylum* (Meliaceae), a species-rich tropical rainforest tree genus

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In this study, we tested the suspected polyphyly of *Dysoxylum* Blume ex Raspail (Meliaceae), as currently circumscribed. *Dysoxylum* is one of largest genera of Meliaceae in SE Asia, with a distribution from continental Asia through Malesia and Australasia into the Pacific. Analyses based on nuclear ribosomal ITS, ETS, the plastid *trnL-trnF* intron and intergenic spacer as well as *rps15-ycf1* intergenic spacer support the polyphyly and recover six strongly supported clades within *Dysoxylum* s.l., in large part supporting the classification of Harms. Based on the largest molecular phylogenetic tree assembled to date, and morphological considerations, a revised disposition of 94 currently recognised *Dysoxylum* species is presented, re-instating the genera *Didymocheton* Blume, *Epicharis* Blume, *Goniocheton* Blume, *Prasoxylon* M. Roem., and *Pseudocarapa* Hemsl. Forty-three new combinations at species level and two at infraspecific level are proposed.

Phylogenetics of the Neotropical montane tree genus *Ruagea* (Meliaceae)

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Ruagea (Meliaceae) comprises ca. 15 species of small or medium sized trees distributed in Central and South America, predominantly occurring in Andean montane rain forests and cloud forests. The taxonomic position of *Ruagea* has changed throughout history, being previously included in *Guarea*. *Ruagea* is currently accepted as a separate genus based on morphology and molecular phylogenetic analyses at the family level. However, its monophyly has not been accurately tested and phylogenetic relationships among species are still largely unknown. In addition, delimitation of species boundaries is not straightforward due to morphological diversity within species. Here, we present the first phylogenetic reconstruction of *Ruagea* based on two nuclear (ITS and ETS) and two plastid DNA regions (*rps4-trnT* and *trnH-psbA*). Our results show that *Ruagea* is monophyletic and composed of four main clades (A, B, C, and D). Clade D constitutes the earliest diverging lineage comprising the Ecuadorian endemic *Ruagea membranacea*, one Colombian population of *R. glabra* and a potentially new species from Colombia. Accessions from species recovered in clade A are highly intermixed. Our results demonstrate that *R. membranacea* and *R. insignis* are monophyletic and provide support for the recognition of two new species with divergent morphologies. The delimitation of the remaining species, including the widely distributed *R. glabra*, remains unresolved as they are recovered as either poly- or paraphyletic. Our results highlight the complexity of the taxonomy of *Ruagea*, as found in other rainforest taxa, and the need of further detailed analyses to delimit these taxa. This study provides the first and most extensive phylogenetic analysis of the genus so far, representing a contribution toward understanding the evolutionary history of *Ruagea*.

S2: Symbiont recognition and establishment in the nudibranch *Berghia stephanieae*

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The ability to associate with photosynthetic organisms and establish a photosymbiosis, is present throughout the animal kingdom. While in most photosymbiotic animals, the symbiont is commonly acquired directly from the environment, in nudibranchs the symbiont is sequestered from the food source, usually photosymbiotic cnidarians. Once the prey is ingested, the symbiont is selectively kept in epithelial cells of the nudibranch's digestive gland system. How the symbiont is recognized and not digested along with the photosymbiotic prey, and how the symbiont is maintained intracellularly are questions still unknown in the model Nudibranchia-Photosymbiont. To approach these questions, we used the aeolid nudibranch *Berghia stephanieae* as a model organism. This photosymbiotic nudibranch feeds exclusively on sea anemones from the genus *Exaiptasia*, that harbor the dinoflagellate *Symbiodinium* as an intracellularly symbiont. We sequenced the transcriptome of *B. stephanieae* under three conditions: continuously fed, starved for seven days, and re-fed after seven days of starvation. We analyzed the gene expression focusing on the genes related to the innate immune system that have been previously linked to symbiont recognition and maintenance in photosymbiotic animals. We found potential recognition receptors that were upregulated when *B. stephanieae* fed after seven days of starvation. Among them are the scavenger receptor class B (SR-B), class E (SR-E), C-type lectins, proteins with a thrombospondin domain (TSRs). In contrast, we found down-regulated elements of the Transforming Growth Factor β (TGF β) pathway, which is thought to be involved in the symbiont tolerance and maintenance. We also detected down-regulation in other components that inhibit phagocytosis. The symbiont recognition machinery in *B. stephanieae* might be similar to other photosymbiotic animals, however it seems that known pathways involved in symbiont maintenance and tolerance are not activated in *B. stephanieae*, suggesting a continuous symbiont digestion.

Tracing sponge (palaeo)eco-evolutionary drivers through deep time

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Sponges (Phylum Porifera) form the earliest branch of the animal evolutionary tree and likely resemble some of the first animals. Identifying how past environmental conditions and tectonics shaped their evolution, diversification and distribution through deep time provides a framework for predicting their persistence and successful adaptation to changing ocean chemistry and thus can inform about the future of global coral reef ecosystems. Some sponge lineages of Demospongiae and Hexactinellida have a remarkably continuous fossil record dating back to 550 Ma. Still, little is known about their biodiversity throughout the Phanerozoic Eon and which environmental parameters influenced their diversification, distribution, extinctions and originations. Surprisingly, no attention has been given to understand sponge palaeobiodiversity in relation to plate tectonic changes. In particular, deep-time dynamics of the latitudinal diversity gradient (LDG) around the P/T extinction crisis, which had a profound impact on the biogeographic distribution of many other marine organisms, remain unexplored for the class Porifera. Therefore, in this study we extracted a total of 11,622 fossil occurrences from 3,400 collections from the Paleobiology database. A curated dataset accounting for spatial and temporal inequities in quantity or quality was used to calculate the palaeodiversity, origin and extinction of several sponge groups throughout the Phanerozoic Eon and to correlate this to potential driving factors such as oxygen, silica, nutrients, tectonic fragmentation, paleoclimate, and competing organism (diatoms, corals). We find a positive correlation between the global sponge genus richness and the assembly and disassembly of supercontinents, particularly during the breakup of Pangaea. Periods of anoxic/hypoxic events during the Mesozoic had a negative effect on the sponge diversity resulting in higher extinction rates, however, some lineages recovered and diversified afterwards. No correlation was observed between DSi concentration and hypersilicified sponge diversity, but the rise of diatoms during the T/J caused a drastic decrease of DSi in the ocean. The causes of the observed shrinking of sponge spicules during the T/J remain obscure and await further investigation. Our data support the overall biodiversification events: Cambrian to M. Ordovician, in E. Silurian, from L. Carboniferous to Cisuralian and M. Jurassic to M. Cretaceous, and provide novel, in-depth insights into origin and extinction rates of sponge lineages in relation to changing ocean chemistry.

Holistic description of new deep sea macrofauna (Cephalopoda: Cirrata) using a minimally invasive approach

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In zoology, species descriptions conventionally rely on invasive morphological or anatomical techniques, frequently leading to the destruction of specimens and thus only a partial understanding of their structural complexity. More recently, non-destructive imaging techniques have successfully been used to describe smaller fauna, but this approach has so far not been applied to identify larger animals. Here, we present a combination of digital non-invasive as well as minimally invasive methods that permit taxonomic descriptions of large zoological specimens in a more comprehensive manner. Using the single available representative of an allegedly novel species of deep-sea cephalopod (Mollusca: Cephalopoda) macrofauna, photography, morphometrics, high-field magnetic resonance imaging, micro-computed tomography, and DNA barcoding are combined to gather all data relevant for a full species description. The results show that this specimen belongs to the cirrate octopod (Octopodiformes: Cirrata) genus *Grimpoteuthis* and is here identified as the holotype of a new species of dumbo octopus. Due to the digital nature of the acquired structural and molecular data, the first cephalopod cyber-type is designated through online provision of all raw and derived datasets. Potentially harmful effects on this unique deep sea specimen were avoided by scanning the fixed animal without addition of any contrast agent. Using high-resolution imaging systems originally intended for analysis of larger objects such as humans, all internal structural data relevant for the identification of a new cephalopod species were successfully obtained. Additional support for the taxonomic placement of the new dumbo octopod species *G. imperator* sp. nov. was obtained through DNA barcoding, further underlining the importance of combining structural and molecular data for a holistic identification of zoological specimens.

Tuesday 2/3/2021	
09:15–10:00	Main lecture 2: Botany Dirk Albach: Using collections efficiently, non- to minimal destructively (Chair: Marc Appelhans)
10:15–10:30	S3: How often do they do it? An in-depth analysis of the hybrid zone of two grass snake species (<i>Natrix astreptophora</i> , <i>N. helvetica</i>) <u>Asztalos</u> , M., Schultze, N., Ihlow, F., Geniez, P., Berroneau, M., Delmas, C., Guiller, G., Legentilhomme, J., Kindler, C. & Fritz, U.
10:30–10:45	S4: Adaptive introgression or parallel evolution – tracing the origin of a novel reproductive strategy in Sulawesi ricefishes <u>Flury</u> , J.M., Meusemann, K., Nolte, A.W., Hilgers, L., Herder, F., Spanke, T., Misof, B. & Schwarzer, J.
10:45–11:00	S5: Quantitative analysis of spore shapes improves identification of fungi <u>Ordynets</u> , A. & Kessler, S.
11:00–11:15	Breakout rooms: Main lecture / Talk 1-3 to meet the speakers / Café A, Café B, Café C
11:15–11:30	Adding leaves to the Lepidoptera tree: Capturing hundreds of nuclear genes from old museum specimens <u>Mayer</u> , C., Dietz, L., Call, E., Kukowka, S., Martin, S. & <u>Espeland</u> , M.
11:30–11:45	S6: Plastid phylogenomics of the Gynoxoid group (Senecioneae, Asteraceae) highlights the importance of motif-based sequence alignment amid low genetic distances <u>Escobari</u> , B., Borsch, T., Quedensley, T.S. & Gruenstaeudl, M.
11:45–12:00	Why all Codes of Nomenclature, not just the Zoological Code, should allow DNA sequences (or assembled genomes) as sole or additional type material of species names <u>Renner</u> , S.S.
12:00–12:15	Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C
12:15–12:30	S7: Biodiversity patterns of herbivore scarab chafers (Coleoptera: Scarabaeidae) in Sri Lanka <u>Ranasinghe</u> , U.G.S.L., Eberle, J., Bohacz, C., Benjamin, S.P. & Ahrens, D.
12:30–12:45	Evolutionary trends of antennal surface structures in scarab beetles Bohacz, C., Pacheco, T.L. & <u>Ahrens</u> , D.
12:45–13:00	Insights into the mechanisms of sex bias in the hybridogenetic flea beetle, <i>Altica lythri</i> <u>Rohlfing</u> , K., You, L., Franke, S. & Dobler, S.
13:00–13:15	Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C

Main lecture 2:

Using collections efficiently and non- to minimal destructively

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The approx. 3000 herbaria worldwide are home to about 400 million plant specimens. Whereas herbaria are sometimes believed to be outdated, modern research demonstrates that herbaria are more important and valuable than before. Traditional uses of herbaria, such as documentation of distribution, morphological variation, storing type specimens and teaching plant identification, may have mostly been substituted by providing information for large data bases, DNA barcoding etc. However, herbarium specimens are increasingly used as genomic resources to access DNA otherwise inaccessible due to legal restrictions or extinction of populations or species. Herbarium genomics further provide insights into the past and allow tracking the evolution over time of hybrids, domestication, and invasions, sometimes even answering functional genomics questions. Combined with digitization and accumulating data from hundreds of herbaria, thus, allow novel and otherwise inaccessible insights to answer questions relating to biodiversity conservation, climate change and other pressing research questions. Nevertheless, methodologies will need to be improved to utilize these resources optimally. Since DNA extraction is a destructive sampling method, it needs to be optimized. DNA degradation, fragmentation and mutation during storage need to be considered. Finally, analytical methods need to be adapted to the condition of DNA. Whereas several general recommendations can be made based on various studies and own experiences, many aspects are taxon-specific. Nevertheless, there is pressing need for non-destructive methods. Spectroscopy may offer such a method and initial results demonstrate its potential. Consequently, herbaria will need to be incorporated into university teaching as an important resource providing opportunities for research-oriented teaching and transdisciplinary research as exemplified by a couple of student research projects in Oldenburg.

S3: How often do they do it? An in-depth analysis of the hybrid zone of two grass snake species (*Natrix astreptophora*, *N. helvetica*)

Asztalos, M.¹, Schultze, N.¹, Ihlow, F.¹, Geniez, P.², Berroneau, M.³, Delmas, C.⁴, Guiller, G.⁵, Legentilhomme, J.⁶, Kindler, C.¹ & Fritz, U.¹

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We examined the contact zone of two parapatric species of grass snake in southern France (*Natrix astreptophora* and *N. helvetica*). To this end, we used comprehensive sampling, analyzed mtDNA sequences and microsatellite loci, and built Species Distribution Models for current and past climatic conditions. The contact zone established by the mid-Holocene during range expansions from glacial refuges in the Iberian Peninsula (*N. astreptophora*) and southern or western France (*N. helvetica*). The contact zone represents a narrow bimodal hybrid zone, with steep genetic transition from one taxon to the other and rare hybridization, supporting species status for *N. astreptophora* and *N. helvetica*. Our results suggest that the steepness of the clines is a more robust tool for species delimitation than cline width. In addition, we discovered in western France, beyond the hybrid zone, a remote population of *N. helvetica* with genetic signatures of hybridization with *N. astreptophora*, most likely the result of human-mediated long-distance dispersal. For *N. helvetica*, we identified a southern and a northern population cluster, connected by broad-scale gene flow in a unimodal hybrid zone running across France. This pattern either reflects genetic divergence caused by allopatry in two microrefuges and secondary contact or introgression of foreign alleles into the southern cluster.

S4: Adaptive introgression or parallel evolution – tracing the origin of a novel reproductive strategy in Sulawesi ricefishes

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Adaptive radiations are one key source of species diversity. On Sulawesi, an Indonesian Island close to Borneo and Papua, an endemic radiation of ricefishes (Adrianichthyidae) started to evolve about 20 million years ago, when their most recent common ancestor colonized Sula Spur from Java or the Asian mainland. The family comprises two genera, *Adrianichthys* and the paraphyletic genus *Oryzias*. *Adrianichthys* species are sistergroup to a radiation of Sulawesi *Oryzias* species. In *A. oophorus* as well as in the only recently diverged *O. eversi* and *O. sarasinorum* a novel reproductive strategy has evolved, where females carry an egg cluster beneath the belly. The eggs are connected to the females' oviduct via filaments and remain there until the fry hatches. All described so called pelvic-brooding species share a set of morphological traits, like elongated pelvic fins and shorter ribs that form a ventral concavity, even though they are not each other's closest relatives. In the present study we investigate by means of phylogenetic analyses and ABBA/BABA statistics whether the parallel appearance of the same reproductive strategy in two distantly related lineages might be related to gene-flow and/or introgression of genetic material from *Adrianichthys* species into the Sulawesi *Oryzias* radiation. We found signatures of introgression between *A. oophorus* and *Oryzias* species from different regions and drainage systems on Sulawesi, including pelvic brooding species. This high frequency of introgression leads to the assumption that secondary contact was rather the rule than the exception in Sulawesi ricefishes. Thus, the introgression of pelvic brooding from *Adrianichthys* into pelvic brooding *Oryzias* species is a possible scenario.

S5: Quantitative analysis of spore shapes improves identification of fungi

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Morphology of organisms is an important source of evidence for biodiversity assessment, taxonomic decisions and understanding of evolution. It is easier to work with the linear measurements of organisms. However, the size alone is often insufficient for delimitation of species or populations. Working with quantitative shape data (geometric morphometrics) is more challenging but provides more comprehensive information on morphology. While geometric morphometric is commonly applied to zoological and botanical objects, it was almost ignored in the studies of fungi. In fungal taxonomy, the features of the disseminated propagules, the spores, are of highest priority among phenotypic characters. In this study, we explore how much we gain in the automated identification of fungal species when working with quantitative shape data versus linear size data on fungal spores. We used the fungi of the genus *Subulicystidium* (Agaricomycetes, Basidiomycota, Fungi) as a study object. We analysed spore shape (outline) data via Elliptic Fourier and Principal Component analyses. With flexible discriminant analysis, we achieved slightly higher species identification success rate for shape predictors (61.5%) than for size predictors (59.1%). However, the highest identification success rate was achieved for a combination of both (64.7%). We conclude that working with fungal spore shapes in quantitative way is worth the effort. We hope to stimulate a broader use of quantitative spore shape analysis in fungal taxonomy.

Adding leaves to the Lepidoptera tree: Capturing hundreds of nuclear genes from old museum specimens

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Museum collections around the world contain billions of specimens, including rare and extinct species. Retrieving genetic information from such samples at a large scale, would highly support evolutionary, ecological and systematic studies. We here present a target enrichment kit (LepZFMK1.0) including over 2000 nuclear loci + COI, for Lepidoptera and demonstrate its utility to obtain large amounts of nuclear loci from dry, pinned museum material. Specimens collected between 1892 and 1940 yielded from 468 loci (>115,000bps), to over 860 loci, and more recent dry material up to almost 1800 loci. We sequenced 37 museum specimens across Lepidoptera, many from families or superfamilies not yet included in high-throughput molecular studies. Furthermore, we present our efficient TEnriAn (Target Enrichment Analysis) workflow for processing such data and adding already available transcriptomes and genomes. The filtered datasets (172 taxa, 234,464AA and corresponding nucleotides) were used to infer a phylogeny of the Lepidoptera, which we compare with previous studies.

S6: Plastid phylogenomics of the Gynoxoid group (Senecioneae, Asteraceae) highlights the importance of motif-based sequence alignment amid low genetic distances

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The sunflower subtribe Tussilagineae includes a species-rich lineage of Andean shrubs and trees, the Gynoxoid species group that comprises the genus *Gynoxys* and several related genera and exhibits low genetic distances. Previous molecular phylogenetic investigations of Tussilagineae have included few, if any, representatives of Gynoxoid group and reconstructed unclear patterns of relationships. In the present study, we sequence and compare complete plastid genomes of 21 species of the Gynoxoid group and related Tussilagineae, including the type species of three out of five genera currently recognized for the group, to clarify the main phylogenetic relationships and the generic delimitations within the group. Moreover, we evaluate the impact of manual, motif-based adjustments of automatic sequence alignments on phylogenetic tree inference. Our results indicate that the plastid genomes of the Gynoxoid group harbor different phylogenetic signal among many of their coding and non-coding regions and that the manual post-processing of multiple sequence alignments demonstrably improves the reliability of the subsequent tree reconstruction. Despite incongruent phylogenetic signal, tree inference on the plastid genomes recovered consistent and strongly supported relationships between members of the Gynoxoid group and indicated that at least three of the genera are polyphyletic in their current taxonomic circumscription.

Why all Codes of Nomenclature, not just the Zoological Code, should allow DNA sequences (or assembled genomes) as sole or additional type material of species names

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I am a member of a Special-purpose Committee on “DNA sequences as Types for Algae and Plants” and would enjoy discussion of this topic. Below is some relevant background.

The Code of Zoological Nomenclature (<https://www.iczn.org>) states that establishing new species names without preserved name-bearing type material is permissible when capture or preservation of specimens is not feasible for technical reasons or for conservation concerns, or when specimens must be destroyed to reliably diagnose a new species. Recommendation 73J explains that authors should provide extensive documentation (e.g., multiple original high-resolution images, DNA sequences, etc.) of potentially diagnostic characters as completely as possible.

The Code of Nomenclature for algae and plants (<https://www.iapt-taxon.org/nomen/main.php>) states that the type of a name of a species or infraspecific taxon must be a specimen or illustration.

Since 2019, the mycologists have their own code (<https://imafungus.biomedcentral.com/articles/10.1186/s43008-019-0019-1>), and they also have a Committee on “DNA sequences as Types for Fungi” that is still discussing detailed recommendations. The arguments in favor are beautifully laid out in Hawksworth, Hibbett, Kirk and Lücking (TAXON 65: 899–900, 2016).

The Code of Nomenclature of Prokaryotes (<https://www.the-icsp.org/bacterial-code>) recommends that the type of a species or subspecies should be a designated strain maintained in pure culture, but there are efforts to modify this code so that DNA becomes permitted as type material for uncultured prokaryotes or to make a new Code for uncultured prokaryotes.

Note that all codes permit DNA characters as sole or additional diagnostic characters, and since 2000, some 150 names of animal, fungi, and plants have been published with DNA-based diagnoses.

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S7: Biodiversity patterns of herbivore scarab chafers (Coleoptera: Scarabaeidae) in Sri Lanka

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Very little is known about factors determining assemblage structure of tropical herbivore scarab chafers (Coleoptera: Scarabaeidae). In this study we examine diversity patterns of scarab chafers at a local scale to infer patterns of species turnover among different sites and habitats. We applied a sampling scheme of six UV-light traps that were placed in different habitat types at each locality to explore the quantitative species composition in sites as well as different forest types, including lowland, sub-montane and montane forests in both dry and wet seasons. Four expeditions were undertaken in 2019 and in 2020 to twelve localities in lowland wet/dry evergreen forests, sub-montane wet evergreen forests and montane forests of Sri Lanka. Results of the first two expeditions revealed a high endemism of the target taxa in the study sites. Continued sampling efforts during two further expeditions demonstrated that we recorded almost the complete species assemblage within a particular site, as the species accumulation curve saturated for several sampling events in the fourth expedition. We examined 4689 scarab chafer individuals and identified 43 Sericini morpho-species and 68 other scarab morpho-species. This included so far 10 new species of Sericini. Our results presume large species turnover among traps set in different habitats in the same locality. However, traps of different localities generally showed more similar faunal composition, than traps of the same locality. Species abundance varied significantly across dry and wet seasons in each locality. This might indicate that habitat determines the assemblage composition more than the locality, which we would like to investigate in more detail: our results shown here are based on morpho-species assignments and will be underpinned in the frame of the project by molecular data.

Evolutionary trends of antennal surface structures in scarab beetles

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The diverse scarab beetles with characteristically clubbed antennae exhibit striking morphological variation and a variety of different antennal sensilla. Here we compare the morphology of the antennal surface between major scarab lineages in the background of their phylogeny. We identified various types of antennal sensilla morphologically and searched for phylogenetic patterns of sensilla within the Scarabaeidae. Sensilla were examined using SEM micrographs and the occurrence of the different types of antennal sensilla. We observed a high diversity of sensilla, including multiple transitional forms. There were also a number of other interesting structures on the antennal surface with adaptive value, such as elongate elevations, serial bags, and fields of setae. Our results reveal beside a clear differentiation of sensilla composition and patterns also a number of parallelisms.

Insights into the mechanisms of sex bias in the hybridogenetic flea beetle, *Altica lythri*

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Altica lythri is a hybridogenetic beetle with unique reproduction anomalies that provide an ideal model for understanding how genetic conflicts shape the sex, and thus evolution, of species. Ancient interspecific hybridization and *Wolbachia* bacterial infections in *A. lythri* resulted in introgression of mitochondrial (mt) DNA (HT1, HT2, HT3). Depending on a female's mtDNA haplotype and *Wolbachia* strain (HT1- wLytA1), the progeny can consist exclusively of daughters. This female bias could either be caused by the *Wolbachia* infection itself, which can intervene at different points in the sex cascade to increase the proportion of female offspring, or by the genetic consequences of hybridization in the form of nuclear-cytoplasmic conflicts between introgressed mtDNA and nuclear genes, which result in the absence of heterogamous males with the mtDNA HT1. To understand the mechanisms that contribute to this sex bias, we must identify the point in the sex determination pathway where sex is altered and the males disappear. This well-conserved pathway in insects involves a cascade of regulators that ultimately control sex-specific splicing of the transcription factor, doublesex (*dsx*). However, since male and female offspring are morphologically indistinguishable until adult molt, it has been unclear when female bias occurs during development. We address this issue in *A. lythri* with transcriptomic and molecular approaches. Using RT-PCR, we established a screening method to unambiguously determine the sex at the egg and larval stages. Our data indicate that the sex bias in these flea beetles occurs during meiosis at the latest, or possibly even earlier. These results provide key insights into how sex determination is initiated and whether combinations of selfish genetic elements and/or reproductive manipulating endosymbionts play the key role in this system.

Wednesday 3/3/2021	
09:15–10:00	Main lecture 3: Palaeontology David Grossnickle: Jaw shapes of extant and extinct mammals provide insight on the origins of mammalian diversity (Chair: Julia Schultz)
10:15–10:30	S8: Morphological and molecular variability in <i>Peridinium volzii</i> (Peridiniaceae, Dinophyceae) and its relevance for infraspecific taxonomy <u>Holzer</u> , V., Kretschmann, J., Owsiany, P.M. & Gottschling, M.
10:30–10:45	S9: Carnassial shape variation in Carnivora, Hyaenodonta and Dasyuromorphia compared by geometric morphometrics <u>Lang</u> , A.J. & Martin, T.
10:45–11:00	S10: Suctorial feeding in millipedes (Myriapoda: Diplopoda): The head morphology of the Colobognatha <u>Moritz</u> , L., Blanke, A. & Wesener, T.
11:00–11:15	Breakout rooms: Main lecture / Talk 1-3 to meet the speakers / Café A, Café B, Café C
11:15–11:30	S11: Comparative skull morphology in typhlopoid blindsnakes of the genus <i>Letheobia</i> via Micro-CT <u>Rech</u> , I. & Koch, C.
11:30–11:45	Morphological boundaries among the species of the Caucasian rock lizards (Genus <i>Darevskia</i>) <u>Gabelaia</u> , M., Misof, B., Tarkhnishvili, D. & Wipfler, B.
11:45–12:00	Dragons in Neglect: Taxonomic Revision of Sulawesi Sailfin Lizards (<i>Hydrosaurus</i> Kaup, 1828) <u>Denzer</u> , W., Campbell, P., Manthey, U., Glässer-Trobisch, A. & <u>Koch</u> , A.
12:00–12:15	Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C
12:15–12:30	S13: How to stay attached – Morphological adaptations in the reproductive system of the female pelvic brooder <i>Oryzias everisi</i> <u>Schüller</u> , A., Herder, F., Spanke, T., Schwarzer, J., Vehof, J. & Wipfler, B.
12:30–12:45	S14: Pelvic brooding in Sulawesi ricefishes (Belontiiformes; Adrianichthyidae): Parallel evolution in a specialized reproductive strategy <u>Spanke</u> , T., Flury, J.M., Hilgers, L., Nolte, A. W., Utama, I. V., Herder, F., Wipfler, B., Misof, B. & Schwarzer, J.
12:45–13:00	S15: Sexual dimorphism in an adaptive radiation: Does intersexual niche differentiation result in ecological character displacement? <u>Wasiljew</u> , B., Pfaender, J., Wipfler, B., Gabelaia, M., Utama, I.V., Wantania, L.L. & Herder, F.
13:00–13:15	Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C

Main lecture 3:

Jaw shapes of extant and extinct mammals provide insight on the origins of mammalian diversity

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Modern mammalian diversity is the result of an immense adaptive radiation. However, there remains considerable debate over the timing and dynamics of the radiation, particularly as it relates to the Cretaceous-Paleogene (K-Pg) mass extinction event 66 million years ago (Ma). This is due in part to difficulties in examining patterns of ecological diversity in deep time, which requires ecological inferences from fossil morphologies. Dental and mandibular elements are the most commonly preserved fossils of early mammals, and molar morphologies often provide ecological evidence via dietary correlates. In contrast, the link between jaw shape and diet has been explored to a lesser degree. Thus, to identify jaw correlates of diet that can be readily applied to fossil mammals, I first examine the association between jaw shape and diet in extant therians (marsupials and placentals). I apply phylogenetic comparative methods to jaw measurements and dietary data for a diverse sample of mammals. The distance between the jaw joint and angular process (JAPr distance) is an especially powerful predictor of diet, increasing with greater herbivory. This distance reflects the attachment area of jaw muscles that are particularly important for masticating plant materials. I then apply these findings to the fossil record by measuring JAPr distances in trechnotherians (therians and close relatives) from the Middle Jurassic through Eocene (i.e., 174–34 Ma). Fossil macroevolutionary patterns suggest that trechnotherians were small insectivores for much of the Mesozoic and experienced a rapid increase in dietary diversity prior to the K-Pg boundary, starting at approximately 80 Ma and coinciding with the ecological diversification of flowering plants. In addition, the diversification of herbivorous mammals accelerated after both the K-Pg mass extinction event and the Paleocene-Eocene Thermal Maximum (56 Ma). Thus, this study demonstrates the strong correlation between jaw morphology and diet, and it offers new insight on early mammal evolution by suggesting a multi-step radiation. Further, these results highlight that convergent evolution of similar jaw traits is especially common among many mammalian subclades. This has important implications for phylogenetic analyses of fossil mammals, which rely on morphological characters, because jaw (or molar) characters that are linked to ecological traits may be more prone to homoplasy, thus skewing phylogenetic results and muddling our understanding of mammalian relationships.

S8: Morphological and molecular variability in *Peridinium volzii* (Peridiniaceae, Dinophyceae) and its relevance for infraspecific taxonomy

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Contemporary delimitation of species and populations in the microbial world relies on an integrative approach combining molecular and morphological techniques. In case of the dinophyte *Peridinium volzii* Lemmerm., a considerable number of taxa such as varieties and forms have been reported, but it is unclear at present whether the corresponding traits are stable within reproductively isolated units or refer to intraspecific variability. We established 27 monoclonal strains from Central Europe with a morphology that is consistent for *P. volzii* and characterised them by sequences gained from the rRNA operon (i.e., SSU, ITS, LSU). Ten of such strains, representative for the entire diversity observed, were investigated in detail morphologically using light and electron microscopy. In the molecular tree, *P. volzii* was monophyletic, sister group of *Peridinium willei* Huitf.-Kaas and four ribotypes could be distinguished. Some traits corresponding to previously described varieties and forms were found in individual cells across the strains under investigation, but not as stable characters correlating to certain ribotypes. We also observed new morphological variability (e.g., unusual shape of plate 4''). Cell size and displacement of the cingulum was significantly different between certain ribotypes but in turn, such diagnostic traits are impossible to assign to the already described taxa having ambiguity. The present data given, we are reserved to accept more than a single reproductive unit for *P. volzii*. Thus, more research is necessary including a focus on species delimitation, also from putative close relatives such as *Peridinium maeandricum* (Lauterborn) V. Brehm.

S9: Carnassial shape variation in Carnivora, Hyaenodonta and Dasyuromorphia compared by geometric morphometrics

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Carnassial teeth, specialized for a cutting function, convergently evolved multiple times in therian mammals as an adaptation to a carnivorous diet. We conducted an analysis of shape variation of the lower carnassials of extant Carnivora, extant Australian marsupicarnivores (Dasyuromorphia) and extinct Hyaenodonta via geometric morphometrics to check for differential morphospace distributions. The study included generalized as well as specialized hypercarnivorous taxa. Carnivorans possess a single lower carnassial (m1) in contrast to multiple carnassials in the Hyaenodonta (m1-3) and the Dasyuromorphia (m2-4), which were all included in the morphospace analysis. A PCA of the aligned shape variables shows that the enlargement of the carnassial cutting blade relative to the talonid crushing basin, indicated by the first principal component, separates the primitive from the specialized carnassials. In unspecialized taxa with multiple carnassials, all carnassials are shifted along PC1 compared to the specialized taxa. In all taxa with multiple carnassials, the most distal tooth is more specialized than the mesial teeth, as indicated by the value distribution along PC1. Unspecialized carnivoran carnassials share a morphospace with specialized carnassials present in some Caniformia (*Canis*, *Lycan*, *Speothos*) when taking PC2 into account, which is associated with a longitudinal elongation and a transversal compression of the teeth. An ancestral state reconstruction indicates that this shape variation may be a plesiomorphic feature of Carnivora, which has been retained in specialized Caniformia and is not found in marsupicarnivores and hyaenodonts. It may pose a functional advantage since this elongated tooth shape enables a balanced presence of a cutting blade in mesio-distal orientation as well as a crushing basin.

S10: Suctorial feeding in millipedes (Myriapoda: Diplopoda): The head morphology of the Colobognatha

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In the four orders of uncertain relationship within Colobognathan millipedes, mouthparts are reduced. Because of this reduction, and due to their head shape and microhabitat, it is assumed that the Polyzoniida, Siphonocryptida and Siphonophorida feed suctorial on fungi or algal films. However, the internal morphology of their heads and their feeding mechanism is unknown. Here we study the skeletomuscular system of these groups with a combination of micro-computed tomography, histology and scanning electron microscopy to infer potential feeding modes. The Polyzoniida, Siphonocryptida and Siphonophorida have internalized, narrow mandibles, which are stylet-like in Siphonophoridae, and show a single chambered preoral sucking pump, unique within myriapods. The sucking pump consists of a rigid sclerotized ventral wall, which is supported by the tentorial complex, and a thinner flexible dorsal wall, on which large dilator muscles insert. Posteriorly the sucking chamber can be closed by a circular sphincter muscle. We suggest that the mandibles are used to penetrate surfaces or to loosen particles, and liquid content is sucked in by activation of dilator muscles, while the sucking chamber is closed posteriorly. Subsequently the food is emptied into the pharynx by the elastic contraction of the dorsal wall or by compressor muscles. Our results represent the first morphological evidence for a suctorial feeding mode within colobognathan millipedes. In addition, their sucking pump shows striking similarities to those of Lepidoptera and Hemiptera: All show a rigid ventral wall, supported by the endoskeleton, an elastic dorsal wall and large dilator muscles to move the pumping mechanism. The apparently convergent evolution of this complex morphology in three unrelated arthropod lineages shows how feeding advantages can lead to similar biomechanical solutions.

S11: Comparative skull morphology in typhlopoid blindsnakes of the genus *Letheobia* via Micro-CT

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Although blindsnakes of the family Typhlopidae look very similar and inconspicuous on the outside, they have a diverse skull morphology. Both the shape of the skull itself and the shape and size of the individual bones can differ between genera, but also species-specifically. Multiple bones may be fused or separated and individual bones may be paired or unpaired. The genus *Letheobia* belongs to the subfamily Afrotiphlopinae within the Typhlopidae and currently comprises 37 species, most of which are relatively well studied externally, however little is known about their cranial morphology. Using micro-CT images, we compared the skulls of the holo- and syntypes of ten *Letheobia* species, housed in the collections of the Senckenberg Museum Frankfurt, Frankfurt (SMF), the Museum für Naturkunde, Berlin (ZMB), and the Zoologisches Forschungsmuseum Alexander Koenig, Bonn (ZFMK): *L. akagerae*, *L. buchholzi*, *L. debilis*, *L. decorosus*, *L. episcopus*, *L. gracilis*, *L. graueri*, *L. lumbriciformis*, *L. pembana*, *L. simoni*.

The skull of each species looks unique, but those of *L. episcopus* and *L. simoni* are remarkably distinguished from the other species by fused frontal and parietal bones and fused basioccipital and basisphenoid bones, which are separate in the other species.

Our results show that the skulls of species within the genus *Letheobia* can vary greatly, and skull characteristics are thus of high systematic value. For this reason, skull morphology should be considered as much for distinguishing blind snakes as external morphology, genetics, and biogeography.

Morphological boundaries among the species of the Caucasian rock lizards (Genus *Darevskia*)

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Rock lizards of the genus *Darevskia* (Arribas, 1999) are genetically diverse group mostly found in the Caucasus Mountains. It is difficult to delimit the four closely related *Darevskia* species due to a high degree of morphological similarity and overlapping identification characters. They hybridize and the individuals with intermediate morphology and genetic characters are found. As a result, it is difficult to assign the individuals to distinct species. This is particularly true for the traditional methods such as qualitative morphometrics, where multiple measurements of the body and scales are compared. In a recent publication (Gabelaia et al. 2018), we showed that 3D geometric morphometrics (GM), i.e. the inclusion of the integral shape of the head, provides better results but still fails to define the morphological boundaries associated with genetically defined species of *Darevskia*. We assume that the skull shape is, differently from the head shape, more species-specific and conservative for delimiting the species' morphological boundaries. The skull shape is less prone to homoplasy than the scalation pattern, involved in the external head shape analysis, which is highly variable in *Darevskia*. In the current study, we conduct landmark based and landmark-free (following the approach of Pomidor et al. 2015) GM analyses on 3D skull and mandible models of the different *Darevskia* species to see if it is more powerful in delimiting the species boundaries than the external head shape, at the same time comparing the two GM methods.

Dragons in Neglect: Taxonomic Revision of Sulawesi Sailfin Lizards (*Hydrosaurus* Kaup, 1828)

Denzer, W.¹, Campbell, P.², Manthey, U.³, Glässer-Trobisch, A.⁴ & Koch, A.⁵

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Currently, three different species are recognized within the Southeast Asian agamid genus *Hydrosaurus*: *H. amboinensis* (Schlosser, 1768) from Ambon, Seram, Sulawesi and New Guinea, *H. pustulatus* (Eschscholtz, 1829) from the Philippines and *H. weberi* (Barbour, 1911) from Halmahera and adjacent islands. Historically, two additional species were described from the island of Sulawesi, but were synonymized with *H. amboinensis* more than a century ago and have been treated as such in most subsequent publications. In order to revise the taxonomy and diversity of these enigmatic agamid lizards, we examined the corresponding type specimens and additional material originating from Sulawesi and compared them with photographs of live specimens from field trips. Due to differences in colour pattern and scalation characters, we resurrect the taxa *celebensis* Peters, 1872 and *microlophus* Bleeker, 1860 from the synonymy of *H. amboinensis*, which in turn is restricted to New Guinea and the central Moluccas. Hence, Sulawesi is currently the only known island within the genus' range to be inhabited by two different species of sailfin lizards. Our systematic investigation brings the number of recognized species within the genus *Hydrosaurus* to five.

References

Denzer, W., Campbell, P., Manthey, U., Glässer-Trobisch, A. & Koch, A. (2020). Dragons in neglect: Taxonomic revision of the Sulawesi sailfin lizards of the genus *Hydrosaurus* Kaup, 1828 (Squamata, Agamidae). *Zootaxa* **4747**(2), 275-301.

S13: How to stay attached – Morphological adaptations in the reproductive system of the female pelvic brooder *Oryzias eversi*

Schüller, A.¹, Herder, F.², Spanke, T.³, Schwarzer, J.⁴, Vehof, J.⁵ & Wipfler, B.⁶

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An enormous diversity of reproductive strategies evolved within teleost fishes. In ricefishes (Adrianichthyidae) a unique reproductive strategy called pelvic brooding is known for the three species *Oryzias sarasinorum*, *O. eversi* and *Adrianichthys oophorus* endemic to freshwaters in Sulawesi. Generally, after spawning female ricefishes carry a bundle of eggs which is attached via filaments that emerge from the genital opening. Transfer brooding ricefish species, like the well-known Medaka, deposit the eggs a few hours after spawning, whereas the eggs of pelvic brooding species stay attached to the female until the juveniles hatch. In the pelvic brooder *O. sarasinorum* a transient structure called plug is known to anchor the filaments inside the female. However, the adaptations in the female reproductive tract of the other two species are unknown. In the present study, we investigated morphological adaptations in the reproductive system of female *O. eversi*, the likewise pelvic brooding sister group of *O. sarasinorum*. We sampled females at several time points over the reproductive cycle and generated histological sections. Over the course of egg carrying, a tangled mass of attaching filaments, epithelia cells, blood capillaries and collagen tissue becomes a compact plug-like structure in the anterior part of the oviduct. Moreover, oocyte maturation in the ovary seems to be suppressed and the structure of the ovarian wall changes during this time. Our results demonstrate a striking resemblance of the adaptations to pelvic brooding in the reproductive system of *O. eversi* with *O. sarasinorum*. This is in line with phylogenetic evidence indicating that pelvic brooding within *Oryzias* shares a common evolutionary origin.

S14: Pelvic brooding in Sulawesi ricefishes (Beloniformes; Adrianichthyidae): Parallel evolution in a specialized reproductive strategy

Spanke, T.¹, Flury, J.M.¹, Hilgers, L.¹, Nolte, A. W.², Utama, I. V.³, Herder, F.¹, Wipfler, B.¹, Misof, B.¹ & Schwarzer, J.¹

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The evolution of similar character traits in different species as a response to common environmental pressures can be seen in various examples throughout the animal kingdom. Highly interesting cases of such convergent or parallel evolutions include reproductive strategies, as they can involve simultaneous adaptations of morphological, physiological or behavioral traits.

Fishes, due to their enormous diversity in reproductive strategies, represent a prime example for this field of study. Ricefishes (Beloniformes; Adrianichthyidae) are a group of small freshwater fishes found in East-Asia. The vast majority of ricefishes are known to be external bearers in which females deposit a cluster of eggs on submerged substrates shortly after spawning. However, for two ricefish lineages endemic to the island Sulawesi, a distinct reproductive strategy called 'pelvic brooding' is described. Females of pelvic brooding species (*Adrianichthys oophorus*, *Oryzias eversi*, *O. sarasinorum*) carry the fertilized egg-cluster for about two weeks until the offspring hatch. The egg cluster, which is situated in an abdominal concavity and covered by elongated pelvic fins, is attached to the female via filaments that originate from each egg. The filaments converge inside the female and form a plug-structure that anchors the entire clutch inside the ovarian cavity.

In a comparative approach involving transfer brooding species and the three pelvic brooders, we employ high-resolution μ CT-imaging, morphometrics and histology to identify the morphological prerequisites associated with this unique reproductive strategy. We found similar adaptations in the two lineages of pelvic brooding ricefishes including the plug-structure, modifications of the ribs forming the ventral concavity and elongated pelvic fins in female pelvic brooders. The insights into the morphological prerequisites of pelvic brooding will add up to a deeper understanding of the evolution of this unique reproductive strategy.

S15: Sexual dimorphism in an adaptive radiation: Does intersexual niche differentiation result in ecological character displacement?

Wasiljew, B.¹, Pfaender, J.², Wipfler, B.¹, Gabelaia, M.¹, Utama, I.V.³, Wantania, L.L.^{1,3} & Herder, F.¹

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Evolutionary radiations are one of the most plausible explanations for the rich biodiversity on earth. Ecological opportunity has been identified as a key factor permitting adaptive radiations, the most studied form of evolutionary radiations, and biotic interactions are a major component of ecological opportunity. Competition among individuals is expectedly highest in populations of conspecifics. Divergent modes of resource use might minimize trophic overlap, and thus intraspecific competition, resulting in ecological character displacement between males and females. However, the role of intersexual differentiation in speciation processes is insufficiently studied. The few studies available suggest that interspecific niche differentiation exists in adaptive radiations, but their role within the radiation, and the extent of differentiation within the organism itself, remains largely unexplored. Here, we test the hypothesis that multiple morphological structures are affected by sexual niche differentiation in “roundfin” *Telmatherina*, the first case where sexual niche differentiation was demonstrated in an adaptive fish radiation. We show that males and females of two of the three “roundfin” morphospecies differ in several structural components of the head, all of them are likely adaptive. Sexual differentiation in the head apparatus is linked to the respective morphospecies-specific ecology, and affects several axes of variation in cranial traits. Trait variation translates into different feeding modes, processing types and habitat usages that add to interspecific variation in all three morphospecies. Intrasexual selection, i.e. male-male competition, may contribute to variation in some of the traits, but appears unlikely in internal traits which are invisible for other individuals. We conclude that intersexual morphological differentiation adds to the adaptive spectrum of “roundfin” *Telmatherina*, and might play a key role in minimizing intraspecific competition in emerging radiations.

Thursday 4/3/2021	
09:15–10:00	<p>Main lecture 4: Biodiversity</p> <p>Pedro Frade: Codiversification and biodiversity loss in reef-building corals</p> <p>Chair: Dominique Zimmermann</p>
10:15–10:30	<p>A change in paradigm: From publications to publishing building blocks of digital accessible biodiversity knowledge</p> <p><u>Agostj, D., Bénichou, L. & Penev, L.</u></p>
10:30–10:45	<p>The Biodiversity Crisis Response Committee of SPNHC: Mitigating biodiversity loss and advocating for the collections community's contributions to conservation efforts</p> <p>Ellwood, L., Bentley, A., <u>Buschbom, J.</u>, Karim, T., Mast, T., Nelson, G., Wheeler, E.K.</p>
10:45–11:00	<p>The Nagoya Protocol – what does it mean for you?</p> <p><u>Karger, E.</u></p>
11:00–11:15	<p>Breakout rooms: Main lecture / Talk 1-3 to meet the speakers / Café A, Café B, Café C</p>
11:15–11:30	<p>National Research Data Infrastructure – how the NFDI4BioDiversity mobilizes and presents valuable community data</p> <p><u>Ebert, B. & Glöckner, F.O.</u></p>
11:30–11:45	<p>Introducing GBOL III: Dark Taxa, targeting Central Europe's unknown insect biodiversity</p> <p><u>Rdudh, V. & Peters, R.S.</u> – on behalf of the GBOL III: Dark Taxa consortium</p>
11:45–12:00	<p>FörTax – Promotion of taxonomic knowledge as a basis for nature conservation: Successes, deficits and prospects</p> <p><u>Waskow, K., Nöske, N., Stehr, K. & Miesen F.W.</u></p>
12:00–12:15	<p>Breakout rooms: Talk 1-3 to meet the speakers / Café A, Café B, Café C</p>
12:15–12:30	<p>Presentation of Student Awards and Laudatio of Rensch Prize Winner by Mark Gottschling</p>
12:30–13:00	<p>Rensch Prize Presentation: Diversity, morphology, and taxonomy of selected dinophytes</p> <p><u>Kretschmann, J.</u></p>
13:00–13:15	<p>Photo session of participants and short break</p>
13:15–14:00	<p>Mitgliederversammlung (General Assembly) & Closing ceremony</p>

Main lecture 4:

Codiversification and biodiversity loss in reef-building corals

Frade, P.R.¹

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I will start by revisiting the current conservation state of coral reefs, and will introduce the coral holobiont concept. I will then present three research topics: 1) the evolutionary ecology of corals and their photoautotrophic symbionts, 2) the deep reef as a climate change refuge for coral biodiversity, and 3) new research findings potentially contributing to increased resilience of corals to climate change. Throughout this presentation, I will bring together personal and professional aspects that have shaped my career as coral reef scientist, including the recent witnessing and reporting of mass coral bleaching events on the Great Barrier Reef, in Australia.

A change in paradigm: From publications to publishing building blocks of digital accessible biodiversity knowledge

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So far, our knowledge about biodiversity is in an estimated 500M annually increasing number of pages starting with Linnaeus' works in 1753 and 1758 respectively. For each species, at least one taxonomic treatment, a clearly dedicated section of a publication, exists. From Linnaeus inset, treatments have further been structured into citations of previous treatments, description, behavioral notes and distributions to name a few, and are based on collections of specimens. These treatment citations, also including statements like synonymies, include the entire catalogue of life, based on a citation network similar to bibliographic citations used in publications. This situation is the best possible prerequisite for leveraging the Internet, even more its aspect of the semantic web, whereby a treatment cites specimens, gene sequences can also be linked back to the citing treatment, the knowledge graph. At the same time, research results about a specimen, a gene sequence are immediately accessible, facilitating many novel opportunities, speeding up taxonomists' work and providing a never seen access to biodiversity data for life sciences, conservationists and beyond. It complements ongoing research on sequencing all species of life (e.g. BioScan), or citizen science initiatives (e.g. iNaturalist). It provides existing knowledge about the identified sequenced or photographed species, a platform to add data about unknown species and include it into the corpus of digital accessible knowledge. Such a system also allows new entries to this knowledge, for example from each specimen, a published figure, a taxonomic or a person's name. This lecture will present two approaches. The first focuses on how to make known biodiversity accessible through the Biodiversity Literature Repository (BLR) and TreatmentBank. The second is based on Pensoft's, the Consortium of European Taxonomic Facilities (CETAF) publishing group's and the European Journal of Taxonomy (EJT) publishing styles, making new data immediately digital accessible knowledge. This includes making treatments, figures, materials citations findable, accessible, interoperable and reusable (FAIR) and therefore making them accessible and reusable in the Global Biodiversity Information Facility (GBF). The ultimate goal of this change in paradigm is to make not only all known data about biodiversity digital immediately accessible knowledge but make use of the authors' already existing structured data in his research environment.

References

Biodiversity Literature Repository: <https://zenodo.org/communities/biosyslit/search?page=1&size=20>

TreatmentBank: <http://plazi.org/>

Pensoft: <https://pensoft.net/browse-journals>

EJT: <https://europeanjournaloftaxonomy.eu/index.php/ejt/issue/archive>

The Biodiversity Crisis Response Committee of SPNHC: Mitigating biodiversity loss and advocating for the collections community's contributions to conservation efforts

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In 2019, the Global Assessment report of the Intergovernmental Panel on Biodiversity and Ecosystem Services (IPBES) called the world to urgent action to avert accelerating biodiversity loss and nature's unprecedented and dangerous decline. In response to this call, The Society for the Preservation of Natural History Collections (SPNHC) initiated the formation of a Biodiversity Crisis Response Sessional Committee.

The committee is tasked with investigating the role of SPNHC and more generally the natural history collections community in mobilizing collections information for effective mitigation of biodiversity loss, and in widely broadcasting the community's positive contributions to conservation efforts.

Over the past two years, the committee conducted a survey on the above topics distributed to SPNHC members and biodiversity scientists via listservs; it submitted, in close cooperation with CETAF, two comments to the public review of the monitoring framework of the post-2020 Global Biodiversity Framework of the Convention on Biological Diversity; and organized a well-attended webinar of panel speakers discussing "Actions to Conserve Biodiversity".

Based on the results of these activities, the committee currently is developing a set of goals and objectives that identifies the foundation for meaningful and sustained organizational and individual action, which promote a transition towards the protection and restoration of biodiversity and nature.

The Nagoya Protocol – what does it mean for you?

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Have you heard of the Nagoya Protocol? If you are doing research on non-human biological material that originally comes from outside of Germany, then you need to know about it! Regulation (EU) No 511/2014 creates compliance obligations for German researchers and the competent authority in Germany, the German Federal Agency for Nature Conservation (Bundesamt für Naturschutz, BfN), is checking universities and research institutes across the country to make sure that basic and non-commercial researchers are following the rules.

Understanding compliance is important but it can be daunting! In this short talk, I will provide a brief overview of researchers' obligations arising from the implementation of the Nagoya Protocol and explain how the German Nagoya Protocol HuB, or GNP HuB for short, is helping the researchers from the German academic research community with understanding their obligations.

I am the manager of the GNP HuB and have previously worked on ABS and Nagoya Protocol related issues for both the Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH and the BfN. In 2018, I co-authored a study for the Secretariat of the CBD on national measures addressing the use of and benefit-sharing arising from the use of digital sequence information on genetic resources (DSI).

I am based at the DSMZ, which is actively involved in issues relating to the Nagoya Protocol and ABS, participating in various projects and studies as well as bringing the perspective of the science community into relevant policy discussions. As registered collection of genetic resources recognized under the Regulation (EU) No 511/2014, DSMZ ensures that all of the biological material it holds is compliant with the Nagoya Protocol.

National Research Data Infrastructure – how the NFDI4BioDiversity mobilizes and presents valuable community data

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NFDI4BioDiversity is a consortium of 49 partners dedicated to deliver practical tools for researchers and improve data availability for environmental studies/ecology. We are part of a greater network within the German National Research Data Infrastructure (NFDI), which is funded through a 10-year-programme of the Joint Science Minister Conference in Germany (GWK). Starting in October 2020, the first funding phase runs for five years until September 2025. At the core of NFDI4BioDiversity are data on the biodiversity of animals, plants and microorganisms. NFDI4BioDiversity builds on previous work by the German Federation for Biological Data, which has been funded by the DFG since 2014. As part of this project, the data centres of natural history museums and established data archives such as PANGAEA and ENA were connected to a common portal, workflows for data submission were standardised, and common (meta)data standards as well as tools and services for research data management (FDM) were established. NFDI4BioDiversity extends the range of activities by incorporating use cases from the broader biodiversity community, including government agencies and citizen science. In the talk, the use cases and IT-based tools will briefly be presented.

Introducing GBOL III: Dark Taxa, targeting Central Europe's unknown insect biodiversity

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Over the last years the GBOL (German Barcode of Life) initiative has set up an efficient infrastructure for DNA barcoding and has built a DNA barcode reference library for the animals, plants and fungi of Germany. While also some species rich taxa of animals are well represented, there are very serious gaps in the reference library in the insect orders Diptera and Hymenoptera. The megadiverse parasitoid wasps and “lower Diptera” contain many so-called Dark Taxa for which only very few or no information are available. Within the new phase GBOL III: Dark Taxa, funded again by the German Federal Ministry of Education and Science (BMBF), we tackle the unknown insect biodiversity of Germany and Central Europe in an unprecedented way, increase the completeness of the DNA barcode reference database and train a new generation of taxonomists. Results of GBOL III: Dark Taxa will heavily improve the significance of future biodiversity studies, including biodiversity monitoring and insect conservation. The project will also focus on knowledge transfer to attract attention for the diversity and importance of Dark Taxa in science and society. Here, we report on the structure and aims, the target taxa and the people and institutions involved in our recently launched initiative.

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 supplies 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.

Rensch Prize Presentation:

Diversity, morphology, and taxonomy of selected dinophytes

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The biodiversity assessment of dinophytes started in the late 18th and early 19th century with light microscopy. For such historical descriptions, drawings have been mostly designated as types, because no original physical material is preserved. Based on these drawings many taxa cannot be unambiguously determined leading to an inconsistent use of names and a considerable taxonomic confusion. The International Code of Nomenclature for algae, fungi, and plants (ICN) provides the tool for designating an epitype to clarify such ambiguous historical names. Epitypification has great potential for a robust taxonomy in the various unicellular organismal groups, and this consists in collecting new material as closely as possible to the type locality. The goal is to capture the original author's intent as inferred from the protologue, specimens and original illustrations, but relatively few such studies have employed this approach in the past. However, we taxonomists are encouraged to acknowledge the work of previous researcher generations and to give the clarification also and particularly of old scientific names in the microbial world at least a try.

My PhD thesis consists of 9 peer reviewed and published papers. Newly established strains of dinophytes provided information for the phylogenetic placement and resulted in the description of a new family, two new genera and seven new species or varieties. Furthermore, the strains were used for the investigations on morphological and molecular intraspecific variability and for reliable inferences on the distribution of dinophytes. Strains, established from samples, collected at the type locality and being morphologically consistent with corresponding protologues, were used for the taxonomic clarification of eight scientific names and the designation of interpretative epitypes. Taxonomic activity in the microbial world is usually the result of considerable work, which is associated with also the gain of new morphological and molecular data.

13.01.2021

EINLADUNG

zur 22. Ordentlichen Mitgliederversammlung der Gesellschaft für Biologische Systematik (GfBS)

2021

Termin: Donnerstag, 4. März (13.15–14:00)

Ort: online

Tagesordnungspunkte:

1. Feststellung der Tagesordnung
2. Bericht des Präsidenten und Aussprache
3. Bericht des Geschäftsführers
4. Berichte der Beisitzer
5. Berichte des Schatzmeisters und der Rechnungsprüfer sowie Aussprache
6. Entlastung des Vorstandes
7. Entwicklung der ODE
8. Beschluss über Tagungstermin und Tagungsort für die nächste Jahrestagung
9. Verschiedenes