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## Public keynotes

### Modern extinctions and what we need to know – and do – to prevent them

Stuart Pimm<sup>1</sup>

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How many species are known, how many remain undescribed, and how many are threatened with extinction? These three questions are inter-related and all depend critically on where species occur. For example, there are approximately 390,000 described vascular plants and models of rates of description predict 70,000 still to be named – a total that matches expert opinions. Those predictions expect the unknown species to be in the biodiversity hotspots where rates of habitat loss are exceptionally high. Not surprisingly, recently described species have smaller geographical ranges than ones described many decades ago. And unknown species are surely unknown because their ranges are also small. Small ranges and high levels of habitat loss combine to make it probably that undescribed species should be added to the total of known species at risk of extinction. A third of plant species are at risk – comparable levels to well-known vertebrate taxa. Comparing rates of extinction to the episodic mass extinctions in the fossil record is fraught with difficulty. Comparisons to rates of diversification derived from molecular phylogenies are much more certain. Species are likely going extinct hundreds to thousands of times faster than they diversify. What can be done to prevent extinctions also depends much on geography. About 10% of species occur on islands as small or smaller than New Zealand. Invasive species constitute a major threat to them. For the remainder, in the key places, continental habitats are massively fragmented. Energetic restorations of habitat connections offer considerable hope to protect species there.

### *Danuvius guggenmosi* and the positional behaviour of the last common ancestor of great apes and humans

Madelaine Böhme<sup>1</sup>

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Many ideas have been proposed to explain the origin of bipedalism in hominins and suspension in great apes (hominids); however, fossil evidence has been lacking. It has been suggested that bipedalism in hominins evolved from an ancestor that was a palmigrade quadruped (which would have moved similarly to living monkeys), or from a more suspensory quadruped (most similar to extant chimpanzees). The discovery of partial skeletons from a new late Miocene ape *Danuvius guggenmosi* challenged these views. In this presentation I will demonstrate the functional morphology of *Danuvius*, which provides evidence of a newly identified form of positional behaviour—extended limb clambering. I will further discuss potential implications for homoplasy within great apes' postcranial skeleton and resulting challenges for fossil hominid systematics.

## The evolution of annelids

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Annelids comprise a group of over 20,000 described species found in marine (benthic and pelagic), limnic and terrestrial habitats. Membership and relationships of this taxon has been matter of debate for decades. Several taxa which have been originally described as separate “phyla” outside of Annelida have been found to represent ingroup taxa in the last two decades, such as Echiura, Sipuncula, Myzostomida or Orthonectida. Phylogenomic analyses of huge data matrices made it finally possible to recover a well-supported and resolved annelid backbone tree. Based on this hypothesis, most of the annelid diversity is comprised in two reciprocal monophyletic groups, Sedentaria and Errantia, which are named after the predominant life style of their members. Several taxa branch successively outside this large radiation. Oweniidae + Magelonidae represent the sister taxon of all other annelids. Among others Chaetopteridae, Sipuncula, and Amphinomida are also part of this basally branching part of the annelid tree of life. Here I will review important steps which led to this phylogenetic hypothesis, explore the evolution of several morphological structures (e.g., nervous system, nuchal organs, parapodia) and highlight reasons for the difficulty of this phylogenetic problem. Finally, I will give an outlook of future tasks.

## Rensch-Award keynote

### **Patterns of morphological evolution in the skull of turtles: contributions from digital paleontology, neuroanatomy and biomechanics**

Gabriel S. Ferreira<sup>1</sup>

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The fossil record is a fundamental facet of evolutionary morphology, since from its study it is possible to retrieve unique data on many evolutionary aspects, e.g., rates of evolution, the role of mass extinctions on diversity, the polarity of character changes, and a glimpse into morphotypes that don't exist anymore. At the same time, new tools and methods, such as computed tomography, digital reconstructions, and Finite-Element Analysis, known collectively as digital or virtual paleontology, have brought novel possibilities on how to formulate and answer paleontological questions. Here, digital paleontological techniques were used to analyze the patterns of morphological evolution of the skull of turtles and provide novel interpretations of the neuroanatomical and functional relations of specific cranial traits to the whole skull architecture. Following an overview of the osteological, muscular, developmental, and functional evolution of the craniocervical system of turtles, computed tomography and other 3-D digital methods, were used to reconstruct the jaw adductor musculature and the neuroanatomical structures of one of the earliest turtles, *Proganochelys quenstedti*, in order to investigate the early evolution of the adductor chamber and the sensorial anatomy in this taxon. Following, Finite-Element models of a series of extinct and extant taxa, together with hypothetical simulated morphotypes, were analyzed to explore the relation between muscle stress distribution patterns and skull architecture in the group. A scenario of

progressive correlation between neck and skull is suggested, in which modifications in one structure opened new paths to the other, and vice-versa. Most of the related evolutionary change happened during the Jurassic and, as such, might have been related to the great diversification experienced by turtles at this time.

## Oral presentations

### Oral Presentation 1

#### **Phylogeny of Sabellida (Annelida)**

Ekin Tilic<sup>1</sup>, Greg W. Rouse<sup>2</sup>

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Sabellida are a diverse group of tube-dwelling sedentary marine worms with an often colorful, feathery crown. The phylogeny of this fascinating taxon still remains poorly understood, with the little available molecular sequence data conflicting with previous morphology-based studies. We present the results of our phylogenomic analyses with 17 new sabellid transcriptomes, and a targeted exon capture analysis, where we sequenced over 500 exons for ca. 100 additional sabellid species. We also conducted a thorough methodological analysis comparing phylogeny reconstruction from gene trees (ASTRAL) and concatenated species tree analyses. The results of our phylogenomic study highly supports the position of Fabriciidae as the sister taxon of a monophyletic clade of Sabellidae + Serpulidae. The new and robust sabellid phylogeny, will not only allow the necessary taxonomic revision of this taxon, but also provides a tool to explore the evolution of the diverse life-history strategies, body size and morphology within Sabellidae. Furthermore, our analyses revealed over 10 new sabellid species, that are yet to be described.

### Oral Presentation 2

#### **Stowaways – marine leeches infecting olive ridley sea turtles entangled in ghost nets**

Stephanie Köhnk<sup>1,2</sup>, Claire Petros<sup>2</sup>, Claire Lomas<sup>2</sup>, Enas Mohamed Riyad<sup>3</sup>, Martin Stelfox<sup>2,4</sup>

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Sea turtles are known to host a wide variety of organisms, including parasitic marine leeches of the family Ozobranchidae. Leeches are sanguivorous (blood feeders) and are subsequently found on soft skin areas of turtles, such as the cloaca and corners of eyes and mouth. Superinfection with this parasite can lead to severe damage to the host, for example sea turtle leech erosion disease (SLED). Turtles suffering from SLED can show severe disfigurement to erosion of skin, muscle and occasionally bone tissue (Bunkley-Williams et al. 2008). Ozobranchidae have been shown to be a potential candidate as a

mechanical vector for the tumour inducing fibropapilloma-associated turtle herpesvirus (Greenblatt et al. 2004). Marine Ozobranchidae have been found in all major ocean basins infecting all hard-shelled sea turtle species. The primary focus of previous investigations has been in the Atlantic and Pacific Oceans. Records from the Indian Ocean are scarce but indicate a widespread distribution with specimens documented in Western Australia, Reunion, Seychelles and India (Baird 1869, Sanjeeva Raj 1959, Reme 1980, Göpper et al. 2018). In this study, we present the first cases of ozobranchid leeches found on sea turtles in the Maldives. The host turtles were entangled in abandoned, lost or discarded fishing nets, so called ghost nets, and treated at the Olive Ridley Project's Marine Turtle Rescue Centre in Baa Atoll in the Maldives. Both hosts were Olive Ridley turtles (*Lepidochelys olivaceae*), which are typically not resident to the country, but are often observed entangled in ghost nets. The entangled turtles are thought to be carried over great distances when floating in various ocean currents. Ozobranchid leeches were identified to the species level with morphological and barcoding methods (Davies 1978, McGowin et al. 2011). The presence of parasitic leeches on entangled turtles may have epidemiological implications for the endemic populations of sea turtle species throughout the Indian Ocean.

### Oral Presentation 3

#### **Exploring species delimitation methods in a Cretan door snail species complex based on RADseq data**

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Even with molecular genetic data, delimiting species in radiations is notoriously difficult because of incomplete lineage sorting and introgression between incipient species. Next generation sequencing of genome-wide markers may help to overcome these problems. We used the door snail genus *Albinaria* from the Eastern Mediterranean, which is one of the most species rich land snail genera, to assess different methods for species delimitation. We generated double digest Restriction site Associated DNA sequencing (ddRADseq) data of 140 individuals of 48 populations of the *Albinaria cretensis* complex from Crete. Competing classifications based on shell characters divided this complex into 5-9 species with up to 18 additional subspecies. Different methods for species delimitation using the ddRADseq data suggested a division of our data set into 14-45 species. There is no clear rationale for rating entire classifications. Rather, we considered the proposed partitions candidate species. We used especially sympatric occurrences or overlapping distribution areas, the results of a novel test that evaluates whether the differentiation between allopatric candidate species can be explained by isolation by distance, and the results of a model-based clustering method that infers population structure and indicates gene flow to assess candidate species. Based on these criteria, we suggest a classification of the species complex into 12 species of which only three correspond to morphologically delimited species, whereas the others have to be newly delimited or represent cryptic species not recognized so far.



#### Oral Presentation 4

### Phylogeography and population structure of the door snail *Charpentieria itala* in the Southern Alps

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The door snail *Charpentieria itala* is widely distributed in the Southern Alps. It comprises two groups of subspecies, which are sometimes considered distinct species. Some subspecies that morphologically resemble *Charpentieria stenzii* occur at exposed rocks at higher altitudes, whereas other subspecies live on more humid rocks and in forests at lower altitudes. The occurrences of the stenzii-like or 'stenzioid' subspecies are concentrated in mountain areas that were not glaciated during the Last Glacial Maximum. It has been hypothesized that the stenzioid subspecies have a common origin and represent relicts of an early colonization wave that survived the ice ages in these isolated mountain refuges within the Alps, whereas the non-stenzioid subspecies survived the ice ages at the margin of the Alps. As a result of the climate warming after the glacial, stenzioid and non-stenzioid subspecies came into contact and hybridized in different regions to different degrees. We generated a data set of genetic markers from 37 Alpine populations of *Charpentieria itala* using a modified double-digestion restriction-site associated DNA (ddRAD) sequencing approach. We study the evolutionary history of the species complex applying phylogeographic and population genetic analyses based on ddRAD data set.

#### Oral Presentation 5

### Species identification beyond barcoding - Multi-locus sequencing in sponges

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Sponges (Porifera) are known for their ecological importance, high diversity and widespread occurrence in all aquatic systems all around the planet. More than 9,000 species have been described so far, entirely based on morphological characters. However, phenotypic plasticity and the paucity of complex diagnostic characters hamper species delimitation in Porifera. In the genus *Tethya* (Demospongiae, Porifera), for instance, the reduced number and conservativeness of morphological and commonly used molecular markers make species identification and delimitation difficult. Since Next-Generation-Sequencing opens up new possibilities in sequencing multiple loci at once, we aimed at developing a genome-wide set of markers to identify species in the genus *Tethya*. Here, we present a proof-of-concept for the use of multilocus coding and non-coding genomic markers for species identification and delimitation in sponges. We analyzed and compared draft genomes of *T. wilhelma*, *T. minuta* and *T. citrina*, and used gene order (synteny) to find conserved ortholog genes in this genus. This set of genes was used to design ~20,000 baits to capture and sequence 7,400 single-copy *Tethya* orthologs. The captured genomic regions span ~5 Mb and contain exon (3.1 Mb) and intron (1.4 Mb) sequences and, ca. 0.5 Mb intergenic genomic regions. Approximately 3,600 captured markers were present all of the captured species (n=3) and were used to build a Hidden Markov Model Profile database to which de novo captured species can

be added in the future. We envisage our system to allow for the quick and accurate identification of *Tethya* species and to provide a robust system for the delimitation of new species within this genus.

#### Oral Presentation 6

### **Understanding Phylogenetic Relationships in Cladobranchia (Nudibranchia, Heterobranchia, Gastropoda) using NGS Data**

Dario Karmeinski<sup>1</sup>, Jessica Goodheart<sup>2</sup>, Tatiana Korshunova<sup>3</sup>, Alexander Martynov<sup>4</sup>, Michael Schroedl<sup>5</sup>, Heike Wägele<sup>1</sup>, Alexander Donath<sup>1</sup>

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The species-rich taxon Cladobranchia (Nudibranchia, Heterobranchia) currently comprises approximately 98 genera from 22 families of exclusively marine gastropods. Despite attempts to shed light on the evolution of the group, the phylogenetic position of most of its families is still subject to debate. While past efforts of gaining a better understanding of the relationships within Cladobranchia using barcoding gene approaches did not result in phylogenies with satisfactory resolution, the first phylogenies using transcriptomic multi-gene approaches only covered a limited number of species omitting many families with uncertain position. To overcome this problem, we sequenced the transcriptomes of 21 species of heterobranch sea slugs and combined our data with raw reads from 40 species of Heterobranchia available from public databases. In order to obtain a high number of genes suitable for phylogenetic analyses, we assembled the raw reads using six different transcriptome assembly tools. For each species, we identified the best assembly using a variety of descriptive parameters. We then searched the assemblies for orthologous genes that are presumed to be single-copy in molluscs and combined them in a phylogenetic supermatrix. Here we show our first results from the broadened dataset.

#### Oral Presentation 7

### **Illuminating the “dark” abyssal biodiversity**

Magdalini Christodoulou<sup>1</sup>, Tim OHara<sup>2</sup>, Andrew F. Hugall<sup>2</sup>, Pedro Martinez Arbizu<sup>1</sup>

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The largest and commercially appealing mineral deposits can be found in the abyssal seafloor of the Clarion-Clipperton Zone (CCZ), a polymetallic nodule province, in the NE Pacific Ocean, where testing of a bus-sized mineral collection system is set to start soon. In anticipation of deep-sea mining impacts, it has become essential to rapidly and accurately assess biodiversity. For this reason, ophiuroid material collected during seven scientific cruises from across the CCZ and the DIS-turbance and re-COLonisation (DISCOL) Experimental Area (DEA), in the SE Pacific Ocean, was examined. The specimens were barcoded (COI) and subsequent species delimitations analyses revealed the presence of 43 deep-sea brittle stars species and thus uncovering an

unexpectedly high diversity. Furthermore, barcodes (COI, 28S) were mapped on a substantial tree of life to show unprecedented levels of abyssal ophiuroid phylogenetic diversity including at least three ancient (>70 Ma), previously unknown clades.

#### Oral Presentation 8

##### **Associated ophiuroid fauna on cold-water corals of the Reykjanes Ridge**

Angelina Eichsteller<sup>1</sup>, Pedro Martínez Arbizu, Saskia Brix<sup>1</sup>

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In this study we focus on the ophiuroid species associated with the corals south of Iceland. The specimens were sampled by the ROV, in 3 different Areas, during the recent expedition MSM75 by the IceAGE\_RR (Icelandic marine Animals: Genetics and Ecology\_Reykjanes Ridge hydrothermal vent activity) project. In each Area, several corals were sampled and the ophiuroid specimens were identified to species level. The integrative taxonomic approach, based on morphological characters and the DNA barcoding with COI of the collected ophiuroids, revealed five species that live on the corals: *Ophiomitrella clavigera*, *Ophiactis abyssicola*, *Ophiocreas Oedipus*, *Ophiacantha bidentata* and *Ophiomyxa serpentaria*. We catalogue each ophiuroid species in a short identification guide. There, we can already see a variability in species occurrence on the corals. Deep-sea corals belonging to the family Plexauridae Gray, 1859 and Acanthogorgiidae Gray, 1859 exclusively host the species *O. clavigera*. The collected species are therefore associated with different corals but don't show a species-specific distribution. The population structures of the two most abundant species, *O. clavigera* and *O. abyssicola*, are presented in a haplotype network. It is shown, that the genetic structure is low for *O. clavigera* and high for *O. abyssicola*. In order to prove the population structure of *O. clavigera*, the recently developed Next Generation Sequencing (NGS) method 2b-RAD was used. In the analyzing, 2 conservative approaches were tested. A clear differentiation between Area 2 and 3 is shown. Also, a tendency to distinguish between the 4 different locations was recorded. We conclude that COI is a good method for species delimitation and 2b - RAD for population genetic studies.

#### Oral Presentation 9

##### **Past, present and future: Integrative taxonomy of barnacles (Crustacea: Cirripedia) from Eastern Indonesia**

Pipit Pitriana<sup>1,2</sup>

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Barnacles are intensively researched globally due to their uniqueness and ecological role. However, research on the taxonomy of barnacles in Indonesia is still very limited. This study was conducted to provide additional contributions to the study of taxonomy and biodiversity of barnacles in eastern Indonesia. The methods used in this research is a combination of classic taxonomic works with modern technologies and connects recent barnacle finds with specimens from the Museum's collection. The preliminary

results indicated more than 90 species of barnacles were found in Moluccas Islands (Eastern Indonesia). While for the molecular results, it may suggest different relationships for some barnacle clades than previously assumed. This study indicates that species diversity of barnacles from eastern Indonesia has been underestimated. This also shows the importance of a more comprehensive approach in sampling and molecular work to explore more the diversity of barnacles in Eastern Indonesia.

Oral Presentation 10

### **Case studies of different crustacean taxa – how reproductive mode influences biodiversity and species distributions**

Saskia Brix<sup>1</sup>, Katrin Linse<sup>2</sup>, James Taylor<sup>1</sup>, Anne Helene Tandberg<sup>3</sup>, Anne-Nina Lörz<sup>4</sup>, Angelina Eichsteller<sup>1</sup>, Annabelle Siebert<sup>4</sup>, Martin Schwentner<sup>5,4</sup>

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The deep-water marine habitats around Iceland are multifaceted, comprising of subarctic and North Atlantic biogeographic regions, influenced by complex oceanographic current and water mass regimes, and shaped by topographic features like the Greenland-Iceland, Iceland-Faroe and Reykjanes Ridges. These factors have a strong influence on regional species diversity and distributions. The comprehensive collections of BIOICE (Benthic Invertebrates of Icelandic waters) and IceAGE (Icelandic marine Animals: Genetics and Ecology) enabled the morphological and molecular analysis of selected benthic crustacean taxa and comparison of phylogeographies in planktonic Cirripedia versus brooding Amphipoda and Isopoda. Results from the balanomorph barnacle *Bathylasma* cf. *hirsutum* show low intraspecific diversity in the COI gene but indicate that geneflow is directed by current direction and past settlement events can be identified. Analyses of morphologically selected amphipod and isopod taxa revealed high intrageneric and -specific diversity. Amphipod specimens from North Iceland morphologically identified as *Rhachotropis helleri* based on no differences in diagnostic characters are a complex of three significantly different COI clades. Morphological species determination in the isopod genus *Oecidiobanchus* relies on minor differences and surprisingly instead of two, three species were delimited in a molecular approach showing different, but partially overlapping geographic distributions. In contrast, the isopod species *Haploniscus bicuspis*, which is known for strong sexual dimorphism in males, shows a wide distribution range from the western Greenland-Iceland to the western Iceland Faroe Ridge.

Oral presentation 11

### **Morphological and molecular diversity of Cumacea (Crustacea; Peracarida) within Northern European Ocean ecoregions**

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The surrounding Sub-Arctic Ocean area of Iceland is among the most special in the world in terms of water mass diversity and is known as the transition zone between North Atlantic and Boreal-Arctic. Peracarid crustaceans often form a major part of macrobenthic communities in diversity and abundance. This study aims to give a first insight into the underestimated morphological and genetic variability of the peracarid order Cumacea in Icelandic and adjacent waters. Cumaceans are small, mostly marine bottom-dwelling crustaceans with a unique comma-shaped body structure and low dispersal abilities. Therefore, they represent ideal model organisms for the investigation of the possible linkage between hydro-geographically parameter and evolutionary processes. So far, 250 cumacean species are known from Arctic Waters. Biogeographic information on cumacean occurrence records were extracted from the publicly accessible platform OBIS and were analyzed for dominating taxa in predefined ecoregions. A new dataset was created in this study, comprising more than 2500 new occurrence records and published data in Nordic Seas and the Arctic Ocean region. A combined approach incorporating traditional taxonomy and modern molecular methods was conducted to investigate the applicability of genetic analyses for cumacean species delimitation.

Oral Presentation 12

### **Surprisingly high variability of the DNA barcode fragment within Central European woodlice species (Crustacea, Isopoda, Oniscidea)**

Michael J. Raupach<sup>1</sup>, Björn Rulik<sup>2</sup>, Jörg Spelda<sup>1</sup>

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The Oniscidea or woodlice are the most successful group of crustaceans that invaded the land by far and represent to humans the most familiar group of isopods. In contrast to other amphibious crustaceans, e.g. land crabs or terrestrial hermit crabs, no developmental stage (egg, juvenile, etc.) of the Oniscidea requires free water and all biological activities are able to be conducted on land. In some ecosystems, e.g., European forests, woodlice perform an essential role in the decomposition, being largely phytosaprophagous and often occurring at very high population densities, but also act as important prey for a broad range of predatory arthropods. Here we present the first comprehensive DNA barcode library for terrestrial isopods, with a focus on Germany as part of the GBOL project. Our analysis revealed unusually high intraspecific distances for numerous species, with maximum distance values >20%. In spite of these high intraspecific variabilities, however, interspecific distances with values between 12% and

30% allowed a valid species assignment of all analyzed isopods. Possible causes for these observations will be discussed. Our study represents the first step in generating an extensive reference library of DNA barcodes for terrestrial woodlice as part of future molecular biodiversity assessment studies of soil organisms.

Oral Presentation 13

### **Song evolution in tits and chickadees (Aves: Paridae)**

Dieter Thomas Tietze<sup>1</sup>

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Passerines are the most successfully diversified bird order (around 60% of all avian species). That is presumably due to their outstanding cognitive abilities. This mental advantage enables them to quickly make new resources accessible and thus to inhabit huge areas. Furthermore, they developed complicated songs to defend their territories and to attract females for mating. Of course, not all passerine species are equally clever. Even within a single family of 50 to 70 species, relevant traits may vary considerably. Tits and chickadees (Paridae) are widely distributed songbirds and exceptionally smart. They evolved in the East Asian mountains (Sino-Himalayas). The earliest splits date back 10 to 15 million years and between 8 and 5 million years ago they dispersed from the Sino-Himalayas and got established also in North America and Africa. Although most species are of similar size, they vary a lot in coloration and plumage pattern. The territorial songs are relatively short and simple and differ hardly within a single male and within a population. I am asking, 1) if despite the quite uniform size the general negative correlation between body size and song frequency can be recovered, 2) which song traits are influenced by distribution and thus by interspecific differences in climate niche and 3) if across species more colorfulness of the plumage coincides with less diversity in song (trade-off under sexual selection). I am approaching the answers to these questions for 55 out of the 64 species with 1084 song recordings retrieved from XenoCanto.org and automated analytical methods including artificial intelligence.

Oral Presentation 14

### **A global review of insular woodiness and its potential functional significance**

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The repeated evolution of woody growth form in herbaceous lineages of flowering plants on islands—insular woodiness—has long been recognized as an iconic island phenomenon. Several hypotheses exist to explain the evolution of insular woodiness, including the release from climate seasonality and herbivore pressure. However, experiments testing these hypotheses are virtually absent and a global synthesis on the biogeography of insular woodiness is missing so far, mainly because information on the identity and geographical distribution of insular woody species is scattered across (grey) literature. Here we present a global database on insular woody species and combine it with the Global Inventory of Floras and Traits (GIFT), georeferenced species

occurrences, and environmental data in a generalized linear modeling framework to identify global diversity patterns of derived insular woodiness and potential environmental correlates. Specifically, we test the fraction of derived woody species in the flora of oceanic islands globally and relate it to island characteristics including island age and isolation, climate, and herbivore presence. The results show a large difference in importance of derived woodiness across islands, supporting several archipelagos known for derived woodiness as diversity hotspots, especially Hawaii and the Canary Islands. Climate emerged as an important correlate of derived woody species diversity, across latitudes. However, the results suggest taxon-specific drivers among evolutionary lineages. In summary, we introduce a novel dataset on derived insular woody species and provide our first results on a global perspective on the biogeography and correlates of insular woodiness.

Oral Presentation 15

### **Geomorphometric analyses of heritable fruit traits in Bottle Gourds**

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<sup>1</sup> CSIR – National Botanical Research Institute, Lucknow, India; <sup>2</sup> University of Nibadan, Nigeria;

*Lagenaria siceraria* (bottle gourd) is a unique member of the economically important Cucurbitaceae family due to the diversity in fruit shape, yet with consistent homologous points. Central to plant classification and identification success in taxonomy are morphological traits of organs such as fruits. We examined 250 fruits from 10 unique bottle gourd accessions using linear measurements and comprehensive morphometric techniques. We identified allometric variation as the result of differing circumference-to-height aspect ratios between accessions and species of bottle gourds. The allometric variation was due to variation in the girth of the fruits, not the environment. Aspect ratio was highly correlated with the first principal components of morphometric variation quantified using elliptical Fourier descriptors. Although, the main source of variation is aspect ratio, complex shape variations is captured by linear measurements. This insights reveal that fruits morphometry can capture complex, heritable phenotypes. Thus, EFD is a technique that provides robustness to data from heritable plant traits.

Oral Presentation 16

### **New results from the *Ochagavia-Fascicularia* group using genome skimming**

Juraj Paule<sup>1,2</sup>, Roswitha Schmickl<sup>3,4</sup>, Tomáš Fér<sup>4</sup>, Sabine Renger<sup>1</sup>, Georg Zizka<sup>1,2</sup>

<sup>1</sup> Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany; <sup>2</sup> Goethe University, Frankfurt am Main, Germany; <sup>3</sup> Institute of Botany, The Czech Academy of Sciences, Pruhonice, Czech Republic; <sup>4</sup> Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic

*Ochagavia* (4 species) and *Fascicularia* (1 species) form a well-supported clade of the early diverging Bromelioideae. The two genera are morphologically similar, but can be easily discerned on the basis of generative characters. Besides the species distributed on the Chilean mainland, the group includes *Ochagavia elegans*, endemic to the oceanic Isla Robinson Crusoe of the Chilean Juan Fernández Islands. The somewhat

enigmatic species morphologically clearly is assigned to *Ochagavia*, but in previous molecular phylogenetic studies formed mostly a sister clade to the remainder of *Fascicularia* and *Ochagavia*. A genomic approach, including whole plastomes (ca 160k bp) and nuclear rDNA cistron (ca 6k bp) was used to analyse the evolution of this clade.

Oral Presentation 17

### **The genus *Sphex* in Sub-Saharan Africa – an integrative taxonomic revision**

Thorleif Dörfel<sup>1</sup>, Michael Ohl<sup>1</sup>

<sup>1</sup> Museum für Naturkunde, Berlin, Germany

*Sphex* is a genus of digger wasps with over 130 species, occurring all over the world. Females prey on various katydids that are used as larval provisions in ground nests. From the Afrotropical region, 31 species and seven subspecies are known, but their descriptions are often vague and there are barely any usable revisions or identification keys. Digital images and molecular data are almost nonexistent. After examining nearly 4,000 pinned specimens and generating sequence data from 30 different species and subspecies, we present a complete taxonomic revision of the region. Eight species and six subspecies are newly described, and numerous taxonomic changes as well as seven additional species groups are proposed, bringing the total for the Afrotropical region up to 37 species and six subspecies in eight groups. All groups are supported in the intrageneric phylogeny we constructed based on sequence data from mitochondrial COI and two nuclear gene regions. Moreover, locality data from all specimens was digitized, translated into coordinates and incorporated into distribution maps. Using morphological characters that were neglected by previous authors, we were able to construct an identification key that covers the entire Sub-Saharan region.

Oral Presentation 18

### **Loss of dicondylic mandibles in hyperdiverse parasitoid wasps**

Lars Krogmann<sup>1</sup>, Thomas van de Kamp<sup>2</sup>

<sup>1</sup> Staatliches Museum für Naturkunde Stuttgart, Germany; <sup>2</sup> Karlsruhe Institute of Technology (KIT), Karlsruhe, Germany

One of the key events in early insect evolution was the development of mandibles with two joints. This allowed for a more powerful bite, but restricted mandibular movement to a single degree of freedom. Insect mouthparts have undergone considerable adaptations in several derived groups with sucking mouthparts, but it is common doctrine that the dicondylic articulation of chewing mandibles remained unaltered during insect evolution. Here we describe highly modified mandibles without the restrictions of a single degree of freedom and hypothesize a major role in insect diversification. This type of mandible seems to be a defining character of chalcid wasps, one of the most species-rich insect superfamilies of primarily parasitoid species. A flexible mandibular movement even allowed for the development of bizarre mandibles, such as unique antler-like mandibular processes in an undescribed species that potentially act as grasping tool. The observed shift from powerful chewing to precise cutting likely facilitated various adaptations to diverse enclosed hosts, which pose different challenges to the emerging



parasitoid wasps. Our study highlights the need for comprehensive anatomical studies even of putatively well-known character systems to identify major steps in insect evolution.

#### Oral Presentation 19

### **First non-feeding species of Sericini chafer from Amazonia (Coleoptera, Scarabaeidae): implications on scarab evolution**

Thaynara L. Pacheco<sup>1,3</sup>, Marcela L. Monné<sup>1</sup>, Fernando Z. Vaz-de-Mello<sup>2</sup>, Dirk Ahrens<sup>3</sup>

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Sericini is a tribe of chafer beetles with around 4000 described species. With a cosmopolitan distribution, the tribe had a Cretaceous origin in the West Gondwana with repeated dispersion out of Africa and is one of the oldest extant chafer lineages. While most part of the recent systematic work on the tribe focus on the Old World Sericini, very little is known about the Neotropical lineages. This includes the scarce knowledge of biodiversity in the number of species, distribution, and ecology habits. So far Neotropical taxa represent only 5% of Sericini species richness. In course of a comprehensive taxonomic treatment of South American species, a few outstanding specimens were discovered for two Amazonian localities. Using comparative morphology and phylogenetic inference, we could place these new taxa in a phylogenetic context and the strong reduction found in mouthparts lead us to assume a non-feeding lifestyle of these species. These discoveries could represent a key piece to a better understanding of the evolution of the scarab beetles and of Sericini, in particular, in the light of the historical biogeography of the Amazon region.

#### Oral Presentation 20

### **Sawfly genomes provide insights into traits that fostered the mega-radiation of parasitoid and eusocial Hymenoptera**

Jan Philip Oeyen<sup>1</sup>, Bernhard Misof<sup>1</sup>, Oliver Niehuis<sup>2</sup>

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Hymenoptera (sawflies, wasps, ants, and bees) are a mega-diverse insect order. The tremendous success of the group is often attributed to the transition from the ancestral phytophagous life style, which is retained in most sawflies ("Symphyta"), to parasitoidism. This transition happened only a single time, in the last common ancestor of the parasitoid sawfly family Orussidae and the wasp-waisted Hymenoptera (Apocrita). However, Orussidae and Apocrita differ strongly in their species diversity. Thus, speciation was likely promoted by the acquisition of further traits. To shed light on early Hymenoptera genome evolution and traits that likely fostered a parasitoid life style, we sequenced the genomes of the phytophagous sawfly *Athalia rosae* and the parasitoid sawfly *Orussus abietinus* and compared them to those of parasitoid and eusocial Apocrita. We found that the genomes of the two sawflies contain genes thought to be absent in Hymenoptera (e.g., CO2 receptors), but also genes and genomic traits thought to be specific to Aculeata (e.g., small immune gene repertoire; low content and

activity of transposable elements). These traits were, therefore, likely a feature of the common ancestor of all Hymenoptera. Furthermore, we found that the evolution of parasitoidism coincided with an increase of storage proteins that are rich in nitrogen, possibly having facilitated the dietary change. We also found that parasitoid and eusocial Apocrita have a significantly larger repertoire of odorant receptors than phytophagous and parasitoid sawflies, which may have enabled the success of the two former groups by facilitating the formation of new ecological niches.

Oral Presentation 21

### **Phylogenomics of Acrididae (Insecta: Orthoptera): More genes, more resolution?**

Oliver Hawlitschek<sup>1</sup>, Ricardo Pereira<sup>2</sup>, Edgardo Ortiz Valencia<sup>3</sup>

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Acrididae is a family of grasshoppers that has posed problems to phylogenetic reconstruction because of widespread incomplete lineage sorting, hybridization, pseudogenes (numts), and possibly *Wolbachia* infection. Nevertheless, earlier DNA barcoding and multigene phylogenies have already suggested that the current taxonomy needs revision. Especially, the current generic assignment of many species has to be revisited. We sequenced transcriptomes of a selection of Central European species of the subfamily Gomphocerinae. Our results confirm the genus *Chorthippus* as polyphyletic, encompassing the genera *Stauroderus*, *Gomphocerus*, and *Gomphocerippus*. Our genomic data also appears to resolve species complexes, e.g., the *Ch. biguttulus* complex, that could not be resolved using DNA barcoding or mitochondrial genomes due to haplotype sharing. The position of some species, e.g., *Ch. apricarius* and *Ch. alticola*, differs significantly between mitogenomic and transcriptomic trees. Our goal is the detection of genomic markers that can be used for resolving the larger-scale phylogeny of this important but poorly studied group.

Oral Presentation 22

### **Diversification in and around the Atlas Mountains: A Review of the genus *Thalpomena* Saussure, 1884**

Lara-Sophie Dey<sup>1</sup>, Axel Hochkirch<sup>2</sup>, Abdelhamid Moussi<sup>3</sup>, Martin Husemann<sup>1</sup>

<sup>1</sup> Centrum für Naturkunde, Universität Hamburg, Germany; <sup>2</sup> University of Trier, Germany; <sup>3</sup> University of Biskra, Algeria

*Thalpomena* Saussure, 1884 is a North African endemic genus, largely restricted to the Atlas Mountains and adjacent mountain ranges. Currently, seven species with four additional subspecies are described from the Atlas Mountains, one species occurs in Libya and one in the Somalian Highlands. The taxonomy of the genus has last been updated in 1949 by Dirsh, who published a revision of the genus including its allies (*Cophotylus*, *Crinita*, *Pseudocoles*). However, in his descriptions he already mentioned the vague status of many taxa. Since then, the taxonomy of the genus has been largely untouched. In our study, we investigate the systematic relationships within the genus for the first time using molecular methods. Our sampling includes all known species with

more than 360 individuals from most of their distribution ranges. We combined molecular data from four mitochondrial (COI, ND2, 16S & 12S) and one nuclear gene (H3) with distribution data from collections and the literature and biometric measurements of 10 characters to obtain a comprehensive view of the interspecific relationships within the genus. Our genetic as well as morphological analyses do not support the current taxonomy and suggests some synonymies. Wing coloration has little meaning for Oedipodinae taxonomy, yet wing-band shape seems to be a more useful trait. The genetic lineages obtained from the phylogenetic analyses correspond well with mountain barriers suggesting that the orography was a driver of diversification in the group.

Oral Presentation 23

### **Researchers staring at snails' tongues – Distinct radular movement patterns in the major gastropod lineages**

Wencke Krings<sup>1</sup>, Carolin Scheel<sup>1</sup>, Stanislav N. Gorb<sup>2</sup>, Matthias Glaubrecht<sup>1</sup>

<sup>1</sup>Centrum für Naturkunde, Universität Hamburg, Germany; <sup>2</sup>University of Kiel, Germany

Mollusca are the second species-rich animal group, containing 80000 species in Gastropoda alone. This biodiversity goes along with the colonialization of diverse environments and with the establishment of various ecological niches: gastropods feed on a range of food sources with different mechanical properties thanks to a key innovation for mechanical food processing, viz. the radula. The radula is an important autapomorphy of the Mollusca, a chitinous membrane embedding small teeth for loosening food from surfaces. Those teeth are well-studied both in taxonomic and biomaterial studies: they can be very distinct in their morphology, in their amount on the radula but also in their mechanical properties. Even though there are intensive studies on the radula, little attention had been paid to its general movement while feeding and to the interaction of the teeth with the food, especially in a phylogenetic context. For this study the radula movement of 20 representative species of the four major lineages of the Gastropoda (Vetigastropoda, Neritimorpha, Caenogastropoda, Heterobranchia) and one species of the Polyplacophora were filmed and analyzed. We identified six different types of radula movements resulting in the rotation, folding, rolling, liking and flapping of the radula or its teeth, which were summarized in schematic illustrations and subsequently reviewed in phylogenetic context. Scanning electron microscope images of the radula were also generated and compared with the video-results which allowed us tracking the action of the distinct radular tooth types. Especially interesting is the fact, that in some taxa we found grasping movement patterns, the radula itself can be twisted and bended or it uses the jaw as counter bearing. Thus the whole organ can act like a pincer, hence food is not only scratched from the surface but can also be teared or ripped apart by the action of certain prominent teeth. This function of the radula was found to be highly convergent in the different major taxa.

## Oral Presentation 24

### **Convergent loss of the mammalian vomeronasal system – combining morphology and genomics**

Ulla Lächele<sup>1</sup>, Nikolai Hecker<sup>2</sup>, Michael Hiller<sup>2</sup>, Heiko Stuckas<sup>3</sup>, Peter Giere<sup>1</sup>

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The perception of pheromones is crucial for mammals to detect the perfect mating partner. The structure responsible for this perception is the vomeronasal system, which includes the enigmatic vomeronasal organ (VNO). The VNO has been an object of investigation for decades and remains still somewhat mysterious. The vomeronasal organ or Jacobson's organ is located in the anterior nose and is lined with sensory epithelium. The organ is connected via the vomeronasal nerves to the accessory olfactory bulb in the anterior region of the brain. The system is present in most mammals, however the anatomical structures are reduced or lost independently in various taxa like whales, higher primates, the manatee and some bats. To understand the evolution and loss of the system, we collected data on the absence or presence of the respective structures for 115 mammalian species by an intense literature research and the investigation of histological serial sections. Subsequently, we applied a new genomic approach "Forward Genomics" to identify inactivated protein coding genes associated with the reduction of the vomeronasal system (VNS). Our results confirm that the inactivation of the well-studied *Trpc2* gene is specific to mammals with reduced VNS. Moreover, we identified the inactivation of the genes *Aox 2*, *Mslnl* and *S100z* to be associated with VNS reduction, which was not known before. These genes serve as marker genes and allow a more detailed investigation of the vomeronasal system in the future. The inactivation of these genes in otters and seals predicts a reduction of the VNS in these species, for which no morphological data is available. This study shows the huge potential of the combination of comparative morphological and genomic approaches.

## Oral Presentation 25

### **Universal single-copy orthologs (USCOs) as markers for species-level taxonomy**

Lars Dietz<sup>1</sup>, Jonas Eberle<sup>2</sup>, Christoph Mayer<sup>1</sup>, Lars Podsiadlowski<sup>1</sup>, Ralph S. Peters<sup>1</sup>, Ximo Mengual<sup>1</sup>, Bernhard Huber<sup>1</sup>, Marianne Espeland<sup>1</sup>, Thomas Wesener<sup>1</sup>, Oliver Niehuis<sup>3</sup>, Bernhard Misof<sup>1</sup>, Dirk Ahrens<sup>1</sup>

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DNA barcoding is a commonly used method of species identification and delimitation. In animals, it is mostly based on nucleotide sequences of the mitochondrial gene CO1. However, especially in groups of recently diverged species using only a single gene may give insufficient or misleading results. Recent advances in nucleotide sequencing technologies have made it significantly easier and less costly to sequence hundreds or thousands of gene loci, which may be used to better resolve species-level taxonomy. Here we report the testing of the taxonomic usefulness of a set of several hundred "Universal Single-Copy Orthologs" (USCOs) that are present as single-copy genes

within the genomes of most animal taxa. The genes were sequenced using a target hybrid enrichment approach, and several different published pipelines as well as newly developed approaches were assessed for assembling the obtained nucleotide sequences. The taxonomic and phylogenetic performance of USCOs was evaluated by analyzing seven different datasets that comprised sequences of species from four different insect orders as well as from myriapods and spiders. Inference of phylogenies using concatenation and coalescent approaches gave a first impression of the amount and utility of USCO DNA sequences obtained via DNA target enrichment. Our results show that USCOs can be used to reliably distinguish known morphospecies and can be used to obtain highly resolved phylogenies even in cases in which CO1 is unable to differentiate between species.

#### Oral Presentation 26

##### **PhylUp: Automated updating of phylogenetic alignments with custom sampling strategies**

Martha Kandziora<sup>1</sup>

<sup>1</sup>Hamburg, Germany

Due to the community effort of making DNA sequences publicly available, phylogenies and alignments often lack taxa that have only recently been made available. I developed a new software pipeline – PhylUp – to add newly sequenced material into existing alignments. PhylUp automates the updating of phylogenetic alignments by adding new sequences based on similarity to existing sequences to the alignment. The user can control the details of the search for additional sequences, for example how many sequences per taxon should be included. Additionally, there is an option to add unpublished sequences. Overall, the program updates alignments and can compute a new phylogeny including support values for phylogenies which then can be used for further analyses. I will present the workflow in more detail and show the ability of the method to update phylogenetic alignments on an Asteraceae sublineage Senecioneae.

#### Oral Presentation 27

##### **From conservation genomic research to highly cooperative application: statistical quality, user acceptance and IT security**

Jutta Buschbom<sup>1</sup>

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At a time of rapidly declining biodiversity, basic research in organismal evolutionary biology often simultaneously becomes involved in the protection of the investigated organisms, their natural populations and ecosystems. Hereby, conservation tasks are cooperative and social endeavors that require interested parties from many parts of society and the world to come together and work towards a shared goal. Moreover, applied tools require very stringent statistical quality measures. This results in the need for large, information-rich datasets, due to distribution-range-wide sampling and the transition to dense genome-wide sequencing. Such standardized and validated

reference datasets in themselves can only be accomplished by cooperation of many. For these purposes, a dedicated work environment is needed that supports and promotes the highly cooperative settings, stringent statistical demands and dynamic objectives of concrete conservation strategies and tasks. At the core of the work environment lies the integration of a modular chain-of-custody, a sample and data infrastructure and an analytical environment. Furthermore, special attention has to be paid to user-friendly interfaces and a versatile access-management, reflecting the needs of data providers and users, ethical guidelines and conservation goals. Quite exceptionally in organismal evolutionary research, questions of security need to be considered from the start for samples, data and IT-infrastructures. Reference datasets of within-species genetic diversity are designed to be very powerful in their applications, resulting in effective economic and sociopolitical impact. The very valuable datasets need protection themselves, for them to support the development of sustainability and thus to safeguard the richness of biodiversity.

Oral Presentation 28

### **Species delimitation and geography**

Bernhard Hausdorf<sup>1</sup>, Christian Hennig<sup>2</sup>

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Despite the importance of the geographical arrangement of populations for the inference of species boundaries, only few approaches that integrate spatial information into species delimitation have been developed so far. Persistent differentiation of sympatrical groups of individuals is the best criterion for species status. Species delimitation becomes more prone to error if allopatric metapopulations are considered because it is often difficult to assess whether observed differences between allopatric metapopulations would be sufficient to prevent the fusion of these metapopulations upon contact. We propose a novel approach for testing the hypothesis that the multilocus genetic distances between individuals or populations belonging to two different candidate species are not larger than expected based on their geographical distances and the relationship of genetic and geographical distances within the candidate species. A rejection of this null hypothesis is an argument for classifying the two studied candidate species as distinct species.

Oral Presentation 29

### **Think global, act local – what the seemingly increasing number of Austrian animal species can tell us**

Elisabeth Geiser<sup>1</sup>

<sup>1</sup>Salzburg, Austria

In 1998 Geiser published that 45870 species of animals occur in Austria. An update after 20 years on behalf of the Zoological Botanical Society Austria (Geiser 2018) resulted in 54125 animal species reported for Austria. Insects alone account for 40 000 species. This increase by 8255 species or 18 % is first and foremost due to an improved

level of scientific knowledge. On the one hand, several projects of pure and applied science provided a lot of new data and lists which can be analysed to gain species numbers of animal groups in Austria. On the other hand, these numbers will be always fuzzy and disputable, to mention only the problems caused by alien species or subspecies status. Also, there are a considerable number of species for which only few individuals have been recorded in Austria. Others have not been recorded in Austria for more than 50 years. Although the species number has seemingly been magnified, it does not mean that the pressure on biodiversity has decreased. On the contrary – biomass is shrinking. Therefore, it is necessary to consider that this seemingly encouraging number of animal species in Austria only reflects a status which includes an increasing number of endangered species.

## Poster presentations

### Poster 1

#### Recent progress in species delimitation in *Subulicystidium* (Trechisporales, Basidiomycota)

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Diversity of corticioid fungi (resupinate Basidiomycota), especially outside the northern temperate climatic zone, remains poorly explored. For many decades, the delimitation of species in *Subulicystidium* (Hydnodontaceae, Trechisporales) was a challenge. The presence of numerous transitional forms as to basidiospore size and shape hindered species delimitation, and almost no data on molecular diversity has been available. We aimed at clarifying the species boundaries and distribution patterns in *Subulicystidium* and providing the key for species identification. Between 2015 and 2019, we examined ca. 200 *Subulicystidium* herbarium specimens mostly from Paleo- and Neotropics but some also from temperate and boreal Eurasia. We recorded the size and shape of basidiospores and cystidia in a systematic way, and applied DNA barcoding and phylogenetic Bayesian and Maximum likelihood approach to assess the variation in the nrDNA (ITS and 28S regions) for the whole genus. We described 11 new species and thus doubled the number of known species in the genus *Subulicystidium*. The main deliverables from analyses of ITS and 28S nrDNA in *Subulicystidium* are: (i) There is no universal barcoding gap applicable for the whole genus; (ii) At the level of individual species, a barcode gap is observable in *S. fusisporum*, *S. parvisporum*, *S. robustius*, and *S. tedersooi*; (iii) Species *S. longisporum*, *S. obtusisporum*, *S. brachysorum* and *S. meridense* are highly polyphyletic; (iv) Species *S. perlongisporum* is monophyletic but includes two sympatric lineages. We found species with transoceanic distribution (e.g. *S. oberwinkleri* and *S. perlongisporum*) but also species known so far from the single isolated area (e.g. *S. parvisporum* on La Réunion Island). The true distribution patterns of *Subulicystidium* species are yet to be elucidated.

## Poster 2

### Potential of micro-CT for taxonomic studies on Staurozoa (Cnidaria)

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Staurozoa, so called “stalked jellyfishes”, is a cnidarian taxon lacking a free-swimming medusa stage. They represent a small taxonomic group currently comprising about 50 valid species. Like many other gelatinous animals, staurozoans have relatively few stable macromorphological characteristics of taxonomic value. However, recent histological studies reveal that internal morphological features have a high scientific value for systematic and evolutionary studies on staurozoans. In the present study, we used micro-CT scans (Xradia MicroXCT-200 X-ray imaging system, Carl Zeiss Microscopy GmbH) of osmium tetroxide stained, critical point dried specimens of the species *Craterolophus convolvulus* to evaluate the potential of micro-CT for the depiction of taxonomically important structures. The results, which were compared to traditional histological technique, demonstrate that micro-CT is particularly useful to comprehend the general body organization of staurozoans. Moreover, targeted placement of virtual cut planes is beneficial for the visualization and understanding of specific morphological features, as the shape and dimensions of the claustra, the canal system at the base of the tentacular clusters, and the delimitation of the manubrium. In conclusion, micro-CT volume renderings are suitable to visualize most taxonomically important structures with limitations in microscopic structures, as for example gametes and nematocysts.

## Poster 3

### *Berghia stephanieae*, a model organism for understanding photosymbiosis in nudibranchs

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Among metazoans, many phyla are able to associate with photosynthetic organisms and are thus benefiting passively from photosynthesis. In sea slugs (Gastropoda), the animal host either forms a symbiosis with unicellular algae, usually *Symbiodinium*, (Nudibranchia-Dinoflagellates) or retains only the chloroplasts of its food source (Sacoglossa). Nudibranchs usually obtain their symbionts from their food prey (anemones, soft and hard corals), becoming the secondary hosts of *Symbiodinium*. Several questions including how the symbiont is recognized by the animal host, how the symbionts are maintained intracellularly, and what the symbiont contributes to the animals' development and reproduction remain unanswered for Nudibranchia. To shed light on these questions, an integrative approach combining techniques of genome and transcriptome sequencing, immunoblotting, and developmental observations, is needed. In order to successfully apply these techniques, a model organism is required. The aeolid nudibranch *Berghia stephanieae* can serve as such model organism, because this species and its food source *Exaiptasia*, can be cultured relatively easily in the laboratory, in both symbiotic and aposymbiotic (dinoflagellate-free) states, and because the slugs



have a short generation time and a fast metamorphosis. Thus, *Berghia stephanieae* can be used to successfully apply these approaches. Here, we present first insights into using *B. stephanieae* as a model organism to understand the (molecular) bases of photosymbiosis in Nudibranchia.

#### Poster 4

### **Quantification of Different Symbiodinium Strains in the Nudibranch *Phyllodesmium briareum***

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Nudibranchia (Mollusca, Gastropoda) are a group of marine sea slugs most famous for their conspicuous colouration – which gave them the term “butterflies of the sea”. Besides, some taxa are able to form a symbiotic relationship with different strains of the unicellular algae *Symbiodinium*. The extent to which the symbiosis is stable among the different species varies from a few days to several weeks. One of the most stable photosymbiotic relationships, lasting several months, is found in *Phyllodesmium briareum*, a species distributed from Indonesia to Northern Australia, retrieving the symbionts by feeding on various species of the soft coral *Briareum*. Which factors underpin this long-term photosymbiotic relationship is still unknown. Here, we investigated the presence of different *Symbiodinium* strains in field collected and laboratory cultured slugs. In order to understand if a specific symbiont is important for this photosymbiotic relationship, we analysed the strain composition upon starvation. For this, we established a (real-time) PCR protocol, which allowed us to qualitatively and quantitatively analyse the respective strain abundance in the different specimens. Our results suggest that in *Phyllodesmium briareum* the abundance of the different strains varies greatly.

#### Poster 5

### ***Elysia viridis* as a promising system to understand kleptoplastid longevity in Sacoglossa**

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Sacoglossa (Mollusca, Gastropoda) are a small group of marine sea slugs with about 400 species described to date. Some members of this group are famous for their ability to steal and incorporate photosynthetically active plastids (then referred to kleptoplastids) from their green macroalgal prey (Chlorobionta, Ulvophyceae) – a unique system of photosymbiosis called functional kleptoplastidy. How the kleptoplastids are maintained in the animals, in some species even over several months, is unknown. However, a factor underpinning functional kleptoplastidy might be based on photoprotection mechanisms the kleptoplastids bring along. To understand if such mechanisms are indeed important in kleptoplastid longevity, *Elysia viridis* is a promising system. This widely distributed species feeds on a variety of green algae including

species possessing or lacking photoprotection mechanisms, such as the Xanthophyll Cycle (XC) and the energy-dependent non-photochemical quenching (qE). Here, we investigated the influence of the presence or absence of the XC and the qE in the respective food algal with regard to kleptoplastid longevity in *E. viridis*. We found evidences that the XC and qE have unexpected little relevance.

#### Poster 6

### **Sperm ontologies and RDF-coding in phylogeny inference - a case study from Nemertea**

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Recent advances in sequencing techniques and computational power have made it possible to compile and analyze genomic data in a reasonable time range. On the other hand, the analysis of morphological data sets has somewhat come out of fashion, mainly due the considerably smaller size of morphological character matrices. Ontology based Resource Descriptive Framework (RDF) statements have been proposed to provide the long-sought inter-subjective transparency to morphological character coding. Additionally, due to the detailed and systematic assessment of characters, it is expected to significantly enlarge morphological data matrices. Nemertean spermatozoa are as a case study for a nemertean sperm ontology. We also propose a way to used RDF statements as a new way to code sperm characters.

#### Poster 7

### **Bridging the gap – Nemertean taxonomy combining barcoding and histology**

Jörn von Döhren<sup>1</sup>

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Nemerteans are worm-shaped nocturnal predators in marine and limnic habitats that are said to be notoriously difficult to identify. Most of the external characters in nemertean are highly variable or lack uniqueness to identify species. Species descriptions have "traditionally" relied on histological techniques in order to document characters of internal morphology. There are only very limited data regarding the molecular markers needed for modern day biodiversity research. To broaden the molecular data base it is necessary to combine histology and molecular analyses. A work flow is presented here to overcome problems in linking classical morphological data to molecular data. This workflow allows tracing sequence data back to series of histological that show relevant characters for species identification. Every barcode therefore has a morphological counterpart. This allows transferring of classical information on the structure and biology of Nemertean into the age of molecular-based identification.

## Poster 8

### **Collettea in the Kuril-Kamchatka Trench**

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To date, all published *Collettea* species have exclusively been delineated by their morphological appearance. It has become obvious in the last years that morphological characters alone are insufficient for species delimitation, as is also shown by reports of cryptic species, potential high intraspecific variability, or the overlap between intraspecific variability and interspecific variation between closely related species. Here we pursued an integrative taxonomic approach to delimitate *Collettea* samples collected during the KuramBio II cruise to the Kuril-Kamchatka Trench. Conventional taxonomical techniques were complemented with the mtDNA markers COI and 16S. This gives a first and unique insight into composition and diversity of *Collettea* species from a deep-sea trench in the Northwest Pacific. Our approach succeeded in delimitation of nine new *Collettea* species as well as one full species description for *Collettea* n. sp. 1 and four rough descriptions for *Collettea* n. sp. 2 – 4. All nine *Collettea* species were unique to a specific area, of which six were singletons. Furthermore, our approach indicated that the number of ventral setae on the cheliped propodus fixed finger is an unreliable character for species delimitation. Molecularly, we unveiled at least one cryptic species and surprisingly high in-generic divergences of 24.7 – 40.3% between COI-sequences. In conclusion, we question the monophyly of *Collettea* and emphasize the need for a thorough phylogenetic analysis and a subsequent revision of the genus - potentially following the approach introduced here.

## Poster 9

### **Deep-sea polychaete species living in two oceans – confirmed by molecular data.**

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Polychaetes are a dominant faunal element in many deep-sea habitats. However, the distribution of deep-sea polychaetes is still largely unknown. This is partly explained by difficulties in identification to species level due to usually poor condition of specimens from deep-sea samples. In recent years new material has been collected from bathyal depths (4000-5800 m) during expeditions to the N and S Atlantic as well as the central and NW Pacific. Based on this material we aim to study the distribution patterns of selected deep-sea polychaete species using an integrative approach including morphological and molecular studies. We focus here on the following taxa: *Sigambra* (Pilargidae), *Octomagelona* (Magelonidae), and *Spiophanes* (Spionidae). New sequences (COI and 18S) supplemented by data from public sources are included in the analyses. First results revealed two general distribution patterns: species present only in the Atlantic or the Pacific *versus* species occurring in both oceans. Potential

explanations could be seen in dispersal capacities of the respective species in combination with life history patterns, ocean currents and bottom topography.

Poster 10

### **Fluorescence microscopy in the field: a tool for improved discovery and identification of meiofauna organisms**

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Field identification of small soft-bodied aquatic organisms can be challenging because in many cases diagnostic characters are either scarce, or not readily observable under normal reflected or transmitted microscope illumination, or require specific preparation techniques in the laboratory. Eliciting autofluorescence of structures such as bristles, cuticles, storage inclusions, glandular secretions, or photoreceptor cells can drastically increase their signal-to-noise ratios and, thus, visibility for taxonomic identification. Furthermore, unprecedented autofluorescence patterns may add new diagnostic characters allowing to taxonomically identify individuals previously deemed indeterminable. Finally, flashy autofluorescence can help to discover inconspicuous or well-camouflaged animals. Due to both their larger footprint and higher technical complexity, however, fluorescence microscopes are rarely used the field. To meet the requirements of air travel and work in remote areas we use a vintage research epifluorescence microscope that has been modified to fit into cabin luggage. White light and fluorescent illumination sources have been replaced by LEDs in order to minimize power consumption and allow operation on battery power. The device additionally features differential interference contrast, dark field and polarisation microscopy. Here we demonstrate the advantages of field application of fluorescence microscopy as exemplified by our study organisms: marine meiofaunal oligochaetes are mainly identified by their genital chaetae, which occur only in specific segments of reproducing individuals and traditionally require fixation and mounting on glass slides in glycerol for inspection. Using blue light excitation these structures can be easily seen in living or lightly narcotised specimens. For some species we discovered characteristic fluorescent patterns in the body wall that are invisible under white light illumination and provide reliable characters to distinguish even non-reproducing individuals of co-occurring species. Other examples include placozoans, which show bright autofluorescence that is useful when substrates are screened for these animals. Although probably not universally applicable, we highly recommend experimenting with fluorescence observation when collecting and identifying small invertebrate animals.

Poster 11

### **Against all odds – The “meiofauna paradox” of *Dinophilus* (Annelida) and its boreal North Atlantic distribution**

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Meiofaunal (microscopic) animals exhibit highly similar and simple morphologies complicating species identification, which has led to the “Everything is Everywhere, but the environment selects” hypothesis that claims ubiquitous distribution of microscopic organisms. However, DNA barcoding and population genetic studies have revealed an unforeseen hidden diversity of cryptic species among microscopic marine benthos, which has led to a paradigm shift, rejecting cosmopolitanism of marine meiofauna until genetically proven. With phylogenetic and species delimitation analyses of worldwide collected genetic samples of the meiofaunal family Dinophilidae (Annelida) we here resolve three genera within the small family and showcase an exceptionally broad, boreal, North Atlantic distribution of a single microscopic marine species with no obvious means of dispersal besides vicariance. With its endobenthic lifestyle, small size, lack of pelagic larvae and limited migratory powers, the broad distribution of *Dinophilus vorticooides* seems to constitute a “meiofaunal paradox”. Its habitat (the biofilm among sand grains, but also on macroalgae and ice) as well as its eggs encapsulated in cocoons and obligatory dormant encystment stages have been interpreted as adaptations to the boreal climate. Additionally, these life cycle peculiarities also point towards a way to survive long-distance rafting dispersal, which might be overcoming their own dispersal limitations. Though often neglected and possibly underestimated among marine microscopic species, dormancy may be a highly significant factor for explaining wide distribution patterns and a key to solving this meiofaunal paradox.

Poster 12

**First evidence of internalization of nanoparticles in the tissue of the limnic rotifer *Brachionus calyciflorus* Pallas, 1766**

Julia R. Geppert<sup>1</sup>

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Artificial micro- and nanoparticles (MPs and NPs, respectively) from human activities of diverse fields including catalysis, electronics, cosmetics and cancer detection are causing increasing pollution of aquatic environments through industrial abrasion processes and sewage. Since it is known that specific NPs such as gold can induce toxicity within organisms, MP and NP pollution in general has received much attention of late. Nevertheless, the actual impact of such particles remains largely unknown, including whether they potentially enter the food chain (e.g., via planktonic organisms). In this study, investigations using light- and transmission electron microscopy (LM and TEM, respectively) verify that the limnic rotifer *Brachionus calyciflorus* does indeed ingest (LM images) as well as internalize (TEM images) citrate stabilized gold NPs (AuNPs) within vacuoles within its stomach cells, possibly via endocytosis. AuNPs of diameters 8.5 and 12.5 nm were both internalized and both showed lethal effects in most of the rotifer individuals. This study provides the first definitive evidence that AuNPs are indeed internalized in the tissue of rotifers and therefore justifies further *in vivo* studies to determine those factors that most influence the uptake of and therefore risk posed by NPs to small, freshwater organisms like the planktonic *B. calyciflorus*.

**Diversity and distribution of Gastrotricha inhabiting different substrata of high arctic submarine seamounts of the Langseth Ridge sampled during expedition PS101 of R/V POLARSTERN**

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The distribution and biogeography of marine interstitial meiofauna - microscopic metazoans and protists that dwell inside the clefts and crevices between sediment grains - is still one of the big enigmas of marine biology. Representatives of almost every phylum may be found in this extraordinary biocenosis and many of them, like the marine gastrotrichs, are amongst others characterized through a life cycle that is strictly bound to the sediment and lacks any active or passive dispersal propagule such as planktonic larvae, dormant stages, or resting eggs. Despite this limited dispersal capacity the majority of species possess rather widespread distributions across whole oceans or even around the globe. Some of these distributions may be artificial, since multiple evolutionary entities (e.g. species, subspecies, cryptic species) with more restricted ranges could be 'lumped' under a single species name. However, even in such a case, the ancestors of, e.g., species complexes must have been dispersed somehow during their evolutionary history. In this context, oceanic islands and seamounts could play an important role for stepwise distribution and/or speciation of marine interstitial meiofauna. In order to explore the 'biogeographic functioning' of these geological structures, several maritime expeditions have been conducted in the past, among them cruise PS101 of R/V POLARSTERN to the high Arctic Langseth Ridge in 2016. 817 gastrotrich specimens of 33 selected samples will be determined to species level in order to analyse and compare community structure between biotopes and with that of other geographic regions. Initial results so far reveal specimens of the genera *Desmodasys*, *Oregodasys*, *Ptychostomella*, *Tetranchyroderma*, *Urodasys* (Macrodasyida), and *Musellifer* (Paucitubulatina). Marine gastrotrichs have never been recorded from such high latitudes before. Felty mats composed of calcareous tubeworm debris and siliceous sponge needles from the dominating local demosponge taxa (*Geodia* spp., *Stelletta* spp.) are inhabited by an obviously much more diverse gastrotrich community, than is the underlying sediment itself. Taxonomically better resolved results of this ongoing project will be used in the near future for zoogeographic analyses.

Poster 14

**A fresh look at Melanopsidae (Caenogastropoda: Cerithioidea): Evolutionary systematics, biogeography and conservation genetics**

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Melanopsidae occur in subtropical and temperate regions of the Western Palearctic and are also reported from Zealandia, which is an unparalleled disjunction among freshwater animals. Melanopsidae also have a rich fossil record. We sequenced nuclear and mitochondrial markers of a representative sample of species/genera covering the entire geographic range of the group. We compare the timeframe for the evolution of major melanopsid lineages with geologic events and elucidate scenarios that may have shaped distribution patterns. Our phylogenetic analyses suggest that Melanopsidae are not monophyletic. *Holandriana* is more closely related to Pleuroceridae and Semisuclospiridae than to Melanopsidae s.str. The Zealandian taxa (Zemelanopsidae) were recovered as the sister group of a clade including *Melanopsis*, *Microcolpia* and *Esperiana* (Melanopsidae s.str.). *Esperiana* branches off first, while *Microcolpia* represents the sister group of *Melanopsis*, which is comprised of three lineages: 1) western Mediterranean region, 2) eastern Mediterranean region and 3) Italy. While the Italian populations show relatively little shell variability, the eastern and western *Melanopsis* lineages are highly variable. Several geographically coherent groups in *Melanopsis* can be ranked as species, but in a number of cases morphologically distinct forms were not recovered as monophyletic units. We used AFLP markers to assess the genetic diversity in two genetically (based on mitochondrial data) well-delimited clades: 1) the Italian narrow-range endemic *M. etrusca*, which was known historically from twelve populations, half of which have already gone extinct, and 2) the Caucasus endemic *M. mingrelica*. The genetic diversity in the remaining populations of *M. etrusca* showed distinct geographic structuring of populations, which should be taken into account for developing recovery plans for the species, which are urgently needed to prevent a further decline. Contrarily, little phylogeographic structure was observed in *M. mingrelica*; especially populations from localities in the Caspian Sea drainage from Georgia and Azerbaijan were not separated from those in the Black Sea drainage of Georgia suggesting a possibly rather recent colonization of the Caspian Sea drainage.

Poster 15

**Monitoring and diversity of marine Heterobranchia in North Sulawesi, Indonesia**

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Marine heterobranch taxa are primary or secondary consumers, thus associated with sessile coral reef organisms. This renders them as good indicators to study the health situation of marine tropical habitats and to become a major target for monitoring programs. Investigation of marine Heterobranchia in several areas in North Sulawesi has

been done between 2015 to 2018, including the first monitoring in Bangka Archipelago (BA) in 2017 and 2018. BA comprises small islands of biogenic reefs, volcanic rocks, mangroves, and seagrass meadows. One particular area was threatened since 2012 by the buildup of mining infrastructure, however mining never started because cancellation of the concession. The aim was to provide a baseline for future monitoring surveys on marine heterobranchs with regard to further environmental changes especially within the BA. In total 484 specimens comprising 149 species (Cephalaspidea, Aplysiida, Sacoglossa, Pleurobranchiida, Nudibranchia and additionally Eupulmonata) of marine heterobranchs were collected in the two sampling events in 2017 and 2018. Thirty-three species are new to science. The species accumulation curve also indicates the increase in species around Bangka Archipelago not recorded before and need to be explored regarding diversity baseline. Marine heterobranchs are not only good targets for monitoring, they are also famous for their compounds, used in defense or antifouling. These compounds additionally provide potential drug leads for medical applications. Since Phyllidiidae is the most common group in North Sulawesi and its compounds of high interest, the first extended result on the phylogeny of this heterobranch family is also presented. We included all available CO1 and 16S sequences from NCBI (106 specimens) and from our studies in Sulawesi (595 specimens). This biggest concatenated data set worldwide shows that these genes are good enough to limit the genera and distinct species clades within Phyllidiidae. However, lack of molecular data from many species in GenBank, and the lack of good morphological descriptions for many species, makes a thorough revision of many species based on both methods necessary. These analyses are in progress.

Poster 16

### **Extreme incongruences in recent taxonomy and molecular genetics of tropical freshwater snails (Gastropoda; Cerithioidea: Thiaridae)**

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Incongruences between morphologically derived taxonomy and molecular phylogenies based on mitochondrial genes are a major hurdle of modern evolutionary systematics. We uncovered a particularly intriguing case in the taxonomically enigmatic thiarid freshwater gastropods. Based on extensive material of all twelve currently accepted genera sampled in most cases from the entire range of a taxon, we included 247 specimens in phylogenetic analyses based on two mitochondrial gene fragments (cytochrome c oxidase subunit I and 16S rRNA genes). The analyses revealed major incongruences of recent taxonomy and our molecular phylogeny, recovering half of the represented genera as non-monophyletic if viewed according to the current taxonomy. Furthermore, we sequenced fragments of the nuclear 28S and H3 genes of 68 specimens, representing overall ten thiarid genera. The phylogeny based on the combined nuclear and mitochondrial gene fragments is largely congruent with the topology obtained from mitochondrial data alone. Reasons for the present incongruences might be manifold: fallacies in current taxonomy (i.e. over- or under-splitting), presence of morphologically cryptic species, differences in mode of mitochondrial DNA inheritance, karyotypic variation, presence of pseudo-genes,



ancestral mitochondrial DNA polymorphisms, introgression and indirect selection of mitochondrial DNA by endosymbiont infections. Unfortunately, our current dataset does not allow for the identification of the cause of these incongruences, though it is very likely, that not only one but several of the aforementioned phenomena played a role in Thiaridae evolution. Our study gravely emphasizes that future studies on this group ought to be based on a genomic approach.

Poster 17

### **Interactive identification keys for easy online use**

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Interactive keys are easy and fast to use, because the characters are illustrated. Correct identification enables further investigations to be soundly based (e.g. modelling the effects of single or multiple stressors in the marine environment, recognising a biosecurity threat, interpreting functional roles within different habitats) as morphologically very similar species may utilize totally different ecological niches, may show different behaviour and can have different physiological requirements. The identification keys currently available for most marine Amphipoda are out of date, only available in linear format that require a lot of taxonomic expertise to use. However, the creation of interactive keys requires taxonomic expertise, the ability to draw / illustrate the relevant characters and the technical know-how of using the software and placing the keys online. We have created interactive keys for two marine families of Amphipoda which are available online: <http://amphipod.dnsalias.net>

Poster 18

### **Pseudo-cryptic diversity in a highly abundant benthic copepod genus of the North Sea uncovered by mtDNA barcoding**

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The species *Leptastacus laticaudatus* Nicholls, 1935 was found 1992 in a mere morphological study as the most abundant harpacticoid copepod species in the entire North Sea. The species stands out in its genus by the peculiar morphology of the 5th leg pair. A recent study combining morphology and mtDNA barcoding for specimen identification in the North Sea found this morphospecies to actually comprise three pseudo-cryptic species with genetic distances in the COI gene fragment ranging between 15 to 30%. Two of the species were found to occur sympatrically whereas detailed morphological examinations revealed none of them to be identical to the original description from the northern British coast, or the re-description of the species from the European continental coast. In the current study we carried out detailed morphological examination, increased the number of investigated specimens by COI barcoding and extended the molecular data set with a nuclear genetic marker, supporting the initial findings of pseudo-cryptic diversity in the genus. Two further new species from the genus are included in the study to emphasize the enormous overseen diversity in this highly abundant animal group.

Poster 19

### **Diversity and phylogeny of anchialine cave copepods**

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Anchialine habitats are costal water-bodies located within crevicular and cavernous karst and volcanic terrains that extend inland to the limits of seawater penetration. Such systems are characterized by limited primary production; however they are inhabited by rich, diverse and specialized fauna, with high levels of endemism, particularly of crustaceans. Copepod orders Platycoepoidea, Misophrioida, Calanoida, Cyclopoida and Harpacticoida have successfully colonized anchialine habitats, in which at least one family has been reported as exclusive to these ecosystems. In a recent survey of anchialine caves in the Yucatán Peninsula, Cuba, Lanzarote and Sardinia, so far 63 species belonging to six copepod orders were found including the first record of the order Canuelloidea in anchialine ecosystems. Among the most interesting discoveries, we present here for the first time a species of the order Platycoepoidea in the Mediterranean basin; a new species of the misophrioid copepods genus *Palpophria* from a locality in Cuba is also presented (previously only known from the type locality in Lanzarote). For cyclopoid copepods, a member of the typically deep-sea benthic family Giselinidae is presented, additionally two new species of the family Speleoithonidae from sinkholes in the Yucatán Peninsula are reported. Two nuclear genes fragments from large and small-subunits (28SrRNA and 18SrRNA) and the mitochondrial marker cytochrome c oxidase subunit I (COI) from 56 species have been sequenced in order to investigate the phylogenetic relationships between anchialine copepods. A comprehensive phylogenetic analysis has been performed here including the molecular data of all copepod orders available from Khodami et al. (2017) to reveal the phylogenetic position of anchialine lineages among other copepod habitants. We discuss the close relationship of anchialine cave copepod fauna with the deep-sea species, and the different possible colonization scenarios from deep-sea to anchialine ecosystems.

Poster 20

### **Morphological investigations into the calceoli of selected Amphipoda (Crustacea)**

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Despite our wide understanding of sensory organs in crustaceans, the enigmatic calceoli of Amphipoda and their function is unclear, although they are known for 200 years. Calceoli are a common feature in fresh water, subterranean and marine amphipods, primarily found on male antennae. Therefore, previous studies indicated a chemosensory function mainly associated with reproduction. However, calceoli have not been studied with advanced microscopical techniques. We use a range of morphological methods to illuminate the structure and function of calceoli: 1) Light microscopy to analyze the location and arrangement of these organs next to sensory bristles along the antennae; 2) Scanning electron microscopy to compare the detailed external

morphology of these peculiar organ with previously published crustacean structures; 3) Confocal Laser Scanning microscopy to visualize internal features, including differences in cuticular composition; 4) Histological section series to enable the 3D-reconstruction of the organ in high detail. Based on our preliminary studies of antarctic *Oediceroides calmani* Walker, 1906, we conclude that the calceoli seem to consist of two subunits with different lamellar organization. The entire unit is connected to the antenna via short stalks, arranged in alternating rows with one calceolus per flagellar segment. Integrating all our morphological data, we hope to understand the purpose/function of the individual compartments as well as their overall contribution to the behavior of Amphipoda.

Poster 21

### **Non-destructive DNA extraction with Chelex for morphological studies**

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Integrative taxonomic approaches, which combine molecular and morphological methods, have become an integral part of modern taxonomy. Especially for small taxa, DNA extraction is usually destructive reducing the value of vouchers for subsequent morphological studies. Whole-body DNA extractions with Chelex offer the possibility to retrieve the complete animal afterwards, however, it is currently unknown whether small structures like setae become damaged or altered. We studied fine setae of three amphipod families – Atylidae, Pleustidae and Podoceridae – before and after Chelex extractions to document potential damages and to evaluate the suitability of this approach for taxonomic studies. Chelex treatment had no negative effect on fine structures like setae, these were unaltered. Chelex is a fast, effective and low-cost method for whole-body DNA extractions for subsequent morphological studies. This is also important for long-term storage of voucher specimens.

Poster 22

### **Necessity of reliable identification as a baseline for conservation - an isopod case study on the genus *Haploniscus* Richardson, 1908**

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Why does conservation need species identification? During the first two IceAGE (Ice<sup>l</sup>andic marine **A**nimals: **G**enetics and **E**cology) expeditions in 2011 and 2013, benthic macrofauna was sampled from various stations surrounding Iceland, specifically along depth transects including the Norwegian Channel, the Faeroe-Iceland-Ridge, South Iceland and East Greenland. Asselote isopods identified as *Haploniscus bicuspis* (Sars, 1877) were closely examined in an integrative approach to solve the question if *Haploniscus bicuspis* is a species complex or one species with different morphotypes. They were found to show high morphological variability in species-specific characters. Different morphological techniques (light-, scanning -and confocal microscopy) are complemented by multiple species delimitation methods based on genetics and

proteomics. Preliminarily, a dataset for mitochondrial COI and nuclear ITS-1 was established. Furthermore, a ddRAD approach is applied, as well as a proteomic approach using the same set of specimens. All data sufficiently contribute to develop a database for the isopod species occurring around Iceland. So far, our results revealed that differences between male individuals regarding the pleopod 1 might represent developmental stages instead of different subspecies or male morphotypes within *H. bicuspis*. However, the analysis of the genomic and proteomic data is still ongoing. These different methodologies are steppingstones towards solving the *H. bicuspis* species' complex puzzle. Regarding conservation issues in such a climatically sensitive region like the subarctic waters around Iceland, a baseline for definitive and rapid species assessment method needs to be developed. In the future, this will aid efficient identification of various isopod species around Iceland.

Poster 23

### **OBIS- A Biogeographic tool for North Atlantic Peracarida**

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“OBIS (Ocean Biogeographic Information System) is a global open-access data and information clearing-house on marine biodiversity for science, conservation and sustainable development”. Here we present the workflow to create data sets for OBIS that are based on different kinds of Metadata, we focus on the peracarid crustacean orders Isopoda and Amphipoda from: 1) BIOICE project (Benthic invertebrates in Icelandic waters). Peracarid crustaceans were collected during 19 cruises. Benthic samples were taken at 579 stations, ranging from 25-3000 m depth. 2) IceAGE project (Icelandic Animals Genetics & Evolution). Over 100 000 peracarid crustaceans were collected during two expeditions. Benthic samples were taken at more than 60 stations, ranging from 100 to 3000 m depth. 3) Literature data. Data from over 20 publications has been included so far. We contribute to a global alliance that collaborates with scientific communities to facilitate free and open access to, and application of, biodiversity and biogeographic data and information on marine life. Our peracarid data are essential to the world's ocean biodiversity and biogeographic data and information required to address pressing coastal and world ocean concerns.

Poster 24

### **An evaluation of the Mediterranean species of the band-winged grasshopper genus *Acrotylus* (Fieber, 1853) using DNA barcoding.**

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The grasshopper family Acrididae is one of the most diverse lineages within the Orthoptera, including more than 6.700 species valid species. Within the Acrididae, the Oedipodinae are one of currently 26 subfamilies. A total number of 137 genera and 794 species are associated with this subfamily. The Mediterranean region represents a

hotspot of biodiversity with a high number of endemic species, whereas the center of biodiversity of the genus *Acrotylus* is located in South Africa, while a number of species can be found in the Mediterranean where they are distributed in dry habitats with sparse vegetation. Although some species are widespread throughout the Mediterranean area, the phylogenetic relationships within this genus are poorly understood due to a long history of conflicting classification schemes, especially between the two widespread species *A. insubricus*, known for its stouter body compared to *A. patruelis*, commonly known as 'the slender burrowing grasshopper'. The body length and width of individuals of both species were measured and compared in order to find a new morphological character to distinguish between these species. Statistically significant differences of the width between both sexes have been recorded which means that on average, *A. insubricus* is wider and has a stouter body than to *A. patruelis*. Additionally, the males of *A. insubricus* turned out to be smaller than the males of *A. patruelis*. In this study, I also present a phylogeny of the genus *Acrotylus* based on the barcoding-gene COI including the Mediterranean species of this genus as well as additional African species in order to test the current taxonomic status of these species. I found that the current species status of *A. innotatus*, *A. insubricus*, *A. longipes* and *A. patruelis* were valid. In contrast, the two species *A. errabundus* and *A. incarnatus* did not represent independent genetic clusters and perhaps need to be synonymized. Moreover, two new clades were recovered which may represent species new to science: one is found in the Middle East (Iran, Afghanistan), the other in the Balkan Peninsula (Bulgaria, Turkey).

Poster 25

**Environmental suitability and biogeographic history of the widely distributed band-winged grasshopper *Sphingonotus (Sphingonotus) rubescens* with a new record from Thailand (Acrididae: Oedipodinae)**

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*Sphingonotus (Sphingonotus) rubescens* (Walker, 1870) presents the broadest continuous distribution, ranging from Southern Europe, Northern Africa, Western, Central, Southern and Eastern Asia. Here we extend the known distribution range to Thailand and explore the species spatial distribution and climatic niche. Using the maximum entropy approach, we project the species distribution model into the past, Last Glacial Maximum (~22,000 yr BP) and Last Interglacial (~6,000 yr BP), to investigate how the species' range would have changed through time, and its possible past climate refugia; and to the present, to identify possible collection gaps and environmental suitability of the new occurrence record in Thailand. Further, we utilize the species known distribution to characterize habitats where the species occurs.

## Poster 26

### **Local and Regional scale patterns of biodiversity of Sericini chafers (Coleoptera: Scarabaeidae) in Sri Lanka**

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Biodiversity of tropical forests varies at spatial and temporal scales. Describing and analysing biodiversity and its major patterns is key to investigate the underlying processes and causes of diversification. Knowledge about assemblage differences between different habitats and the local genetic variation is extremely rare for scarab chafers (Coleoptera: Scarabaeidae), and habitat differences within one locality never has been explored. Therefore, we examined the patterns of diversity and turnover of pleurostict Sericini chafers (Coleoptera: Scarabaeidae) in Sri Lanka, an isolated, geologically very old land mass and one of the world's biodiversity hotspot area. We used six UV light traps at different habitat types, in different forest types in the lowlands and highlands and in different seasons to explore quantitative species composition and to infer at first time habitat and assemblage turnover for herbivore scarabs in a fine scale. From a preliminary investigation in isolated forest sites of Sri Lanka during two field surveys before and after S-W monsoon season in 2019, a total of 1893 specimens were captured, including 12 new species and 29 previously known species. Assemblages are compared here in detail. 15 species were syntopically co-occurred in both seasons, while 7 species disappeared and 13 species emerged after S-W monsoon season. At regional scale, the highest diversity in terms of richness was observed in Nuwara Eliya (wet zone-highlands->1800m) in pre-monsoon season, whereas Dambulla (Intermediate zone- 180m) in post-monsoon season. Number of specimens per trap and day varied significantly in each habitat type with the season. The results presume a large species turnover even within one sampling site: while traps of different localities showed more similar faunal composition with other sites rather than with traps of the same locality. This could indicate that more than the locality determines the assemblage composition.

## Poster 27

### **The evolution of subsociality in tortoise beetles (Coleoptera, Chrysomelidae, Cassidinae): a molecular phylogenetics approach**

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The subsocial behaviour (=parental care) has been recorded in 11 beetle families. Cassidinae and Chrysomelinae are the only leaf beetles (Chrysomelidae) subfamilies in which the parental care is recorded. Although the subsociality in insects has received much attention, there is still little information regarding the evolution of this behaviour based on phylogenetic approaches. Cassidinae is the second larger subfamily within Chrysomelidae and two of their tribes present parental care: Mesomphaliini and

Eugenysini. Here we present the first phylogenetic reconstruction of Mesomphaliini and one of the first in Cassidinae to employ molecular data. We conducted Bayesian inference and maximum likelihood analyses based on concatenated data of four gene regions. We also reconstructed the ancestral character state of the subsociality in Cassidinae. Our results recovered a monophyletic Mesomphaliini when Eugenysini is included, for that reason we proposed the synonymy of Mesomphaliini with Eugenysini n. syn. We also recovered three origins and no losses of the subsociality in Cassidinae evolution, corroborating previous studies that show multiple origins of subsociality in insects.

Poster 28

**Two subfamilies, two strategies – unexpected differences in the effects of miniaturization in Coniopterygidae (Neuroptera: Insecta)**

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The Coniopterygidae, or “dustywings”, can be regarded as the midgets of Neuroptera. While there are singular species with a small body size in different neuropteran families, they are the only family with a small body size throughout all species. The Coniopterygidae comprise three subfamilies, of which representatives of two have been examined regarding their head anatomy. Several structural modifications correlated with miniaturization are recognized: a relative increase in the size of the brain, a reduction in the number of ommatidia and diameter of the facets, a countersunken cone-shaped ocular ridge, and a simplification of the tracheal system. Beside these miniaturization effects, which both families have in common, some structures evolved strikingly different in response to the constraints correlated with a small body size: the relatively increased suboesophagial ganglion in Coniopterygidae necessitates a forward shift of the mouthparts and thus a ventral closure of the head capsule, which is realized as hypostomal bridge in Coniopteryginae, while it is a gula in Aleuropteryginae. Furthermore, the dorsal tentorial arms are reduced in Coniopteryginae, whereas they are directed posteriorly and fused in Aleuropteryginae, forming an arch that fulfills functions otherwise taken by the tentorial bridge; the latter formation is, based on our review of the literature, not known in other insect orders. The unexpected intrafamilial diversity illustrates the increase of variability, observed in other miniaturized taxa, for the first time in insects. As a conclusion we suggest to increase the taxon sampling of miniaturized forms in morphology-based phylogenetic analyses.

## Poster 29

### **Phylogenomic insights into the evolution of Neuropterida (Insecta: Holometabola)**

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The holometabolous insect superorder Neuropterida contains more than 6,500 described species in three orders: Megaloptera, Neuroptera, and Raphidioptera. Previous phylogenomic investigations of Neuropterida have suggested a robustly resolved phylogeny of Neuropterida that is in part incompatible with phylogenies inferred from analyzing morphological characters. Additionally, analyses of different phylogenomic datasets or with different phylogenetic methods have resulted in mutually exclusive, but strongly supported phylogenetic hypotheses. In this study, we generated new transcriptomic data in an effort to resolve the persisting phylogenetic incongruencies. We reconstructed the phylogeny of Neuropterida by analyzing sequences from 3,983 single-copy genes and we also inferred divergence times for the major lineages of the group. Raphidioptera are robustly inferred as sister to Megaloptera + Neuroptera. Within Neuroptera, Coniopterygidae are inferred as sister to all remaining neuropteran families. This phylogenetic relationship cannot be corroborated by morphological analyses and suggests that larval cryptonephry (i.e. fusion of the Malpighian tubules to the hindgut) might be an apomorphic feature for Neuroptera, with secondary modification in Nevrothidae and Sisyridae. Moreover, our results are congruent with previous phylogenomic analyses concerning the monophyly of Osmyloidea (Nevrothidae, Osmylidae, and Sisyridae) and also suggest Ithonidae as sister to monophyletic Myrmeleontiformia. The family Nymphidae is placed as sister to Nemopteridae + (Ascalaphidae + Myrmeleontidae), in accordance with phylogenetic results of recent morphological studies. Despite these robust results, our four-cluster likelihood mapping analyses suggest that the phylogenetic relationships within Osmyloidea remain ambiguous. Our divergence time estimates suggest a common origin of the extant Neuropterida in the middle of the Carboniferous. Overall, our comprehensive phylogenomic analyses suggest a new timeline for the evolution of the major neuropterid lineages and provide a reliable scaffold for the most ancient phylogenetic splits within Neuropterida. Additionally, our four-cluster likelihood mapping analyses help to identify open questions in the phylogeny of the group.

## Poster 30

### **The Entomological Collections of the Zoological Museum Hamburg**

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The Entomological Collection at the Zoological Museum of the Center for Natural History (ZMH) hosts ca. 5 million specimens and more than 10,000 type specimens, being placed among the five largest insect collections in Germany, with a current annual growth of 250,000 specimens. Yet, the ZMH has long been neglected hence it remains nationally and internationally poorly known. Its past is marked by the bombings during



the WW2, which led to the loss of a great share of its specimens, with emphasis on the collection of holometabolous insects – e.g., Coleoptera, Lepidoptera, Diptera, Neuroptera. Fortunately, specimens of other insect groups, and material stored in alcohol were saved, and in subsequent years, complemented by specimens added by vendors, traders or private collectors. Hence, nowadays the ZMH is much larger than before the destruction, including several scientifically historically relevant partial collections; these include the weevil collection of Eduard Voss, the Heteroptera collection of Eduard Wagner, and the Trichoptera from Georg Ulmer, among others. Currently, the ZMH entomological collection remains growing further and is simultaneously, systematically and taxonomically updated, counting on the publication of type catalogs, databasing and reallocation of specimens to proper storage conditions i.e., unit-tray system. Looking into the future, the Entomology Division intends to make the collection more accessible through the digitalization, initially of type specimens and collection of metadata of each specimen, that way promoting a larger recognition of its hosted diversity and treasures.

Poster 31

**Effects of climate change on conservation efforts to preserve the white-headed duck, *Oxyura leucocephala***

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Climate change is expected to substantially alter biodiversity, causing changes in phenology, genetic composition, and most importantly enabling alien species to expand into regions in which they previously could not survive and reproduce. Thus, understanding the effects of the climate change on native and invasive species distribution is key for biodiversity conservation. We used ecological niche modelling to estimate the potential distribution of two hybridizing duck species, the endangered white-headed duck (*Oxyura leucocephala*, Scopoli, 1769) and the invasive ruddy duck (*Oxyura jamaicensis*, Gmelin, JF, 1789), to assess the effects of climatic changes on the species future distributional patterns. Primary occurrence data was obtained from the Global Biodiversity Information Facility. Environmental models were projected using maximum entropy approach, for present and 2050-time horizon climate scenarios using two general circulation models (CCSM4, MIROC5) and three IPCC representative concentration pathways (RPC; 2.6, 4.5, 8.5). Models were run with three regularization multiplier parameters, using three combinations of calibration areas. Results did not show noticeable redistribution of the two species in the future, since the percentage and location of suitable area did not considerably differ between two time periods. However, models showed the substantial overlap in potential distribution of species in both time periods, indicating that hybridization would remain as a threat to conservation efforts to preserve white-headed duck. With further refinement of our models, incorporating the predictions of species potential distribution in the future can aid in prioritizing key areas in the management policies for both species.