

Keynote Speakers

Hadal Crustacea from 6000m to 11,000m deep

Jamieson A¹

¹University Of Western Australia, Perth, Australia

Biography:

*Prof. Alan Jamieson is Director of the Munderoo-UWA Deep Sea Research Centre. He has 23 years of experience in deep-sea science, technology and exploration. He is an authority on the hadal zone (>6000 m) and has published >130 scientific publications and monographed the book *The Hadal Zone: life in the deepest oceans*. He has participated in nearly 70 deep-sea expeditions spanning every ocean and completed 15 deep-sea submersible dives from 500 to 10,700 m. He is currently Chief Scientist of the RV *Dagon* (formally *Pressure Drop*) and the full ocean depth submersible *Baku* (formally *Limiting Factor*).*

Since the first scientific expeditions to the deepest ocean trenches, crustacea have been known to be a dominant hadal group particularly the amphipoda. Amphipods, common to all trenches studied so far, are a conspicuous and significant scavenging group on which many scientific studies at hadal depths have been based. Conversely, until the mid-2000s, decapods were thought to be one of the few deep-sea crustacean groups that had no hadal representatives at all, however, this is no longer the case. Decapods, are also common to all known trenches but are restricted to depth of ~7800m. The last 15 years has seen a renaissance in hadal trench exploration, and the Amphipoda and Decapoda have featured heavily in these contemporary studies. This presentation will document the biodiversity and biogeography of these crustaceans across 16 trenches and the adjoining abyssal plains. It will also showcase some of the latest in situ observations of some key species and their inter-species interactions, including the supergiant amphipod *Alicella gigantea*.

Moving towards re(Indigenising) science: actions for change

McAllister T¹

¹ Victoria University of Wellington, Wellington, New Zealand

Biography:

Dr Tara McAllister is a Māori scientist, interdisciplinary scholar and a mother belonging to the iwi (tribes) of Te Aitanga a Māhaki and Ngāti Porou, with expertise spanning from freshwater ecology to racism in the tertiary sector. Her research has sought to address the underrepresentation of Indigenous scholars in academia and has resulted in changes to policy and practise within the tertiary sector in New Zealand. She earned a Bachelor of Science in ecology and biodiversity and marine biology from the Victoria University of Wellington and a PhD in water resource management from the University of Canterbury.

Dr McAllister will weave her expertise and experience as a Māori scientist and her research into inequities in higher education to discuss re(Indigenising) science. She will explore why re(Indigenising) science is important and draw on examples from Aotearoa of how dominant science has caused harm to Indigenous people. She will discuss the inclusion of Indigenous people and knowledge in science and highlight why to create a better future in science we must go beyond simply including Indigenous people in science.

The evolution of crustacean visual systems: themes, challenges, and remaining mysteries

Porter M¹

¹*University Of Hawai'i at Mānoa, Honolulu, USA*

Biography:

Dr. Megan Porter is a Professor in the School of Life Sciences at the University of Hawai'i at Mānoa. She is a visual ecologist and evolutionary biologist who studies the way animals see the world. Her research is focused on the molecular aspects of vision in a range of crustaceans including decapods, copepods, and stomatopods. As a researcher of animal vision, Dr. Porter is especially interested in the intersection between science and art, and how understanding the visual systems of other animals alter our own perception of the world.

The Crustacea have evolved an amazing array of visual systems, exhibiting a multitude of eye types, optical designs, structures specialized for color and polarization vision, and molecules involved in detecting light. This diversity is compounded by the often distinct eyes found in larval versus adult forms. Yet, knowledge of visual systems is still lacking, particularly with respect to integrating information across biological levels (e.g. molecules, morphology, physiology, behavior) within an evolutionary context. As a first step towards an integrated view of crustacean visual system evolution, we identified the complement of expressed opsin genes, coding for the protein component of light sensitive visual pigments, from 95 species representing 32 orders of crustaceans. Interesting patterns include the retention of opsins from the long wavelength sensitive clade in several orders that have lost eyes (i.e. Mystacocaridida, Podocopida, Nectiopoda, Brachypoda); a clade of putative middle-wavelength sensitive opsins found only within thecostracans; and many species expressing more opsins than predicted based on characterized photoreceptor spectral diversity, with the most extreme example found in stomatopods that express over 30 opsins in a single retina. Building on this foundation, crustacean eyes also exhibit an extreme diversity in eye types, but the link between photoreceptor diversity and opsin diversity is still poorly understood. In situ hybridization studies in stomatopod retinas demonstrate the potential for complex and unexpected patterns of opsin expression and co-expression within spectrally distinct photoreceptors. The convoluted relationship between opsin diversity and photoreceptor diversity extends to even the simplest crustacean eyes. To unravel these remaining mysteries, studies linking opsin expression patterns within photoreceptors to physiology, and physiology to behavior, are needed across the ecological and taxonomic diversity within the Crustacea.

Oral Presentations

Identifying the sediment size preference of coastal horseshoe crab, *Tachypleus gigas* spawning

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Biography:

In 2020, Anis Syahira Abdul Halim graduated from Universiti Malaysia Terengganu (UMT) with a Master of Science in Ecology. She has been working with the Horseshoe Crab Research Group at UMT since 2017 and the NGO, Persatuan Konservasi Belangkas Malaysia (MyHSC), since 2022 due to her dedication to horseshoe crab welfare and conservation. She is currently finishing her Ph.D. study on horseshoe crab spawning in captivity.

Horseshoe crab spawning beaches are shrinking year after year, either due to anthropogenic activities along the coast or natural causes. Reproduction and release of hatchery-reared horseshoe crabs is an effective approach to restore their population in the wild. This research was carried out to determine the sediment size preference for spawning of the coastal horseshoe crab, *Tachypleus gigas*, based on the number of nests and eggs produced per nest in captivity. The natural spawning method was conducted in a concrete spawning tank containing three sizes of sediment (coarse: 0.50–1.00 mm; medium: 0.25–0.50 mm; fine: 0.10–0.25 mm). The number of nests and eggs per nest produced in medium and coarse sediment is significantly higher than in fine sediment, indicating that *T. gigas* prefers to spawn in sediment with particle sizes ranging from 0.25 to 1.00 mm. These findings might serve as baseline information for the hatchery management of horseshoe crab particularly *T. gigas* in future conservation efforts.

The Influence of the Toxin Producing Dinoflagellate, *Alexandrium catenella* (1119/27), on the Feeding and Survival of the Marine Copepod, *Acartia tonsa*

Abdulhussain A^{1,2}, Cook K³, Turner A⁴, Lewis A⁴, ElSafi M⁵, Mayor D³

¹Department of Marine Sciences, Kuwait University, Fintas, Kuwait, ²Ocean and Earth Science, University of Southampton, Southampton, UK, ³National Oceanography Centre, Southampton, UK, ⁴Centre for Environment, Fisheries, and Aquaculture Science, Weymouth, UK, ⁵Oceanography Department, Alexandria, Egypt

Biography:

I am Dr. Ali Abdulhussain, an Assistant professor at the department of Marine Science, Kuwait University. I studied PhD at the University of Southampton, and Graduated on January 31, 2022 focusing of the impact of toxic algae on multiple copepods including *Acartia tonsa* and *Calanus finmarchicus*. My work involved culturing copepods, culturing toxic and non-toxic phytoplankton, running survival, feeding, reproduction, and toxin accumulation, and analysis experiments. My current work at Kuwait university involve research on copepods at the Arabian/Persian Gulf, and also teaching different courses such as Introduction to marine science, marine botany, and Plankton ecology.
And also research

Blooms of harmful algae are increasing globally, yet their impacts on copepods, an important link between primary producers and higher trophic levels, remain largely unknown. Algal toxins may have direct, negative effects on the survival of copepods. They may also indirectly affect copepod survival by deterring feeding and thus decreasing the availability of energy and nutritional resources. Here we present a series of short-term (24 h) experiments in which the cosmopolitan marine copepod, *Acartia tonsa*, was exposed to a range of concentrations of the toxic dinoflagellate, *Alexandrium catenella* (strain 1119/27, formerly *Alexandrium tamarense*), with and without the presence of alternative, non-toxic prey (*Rhodomonas* sp.). We also present the toxin profile concentrations for *A. catenella*. The survival and feeding of *A. tonsa* was not affected across the range of concentrations recorded for *A. catenella* in the field; increased mortality of *A. tonsa* was only discernible when *A. catenella* was present at concentrations that exceed their reported environmental concentrations by two orders of magnitude. The observed lethal median concentration (LC50) for *A. tonsa* exposed to *A. catenella* was 12.45 ng STX eq L⁻¹. We demonstrate that *A. tonsa* is capable of simultaneously ingesting both toxic and non-toxic algae, but increases clearance rates towards non-toxic prey as the proportional abundance of toxic *A. catenella* increases. The ability to actively select non-toxic algae whilst also ingesting toxic algae suggests that consumption of the latter does not cause physical incapacitation and thus does not affect ingestion in *A. tonsa*. This work shows that short-term exposure to toxic *A. catenella* is unlikely to elicit major effects on the grazing or survival of *A. tonsa*. However, more work is needed to understand the longer-term and sub-lethal effects of toxic algae on marine copepods.

Intersexuality could give rise to all female offspring in the red claw crayfish *Cherax quadricarinatus*

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¹Ben-Gurion University of the Negev, Beer-Sheva, Israel, ²Achva Academic College, Arugot, Israel, ³Stanford University, Monterey, USA

Biography:

Comparative and applied endocrinology, Crustacean Sexual plasticity, Regulation of sex-differentiation, Reproduction and growth. Biocontrol and Aquaculture.

Culturing monosex crustacean populations presents a promising sustainable avenue for aquaculture and biocontrol. The redclaw crayfish, *Cherax quadricarinatus* is a widely grown species around the world. It is a ferocious omnivore considered as a classical invasive species hence, monosex populations (all female or all male) that do not reproduce could suggest solutions for aquaculture escapees and unwanted settling of biocontrol agents.

In *C. quadricarinatus* intersex individuals are naturally occurring and known to exhibit mix sex phenotypes including different combinations of male and female gonopores. More importantly, a simple chromosome-based sex-determination model showed that *C. quadricarinatus* intersexual individuals are genetically females, bearing heterogametic sex chromosomes (WZ), but function as males. In such intersex individuals bearing both, male and female reproductive systems, manipulating the insulin-like androgenic gland (IAG) hormone, comprising the crustacean sex-controlling switch (IAG-switch), resulted with a shift in reproductive outputs from maleness (active testes) to femaleness (active ovaries).

Crossing intersex individuals with females resulted with offspring with femaleness tendency with the presence of individuals bearing WW chromosome ('super-females'). Evidently, using genomic sex markers we validated the presence and viability of WW females in the laboratory and more importantly in redclaw populations in nature. Identifying such viable WW females pave the way to the establishment of a production scheme for all-female *C. quadricarinatus* populations. Establishment of such production schemes through crosses of WW females and intersexual active male individuals will be discussed for improved environmentally sensitive aquaculture and biocontrol.

Recent development of Carcinological Society of Japan, with special emphasize of international activity

Asakura A¹

¹*Seto Mar Biol Lab, Kyoto University, Shirahama-cho/Nishimuro-gun, Japan*

Biography:

2012 - present. Professor, Kyoto University

2012 - 2020. Director, Seto Marine Biological Laboratory, Kyoto University

2021 - present. Director, Field Science Education and Research Center, Kyoto University

2010 - 2011. President, The Crustacean Society (USA)

2012 - present. President, Carcinological Society of Japan

In April 1961, the Japanese Emperor Hirohito celebrated his 60th birthday, who was a renowned marine biologist. In honor of his birthday, Dr. Isabella Gordon, British Museum of Natural History, was invited to Japan for a face-to-face talk with Hirohito. This meeting was also attended by several Japanese carcinologists, including Prof. Tsune Sakai (Yokohama National University), Prof. Itsuwo Kubo (Tokyo University of Fisheries), and Dr. Yo K. Okada (National Science Museum, Tokyo), which led to the formation of the Carcinological Society of Japan (CSJ).

Recently, CSJ have making great efforts to internationalization of the society to promote international communications and activity. In 2009, a joint international conference was held by The Crustacean Society (USA) and CSJ in Tokyo. Another joint international conference was held by International Association of Astacology and CSJ in 2014 in Sapporo. International Symposium on Barnacle Biology was held in 2014 in Shirahama and Tokyo and 2019 again in Tokyo. "International Symposium: Frontiers in Crustacean Biology: Asian Perspectives" was held in Tokyo and in 2019 in Hong Kong during TCS Summer Meeting. "International Symposium: Symbiosis and Parasitism in Crustacea: Diversity and Ecological Studies in Asian Region" was held in Taiwan during Asian Marine Biology Symposium in 2019. CSJ and Malacological Society of Japan hold International Symposium on Evolutionary Biology of Parasitic and Symbiotic Relationships between Molluscs and Crustaceans in 2017. International Symposium "Biology of the EBI (prawn, shrimp, and lobster)" dedicated to Dr. Ken-Ichi Hayashi, Emeritus Professor of National Fisheries University was held in Kagoshima.

CSJ is now at a turning point. We believe that collaboration between CSJ and other related academic societies in the world are important for future development of crustacean biology.

Meiuran evolution in light of genomic applications

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Biography:

Greetings, my name is Lauren Ballou and I am a post-doctoral associate at Florida International University. Throughout my studies, I have been greatly interested in the biogeography, systematics, and evolution of crustacean fauna. Using an integration of both morphological and molecular approaches, I have had the opportunity to ask exciting questions across Pancrustacea; such as exploring the deep relationships within Meiura and investigating speciation within the stygobitic clade Remipedia.

The clade Meiura is comprised of both “true” (Brachyura) and “false” (Anomura) crabs. This fascinating group boasts high degrees of diversity and is well-known for its habitat ingenuity across freshwater, marine, and terrestrial systems. While meiuran evolution has been investigated for decades using multiple lines of evidence, the deeper relationships within the clade remain conflicting and largely uncertain. In this study, we seek to better examine the family relationships across true and false crabs via two molecular approaches. Firstly, we used Sanger sequencing to compare 10 genes across 344 taxa representing 88 of 109 families within Brachyura. We constructed a phylogeny via Maximum Likelihood (ML) and Bayesian Inference (BI), recovering a paraphyletic “Podotremata”, with Thoracotremata nested within “Heterotremata”. As expected, the resolution at deeper nodes was relatively ambiguous, suggesting more data and taxa were necessary. Using an integration of molecular and ecological datasets, we estimated that habitat transitions from marine systems have occurred between 5–15 times within Brachyura. To better elucidate the deeper relationships of the groups, we applied a second approach using next-generation Capture-Seq across 700 taxa, representing nearly every meiuran family (131). Probes are being designed to target thousands of randomized loci (ultra-conserved elements) and full mitochondrial genomes. Additionally, we targeted 41 genes of functional interest to better examine the physiology and development of crabs (HOX, opsins, circadian rhythm). With these data, we will use phylogenetic analyses to recover incongruence with previous topologies largely dependent upon the type and quantity of data utilized (mitochondrial genomes, nuclear protein-coding genes, randomized loci). Finally, we will trace functional genes across the tree to provide insight into the macroevolutionary strategies employed within Meiura.

Consequences of Heat Spikes on Crustacean Burrowers and the Communities they Engineer

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¹National Institute of Water and Atmospheric Research, Hamilton, New Zealand, ²University of St. Andrews, St. Andrews, UK

Biography:

Thomas is on a placement year working in the marine ecology lab at NIWA Hamilton as part of the Integrated Masters in Marine Biology course delivered by the University of St. Andrews. He has particular interest in decapods, especially their behaviour, ecology, evolution and functioning in the context of the habitats and communities they reside.

Global warming is increasing mean air and water temperatures, resulting in an increased frequency, duration and magnitude of heat wave and temperature maxima events. Due to their position at the interface of land and water, intertidal habitats are particularly sensitive to these challenges with shallow areas facing amplified heating compared to deeper waters. Middle of the day low tides result in long periods of sun exposure, with summer temperatures able to reach over 40°C in New Zealand estuarine soft sediments. To examine the influence of these heat spikes we conducted a series of laboratory and field experiments intensifying these temperatures to levels likely experienced in the future with particular focus on the response of the functionally significant burrowing crab *Austrohelice crassa* (Decapoda: Varunidae). Temperatures in air and sediment were recorded using loggers deployed to a range of sediment and habitat types, and point measurements were collected inside and outside of crab burrows during midday low tides. This was used to inform experimentation using a gradient of temperature in a temperature controlled room rising from average summer temperatures to those experienced at extreme heat spike events to examine behavioural response and thermal microhabitat selection of *A. crassa*. Furthermore, open top chambers were utilised in field experiments to artificially increase temperatures beyond heat spike events and the behaviour of the crabs recorded in addition to overall community response in areas with and without burrows to identify the impact these have as refugia from, or distributors of, heat in these extreme events.

The road to success – global dispersal and ecological footprint of the amphipod super-crustacean *Jassa*

Beermann J¹

¹*Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany*

Biography:

Started working with amphipod crustaceans (ecology and taxonomy) in 2007.

*PhD in Zoology from Free University of Berlin (Germany) in 2013; topic: ecology of coexisting *Jassa* species in the North Sea.*

Researcher at AWI Bremerhaven (Germany) since 2015.

The establishment of artificial hard substrates in marine environments (e.g. harbours/pontoons, offshore wind farms, oil and gas platforms) provides suitable habitat for particularly adapted invertebrate communities. In temperate to warm seas, these fouling communities are often dominated by species of the genus *Jassa* in terms of abundance and sometimes even biomass. Densities of these amphipods are known to exceed 1 million individuals per m². *Jassa* species discrimination has had a problematic history which is why species' occurrences have often been undetected. Nonetheless, some *Jassa* species have been transported by human shipping activities since at least the 19th century and now occur widely in coastal waters across the globe. Recent molecular data support a scenario of still ongoing dispersal of at least three *Jassa* species all over the world as evidenced by the genetic connectivity of conspecific populations from geographically distant regions. Further, as some species of *Jassa* are typical colonizers of artificial hard substrates, they profit from the anthropogenic transformation of marine habitats. As a result, facilitated by some partitioning of resources, several species can now be found coexisting in dense amphipod fouling assemblages. *Jassa* species can be highly effective suspension feeders with a potentially significant impact on neighbouring communities due to their high abundances. Results of a recent feeding experiment suggest that in the southern North Sea alone, *Jassa* filters almost 5 km³ of water per year. At the same time, these amphipods release up to 547 tons of carbon per year in the form of feces, thus enriching surrounding soft sediment communities with organic matter. Given the wide dispersal of *Jassa* species around the world and the ongoing anthropogenic transformation of marine environments, these tiny (neo)cosmopolitans may increasingly have profound impacts on coastal ecosystems.

Microplastics ingestion by the Pacific mole crab *Emerita analoga* from Monterey Bay, California, U.S.A.

Bhaduri R¹

¹California State University Stanislaus, Turlock, United States

Biography:

Dr. Ritin Bhaduri is an Associate Professor in the Department of Biological Sciences at California State University Stanislaus, Turlock, U.S.A. He received his Ph.D. in Biological Sciences from George Washington University in Washington, D.C. He is a recipient of the Fulbright U.S. Scholar Academic and Professional Excellence Award in 2022. His research focuses on the ecology, behavior, and parasitism of marine crustaceans. He is currently teaching Invertebrate Zoology, Parasitology, and Marine Ecology. Why am I interested in crustaceans? They are abundant, diverse, and make excellent research subjects for scientific investigations.

Contamination by microplastics (MPs) is a major emerging hazard to global environmental health. Millions of tons of plastic are produced annually and remain in the environment, breaking down into microscopic fragments over time. These compounds have the potential to bioaccumulate and adversely affect animal health at higher trophic levels. The Pacific mole crab *Emerita analoga* is one of the most abundant crustaceans in the swash zone of sandy beaches along the Pacific coasts of North and South America. Adult crabs feed on various plankton, and are themselves prey for shore birds, fishes, and marine mammals. This study examined the presence of MPs in *E. analoga* and its surrounding natural environment (beach sediment and seawater) in Monterey Bay, California. Crab weight and carapace length were quantified, and their internal contents were further processed for detecting/quantifying MPs. Crab tissues were chemically digested using 30% hydrogen peroxide, sifted using 50µm sieve, filtered via membrane filter of 0.47µm, stained with Nile red dye, observed under a fluorescence microscope, and MPs quantified with regards to shape, size and abundance. Results showed that 74% of crabs tested positive for MPs. Such a high proportion can be explained by the facts that mole crabs are sediment dwellers and >85% of beach sediment and seawater samples contained MPs. Regression analyses revealed significant correlations between MPs abundance and crab weight/length. The composition of MPs showed consistency in crabs, beach sediment, and seawater, with fibers, particles, and beads as the dominant types. Our findings suggest that *E. analoga* may serve as a potential bioindicator species for evaluating plastic pollution and confirm MPs as a common environmental contaminant that poses a serious threat to aquatic organisms across all trophic levels.

New Zealand and the UN Decade of Ocean Science for Sustainable Development (2021 - 2030)

Bieda S¹

¹*New Zealand National Commission For UNESCO, Wellington, New Zealand*

Biography:

*Silke has a background in museums and heritage conservation. From 2004 she led a team of museums educators at the multimedia history exhibition *The Story of Berlin* before moving to New Zealand in 2007. For a decade she worked in management roles with *Heritage New Zealand* and was the manager of national heritage icon *Old St Paul's*, Wellington.*

Silke has a Masters in Museums & Media Studies, Linguistics and English Philology from the Free University of Berlin.

For the past three years she has been working on Aotearoa's contribution to the UN Decade of Ocean Science for Sustainable Development.

The UN Decade of Ocean Science for Sustainable Development (2021-2031) grew out of the recognition that much more needs to be done to reverse the decline in ocean health through the implementation of new multidisciplinary approaches. The New Zealand National Commission for UNESCO has been supporting a multidisciplinary contribution to the Decade with indigenous knowledges at the core. This is demonstrated with the establishment and membership of the New Zealand Decade Committee to engage national stakeholders with the Decade, through the development of an online platform to showcase ocean science projects from New Zealand and in the contributions from New Zealand to the international virtual lab series. Weaving knowledge systems together has generated a distinctive approach to how New Zealand undertakes science and research and how we collaborate with one another. Future Oceans Decade work will be deepening international connections in relation to weaving together knowledge systems to support contributions to the Decade including links to the International Decade of Indigenous Languages.

Additions and revisions to the squat lobster fauna (Anomura: Chirostyloidea and Galattheoidea) of South Africa

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Biography:

Thomas (Arno) is a PhD student at the University of Cape Town, South Africa. He is currently supervised by Emeritus Professor Charles Griffiths, Dr Lara Atkinson and Professor Enrique Macpherson. Thomas is a keen crustacean taxonomist who reviewed the Acrothoracica of South Africa during his master's research and is now busy revising the squat lobsters and porcelain crabs of South Africa. Thomas is a keen squash player and avid hiker who loves to explore the beauty of the Western Cape. This conference is an excellent opportunity for Thomas to gain valuable experience and network with the world's leading carcinologists.

Squat lobsters (Superfamilies Chirostyloidea and Galattheoidea) are among the most abundant, cosmopolitan and diverse macrobenthic invertebrate groups, with over 1500 species known globally. The squat lobster fauna of South Africa has never been formally collated and existing species descriptions have either formed part of larger works on crustaceans (such as Barnard's 1950 monograph) or been published as ad-hoc species descriptions. South Africa's marine life is known to be remarkably diverse due to its unique geography and it is concerning that there is such a deficiency in taxonomic knowledge in South Africa of such a speciose group. Furthermore, almost a quarter of the 32 known South African species have a dubious taxonomic status. There is thus a pressing need for a revision of this group in South Africa. By examining material housed in the collections of the Iziko Museums of South Africa, as well as new material collected on an ad-hoc basis, this study aims to revise the squat lobster fauna of South Africa using both morphological and molecular techniques (where possible). These ongoing analyses have so far resulted in resolution of the taxonomic status of seven species, with six species being removed from the fauna list due to misidentifications. Moreover, eleven new species distribution records (all from the east coast) have been identified. Lastly, two new Galathea species and a species of Raymunida are currently being described. To date, this research has increased the tally of South African squat lobster species from 32 to 43 confirmed species.

To cut a long-armed story short: cryptic diversity in endoparasitic isopods from mud crabs along the US Atlantic coast revealed by molecular and larval characters

Boyko C¹, Williams J¹, Tepolt C², Blakeslee A³

¹Hofstra University, Hempstead, USA, ²Woods Hole Oceanographic Institution, Woods Hole, USA, ³East Carolina University, Greenville, USA

Biography:

Dr. Boyko's interests include the taxonomy, ecology, phylogenetic systematics of crustaceans, and host/parasite co-evolution. He has published over 140 papers on a variety of invertebrate subjects, described 135 new taxa (species to family level), and has served as a consultant for several museums. He is currently the Laboratory Director for the Department of Biology at Hofstra University and a Research Associate at the American Museum of Natural History and Yale University and teaches in an adjunct capacity. He is currently the Vice Chair of the Steering Committee for the World Register of Marine Species (WoRMS).

This study documents two endoparasitic entoniscid isopods, *Cancrion carolinus* and the recently described new genus and species *Cryptocancrion brevibrachium* from western Atlantic mud and stone crabs, based on molecular and morphological data, including descriptions of their epicaridium larvae. Although these species cannot be distinguished based on adult female characters, molecular data plus larval and male morphology show that two species are present, sometimes sympatrically. As is suspected for nearly all entoniscids, these species use copepods as their intermediate hosts and the epicaridium larvae seek out and clutch onto the copepods, likely involving the use of their modified sixth pereopods. *Cryptocancrion brevibrachium* is documented to have epicaridium larvae with a "short-armed" morphology (sixth pereopod subequal in length to pereopods 1–5), and the adults parasitize at least three species of western Atlantic mud crabs. In contrast, *Cancrion carolinus* has epicaridium larvae with a "long-armed" morphology (sixth pereopod approximately twice the length of pereopods 1–5) and is found in at least three mud crab and one stone crab host species. Two of these hosts are reported as infested by entoniscids for the first time. This study highlights the cryptic and morphologically reduced nature of adult entoniscids, thus accurate identification of the parasites from these ecologically important host species requires examination of epicaridium larvae and/or molecular data.

A deep-sea game of hide and glow: Light organ function and diversification in sergestid shrimps

Bracken-Grissom H¹

¹Florida International University, North Miami, United States, ²National Museum of Natural History-Smithsonian, Washington DC, United States

Biography:

My name is Heather Bracken-Grissom and I am an Associate Professor in the Biology Department and the Assistant Director of the Coastlines and Oceans Division at Florida International University. My current research involves describing and documenting biodiversity and studying the evolution of bioluminescence and vision in the deep sea. To study these questions, I use crustaceans as model organisms in combination with genomic tools. Lastly, I am also the North American Governor for the Crustacean Society and enjoy thinking about opportunities to promote early career researchers from diverse backgrounds and cultures.

Deep-sea shrimp belonging to the family Sergestidae provide a unique system for studying the evolution of bioluminescence. Most species within the family have one of three distinct forms of photophores including lensed photophores, unlensed photophores or internal organs of Pesta, while other species lack light organs completely. In this group, photophores are known to function in counterillumination, in which they can alter light emission to match downwelling sunlight and camouflage themselves from predators below. Over the past few years, our research group has used integrative methods (genomic + morphology) to study the diversification of photophores and their role in counterillumination and congeneric recognition. Genomic skimming and phylogenomic investigations suggest light organ type may be correlated with species' depth distributions. Non-lensed photophores evolved once across the family but were lost in the deepest living genus. Lensed photophores also evolved once within benthopelagic genera, suggesting a potential link between the evolution of lenses and the seafloor. The internal organs of Pesta represent the ancestral state for the family and can be found in species with the shallowest depth profiles. Photophore diversity extends beyond light organ type, as each species displays unique light organ patterns. We investigated if species-specific arrangements play a role in conspecific recognition, as darkness and low biomass make it challenging for animals to identify one another in the deep sea. By combining morphology and visual modelling we found sergestids to be capable of detecting bioluminescence over ecologically relevant distances, however they cannot resolve organ pattern. More recent studies suggest light organs play a role in eye size evolution, with larger eyes being found in shrimp with lensed and unlensed photophores. These results suggest a potential role in bioluminescent signaling and an expanded role beyond counterillumination.

Importance of nationally Red Listed species in biodiversity conservation: a case study of freshwater decapods in Singapore

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Biography:

Cai Yixiong is at the National Biodiversity Centre, National Parks Board, Singapore, where he works on conservation of freshwater biodiversity, with research focusing on the ecological and hydrological characteristics of tropical freshwater streams. His primary research interest is on taxonomy, ecology, biogeography, and conservation of freshwater shrimps in East and Southeast Asia.

The distribution, abundance, and conservation status of freshwater decapod fauna of Singapore are updated based on results of comprehensive freshwater habitat survey conducted in the last decade, with 25 species recorded, including six species of shrimps that were officially assessed as extinct in Singapore Red Data Book (3rd edition; Dec 2022), namely *Macrobrachium rosenbergii*, *M. scabriculum*, *M. neglectum*, *M. idea*, *Caridina sumatrensis*, and *C. bruneiana*, representing 24% of total known native fauna. All of them are with small eggs, required to undergo pelagic larval development stages at downstream with tidal influence to complete their life history. Conversion of earth streams to concrete drains and impoundment of rivers to reservoirs in the last five decades are believed to be responsible for their extinction. Of the 19 extant species, six are crabs and 13 are shrimps. Three species of freshwater crabs, *Johora singaporensis*, *Parathelphusa reticulata* and *Irmengardia johnsoni*, are endemic to Singapore, with first two being restricted in very small areas and to be assessed as nationally Endangered, and the third one being nationally Vulnerable, with a relatively wider range. Of the 13 extant species of freshwater shrimps, two (*Macrobrachium platycheles* and *Caridina gracilipes*) are nationally Critically Endangered, and seven (*Macrobrachium equidens*, *M. pilimanus*, *Caridina gracilirostris*, *C. peninsularis*, *C. temasek*, *C. malayensis*, and *Potamalpheops amnicus*) are nationally Endangered. In highly urbanised Singapore, habitats that supports freshwater decapods are relatively rare, especially for those with tidal influenced to support amphidromous species. Red Listed species of freshwater carbs have previously contributed significantly on hill streams protections. With the updated nationally Red Listed species of freshwater decapods, associated freshwater habitats in Singapore will receive much more environmental attention, stronger public feedback to inform management, resulting in higher opportunity to be preserved or enhanced for aquatic biodiversity conservation.

How phylogenetic disparately related coral associated barnacles starting their symbiotic life with their hosts? – An example of adaptive evolution

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Biography:

Benny K.K. Chan is interested in the ecology of barnacles and larval biology. His recent research focuses on larval biology and behaviour of coral associated crustaceans.

The invasion of novel habitats is recognized as a major promotor of adaptive trait evolution in animals. Understanding whether similar ecological niches entail independent and adaptive evolution of key phenotypic structures related to larval host invasion in distantly related taxa still at a preliminary stage. In the barnacle molecular phylogeny tree, there are disparately related clades of coral associated barnacles, the Acrothoracican *Berndtia* and the Thoracican Pyrgomatid species. The larval antennular phenotypes (attachment organ) and its functional morphologies facilitating host invasion of these two distantly related coral associated barnacles were investigated. Extensive video recordings show that coral host invasion is carried out exclusively by cypris larvae with spear-shaped antennules in these two distantly related barnacle species. The settlement process first exercises a series of complex probing behaviors followed by repeated antennular penetration of the soft host tissues, which subsequently facilitates permanent invasion. Phylogenetic mapping of larval form and function related to niche invasion in barnacles (Thecostraca) compellingly shows that the spear shaped attachment organs is uniquely associated with corals and penetrative behaviors. These features evolved independently in the two coral barnacle clades and from ancestors with fundamentally different antennular phenotypes. The larval host invasion system in coral barnacles likely evolved adaptively across millions of years for overcoming challenges associated with invading and entering demanding coral hosts.

Abnormal or the new normal? Assessing the degree of intersexuality in pelagic ostracods from the Arctic and Southern Oceans

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Biography:

Emily Chen is a PhD candidate at the Institute of Oceanography, Polish Academy of Sciences researching Arctic and Antarctic ostracods. Originally from New Jersey, Emily had early exposure to the field by attending a marine science high school with access to research vessels and NOAA facilities. Since gaining undergraduate degrees in marine biology and Spanish, Emily is always looking to merge natural and social sciences. She completed her Master's in applied marine ecology and conservation through an international program, with 11 partner universities across Europe. Currently, Emily's PhD combines genetics, taxonomy, and ecology to understand spatiotemporal shifts in polar ostracods.

Knowledge of polar zooplankton communities is far from adequate, and ostracods are a commonly overlooked group. With seven life stages and a shortage of taxonomic experts, ostracods are challenging to identify to the species-level. Sexually dimorphic characteristics (e.g., carapace size and shape) are routinely used to confirm species compositions; however, if there are phenotypic changes and shifts in sex determination resulting from environmental pressures, it could signal problems for taxonomic and ecological research. Our study is based on 1) Arctic zooplankton samples collected in 2001-2006 and 2010-2019 along the west coast of Svalbard and 2) Antarctic zooplankton samples collected during the Discovery Investigations from the 1920s-1930s. Ostracods were initially sorted and subsequently identified using image analyses. Approximately 15% of pre-mature Arctic ostracods from the last decade were found to exhibit a mixture of male and female features, whereas no such intersex specimens were observed in the samples from 2001-2006. For a comprehensive assessment of the presence and extent of intersex ostracods in polar waters, ostracods in Antarctic zooplankton samples were also morphologically analyzed. Ostracods have not yet been documented to display intersexuality, and for confirmation of novelty, taxonomic experts of Ostracoda were contacted during preliminary research and provided with photo evidence and/or preserved whole specimens. Scanning and transmission electron microscopy was then used to determine whether the abnormal reproductive appendages were functional. These baseline data on ostracods are important since environmental stressors may exacerbate the rate of intersexuality, and as important links in the food web, this could potentially have a negative impact for ecosystem functioning.

Environmental Factors in Affecting the Infestation and the Larval Sex Ratio of the Rhizocephalan Barnacle *Polyascus planus*

Chen Y^{1,2}, Chan K¹

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Biography:

Yu Hsuan Chen is a master student in Biodiversity Research Center, Academia Sinica, Taiwan. She is interested in intertidal crabs feeding habits and larval biology. Seasonal variation of rhizocephala larval sex ratio is her current research.

Rhizocephala is a barnacle that parasitizes decapod crustaceans and lower the fitness of the host. Rhizocephala are dioecious have male and female planktonic naupliar and cyprids. Female cyprids infest the crustacean host and develops reproductive organ, the externa. Virgin externa can incorporate male cyprids, undergo fertilization inside the externa and produce embryos.

Previous study showed the larval sex ratio of rhizocephala has seasonal variation. *Polyascus planus*, for example, they have more female cyprids in summer and vice versa in winter. Factors affecting the rhizocephalan larval sex ratio varies with season is still unknown. Currently, environmental factors including temperature and the length of light-dark cycle can affect larval sex ratios but no extensive manipulative experiments have been conducted to test this hypothesis.

The present study is to examine if the temperature and light-dark cycle will alter the larval sex ratio of rhizocephalan, *Polyascus planus*, infesting the crab *Metopograpsus*. Annual collection of host crab is conducted from May 2022 to April 2023 in Keelung and Yilan, Taiwan. The host crab with mature externa is being cultured in the laboratory until first brood of larvae is released under room temperature and pressure and light-dark cycle 9:15. After the first brood, the host crabs with externa are transferred into the treatments with different temperature (28 °C – summer temperature, 18 °C – winter temperature, n > 10 in each level of treatment) and light-dark cycle (13:11 summer, 10:14 winter, n > 10). The larval sex ratio of each month's brood is recorded. Preliminary results (May to September 2022) showed that temperature can affect the larval sex ratio of Rhizocephala. This pattern will be finally confirmed after having a complete year's sampling and experiments.

What the Shell: Skeletal mineralogy of the New Zealand Spiny Rock Lobster (*Jasus edwardsii*)

Conroy A¹, Smith A

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Biography:

Aaron Conroy is an MSc Candidate in the University of Otago Marine Science Department looking at the biogeochemistry of the New Zealand Spiny Rock Lobster. Growing up in Auckland, boating and fishing from a young age, and eventually learning to dive, he has always had the ocean in his life. He moved to Dunedin to study Oceanography and Marine Science, then followed on with an MSc in crayfish biogeochemistry, learning the ins and outs of the physics, biology, and now chemistry of the ocean. He is an avid ocean hunter-gatherer and a PADI SCUBA Instructor.

The spiny lobsters (Palinuridae) are a relatively understudied group. *Jasus edwardsii* (the New Zealand red rock lobster) has not yet been studied regarding carbonate mineralogy. *J. edwardsii*, like other lobsters, has the potential to manifest complex mineralogy, which could include a) variation among body parts of the individual (uses, strengths, formation); b) changes in mineralogy over time from juvenile to adult; c) variation from environmental variables (and therefore a difference in populations). In addition, the presence of a similar species, *Sagmariasus verreauxi* (the packhorse lobster), in similar environments permits comparisons between species. The goal of this MSc project was to examine and identify differences and influences on the skeletal mineralogy of the red rock lobster. X-Ray Diffraction was used to determine the calcium carbonate composition across 13 different sub-locations on each organism's body and then compared between three organisms across two locations. Moults and deceased individuals were sampled to see if the composition of the moults was a duplicate of the whole organism. Results showed that the moults and the entire organisms are very different, finding an unexpected calcium carbonate compound. Understanding the calcium carbonate composition of this economically important species allows predictions for what changes could be expected in a changing climate and ocean.

First evidence supporting the conservation of physiological mechanisms behind extreme dormancy in crustacean zooplankton

Covi J¹, Reed K

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Biography:

Dr. Joseph A. Covi began conducting research within the Pancrustacea as an undergraduate, where he gained an interest in using insects and crustaceans as indicators of water quality. For his Ph.D., Dr. Covi investigated dormancy in brine shrimp embryos with Dr. Steven C. Hand. He then completed a four-year postdoctoral fellowship in the lab of Dr. Donald L. Mykles, where he developed novel models of molting physiology in decapod crustaceans. As faculty at the University of North Carolina Wilmington, Dr. Covi currently investigates topics in crustacean physiology and the susceptibility of crustaceans to climate change and anthropogenic chemicals.

The vast majority of coastal and inland crustacean zooplankton use an extreme state of dormancy to survive decades to centuries of burial in anoxic environments. Daphnids are the current record holder with successful hatching after 700 years of continuous dormancy in the embryonic stage. Copepods are in second place at over 330 years of dormancy. However, almost all research on the physiology of dormancy is conducted on one distant relative, *Artemia franciscana*. Historically, this species was the only zooplankton to produce embryos in the abundance needed for biochemical and molecular experiments. Because other species are almost always found in diverse communities, it is nearly impossible to identify their embryos to the species level. Even when identification is possible, the embryos must then be activated so development is synchronized. Unfortunately, activation methods are not yet available for most species of zooplankton. To solve these problems, embryos of the copepod, *Boeckella poppei*, were collected from Antarctic lake sediments, where they are the only species of crustacean zooplankton present. Embryonic development in *B. poppei* appears to continue under very low oxygen tension, but is eventually arrested under anoxia while the embryos are still partially syncytial. This partially syncytial embryonic state is similar to that of the anoxia-tolerant anostracan, *A. franciscana*. Both *A. franciscana* and *B. poppei* experience intracellular acidification under anoxia. Levels of nucleoside triphosphates (NTPs), which includes adenosine triphosphate (ATP), also decrease dramatically under anoxia in both species. When oxygen is returned, intracellular pH and NTP levels are restored. This large reversible acidification with a depletion of ATP would cause mortality in most eukaryotic species, and may be unique to crustacean zooplankton. These data provide the first comparative evidence that anoxia-induced cryptobiosis in diverse crustacean zooplankton is associated with intracellular acidification and an ability to recover from the depletion of NTPs.

Protecting coastal diversity by including the living dead: dormant zooplankton in the Anthropocene

Covi J¹

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Biography:

Dr. Joseph A. Covi began conducting research within the Pancrustacea as an undergraduate, where he gained an interest in using insects and crustaceans as indicators of water quality. For his Ph.D., Dr. Covi investigated dormancy in brine shrimp embryos with Dr. Steven C. Hand. He then completed a four-year postdoctoral fellowship in the lab of Dr. Donald L. Mykles, where he developed novel models of molting physiology in decapod crustaceans. As faculty at the University of North Carolina Wilmington, Dr. Covi currently investigates topics in crustacean physiology and the susceptibility of crustaceans to climate change and anthropogenic chemicals.

As a strategy to maintain populations in a variable environment, zooplankton species on all seven continents of the world produce embryos that survive decades to centuries in a dormant state termed cryptobiosis. Evolutionary biologists and ecologists have clearly demonstrated the importance of cryptobiotic “egg banks” to lacustrine and estuarine communities over the last century. However, the impacts of human activities on these embryonic storehouses of genetic diversity remain largely unknown. This is concerning, because the list of lipophilic chemicals of anthropogenic origin in water resources is expanding rapidly. Persistent organic pollutants accumulate in bottom sediments of water resources where the dormant embryos rest. Legacy chemicals, like PCBs, are now found in bottom sediments of the most remote locations of the world. Unfortunately, despite the alarming accumulation of anthropogenic chemicals, almost nothing is known about their effects on the recruitment of zooplankton from dormant egg banks. The effects of coal-ash and rotenone on zooplankton recruitment and community structure will be presented. Novel toxicology assays demonstrate that cyclone activity decreases zooplankton diversity in coastal lakes contaminated with metals. Rotenone has a similar effect, but operates by locking embryos in a permanent state of dormancy. The long-term implications of lipophilic chemical accumulation in maritime lakes of the Southern Ocean will be discussed. The broad goal of this presentation is to raise awareness of vulnerabilities in the most resilient life-stage for lacustrine and estuarine zooplankton. The data demonstrate an immediate need to consider dormant life stages in ecological assessments. Standardized toxicology assays that include dormant life stages of zooplankton provide a large step toward protecting zooplankton diversity in coastal communities.

Major revisions in pancrustacean phylogeny through improved taxon sampling with recommendations for resolving remaining difficult nodes

Crandall K¹

¹*George Washington University*

Biography:

Keith A. Crandall, PhD is the Founding Director of the Computational Biology Institute and Professor in the Department of Biostatistics and Bioinformatics at George Washington University. Professor Crandall studies the computational biology, population genetics, and bioinformatics, developing and testing methods for DNA sequence analysis. He applies such methods to the study of the evolution of both infectious diseases (especially microbiome diversity) and crustaceans (especially Decapod crustaceans). Professor Crandall has published over 370 peer reviewed publications, as well as three books.

The clade Pancrustacea, comprising crustaceans and hexapods, is the most diverse group of animals on earth, comprising more than 80% of animal species, and has dominated much of the planet for over 500 million years. It has been the subject of several recent phylogenomic analyses, but despite multiple analyses of hundreds of genes, relationships within Pancrustacea show a notable lack of stability. In this study, the pancrustacean phylogeny is estimated with expanded taxon sampling, particularly of malacostracans, using 106 transcriptomes and genomes and a precise tree-based approach to orthology inference. We completed more than 50 independent tree searches on continually expanded taxon sets using ML, BI, and coalescent-based methods, and our results show that outgroup selection and changes in taxon sampling have a large impact on the topologies recovered. We show that small differences in taxon sampling have a large impact on ortholog identification and phylogenetic estimation. By analyzing only shared orthologs between two slightly different taxon sets, we show that the differences in the resulting species trees are due to the effects of taxon sampling on the phylogenetic estimation, not on ortholog identification. In our final taxon set, we identify 576 protein-coding orthologs comprising 121,508 amino acid positions. Our results reject a number of clades including Caridoida, Eucarida, Multicrustacea, Vericrustacea, and Syncarida but support other classically recognized taxa, such as the Peracarida, and suggest some new clades. In contrast to the traditional Eucarida, we recover a novel relationship between decapods, euphausiids, and two clades of syncarids that we refer to as the Syneucarida. Additionally, with denser taxon sampling, we find Stomatopoda as sister to this clade. In recognition of these new relationships, we propose the name Stomatocaridea for Stomatopoda, Eucarida, and the two separate clades of "Syncarida", which divides Malacostraca into three clades: Leptostraca, Peracarida, and Stomatocaridea.

DecaNet - bringing together data and digital resources for Decapod Crustaceans

Crandall K¹

¹George Washington University, Washington, United States

Biography:

Keith Crandall is the founding Director of the Computational Biology Institute at George Washington University and a Research Associate in the Department of Invertebrate Zoology at the US National Museum of Natural History, Smithsonian Institution. A prolific researcher, Dr. Crandall has published over 370 papers and 3 books, including "Decapod Crustacean Phylogenetics". Dr. Crandall was a Fulbright Scholar at Oxford University, a recipient of the Edward O. Wilson Naturalist Award, an elected Fellow of the American Association for the Advancement of Science, and an Allen Wilson Centre Sabbatical Fellow at the University of Auckland.

DecaNet is a World Registry of Marine Species (WoRMS) group with the goal of establishing a Global Species List of Decapoda, which not only will incorporate all the basic taxonomic information, but will also host all the literature records (including an extensive pdf library), document the distributions of the species, as well as list their ecological (depth, habitat, etc.) attributes in a uniform and hierarchical way. We strive to use the WoRMS platform to integrate with other digital resources, especially the IUCN RedList which is currently out of date taxonomically due to the lack of communication between these digital resources. In general, we argue for better linkage amongst such digital resources to capitalize on the extensive taxonomic, ecological, and descriptive information available through the hard work on the crustacean community. We welcome all carcinologists with an interest in decapod species lists, attributes, photos, and conservation to join us in these efforts.

Assessing symbiosis using observational data: Crustacean symbiont diversity and spatial variability in an ascidian host

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Biography:

Edwin Cruz-Rivera is an Associate Professor in the Department of Biology at Morgan State University and an Adjunct Associate Professor at the University of the Virgin Islands. His interests focus on the trophic ecology and feeding behavior of invertebrates in marine and freshwater ecosystems.

Associations between multiple crustacean species and host ascidians have been documented worldwide for many decades but the nature of these symbioses remains poorly understood. In the Egyptian Red Sea, the solitary ascidian *Phallusia nigra* hosts a symbiotic amphipod and four copepod species, with densities as high as 68 symbionts per host. We analyzed the relationships between symbiont densities and host parameters to evaluate the nature of the symbioses and tested whether these relationships varied spatially. Patterns of species abundances suggested no competition or antagonism between symbionts. Ascidian mass, ash-free dry mass per wet mass (AFDM/WM), and both symbiont density and diversity per host, differed significantly among three reefs from El Gouna, Egypt. However, there was no correlation between amphipod, total copepod, or total symbiont densities and host mass or AFDM/WM. A host condition index based on body to tunic mass ratio was significantly related to symbiont density overall, but this positive pattern was only strong at a single site studied. Despite assumptions based on the habit of some of the symbiont groups, our analyses detected little effect of symbionts on host health, suggesting a commensal relationship.

Predator-prey relationship of snailfish and amphipods in deepest known hadal whale fall events

Dasgupta S¹

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The initial stages of the deepest hadal zone whale falls were recorded at the Western Philippine Basin (WPB) and the Mariana Trench (MT). The two carcasses belonged to Fraser's dolphin (*Lagenodelphis hosei*), and were implanted at water depths of 7729 m in WPB (16°56.964'N, 129°44.244'E) and 8200 m in MT (11°08.058'N, 142°09.654'E). The depths were chosen strategically to understand the species distribution and behavior patterns during the decomposition of the carcass. During an 86-day observation period in the WPB (Day-1, 5, 10, 60, and 86), the carcass was instantly pounced on by lysianassid amphipods on Day 1 in the first stage of mobile-scavenging, followed by the arrival of predatory snailfish to feed on the amphipods. On Day 10, a drastic drop in the number of both amphipods and snailfish was noted, when, unlike in shallow water, there occurred a pause in the feeding phenomenon, as the carcass was left mostly unattended by both the species. This is a unique phenomenon never observed before in other whale fall communities reported elsewhere. Heterotrophic grazers appeared within 1–4 m of the whale carcass, indicating arrival of the second stage, the enrichment-opportunist stage. At the site in MT, observed through 50 days (Day-1, 2, 23, 50), due to the absence of snailfish, the soft tissues were entirely removed by the amphipods within the first few days. Apart from the exposed skeleton, amphipods were observed on the sediments in Day-50. Other visible animals included a sea anemone, which possibly suggest an ongoing enrichment-opportunist stage, or an overlap of stages one and two. Our observations show that at hadal depths, the feeding ecology of snailfish and amphipods plays the major role in degradation and consumption of a large food source. Being the sole predator, snailfishes hover around the whale carcass in the WPB till our last observation on Day 86, possibly looking to intercept any amphipods that may come near the decaying whale tissues. The presence or absence of snailfish at hadal depths influences the rate of decay of a sunken carcass in the initial stages. It could further affect how fast and efficiently the dispersed organic matter or energy-rich lipids in the whale skeleton will be available to other macrofaunal communities, chemoautotrophic bacteria, and bacterial grazers that are able to tolerate elevated sulfide concentrations. Taking into account the food scarcity and limited species diversity in hadal zones, supremacy of depth-controlled predatory snailfish might be the deciding factor influencing the initial stages of a whale fall within 6,000 to 8,200 m in the hadal zone.

Ecomorphological aspects in the evolution of endosymbiotic crabs and shrimps

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Biography:

Werner de Gier is a Dutch PhD candidate at Naturalis Biodiversity Center and Groningen University, studying the ecomorphological aspects in the evolution of symbiotic crustaceans. He mainly focusses on two clades of endosymbiotic shrimp (Palaemonidae), and endosymbiotic pea crabs (Pinnotheridae). Using the famous Holthuis-collection and -library in Leiden, he mixes collection-based studies with new methods like microCT-scanning. Additionally, he tries to combine his project with a healthy dose of education and science-communication tasks.

Inter-phylum host switches play an important role in the evolution and diversification of symbiotic shrimps (Caridea: Palaemonidae) and pea crabs (Brachyura: Pinnotheridae). When switching from one host phylum to another, new selection pressures may result in morphological adaptations that deal with the recently colonised habitat. If this host switch is accompanied by a shift from an ecto- to an endosymbiotic lifestyle (within the hosts' body), the symbionts may evolve a wide range of ecomorphological features most notably seen in their carapace, abdomen, and pereopod morphology. Here we report on studies that were conducted to investigate the evolution of host switches and their connection to morphological adaptations and convergence in two shrimp clades (*Conchodytes* and *Anchistus* 'species groups') and in an endosymbiotic subfamily of pea crabs (Pinnotherinae). Complete phylogeny reconstructions of the shrimp clades show various inter-phylum host switches between multiple, morphologically similar but phylogenetically distantly related, endosymbiotic microhabitats: the internal cavities of (mainly bivalve) molluscan and ascidian hosts. Using a combined SEM and 2D morphometric study on the dactyli of the available shrimp species, host-specific adaptations could be identified. In addition, a 3D morphometric study was done to study the carapace shapes in detail, and link these to the phylogenetic tree to detect converging patterns within and between the clades. A similar 'phylomorphospace' study was also performed for a wide selection of pea crab species, of which pictures from literature sources were used. In this case, a 2D morphometric study was used to landmark carapace shapes of adult females and link the shapes to their presumed host choices. A recently published phylogeny tree was used to also find morphological convergence in the collected data. This demonstrates that shifts in lifestyles, which are also found in symbiotic shrimps, have major effects on the body shapes of pea crabs.

A comparative study of the combined effects of temperature and salinity on performance of larvae of the invasive *Hemigrapsus sanguineus* and the native *Carcinus maenas*

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Biography:

I am a PhD candidate working in the Alfred-Wegener-Institut in the Department of Shelf Seas Systems Ecology. I graduated in Biological Sciences at Faculty of Sciences in Universidad de la República, Uruguay. I did my Masters working in a coastal lagoon located in the south-east coast of Uruguay evaluating the contribution of a key species to the carbon fluxes of the lagoon during an annual cycle. I am working with decapods crustacean larvae, investigating the effects that changes in different environmental drivers (temperature, salinity, food availability) have on larval survival, development and growth.

Quantifying species responses to the combined effects of multiple environmental drivers is critical to better understand the effects of climate change on the performance of native and invasive species. We studied the ontogeny of osmoregulation in the invasive Asian shore crab *Hemigrapsus sanguineus* at an invaded area in the North Sea with animals exposed to acute changes in salinity (0-39‰). The effects of temperature (range 15-24°C) and chronic exposure to low salinities (20, 25, 32‰) on survival, development and growth rates were quantified in the megalopa. We compared these results with published data for the native European shore crab *Carcinus maenas*. *H. sanguineus* and *C. maenas* coexist and overlap in diet and habitat use with the invasive affecting the recruitment of the native. Larvae of *H. sanguineus* were able to hyper-osmoregulate at low salinities (15, 20‰) over the complete larval development; at higher salinities (25–39‰), all larval stages osmoconformed. In *C. maenas* only zoeae I slightly osmoregulate at low salinities and osmoconform at higher salinities, while zoea II-IV osmoconform at all salinities. When reared in seawater, survival of *H. sanguineus* increased with temperature; in *C. maenas* survival was not affected by temperature. In *H. sanguineus*, tolerance to low salinity was depressed at the lowest tested temperature but it was high in the range 18-24°C; in *C. maenas* tolerance to 20‰ was low across temperatures. In *H. sanguineus*, the effects of salinity on dry mass and elemental composition were weak irrespective of temperature. In *C. maenas*, exposure to low salinity resulted in reduced dry mass, C and N content. Overall, the capacity of *H. sanguineus* to osmoregulate at low salinities could explain a relative lower sensitivity to reduced salinity, as compared to *C. maenas*. Osmoregulatory capacity may promote invasion and expansion of *H. sanguineus* in warming coastal zones.

Long-term climate events affecting the larval distribution of the invasive Chinese mitten crab, *Eriocheir sinensis*, in the San Francisco Bay Delta

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Biography:

Master of Science in Biology 2023

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The Chinese Mitten Crab (CMC), *Eriocheir sinensis*, invaded the San Francisco Bay Delta system in 1992, due to human introduction. Since the establishment of this invasive species, there have been many negative environmental and economic impacts surrounding the San Francisco Bay. Explosions in adult populations can potentially have negative effects on native species through competition and predation. Other effects of the mitten crab are caused by juveniles that include stream bank and levee erosion through burrowing behavior that could potentially destroy future housing developments and erode natural ecosystems. Monthly plankton tows taken from the California Department of Fish and Wildlife (CDFW) station D41 were analyzed for *E. sinensis* zoeae. Brachyuran zoeae and megalopa were keyed to species with the use of a dichotomous key (Rice and Tsukimura, 2007; Gonzales et al, 2009). In April 2003, was the highest number of mitten crab zoeae where they recorded a total of 407 larva samples (CPUE = 4064.5). In 2005, no adult crabs were found in Otter trawls conducted by the CDFW and by 2008, no mitten crab zoeae were found in plankton tow surveys. However, in 2012 a total of 26 mitten crab megalopa were discovered and in 2013, another 9 mitten crab megalopa were found. Temperatures below 11.8°C and salinities below 15 psu are associated with declines in CMC abundances. Strong La Niña intensities are associated with increased abundances of CMC. If population explosions can be predicted, preparations can be made for the negative effects caused by the downstream migration of mitten crab juveniles. We are continuing to sort and identify crab zoeae for the years of 2014 and on to keep a record for all the invasive crab species in San Francisco.

Comparative population genomics in wide ranging spiny lobster species

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¹*School of Biological Science, University Of Auckland, Auckland, New Zealand*, ²*Department of Natural Resources and Environmental Engineering, Shiraz University, , Iran*

Biography:

Ahmad Farhad is a PhD graduate with interest in crustacean biology. He is interested in application of genetics and genomics in understanding and management fisheries, aquaculture and conservation issues.

Spiny lobsters (Palinuridae) are among the most economically and ecologically important crustaceans in the world. They found mostly in shallow tropical and temperate waters in many parts of the world. Two widely distributed species, *Panulirus ornatus* and *P. homarus* are key species for fisheries and aquaculture in the Indo-Pacific region, extending from South Africa to French Polynesia. Understanding population structure of are important for guiding sustainable fisheries and aquaculture management. Genome-wide SNPs from DArTseq sequencing of over 400 specimens of the two species taken from 20 locations across their extensive range was used to locate the genetic breaks. SNPs revealed a highly significant genetic structure for both species with pairwise genetic differences among the majority of sampling locations. A pattern of divergence pattern and secondary contact pattern was observed in both species but at two different levels. In *P. homarus* these was very strong divergence between central and marginal populations in both longitudinal margins of the population with recent secondary contacts in the Western Indian Ocean. In contrast, *P. ornatus* showed similar but more recent divergence and secondary contact. These divergence and secondary contact events appear to have created genetic breaks within the population over large geographic scales of the distribution of these species. Moreover, small scale genetic structure over small geographic scales (<1500 km) were also observed that may arise as the result of local adaptation. Overall, the results of genome-level SNPs and other genetic data from previous studies identify at least nine management units across Indo-Pacific for both lobster species, some of which were common between species. The results have implications for fisheries management of these two species and other less studied *Panulirus* species. It also has implications for transfer of seed or broodstock among the management units for an emerging lobster aquaculture focused on these two species.

The adaptationist programme in the crustacean physiology

Faria S¹

¹*Center For Marine Biology, University of São Paulo, São Sebastião, Brazil*

Biography:

PhD in Comparative Biology and Professor of Ecophysiology and Evolutionary Biology. My research focuses on the physiological evolution associated with habitat diversification or climate changes using decapod crustaceans, scleractinian corals and dinoflagellates as system models.

The current physiological diversity reflects a temporal moment of the entirety of life history, and “species” that are recognized as discrete units actually represent a continuum of biological forms and functions linked to each other through space and time. Closely related species are more similar due to a recent divergence, while those more distantly related tend to share functional dissimilarities. Thus, physiological characteristics observed in living species can be inherited directly from their ancestors, without an ad hoc environmental reason. Thereby, the evolutionary process generates two statistical implications in the comparative physiology: the non-configuration of “species” as statistically independent units, and the correlation between physiological traits and historical patterns of speciation. In the scientific literature regarding crustaceans, physiological data sets derived from multiple species have been traditionally interpreted as “states matched to specific environmental conditions”, evoking adaptation and propagating bias in designating natural selection as the formative agent of better organic horizons. Such traditional thinking suggests that a graduated series of successively stronger adaptive mechanisms may have driven habitat diversification, however such linking becomes questionable and may hold true only in specific cases after considering the phylogenetic history. Here, I illustrate such epistemological understanding using osmoregulation in decapod crustaceans from marine to fresh water and terrestrial travellers. I will exhibit how a hierarchical perspective on physiological diversity can answer evolutionary questions and re-examine old paradigms.

What does the future hold for a small, but powerful, amphipod bioturbator in the Wadden Sea?

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Biography:

*Eilish Farrell is a PhD candidate at the Alfred-Wegener Institute, Helmholtz Centre for Marine and Polar Research (AWI), in Germany. She completed her undergrad at the University of Auckland, and her MSc in Marine Biology at the University of Bremen and AWI; doing her thesis research on burrowing and nutrient cycling activities of benthic bioturbators. Currently Eilish's PhD research involves identifying important benthic feeding areas for flatfish in the North Sea, using DNA metabarcoding, experimental, and modelling techniques. During her MSc she worked regularly with the amphipod *Corophium volutator*, becoming best friends with this species over covid lockdowns.*

The amphipod crustacean *Corophium volutator* is a ubiquitous amphipod in the expansive mudflats of the Wadden Sea. It turns over copious amounts of sediment for its small individual size, deeming it a dominant bioturbator in its ecosystem. As an ecosystem engineer, *C. volutator* facilitates ecosystem functions such as nutrient recycling and carbon sequestration. There are, however, many anthropogenic factors that directly impact the environment of *C. volutator*, such as warming temperatures, coastal organic enrichment, and noise pollution. Here, we assess the future outlook of *C. volutator*'s bioturbation activity in the Wadden Sea (German Bight, North Sea) using experimental setups with these three stressors. Fluorescent tracers and sediment profile imaging were used to quantify bioturbation in controlled laboratory experiments. Bioturbation by *C. volutator* was markedly affected by the interaction of temperature and algal enrichment. Bioturbation rates were increased with added algal enrichment at 15°C, however higher enrichment levels at the same temperature did not yield higher bioturbation rates. Temperature rise alone also enhanced bioturbation rates, underlining that bioturbation activity of *C. volutator* can be limited by temperature during colder seasons and by algal enrichment during warmer ones. Furthermore, *C. volutator* was negatively affected by low-frequency noise in terms of lower bioturbation rates and shallower average burial depths. Given the recent trends and developments in the age of blue growth and climate change, this amphipod may suffer with pervasive and persistent anthropogenic effects in its environment. Ultimately, contributions from its bioturbation towards ecosystem functioning could become endangered.

Microsporidian parasite in *Metanephrops challengeri*: implications for a valuable fishery in Aotearoa.

Pande A, **Fenwick M**, Lane H, Madita Wieczorek A, Parkinson D

¹NIWA, Wellington, New Zealand

Biography:

Marks role at NIWA involves the identification and ecology of marine and freshwater invertebrates and fish from shallow water to abyssal depths. He has a good general knowledge of marine and freshwater animals specializing in bi-valves and octopus taxonomy. He is an expert on kākahi, the native New Zealand freshwater mussel.

Mark has spent over a decade working on rock lobster and scampi stock assessments, traveling to the Auckland Islands and the east coast of the North and south Islands.

Mark has strong links to local iwi and is a kaitiaki of Whanganui-a-Tara, a role he takes very seriously.

The emergence and spread of aquatic diseases in response to changing ocean climate poses a threat to wild populations, impacting economic, environmental, and sociocultural wellbeing.

First described in Aotearoa in 2007, *Myospora metanephrops* infects *Metanephrops challengeri* a nephroid lobster popularly known as scampi. Very similar to Northern Hemisphere langoustine, scampi is a high value low volume fishery in Aotearoa. Fished by smaller fishing vessels (20-30 m) using light trawl gear, scampi could be considered a “niche” fishery, meeting demand from an almost exclusively export market.

Myospora metanephrops was first found in the south-eastern Auckland Islands scampi grounds. Infection from *M. metanephrops* is not fatal, but it has a marked effect on fish quality resulting in translucent flesh with an unappealing presentation. This lowers the market value of the fish resulting in lost revenue for the fisher and lost returns for the quota owners. There has been a persistent presence of the disease in the commercial fishery and research catches. Indications are that the prevalence varies from year to year.

Although generally observed at low prevalence, there have been some years where anecdotal information suggests a higher prevalence than is usually seen. However, the distribution and prevalence of *Myospora* has not been properly quantified. Risk factors for increased prevalence have not been determined, although ocean warming is often associated with increased emergence of aquatic diseases. Economic losses to the fishery because of the unappealing presentation are yet to be quantified. The first step to is to determine the geographic range of *Myospora metanephrops* and to establish a prevalence baseline to better understand disease progression and spread dynamics. This may help manage any implications for the wellbeing of the scampi fishery. Monitoring and documentation of any changes in the spread or presentation of the disease are critical. This is an example of how effects of climate change can affect wild caught fisheries globally.

Here we present photographic evidence of the disease and discuss future for mitigation and control.

Predation by invasive portunid crabs on functionally and culturally important bivalves in New Zealand

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Biography:

Michal is a Marine Ecology Technician at the National Institute of Water and Atmospheric Research (NIWA) in Hamilton, New Zealand. Her interests include taxonomy, microscope photography, animal behaviour, and benthic ecology, in particular Amphipoda and Decapoda. She has earned a Master of Science (Research) with First Class Honours in Ecology and Biodiversity from the University of Waikato.

Charybdis japonica (Portunidae), a predatory crab native to Asia, was first reported in Auckland in 2000. *C. japonica* populations have subsequently spread throughout much of northern New Zealand (both east and west coasts). Although most common in submerged habitats, *C. japonica* also occurs in intertidal areas, raising questions about its impact on intertidal prey species. Therefore, an experimental study was designed to evaluate its impact on intertidal sandflat assemblages, specifically those dominated by ecologically and culturally important bivalve species *Macomona liliana* (Tellinidae) and *Austrovenus stutchburyi* (Veneridae).

To understand feeding patterns and impacts on soft-sediment assemblages, we exposed twenty-five 0.30m² patches of sediment to predation by large adult *C. japonica* for 48 hours. Bivalve densities were increased in some treatments to see if prey availability affected predation rate. We analysed final densities of bivalves in cages with and without *C. japonica* and used gut content analysis to determine the prey consumed during this time.

The proportional contribution of prey species to the diet of *C. japonica* was calculated using stomach fullness as a weighing factor. A total of 45 crabs were dissected for gut content analysis, with only 18 of these containing food material at 5 – 30% capacity. The consumption of *A. stutchburyi* and *M. liliana* represented approximately 70% of the gut contents, with the remainder consisting of gastropod species *Diloma subrostratum*, *Cominella glandiformis* and other unidentified soft-bodied macrofauna.

At present, *Charybdis japonica* appears to have little to no broad-scale impact on bivalve populations within the intertidal area. However, with a continuing increase in *C. japonica* populations, these invasive crabs may add pressure to already stressed habitats. Further research on the consumption of key prey species by *C. japonica* is critical to effective management and planning.

Research on sea spiders (Chelicerata; Pycnogonida) in the era of single ship oceanographic voyages (1870-1915)

Fornshell J¹

¹*Smithsonian Institution, Washington, US*

Biography:

PhD 1975 in Oceanography Florida State University

Oceanographer at the U.S. Coast Guard Oceanographic Unit, Washington, DC 1976-1981

Research Faculty University of Puerto Rico, Mayaguez, Puerto Rico 1981-1983

Science instructor Fairfax County Public Schools/Paul VI High School/ Prince Georges Community College 1983-2012.

Visiting Scientist NURC 2009

Research Associate in the Department of Invertebrate Zoology, U. S. National Museum of Natural History 1988-2023.

Research interest(s) microplankton, Copepods, invertebrate larvae, pycnogonids and bioacoustics

The Pycnogonida Latreille, 1810 were known in the first decade of the nineteenth century from collections made in coastal waters. Knowledge of the distribution and diversity was not well known until the latter part of the nineteenth century and first two decades of the twentieth century. The rapid expansion of knowledge about the sea spiders was made possible by the availability of research ships with powered winches or capstans capable of manipulating heavy dredges used to sample the benthic fauna. Also necessary was the wealth either private or governmental to fund major oceanographic research expeditions. The forty-five-year period from 1870 to 1915 witnessed the rapid expansion of knowledge of all benthic and planktonic marine life. This era of single ship voyages of exploration included thirteen expeditions which added materially to the study of the Pycnogonida. The 13 ships and cruise dates were VORINGEN (1875), HMS CHALLENGER (1873-1876), BLAKE (1875-1878), WILLEM BARENTS (1878 and 1879), INGOLF (1895-1896), GEORGE W. ELDER (1899), SOUTHERN CROSS (1899-1900), SIBOGA (1899-1900), RRS DISCOVERY (1901-1904), SCOTIA (1902-1904), ALBATROSS (1905-1906), TERRA NOVA (1910-1914) and AURORA (1911-1914). The results of these cruises established the existence of twelve families of Pycnogonida, ten of which are recognized today. Their distribution in the Arctic, Antarctic, Tropical and Boreal seas was also established. Finally, the vertical abundance and distribution of seven families was also established. A fourteenth voyage of discovery on which sea spiders were collected was the Russian Arctic Ocean Hydrographic Expedition 1910-1915 for which no record of the results appears to have been published in the scientific literature.

The Micronektonic Crustacean Assemblage in the Gulf of Mexico: Temporal Changes Since the Deepwater Horizon Oil Spill

Frank T¹, Milligan R¹, Sutton T¹

¹*Nova Southeastern University, Davie, USA*

Biography:

I am a professor at Nova Southeastern University at the Guy Harvey Oceanographic Center. The two major areas of research in my lab currently are 1) how deep-sea crustacean distribution patterns are affected by anthropogenic stressors and 2) photoreceptor adaptations to dim light (both downwelling light and bioluminescence) environments. We have been studying changes in the micronektonic crustacean ecosystem in the Gulf of Mexico since the 2010 DeepWater Horizon oil spill using traditional trawling techniques. The visual physiology studies are conducted using special temperature insulated, light-tight collectors deployed from opening/closing Tucker Trawls and ROVs.

The Deepwater Horizon disaster released 5 million barrels of oil in the Gulf of Mexico at a depth of 1480m from April – September 2010. The first trawling cruises to quantify the faunal assemblages in this region were in 2011, 3 to 12 months after the oil spill cessation; therefore, these data have to be considered a contaminated baseline against which to examine temporal shifts that may have occurred after the oil spill. The families of micronektonic crustaceans examined in this study include: Benthescymidae, Eucopidae, Euphausiidae, Oplophoridae sensu lato (now split into Acanthephyridae and Oplophoridae) and Sergestidae. Between 2011 and 2015, each family experienced significant declines in abundance, ranging from 70% (Euphausiidae) to 45% (Eucopidae), with no indication of recovery as of August 2022. These differences in vulnerabilities will be discussed with respect to differences in life histories and food preferences.

Deep-sea suprabenthic peracarids from New Caledonia: exploring diversity in the Coral Sea (SW Pacific)

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¹University of Lodz, Lodz, Poland, ²Muséum National d'Histoire Naturelle, Paris, France

Biography:

Inmaculada Frutos obtained her PhD from the University of Alcalá (Spain). Her research is focused on the characterization of suprabenthic crustaceans (mainly peracarids) in deep-sea waters: study of biodiversity within an ecological approach, spatial and temporal evolution of assemblages in relation to abiotic variables and its trophic role in the marine benthic food webs. All of them within a robust systematic knowledge which achieves the description of new species. Active participant in more than 30 expeditions sampling with benthic sledges, she has enhanced her qualification visiting collections at International Institutions from Smithsonian to Melbourne Museum

The central Indo-Pacific is a global hotspot of marine biodiversity and center of endemism where most marine families have their greatest concentration of species in a comparatively small area: The Coral Triangle. Located close to its center, New Caledonia is considered as a unique place of high diversity and endemism where the lack of knowledge on Peracarids is critical.

With about 25000 known species, Peracarida is considered a hyper-diversified group with many more species yet to be discovered. So far, only a few hundred of deep-sea peracarids are known from New Caledonia. Through the deep-sea cruise KANADEEP2 (September 2019, R/V l'Atalante), several sampling methods were performed in order to provide new taxonomic data for filling the gaps of knowledge in peracarids and question biodiversity patterns, endemism and connectivity in deep-sea environments of New Caledonia.

The implementation of complementary sampling devices (sledge, beam trawl, dredge and ROV) allowed the collection of 5106 specimens of peracarids in a depth range from 314 to 3226 m; where 72.6% of individuals were sampled by sledging, suggesting its efficiency for small-sized and fragile suprabenthic fauna. Main taxonomic groups are represented by isopods (2088 individuals, 40.9% of the total peracarids; 33 families), and amphipods (1510 ind., 29.5%; 50 families), followed by cumaceans (1152 ind., 22.6%; 6 families), tanaidaceans (300 ind., 5.9%; 16 families) and mysids (58 ind., 1.1%; 2 families). Munnopsidae, Oedicerotidae, Nannastacidae, Typhlotanaidae and Mysidae were the most represented families from each peracarid group.

First taxonomical approach already suggests a high potential of species new to science. Diversity and composition of peracarids is analysed and compared according to sampling gears, environmental parameters as well as habitats. This New Caledonian fauna will be also recontextualised in the global knowledge of Southwestern Pacific peracarids from previous cruises of Tropical Deep-Sea Benthos program led by MNHN.

Molecular taxonomy of the *Macrobrachium pilimanus* species complex in the southern Malay Peninsula

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Biography:

I am currently a Research Associate in the Lee Kong Chian Natural History Museum. My background and interest are in freshwater ecology, and my M.Sc. broadly examined the conservation and ecology of Macrobrachium shrimps in Southeast Asia.

The genus *Macrobrachium* Bate, 1868, is one of the most diverse groups of freshwater shrimps. Taxonomic complexity within the genus is often masked by interspecific conservatisms and high intraspecific variations due to a limited suite of diagnostic morphological features. Systematic relationships within the *Macrobrachium pilimanus* species complex are especially unclear and this complex remains taxonomically recalcitrant. This study aims to clarify phylogenetic relationships among members of the *M. pilimanus* species complex from the southern Malay Peninsula. Four species from the complex were included in the present analysis, viz., *M. ahkowi*, *M. dienbienphuense*, *M. pilimanus* and *M. platycheles*. An additional, often syntopic species, *M. malayanum*, was also included on account of its previously complicated taxonomy and superficial resemblance to members the complex. Phylogenetic trees were generated on a concatenated dataset of mitochondrial cytochrome c oxidase subunit I (COI), 16S ribosomal RNA and 18S ribosomal RNA genes, using Maximum likelihood (ML) and Bayesian inference (BI) models. *Macrobrachium ahkowi*, *M. pilimanus* and *M. platycheles* formed distinct, well-supported clades. There were inconsistencies in the placement of *M. dienbienphuense*, suggesting possible cryptic speciation and a need to re-examine this species. The COI and 16S phylogenetic trees also support the taxonomic revision and exclusion of *M. malayanum* from the *M. pilimanus* complex. *Macrobrachium pilimanus* itself has an interesting history in Singapore; though first reported in 1960, the record proved to be erroneous, as the specimen was misidentified. This study confirms for the first time its presence—and rarity—in Singapore, with implications on its management and conservation.

Adapted to the cold? Larval thermal tolerance across the native range in the European shore crab *Carcinus maenas*

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Biography:

As a PhD student at the University of Greifswald and Alfred-Wegener-Institute on Heligoland, Germany, he investigates the (combined) effects of ocean warming and other environmental drivers on the development and physiology of early life stages of marine crustaceans and potential effects on their distribution and range shifts. He holds an M.Sc. in marine biological resources (IMBRSea) and worked as a research assistant at the AWI in Bremerhaven and the Leibniz-Center for Tropical Marine Research (ZMT) in Bremen, and took part in scientific cruises. His research interests lie in ecology, physiology and conservation of temperate and high latitude animals.

We studied the variation in larval thermal tolerance among five populations of the European shore crab *Carcinus maenas* spanning a 27° latitudinal gradient from Vigo (Northern Spain) to Tromsø (Northern Norway) including two Arctic populations from the northern edge of the distribution. In a laboratory common-garden setup, we exposed freshly hatched larvae obtained from two to six females per population, to eight temperatures (6 – 27 °C) to quantify survival and development to the zoea II. Experiments were carried out in natural seawater (32.5 PSU), and under ad libitum food conditions (freshly hatched *Artemia* nauplii). Larvae were reared in glasses (60 ml) in five replicate groups of ten individuals each; dead individuals were recorded and removed, and larvae were checked for moulting.

Our results show differences in larval performance among populations. At 6°C all larvae died, but higher tolerance to such temperature was found for the Norwegian populations, especially in those from the northern distributions' limit (Bodø and Tromsø). The Norwegian populations (except the one from Tromsø) showed higher survival in 9° than that from Spain. Generally, the population from the northern range limit (Tromsø) exhibited the lowest survival to zoea II. In addition, all populations showed very low survival at the maximum tested temperature (27°C). We conclude that zoea I of *Carcinus maenas* are eurythermal (range 12 – 24 °C) along most of the distribution range. In addition, we found evidence for higher tolerance to low temperatures in the Norwegian populations. Based on this result, in a further study we want to use phenological modelling to further explore the species potential for poleward range expansions following the warming of the Barents Sea and the Atlantification of the Arctic.

Acknowledgement: this study was funded by DFG-RTG-2010 "RESPONSE" and supported by the Helmholtz graduate school for polar and marine research POLMAR.

Phylogeny relationship and diversity of deep-sea crustaceans from the family Typhlotanaidae Sieg, 1984 (Tanaidacea: Crustacea) and new families: Hamatipedidae, Meromonakanthidae and Paratyphlotanaidae.

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¹Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland, ²Independent Researcher, Waikanae, New Zealand

Biography:

Marta Gellert is a young scientist (PhD student), working on a highly diverse family of marine crustaceans in the family Typhlotanaidae. So far, she has described 31 species and 20 genera, which she has identified in collections from waters around Australia, the west Atlantic, the Kuril Trench-Kamchatka Trench, and waters off Iceland. In addition, using molecular methods for the first time, she discovered that the family she studied (Typhlotanaidae) is not monophyletic and can be divided into at least four families. Three of them are now formally distinguished.

The family Typhlotanaidae Sieg, 1984 (Tanaidacea) is a ubiquitous and diverse group benthic small and unselective detritivorous peracarids. The family is defined mainly by the presence of a three-articulated antennule and unique structures on the carpus of pereopods 4–6, commonly called a ‘clinging apparatus’ that is composed of variety of hooks, spines, tubercles, and thorns, which is a morphological adaptation to their tubicolous life. The first definition of Typhlotanaidae was profoundly unspecific, the group losing and regaining family rank several times in its history. In total, we have examined over 11,000 individuals of Typhlotanaidae family collected from depths of 200–6000 m, covering the period 1960–2021, using an integrative taxonomy approach that combines morphological, morphometric, environmental, and genetic data (i.e., the mitochondrial subunit I of the cytochrome oxidase (COI), histone H3 and the 18S rDNA nuclear gene). For the first time, two classes of data (the morphological and the molecular) were combined to validate the results from both approaches. Our genetic results are consistent with the view of the polyphyletic nature of the Typhlotanaidae and highlight a serious underestimation of taxonomic diversity in this family and during this study three new families, 13 genera and 24 species were discriminated. This collection expands our current knowledge on the diversity and distribution tanaids, significantly increasing the number of deep-sea species and genera of typhlotanuids: in the NW Pacific species by 42%, and genera by 40%; in the N Atlantic species by 67% and genera by 130%.

Cumaceans: Contumacious No More

Gerken S¹

¹*University of Alaska, Anchorage, United States*

Biography:

*When I was 10, I decided to be a marine biologist, although I was not sure what that really involved except learning about marine organisms. I proceeded to do a BS in Marine Biology, an MS in Marine Science, and PhD in Oceanography. My crustacean journey started with my masters thesis, "Population ecology of the lepstracan crustacean *Nebalia pugettensis*). My PhD dissertation was on the cumacean family *Gynodiastylidae*, and I have continued to work on cumaceans for the past several decades, from the Arctic to the Antarctic and places in between.*

Cumaceans are small, relatively obscure peracarid crustaceans. Despite being common in soft sediments, occasionally very abundant (up to ~90,000/ m²), and prey for many other organisms, even most crustacean workers are unfamiliar with cumaceans. Presumably this stems from a combination of the size of the organisms (1–30 mm) and patchy distributions and abundances. It is difficult to study organisms that are frequently not readily accessible nor reliably available, require good microscopes, and about which little is known. In addition, until recently, cumaceans have been resistant to common molecular techniques, even more so than other peracarids. However, new techniques are yielding good results and have led to achievements such as the first well resolved multigene phylogeny, confirming monophyly of the order, most of the families, and a single evolution of the pleotelson, providing a solid foundation for future work within the order.

As organisms that are sensitive to environmental parameters and weak dispersers, cumaceans have the potential to be excellent environmental indicators, especially for the parameters they are sensitive to, such as changes in sediment quality (grain size, organic content) and water temperature. This potential has not been exploited before, due to the lack of information about the group. Given the recent advances, we will be using cumaceans as model organisms to look at responses to climate change around the Antarctic, using a combination of morphology, population level markers (COI, 16S), and transcriptomes, to explore the responses of cumaceans to increasing temperatures and related environmental shifts around the Antarctic.

Peptide hormone expression and synthesis in the reproductive tissues of the Ornate spiny lobster, *Panulirus ornatus*

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Biography:

Susan did her PhD at the University of Bristol, UK, with Professor Steve Morris on understanding the mechanisms and effects of trace metal uptake on freshwater crab osmoregulatory physiology, awarded in 2005. Following work on transport of pollutants across the placenta and then a postdoc at the University of Bath investigating drug resistance using C. elegans, she has recently returned to academia after a career break. She now works on the reproductive endocrinology of spiny lobsters and crayfish at the University of the Sunshine Coast, Australia, focusing on transcriptomics in Tomer Ventura's aquaculture biotechnology group.

Peptide hormone production is not confined solely to the central nervous system of crustaceans. Here, using transcriptomic analysis, we have recently quantified the expression of neuropeptide precursors in the reproductive tissues of the ornate spiny lobster, *Panulirus ornatus*. Precursors of diuretic hormone 44 (DH44), pigment dispersing hormone 3 (PDH3), SIFamide, an insulin-like peptide and members of the neuroparsin family were present in the ovary. The expression of adipokinetic hormone/corazonin-like peptide (ACP) precursor was exceptionally high in the medial sperm duct of *P. ornatus*, an unexpected finding which we validated using qPCR and RT-PCR. The synthesis of mature ACP from the precursor is likely to involve cleavage by prohormone convertase 2 (PC2), however we found no evidence for the digital expression of PC2 in the medial sperm duct. The medial sperm duct of this species contains structures perhaps specialised for spermatophore storage and therefore roles for the ACP precursor in the sperm duct could include regulation of storage or transport of the spermatophore. Other potential roles for the ACP precursor include influencing female lobster behaviour in a similar manner to sex peptide in *Drosophila melanogaster*.

Functional domains of ecdysteroid receptor gene of a field crab inhabiting Indian peninsula: Sequencing and phylogenetic analyses

Lal N¹, **Gopinathan A**¹

¹Vellore Institute Of Technology, Vellore, India

Biography:

A PhD student at the School of Biosciences, Vellore Institute of Technology, Ms Nishita Lal has been pursuing her research for the past six years. Results of her sequencing analysis of the ecdysteroid hormone receptor gene (EcR) have been accepted for publication in the Indian Journal of Biotechnology; another of her manuscript has been communicated to ASEAN Journal of science and technology for development. She has also to her credit, three more publications related to crustacean molecular endocrinology, that were presented in international conferences at Osaka Japan (2018), Bangkok, Thailand (2019) and Malaysia (2022).

This study reports sequence information on the functional domains such as DNA binding domain (DBD) and ligand binding domain (LBD) of the ecdysteroid receptor gene (EcR), of a field crab (*Paratelphusa hydrodromous*) inhabiting the Indian peninsula. Oligo(dT) primed cDNA synthesis, PCR amplification and sequencing, and subsequent bioinformatics studies have shown PhEcRDBD to be comprised of 189 bp, showing 100% identity in its amino acid sequence with those of all the six brachyuran crabs studied till date. The SMART-EMBL analysis revealed that DBD plays a vital role in DNA-binding transcription factor activity and sequence-specific DNA binding at molecular and cellular levels. SMART EMBL analysis of LBD recognized it as HOLI domain, playing crucial role in ligand-mediated Nuclear Receptor activity, ligand recognition and their interaction with co-regulatory proteins, and recruitment of transcriptional factors to trigger induction or repression of target genes. LBD of *P. hydrodromous* (PhEcRLBD), however, has shown maximum identity (90-99%) with only among Gecarcinucid crabs; with other brachyuran and the non-brachyuran crustaceans, the percentage of identity declined significantly (~73-90%). Compared to PhEcRDBD, PhEcRLBD is less conserved, apparently due to its multiple functions such as homo/heterodimerization and transcriptional activation/repression, in addition to ligand binding. Multiple Sequence Alignment performed in this study could locate non-synonymous substitutions, signifying differences in amino acid content existing among various taxa. In addition to providing us with basic information on the endocrine mechanism of crustacean growth, the present study implicates the existence of parallelism between LBD sequence diversity and the habitat of the animal in question, in the order of – gecarcinucid (field) crabs, non-gecarcinucid (estuarine and marine crabs), non-brachyuran crustaceans (inhabiting varied aquatic habitats) and non-crustacean arthropods, respectively. This example of phylogeny-habitat association has not been seriously attempted in crustaceans, but is reminiscent of the eco-evolutionary processes reported from marine bacterial communities and trichopteran insects.

Collecting deep-sea amphipods in sediment traps in the subantarctic Southern Ocean

Halfter S¹

¹NIWA, Wellington, New Zealand

Biography:

Svenja Halfter works at NIWA Wellington as zooplankton ecologist. Svenja's research focuses on diversity and physiology of crustacean and gelatinous plankton of the Southern Ocean, their role in the carbon cycle, and their response to climate change.

Amphipod diversity and population dynamics remain largely understudied, especially in the deep Southern Ocean. Our understanding of inter-seasonal and -annual changes is hampered by logistical challenges that come with working in this remote oceanic region and at depth. Here, we present a long-term record of amphipods intercepted by sediment traps, tools that are usually used to measure time-series of downward carbon flux. At the Southern Ocean Time Series (SOTS) site (47°S, 140°E), south of Australia, sediment traps have been deployed in the meso- and bathypelagic zone since 1997, resulting in one of the longest time-series in the Southern hemisphere. Analysis of the archive from 1997-2020 indicate that amphipods, despite not being dominant in surface waters, are frequently caught in the deep sea. High influxes of certain amphipod species, e.g. *Abyssorchomene abyssorum*, *Primno* spp. and *Eurythenes* spp., have potential negative impact on collected material in the trap and, hence, particulate carbon flux estimates, and require further investigation. Finally, we present biases and opportunities for using sediment traps to collect deep-sea amphipod community data, as well as capturing potential community shifts caused by climate change in the Southern Ocean.

Reproductive indicators of a small-scale crab fishery across a latitudinal gradient in the South-East Pacific

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⁶Departamento de Pesquerías, Instituto de Fomento Pesquero, Valparaíso, Chile

Biography:

I am a marine biologist, with a master degree in biological oceanography and environmental science. Currently I am finishing my doctorate studies at the Department of Earth, Environmental and Life Sciences of Genova University. Since 2008 I have been working at the artisanal fisheries department in a small research center (CIEP) at southern Chile (Chilean Patagonia). I have been working for a few years in developing biological and reproductive indicators for crab's fisheries. I am also very interested in studying reproductive cycle associated to larval stages of marine fisheries.

Reproductive potential is a key trait in the life history of exploited marine populations since it can change due to local environmental conditions including different degrees of fishing intensity. The common strategy of most decapods to brood their eggs prior to hatching, presents an opportunity to estimate potential fecundity. The capacity of crab males and females (eubranchyuran) to store sperm in specialized organs also can be used as reproductive indicator associated to sperm transference capacity. In this context, the present study estimated these reproductive indicators on local populations of crabs supporting a small-scale fishery (*Metacarcinus edwardsii*) along a latitudinal gradient (between 36° and 45°S) in three zones along the Chilean coast that represents comparatively different fishing intensities. Namely, these indicators were (1) Size at the onset of maturity, which was estimated associated to physiological and morphometrical sexual maturity of females and males separately; (2) Sperm transference capacity, which was evaluated through Vaso-Somatic and Receptacle-Somatic indices and (3) Fecundity potential, in terms of number of eggs per ovigerous female. Results indicated that differences in size at maturity along the latitudinal gradient were minimal and within the range estimated by other studies. Reproductive cycle also showed no differences with latitude. Sperm transference capacity showed no clear latitudinal pattern and no differences between low and high fishing intensity zones. The exception was the gonadal size at maturity in males in the southernmost area that where in the lowest range estimated, which in conjunction with low females' fecundity could be suggesting that the fishery is affecting its reproductive condition. Local environmental adaptations are not ruled out since this area is in the southern range of this species distribution.

Marine protected areas provide unfished reference information to empirically assess fishery status

Hanns B¹, Shears N¹, Nessia H¹

¹University of Auckland, ,

Biography:

Benn Hanns is a marine ecologist based in Auckland, New Zealand. His research has examined the effectiveness of New Zealand marine reserves at protecting lobster populations and investigated the drivers and implications of long-term changes in protected lobster populations.

Fisheries stock assessments will typically determine stock-status using estimates of unfished biomass generated from fisheries dependent data. Due to limitations in these data, modelled unfished estimates are reliant on assumptions regarding stock ecology. This can lead to uncertainty in estimates of unfished biomass and can compromise sustainable management. We propose using the biomass of exploited species in no-take marine reserves as a proxy for unfished biomass to empirically assess stock status. Marine reserves provide contemporary examples of exploited populations in the absence of fishing under current conditions, in physical environments comparable to neighbouring fished areas. Using lobster (*Jasus edwardsii*) potting and diver-based survey data from 2018 and 2019 we calculated fisheries relevant metrics from inside and outside two Hauraki Gulf marine reserves. Based on marine reserve reference points, we found spawning stock catch rates and biomass of lobster in adjacent fished areas were 3% and 2% of unfished levels. The comparability of potting and dive survey estimates validates using dive survey data to inform on stock status, while differences in population information between survey methods highlights the limited ability of catch data to accurately inform on sub-legal abundances. Further analysis of dive survey data collected between 2020-22 over a more expansive area, including three marine reserves and 8 comparable fished locations, indicated the fished population is still below 7% of unfished levels. This is despite significant cuts to the total allowable commercial catch in 2018. This study demonstrates how marine reserves can provide information on key parameters which can be incorporated into traditional stock assessments and highlights the critical status of north-eastern New Zealand lobster fishery. Planning for future marine reserves should consider the value of protected areas as tools to help manage fisheries in addition to protecting exploited species.

Exploring the origins of sponge symbiosis within the Balanoidea and the phylogenetic placement of the Acastinae

Hosie A^{1,2}, Fromont J¹, Munyard K², Jones D¹

¹Western Australian Museum, Welshpool, Australia, ²Curtin University, Bentley, Australia

Biography:

Andrew Hosie has been the Curator of Crustacea and Worms at the Western Australian Museum for 14 years. His primary research interests lie in the taxonomy of barnacles, the evolution of symbiosis and the biodiversity of Western Australia.

The evolution of symbiosis has proven to be a successful strategy within the Balanoidea, with barnacles inhabiting the Porifera being particularly speciose. Phylogenetic placement of these symbiotic groups has proven difficult, as morphological adaptation to the hosts are often characterised by the simplification or secondary loss of the characters present in free-living relatives or the result of convergent evolution driven by similar selection pressures. The sponge-inhabiting barnacles in particular have not received as much attention as the free-living or scleractinian symbionts within the Balanoidea. Nuclear (28s, RPII, H3) and mitochondrial (COI, 12s) sequences from 145 species were used to reconstruct a phylogeny of sponge-inhabiting balanoid barnacles to explore origins of sponge symbiosis and the relationship of these barnacles to both free-living and other symbiotic species within the superfamily. The results indicate that sponges were colonised independently three times, two of which resulted in a significant radiation. The first of these significant clades consisted of Membranobalanus-Pyrgospongia, which primarily inhabit sponges of the order Clionaida. This clade was well separated from the much more diverse clade consisting of the Acastinae and Bryozobiinae. Within this latter clade host use was spread across 16 sponge orders as well as octocorals (Cnidaria). A diversity of host fidelity is exhibited by this group of barnacles, with several lineages showing a close correlation to that of the hosts.

The phylogenetic trees support aspects of the subfamily arrangement within the Balanidae, however relationships between them and that of the Pyrgomatidae were not resolved. The Archaeobalaninae was the least supported, with species recovered within or sister to other major clades. This included some members of the octocoral-inhabiting Conopea found nested within the otherwise scleractinian-inhabiting Pyrgomatidae. These results indicate that the evolution of symbiosis within the superfamily is more dynamic than the current classification would suggest.

Amphipoda Type Catalogue of the Natural History Museum, London

Hughes L¹, Herdman A

¹*Natural History Museum, London, South Kensington, United Kingdom*

Biography:

Lauren Hughes is the Principal Curator in Charge of Invertebrates (non-Insects), at the Natural History Museum, London. I am an Amphipod taxonomist with interests across biodiversity, data platforms, natural history and museum studies. I focus on Indo-Pacific and Atlantic marine environments, with projects across shallow-water and deep sea fauna. I have recently been elected to the Steering Committee for the World Register of Marine Species (WoRMS). My current projects include Vessels and Expeditions of the 19th Century, Beach hoppers of California, Australian deep sea fauna and museum projects around data cleaning scientific names, geographic sites records and collections history.

Marine Invertebrate collections at the Natural History Museum, London include specimens collected in the late eighteenth century through to the present year. While the early Porifera, Mollusc and Decapod collections are much discussed and catalogued in various decades, an amphipod type catalogue is yet to be comprehensively completed. The current project continues the work commenced by Thurston & Allen in 1969 which covered Lysianassidae, Stegocephalidae, Ampeliscidae and Haustoriidae.

The NHM collection contains early specimens of little known material studied by William Elford Leach to establish the foundations of higher classification in Carcinology and includes dry pinned amphipod types, microscope slide preparations and alcohol preserved collections. Using museum labels, old registers, index cards and published catalogues, the project enhances the known history of specimens which were previously accompanied by only partial data.

The project improves the records of amphipods across three areas: 1) documenting the collecting efforts of leading nineteenth century UK naturalists Col. George Montagu, Charles Spence-Bate and Alfred Merle Norman; 2) acknowledging early curators of the collection William Elford Leach, Adam White, John Edward Grey and Edward John Miers; and 3) connecting collections from major marine expeditions of the early nineteenth and twentieth century including the HMS Challenger, HMS Erebus & Terror, HMS Sealark, Terra Nova, the Great Barrier Reef Expedition, William Scoresby and RRS Discovery which represents some of the earliest collecting of Amphipoda from the 'Southern Seas' including the Philippines, Fiji, Java, New Zealand, Van Diemen's Land [Tasmania] and New Holland [Australia]. The project has highlighted previously unrecognised Type material; specimens with probable Type provenance (where authors did not explicitly designate a Type series or in collections which pre-date the formation of the International Code of Zoological Nomenclature (ICZN) in 1895) and provides additional commentary on nomenclature of historic amphipod manuscript names.

Pseudotanaidae (Tanaidacea) diversity in North Atlantic

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²Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland, ³Independent Researcher, Waikanae, New Zealand

Biography:

I completed my doctoral thesis in 2020 with the title Diversity and distribution of deep-sea Pseudotanaidae.

(Tanaidacea, Peracarida). In my dissertation, I described one genus and 23 species of crustaceans belonging to the family Pseudotanaidae. I am currently a postdoc at the Department of Genetics and Marine Biotechnology, Institute of Oceanology Polish Academy of Sciences where I continue to study the diversity of the Pseudotanaidae fauna, using an integrative taxonomy approach, combining morphological, genetic and ecological analyses.

The subject of this study is the family Pseudotanaidae of the order Tanaidacea. These crustaceans belong to the Peracarida, so they do not have planktonic larvae, and the female lays her eggs in a brooding pouch. The female lives inside a self-built tube, while the males swim in search of females for mating. These two aspects of their biology make tanaids a type of organism with limited dispersal potential and so an ideal group for studying distribution, diversity and genetic connectivity. The family Pseudotanaidae is widely distributed, highly diverse and often the most abundant tanaid group in deep-sea samples. The seas around Iceland are characterized by a wide variety of environmental factors, and the bottom is separated by several zoogeographic barriers, such as the Greenland-Iceland-Faroe Ridge. The Pseudotanaidae fauna of Iceland is fairly well understood and represented by 20 species (out of 94 described), often widely distributed. Using integrative taxonomy in combination with traditional taxonomy, environmental variables and genetic methods (Bayesian and species delimitation methods, like abgd, gmyc, based on COI and 18s genes), we analyzed the distribution of Pseudotanaidae around Iceland, proving their high diversity and the presence of cryptic groups of species that inhabit distinct areas defined by the complicated hydrography and topography of the Icelandic seas. Our results indicate that the group of cryptic species recognized as the *affinis+longisetosus* morphogroup, truly constitute a single clade in which species are distributed over a wide bathymetric range (300–2700 m).

The responses of crabs (Crustaceans) to anthropogenic vibrational and acoustic disturbance

Joo S¹, Kim T¹

¹Program in Biomedical Science & Engineering, Inha University, Michuhol-gu, Republic of Korea

Biography:

Soobin is a Ph.D student in Marine Zoology Lab at Inha University. He studies to understand the effect of anthropogenic vibration and underwater noise on marine animals. His motto as a researcher is "Human activity could be dangerous to animals; danger to animals could also threaten humans." Because he is interested in conserving marine animals like this, he has participated in various activities, such as participating in large marine animal autopsy research or giving lectures to the public. He dreams of becoming a science communicator who conveys these contents to the public as a scientist.

Vibration and acoustic disturbances induced by anthropogenic activity such as construction, military training, ship noise, offshore wind power, and oceanographic observation cause a noisy marine environment. Recently, an increasing number of studies were conducted to understand the effect of such disturbance on marine mammals and fish, but the number of studies to understand the effect of vibration on invertebrates, including crustaceans, are comparatively low. To investigate the effect of anthropogenic vibrational and acoustics disturbance on crabs, we conducted two exposure experiments mimicking two types of sources: seismic vibration from pile-driving and underwater oceanographic observation sound. The anthropogenic construction activity on the coasts, such as pile-driving, generates seismic vibration that propagates through the substrate, and underwater oceanographic observation sound also could influence marine animals in the underwater environment. First, to determine if seismic vibration induced by pile-driving influences the semi-terrestrial fiddler crab (*Austruca lactea*), locomotion response was measured under 35, 120, 250, 500, and 750 Hz of vibration generated by a vibrator. Secondly, we measured locomotion and physiological conditions of Asian paddle crab (*Charybdis japonica*) exposed to 5 kHz of underwater sound, and this sound was gradually attenuated by the soundproof board and propagated to the three sectors in an aquarium. Our results of two experiments indicate that *A. lactea* and *C. japonica* could detect seismic vibration and underwater sound respectively within certain ranges of frequency and intensity. Additionally, each disturbance could induce behavioral responses, suggesting that anthropogenic vibrational and acoustic disturbance may act as stressors to crabs by letting them consume more energy.

Crustacean microbiome research: past, present and future

Jung J¹, Shields J², Gillevet P³, Song B², Sikaroodi M³, Andrews J³

¹*Ewha Womans University, Seodaemun-gu, Republic of Korea*, ²*Virginia Institute of Marine Science, College of William & Mary, Gloucester Point, USA*, ³*Microbiome Analysis Center, George Mason University, Fairfax, USA*

Biography:

Received Ph.D. in Paguroid phylogeny from Seoul National University

In Jeffrey Shield's lab, conducted lobster microbiome study as a visiting researcher

*In the laboratory of Paul Hebert, who established the concept of DNA barcodes, conducted population genetics research on invasive species *Eriocheir sinensis* as a visiting researcher*

Served as a research professor at Ewha Womans University after returning to Korea

Currently, studying not only crustacean phylogeny and population genetics, but also parasitic barnacle phylogeny and mitogenome, and microbiome of various organisms

Numerous microbiome studies have been conducted focusing on humans and organisms highly related to human life due to the recent development of NGS technology.

Despite the unique characters and close relevance to the human life of crustaceans, only a few studies have been conducted on their microbiome. Herein, to promote the study of crustacean microbiome, I will briefly introduce the microbiome and related studies including the comparative study of hemolymph microbiome according to the survival status of American lobsters that I conducted with Jeff. In this study, the hemolymph microbiome indicated significant differences between living and dead lobsters. In the case of living lobsters, the diversity of the hemolymph microbiome was high, and it maintained homeostasis different from the microbiome in the surrounding environment. On the other hand, in the case of dead lobsters, the diversity of the hemolymph microbiome was low with certain pathogens dominating the microbiome, and these results are regarded to be the result of succession. Lastly, I will present the direction for future research on the crustacean microbiome.

Abyssal-hadal connections: Delving deep into benthic isopod diversity of the northern Pacific Ocean

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¹Senckenberg Research Institute and Natural History Museum, Frankfurt a.M., Germany, ²Goethe-University of Frankfurt, Frankfurt a.M., Germany, ³University of Bremen, Bremen, Germany

Biography:

I'm a deep-sea biologist currently based at the Senckenberg Research Institute in Frankfurt am Main (Germany) with a keen interest in the taxonomy, systematics and diversity of deep-sea benthic isopods. In particular, I explore the likely responses of fauna to human impacts, especially those related to the extraction deep-seafloor minerals and climate change. My current research spans morphological, molecular and phylogenetic data to define species boundaries in selected isopod taxa. This should help to better understand patterns and drivers of the diversity and geographic distribution of deep-sea benthic organisms and, ultimately, to more accurately predict their responses to environmental changes.

Beyond a doubt: isopods are among the most diverse macrofaunal taxa across deep-sea benthic habitats. However, the mechanisms governing this diversity and the distribution of isopod species in the deep sea are still unclear, but it is assumed that spatial distance, the presence of biogeographic barriers, and adult dispersal capacities (all isopods are brooders) are likely important drivers. Here, we examine deep-sea isopod communities from abyssal and hadal areas of the North Pacific, where topographic and hydrographic discontinuities introduce dispersal barriers that are likely to limit species distribution. We used evidence from morphological and genetic characteristics to derive species limits and patterns of diversity in selected isopod families with different mobilities. In particular, we aimed to investigate the influence of bathymetric obstacles, such as the presence of trenches and ridges in the region, as well as geographical distance between sites on species divergence. While the study will contribute to our understanding of how deep-sea diversity is generated, it is also sought to provide pending biodiversity estimates in a region undergoing substantial environmental changes.

Evolution of freshwater crayfish (Decapoda: Astacidea)

Kawai T¹

¹Hokkaido Research Organization, Yoichi, Japan

Biography:

Tadashi Kawai is Chief Researcher of the Fisheries Research Development, Central Fisheries Research Institute, Japan, and present Asian Governor of The Crustacean Society. Dr. Kawai has published over 200 scientific papers with 4 monographs of the freshwater crayfish and 3 freshwater crustacean monographs including Advances in Crustacean Research 22 (Series Editor: Ingo S. Wehrtmann) "Recent Advances in Freshwater Crustacean Biodiversity and conservation (Edited by Tadashi Kawai and D. Christopher Rogers)". Dr. Kawai has held total 5 symposia in the summer meeting in The Crustacean Society and International Crustacean Congress since 2008.

Astacidea contains four superfamilies, Enoplometopoidea and Nephropoidea in the marine, Astacoidea and Parastacidea in the freshwater. Astacoidea has three families, Astacidae, Cambaroididae, and Cambaridae in northern hemisphere, Parastacidae contain only member of family Parastacidae in southern hemisphere. The two superfamilies are called as freshwater crayfish and they have contained approximately six hundred species, distribute in north, middle, and south America, Australia with New Zealand and New Guinea, Malagasy Africa, far-east Asia, Europe. Ancestor of the freshwater crayfish has been evolved from ancient of the marine Astacidea members in Mesozoic era, the single ancestor of freshwater crayfish invades into freshwater area in Super-continent Pangea from marine. This mono-invasion of the freshwater crayfish creates their several adaptations for the freshwater environment. Present study shows functional morphology of respiration and feeding and sensor, calcium metabolism of their gastrolith in stomach, their burrows in natural habitat, mating behavior and direct development of reproductive biology. Those are compared with that of Enoplometopoidea in coral reef and Nephropoidea in deep sea to clarify adaptation for the freshwater environment. The evolution of the freshwater crayfish among Astacidea members were discussed with their molecular biology, paleontology, and zoogeography.

Towards passive traps for marine pest species using novel acoustic methods

Keeler S¹

¹*National Institute of Water and Atmospheric Research*

Acoustic or sound-baited traps that attract pest species are highly effective in detecting incursions of pest species, even at low densities. Such traps have proven highly effective in monitoring and eliminating terrestrial arthropods such as fruit flies and crickets. The use of electronic sound synthesisers to reproduce the sound of conspecifics or hosts has proven highly successful, however this technique has not been utilised in a marine setting as a novel acoustic method for pest control. Here we explore sound production by an invasive marine arthropod, the Asian paddle crab *Charybdis japonica*. Sound production in crustaceans is widely documented and accepted as a means of communication. However, the mechanisms and behavioural function of sound production has never been described in *C. japonica*. The sound produced by *C. japonica* may provide a mechanism to produce sound traps which mimic the sound made by conspecifics and attract these pest species. We describe two distinct sounds being produced by *C. japonica* (a click and a rasp) and suggest two potential methods of sound production based on external shell morphology and the structures of the gastric mill. We also provide some evidence of behaviours which may be used in the generation of these sounds, consisting of leg flicks and clicks, and feeding (gastric mill processing). We explore the possibilities of using acoustic technology such as hydrophones as sound traps for the detection and attraction of these and similar species.

Creative application of crustacean evolution to new generational breakthrough: case studies of environmental assessment and biomimetics

Kim T¹, Joo S¹, Kim M¹, Cho B¹

¹*Inha University, Incheon, Republic of Korea*

Biography:

Dr. Taewon Kim is an associate professor at the Department of Ocean Sciences, Inha University and a leader of Marine Zoology Lab (MaZooL). After getting Ph. D. at Seoul National University based on evolution and ecology of fiddler crabs, he studied the effects of climate change and ocean acidification on marine invertebrates at Stanford University and Monterey Bay Aquarium Research Institute. Taewon is now interested in how environmental stressors influence behavior and physiology of marine animals. He also has a dream to contribute to conservation policy and biomimetics based on ecology and evolution of marine animals.

Crustaceans are successful animals in the aquatic environments and their evolution can be applied in a variety of ways to diverse fields. Here two fascinating examples are introduced. First, some crustaceans have evolved their vibroacoustic communications and recently it has been revealed that those crustaceans are sensitive to anthropogenic sounds. Fiddler crabs are one of those species which communicate using drumming signals with the frequency between 300~500 kHz. Therefore, anthropogenic vibration within those frequencies can interrupt not only their communication but also their behavior. Evaluation on the responses of these crabs can be used in the new generational criteria for anthropogenic activity such as construction and leisure activity. Second, crustaceans have evolved in the extreme environments such as deep-sea hydrothermal vent. To endure such environment, they need hyper-resistant exoskeletons. The understanding on the protective mechanism can be applied to biomimetic materials. We have studied the exceptional properties of crustaceans in the hydrothermal vents and aimed to apply these to new biomaterial for heat resistance and endurance.

Were decapod crustaceans affected by the Cretaceous-Paleogene mass extinction?

Klompmaker A¹, Jakobsen S², Milàn J², Sheldon E³, Jørgensen A², Martin G¹, Portell R⁴

¹Department of Museum Research and Collections & Alabama Museum of Natural History, University of Alabama, Tuscaloosa, USA, ²Geomuseum Faxe, Østsjælland Museum, Faxe, Denmark, ³Geological Survey of Denmark and Greenland, Copenhagen, Denmark, ⁴Florida Museum of Natural History, University of Florida, Gainesville, USA

Biography:

*Adiël Klompmaker serves currently as a Curator of Paleontology at the University of Alabama Museums, where he is involved in the curation of a large fossil collection, research, teaching, outreach, and management of Harrell Station Paleontological Site. His research focuses on biotic interactions among marine animals throughout the Phanerozoic and the many aspects of the fossil record of crustaceans, including taxonomy, diversity, taphonomy, and paleoecology. Thus far, he has published > 70 scientific articles. He serves as an associate editor for the journal *Palaios*.*

The Cretaceous-Paleogene (K-Pg) extinction is one of the most severe mass extinctions in Earth's history linked to a meteorite impact near Chicxulub in Mexico and Deccan Trap volcanism in India. Many major groups became extinct (ammonites, belemnites, non-avian dinosaurs, etc.) or experienced major losses in their biodiversity (bivalves, insects, echinoids, etc.). Conversely, decapod crustaceans, major contributors to marine ecosystems since the Mesozoic Decapod Revolution, are thought to have experienced limited to no extinction based on global analyses. There are, however, multiple explanations for this apparent lack of extinction: (1) decapod diversity was indeed not affected much if at all by the K-Pg event, (2) there was a substantial loss in diversity, but taxon richness rebounded rapidly and was not detectable in global analyses, or (3) uneven sampling has distorted the true signal. Distinguishing between these scenarios has never been carried out thus far by controlled, quantitative sampling on either side of the K-Pg boundary locally at sites where both latest Cretaceous (Maastrichtian) and earliest Paleogene (Danian) decapod-bearing sediments are exposed. Previous research has attempted to assess a possible crustacean K-Pg extinction at a more regional scale, but sampling strategies were not provided and/or only very few decapod species were encountered on either side of the boundary insufficient for comparative analyses. We sampled extensively from two decapod-bearing sites, one in Alabama (USA) and one in Denmark. Collecting took place from sediments that are relatively comparable on both sides of the boundary (fine-grained siliciclastics in Alabama and limestones in Denmark). Specimens from museum collections from those sites augmented the new specimens collected during our recent fieldwork. After working out the taxonomy, we will assess possible changes in diversity, abundance, composition, and body size. The preliminary results will be presented during this conference.

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

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¹Department of Marine Zoology, Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany, ²Department of Biological Sciences, Institute of Ecology, Evolution and Diversity, Johann Wolfgang Goethe University, Frankfurt am Main, Germany

Biography:

Henry Knauber is a crustacean taxonomist and PhD candidate in deep-sea biology working at the Senckenberg Research Institute Frankfurt, Germany. He is enrolled as a PhD student under a PhD-scholarship at the Goethe-University Frankfurt, where he also completed his graduate studies. His scientific work on deep-sea isopods began during his bachelor thesis and since then gradually extended in terms of scope and aims. In his PhD project, Henry investigates deep-sea isopod families with different dispersal abilities using integrative taxonomy and population genetics to unravel the effects of depth, distance and geomorphological features (e.g., trenches and ridges) on benthic speciation processes.

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

Toward resolving the phylogeny of Peracarida using a phylogenomic approach

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¹University Of Alabama, Tuscaloosa, United States, ²Natural History Museum of Los Angeles, Los Angeles, United States, ³University of Alaska Anchorage, Anchorage, United States

Biography:

Kevin Kocot is an Associate Professor in the University of Alabama Department of Biological Sciences and Curator of Invertebrate Zoology in the Alabama Museum of Natural History. Research in the Kocot lab focuses on the biodiversity, systematics, and genomics of understudied invertebrates using both molecular and morphological approaches.

Peracarida is a diverse clade of ~26,000 described extant species in 12 orders representing 39% of all non-hexapod crustacean diversity. Phylogenetic relationships among peracarid orders remain unresolved, hindering understanding of their evolution. Molecular phylogenetic studies addressing higher-level peracarid relationships to date have had limited taxon sampling and inadequate phylogenetic signal from datasets dominated by nuclear ribosomal and mitochondrial genes. Recent phylogenomic studies leveraging hundreds of nuclear-protein coding genes have significantly advanced understanding of higher-level pancrustacean phylogeny and relationships within other crustacean clades, but no such studies focused on Peracarida have been conducted. We are working to leverage publicly available and new transcriptomes and genomes (85 amphipods, 24 tanaids, 12 isopods, five cumaceans, two mysids, and one stygiomysid currently in hand) to reconstruct higher-level peracarid phylogeny and design probes to enable broader sampling across the diversity of Peracarida with a target-capture phylogenomic approach. Preliminary analysis of available transcriptomes and genomes (130 genes, 50,258 positions, 28% missing data) recovered a strongly supported topology with Amphipoda sister to all other sampled peracarids with Mysida+Stygiomysida sister to a clade in which Tanaidacea was sister to Isopoda+Cumacea. To design probes for target-capture, we used ProteinOrtho to identify homologous sequences in available peracarid transcriptomes and genomes. These were aligned and low-quality sequences excluded using a profile hidden Markov-model based approach implemented in Prequal. Maximum likelihood trees were reconstructed for each alignment and strictly orthologous groups were identified and retained using PhyloPyPruner. This pipeline identified 2,346 genes totaling 3,188,614 nt suitable for probe design. This project will apply modern genomic approaches to deciphering peracarid phylogeny, yielding a phylogenetic framework to facilitate understanding of the incredible diversity and morphological disparity of this fascinating clade.

History of taxonomic study of gammaridean amphipods in Japan

Kodama M¹

¹*Kagoshima University, Shimoarata, Kagoshima, Japan*

Biography:

Masafumi Kodama is an assistant professor in the Faculty of Fisheries, Kagoshima University. He has been involved in research on the taxonomy and ecology of amphipod crustaceans, and received his PhD from the University of Tokyo in 2020. His primary research focus is on amphipod crustaceans that inhabit seagrass and/or seaweed beds.

The order Amphipoda is one of the most diverse orders of crustaceans with more than 10,000 species. Although a considerable number of species have been described, there are still many undescribed species, and papers describing new species continue to be published. Among amphipods, gammaridean amphipods (= members of the historical suborder Gammaridea) are a group to which taxonomic studies have been devoted in recent decades in Japan. About 500 species have been documented in Japan, but there are still many undescribed species remain waiting to be described. Taxonomic studies of gammarids in Japan began in the 19th century, but it was not until the second half of the 20th century that research became more and more active. Since the 1960s, taxonomic studies of gammarids have been actively carried out by various authors such as: Kizo Nagata in the 1960s; Akira Hirayama, Shin-ichi Ishimaru, Takehiko Hiwatari, Hiroshi Morino, and Shigeyuki Yamato from the 1970s to the 1990s; Hiroyuki Ariyama and Ko Tomikawa after the 2000s. As a result of the considerable efforts of these authors, the taxonomic study of gammarids in Japan has made great progress over the past half century, and the number of species has increased remarkably. In this presentation, we herein review the study of the taxonomic study of gammaridean amphipods in Japan.

Breaking the assumption in sexual biology models in barnacles – movement, growth and sex change of dwarf males of the androdioecious turtle barnacle *Chelonibia testudinaria*

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Biography:

Diana Kortchemny is a master student in the Ecology and Evolutionary Biology program in the department of Life Science in National Taiwan University. Currently she is working on research of barnacle sexual plasticity and phylogeography and phylogeny of barnacles in the Coastal Ecology Lab in Academia Sinica. Previously she acquired a dual major undergraduate degree in Biology and Philosophy from Tel Aviv University, focusing on the study of marine biology and animal behavior and consciousness.

Previous barnacle reproductive models considered dwarf males of androdioecious barnacles cannot grow up to large size, are not able to change sex, and can only attach on the hermaphrodite for mating. One year monitoring was conducted to examine the reproductive system of the androdioecious turtle barnacle *Chelonibia testudinaria*, providing evidence of growth and translocation of the dwarf males. Three types of dwarf male growth patterns were noticed. Type A dwarf males translocated while growing, until detached from the hermaphrodite, then moved farther. Type B dwarf males grew up but did not translocate. Type C dwarf males grew up blocking the operculum of the hermaphrodite, which resulted in the death of the hermaphrodite. The rate of increase in basal area was significantly different among the three types. Dwarf males of type A and B develop their ovary, become hermaphrodites and have fertilized embryos in the mantle cavity.

Further experiments were conducted to test whether food availability is a key environmental factor to affect the growth, movement, and sexual plasticity of *C. testudinaria* dwarf males. Growth of barnacles with dwarf males was monitored under three treatments differing in food availability (low, normal and high food levels). Preliminary results indicate that increasing food availability affect the size, growth and movement of *C. testudinaria* dwarf males. Movement direction of dwarf males is achieved from greater growth of the shell plates that face the direction of translocation. Dwarf male movement and detachment from the hermaphrodite requires the dwarf male to reorient its shell plates, this process seems to be determined by the size of the dwarf male and the angle between the hermaphrodite to the substrate. Since growth patterns and movement of dwarf males can affect its reproductive success, further studies in barnacle reproductive modeling should consider these patterns in the assumption generations.

Imaging of the digestive glands and gut morphogenesis in the terrestrial isopod *Porcellio scaber* by a combination of micro-CT, light microscopy and transmission electron microscopy

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Biography:

*Katja Kunčič is a young researcher at the Biotechnical Faculty, University of Ljubljana (Slovenia). She completed her bachelor's degree in laboratory biomedicine in 2016 and her master's degree in biochemistry in 2020. Her PhD thesis focuses on the formation and remodelling of cell junctions in arthropod epithelia, so far mainly in the epidermis of the isopod crustacean *Porcellio scaber* (Kunčič et al., 2022). Her expertise includes histological analysis, immunofluorescence, micro-CT and ultrastructural analysis with the transmission electron microscope. She gained experience with optimization of these techniques for analysis of developmental stages of *P. scaber* (embryos, manca) and insect larvae.*

Morphogenesis of the crustacean digestive glands and gut is a complex process of epithelia invagination and structural modification, involving changes in cell shape and ultrastructural differentiation. Concurrently with these structural modifications, the functions of distinct epithelia of the digestive system are established. The formation of occluding intercellular junctions, i.e., septate junctions (SJs), remodelling of apical and basal plasma membranes, and formation of the cuticle are key differentiation processes that enable the barrier and transport functions of epithelia. We evaluated these ultrastructural characteristics in relation to tissue and organ modifications during organism development using an integrative imaging approach. Transmission electron microscopy (TEM) and light microscopy were used in combination with micro-computed tomography (micro-CT) to image the digestive glands and hindgut in selected embryonic and early postembryonic stages of the terrestrial isopod *Porcellio scaber*. With micro-CT, we were able to determine the morphology of the digestive glands and alimentary canal in embryos that are 1 mm in size. In late embryos, the digestive gland lobules are filled with yolk and occupy most of the body, the foregut and hindgut are already fused and the dorsal cells in the hindgut anterior region form a continuous ridge, the typhlosolis. TEM analyses have shown that the length and ultrastructure of the SJs between the digestive glands' cells in late embryos resemble those of adult animals, whereas the SJs in the hindgut epithelium are much shorter than in adult animals. In early postembryonic development, the shape of the lateral and ventral hindgut cells changes from columnar to dome-shaped and the SJs are longer than in previous stages which coincides with the onset of active feeding. The combination of micro-CT imaging of the whole embryos and electron microscopy of sections in selected regions of the embryo provides a valuable integrative insight into morphogenesis at different size levels.

Binding efficiencies of ecdysteroid receptor (EcR) with 20-hydroxyecdysterone and Ponasterone A: a comparative study with 14 brachyuran species

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Biography:

Anilkumar Gopinathan, FRSB, a Senior Professor at the Vellore Institute of Technology (India), and a PhD under the mentorship of Professor KG Adiyodi, has been researching on Crustacean Endocrinology for over three decades. Focussing currently on hormone receptor genes and expression, and WGS, his results have been published in journals of repute such as Molecular and Cellular Endocrinology, General and comparative Endocrinology, Journal of Crustacean Biology and Hydrobiologia. Two times grantee under the International Foundation for Science (IFS, Stockholm), and Scientific Advisor to the IFS, he has also successfully handled Projects from national/international agencies including DST-NSF, DBT, MoES and DAE.

20-hydroxyecdysone (20HE) and Ponasterone A (PoA) are found to be endogenous to insect and crustacean systems, playing central role in the major physiological processes such as molting, reproduction and development. These steroids bind with their respective nuclear receptor(s), leading to allosteric changes in the hydrophobic pockets of the ligand binding domain (LBD), to induce transcriptional activities, leading to gene expression at the target tissue(s). The present study examines the binding efficiencies of both 20 HE and PoA to the LBD of the ecdysteroid receptor (EcR) of the field crab, *Parathelphusa hydrodromous* (Decapoda: Brachyura). The results have also been compared with those of 13 other brachyuran crabs, through protein homology modelling and molecular docking. The efficacy of the receptor active sites for binding with 20HE and PoA has been assessed through computation of the net binding energy (AutoDoc Tools Version 1.5.6) and the amino acid residues involved (PyMOL 2.5). Significantly, in all the 14 brachyuran species studied, the net binding energy was more favourable ($p < 0.01$) for binding with 20HE than with PoA. Although the amino acid residues of EcR, involved in the ligand binding were found to be generally comparable for both the ligands, those for 20HE binding were seen to be more “conserved” than those of PoA. Glutamic acid, threonine, arginine, glycine, tyrosine and asparagine were found to be the amino acid residues primarily involved in ligand binding. Threonine and arginine, however, were seen lacking for PoA binding in some brachyurans. The results of the present study, on the one hand, would contribute to our understanding on the receptor – ligand binding in the mode of hormone action in general, while on the other hand, it could explain why 20HE is preferred over PoA in binding with EcR to accomplish the major metabolic functions in crustaceans.

Long-term changes in estuarine Crustaceans: evaluating the effects of the changing environment

Lam-Gordillo O¹, Lohrer A¹

¹NIWA, Hamilton, New Zealand

Biography:

Orlando is a research scientist at the National Institute of Water and Atmospheric Research (NIWA) in Hamilton, New Zealand. He is broadly trained in marine biology and ecology, with particular interest in biodiversity, ecosystems functioning, restoration, and conservation.

Worldwide trends indicate a decline in marine biodiversity due to a wide range of anthropogenic impacts and modifications, such as climate change effects, fishing, habitat disturbance, increased nutrient loads, and pollution. In coastal ecosystems, these anthropogenic pressures are important drivers of environmental change, influencing the abundance, distribution, and structure of the benthic communities that inhabit these ecosystems. Crustaceans play a major role on ecosystem functioning, transferring energy to different trophic levels, and modifying the sediment through biological processes, which enhances nutrients cycling. Here, we investigated the effects of climate changes (using the Southern Oscillation Index (SOI) and sea surface temperature (SST) at the estuary mouth as proxies) and local environmental variables (i.e., sediment organic matter, chlorophyll-a and mud content) on the abundance and diversity of estuarine Crustaceans across New Zealand. Long-term crustacean data (1987-2022) across 14 sites within four estuaries in New Zealand were analysed. A total of 307,802 crustaceans were collected, belonging to eight different Orders. Amphipoda showed the highest abundance, followed by Balanomorpha, and Cumacea. Linear trend analyses revealed that crustacean abundance and richness increased over time. GAMs showed that Chlorophyll-a, mud content in sediment, SOI, and SST, influence the abundance of crustaceans, yet the influence of these environmental variables was site-dependent. Overall, our study suggests that estuarine crustaceans are affected by the changing climate and resulting environmental pressures.

Crustacean data in the Ocean Biogeographic Information System (OBIS): Current state and future developments in training and community support

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¹UNESCO / IOC Project Office for IODE, Oostende, Belgium

Biography:

Elizabeth is an ecologist by training, with a background in biodiversity, macro-population genetics, and marine biology. She completed her PhD in Biology at Concordia University, Montreal, Canada. She is currently working with OBIS to develop training resources for data providers and users.

The Ocean Biodiversity Information System (OBIS) aims to be the most comprehensive database for the world's ocean biodiversity and biogeographic data. OBIS accepts many kinds of marine biodiversity data, beyond just occurrence records. As of January 2023, OBIS contains 11,458,174 global records of Crustacea, from 33,217 species. The top three most represented species are the Ocean shrimp (*Pandalus jordani* Rathbun, 1902), the American lobster (*Homarus americanus* Milne Edwards, 1837), and the Sidestriped shrimp (*Pandalopsis dispar* Rathbun, 1902), all which have occurrences on the North American coasts. OBIS recognizes the challenges in providing and submitting standardized data and has been developing training resources to guide data providers and users through the entire life cycle of data in OBIS. This simplification into a step-by-step process for publishing data to OBIS will support and encourage the crustacean community to further contribute their valuable data to OBIS. Publishing data to OBIS ensures your data becomes part of the global picture of biodiversity, allowing more vital information to be available for addressing global ocean concerns. OBIS provides open access to this data, allowing users to access Crustacean-specific data that might not be available otherwise. In this presentation, we review the improved process for publishing data to OBIS and the process of obtaining specific data of interest.

Pandalus platyceros – a protandric shrimp as a model to explore the IAG-switch and crustacean sexual plasticity

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Biography:

Tom Levy is a Postdoctoral Researcher at Stanford University. Tom's expertise focuses on reproductive physiology and endocrinology of crustaceans. During his PhD, Tom studied genomic, transcriptomic, and physiological aspects of crustacean sexuality. Using gene manipulations and extensive fieldwork worldwide, he contributed to the development of a novel all-female biotechnology in prawns, revealed molecular insights behind naturally occurring sex-transformation in Alaskan and Mediterranean shrimps and performed a genetic study on intersexuality in the Australian redclaw crayfish that yielded a patent application valuable for aquaculture. Dr. Levy is currently studying gonadal development and germline stem-cell competition mechanisms in tunicates at Stanford University.

The insulin-like androgenic gland hormone (IAG) secreted from the androgenic gland (AG) is a unique endocrine controller (the IAG-switch) of crustacean sexual differentiation. While previous studies of the IAG-switch focused mainly on early developmental stages of gonochoristic species, the high degree of sexual plasticity presented by protandric species makes them ideal models to study this mechanism in adults while transitioning from males to females. Such a species is the Northern spot shrimp, *Pandalus platyceros*, which is of commercial importance in the Eastern Pacific and the primary target species for shrimp fisheries within Southeast Alaska. Different stages of spot shrimp including reproductive males and females and also transitional phase shrimp were collected in Southeast Alaska. A transcriptomic library from tissues associated with the endocrine axis upstream and downstream the IAG-switch (AG, eyestalk, gonad, and hepatopancreas) yielded numerous genes, including IAG, that are differentially expressed between males, females and transitional phase shrimp. The function of the IAG-switch during the life history of this protandric species was demonstrated through measuring the highest transcript levels of IAG gene expression at the juvenile stage, that decreased significantly in mature males and decreased to negligible levels in the transitional and female stages. Moreover, six of the differentially expressed genes in the AG, whose homolog sequences are found in 17 other decapod species, seem to correlate with the expression pattern of IAG thus suggested to be conserved factors associated with the IAG-switch and universally involved in crustacean sex-differentiation. Moreover, IAG loss of function in males through RNAi, induced the sexual transformation that naturally occurs in this species. This included reduction in IAG transcript levels in males, elevation of vitellogenin gene expression in hepatopancreas and transformation of the gonad from an ovotestis containing both ovarian and testicular tissue to a true ovary with vitellogenic oocytes.

Androgenic gland in neo-male prawns lacking male chromosomes – where does it come from and how is it possible?

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Biography:

Tom Levy is a Postdoctoral Researcher at Stanford University. Tom's expertise focuses on reproductive physiology and endocrinology of crustaceans. During his PhD, Tom studied genomic, transcriptomic, and physiological aspects of crustacean sexuality. Using gene manipulations and extensive fieldwork worldwide, he contributed to the development of a novel all-female biotechnology in prawns, revealed molecular insights behind naturally occurring sex-transformation in Alaskan and Mediterranean shrimps and performed a genetic study on intersexuality in the Australian redclaw crayfish that yielded a patent application valuable for aquaculture. Dr. Levy is currently studying gonadal development and germline stem-cell competition mechanisms in tunicates at Stanford University.

The androgenic gland (AG) and its prominent secreted factor, the insulin-like androgenic gland (IAG) hormone, that act as a crustacean sex-controlling switch (IAG-switch) are being studied since late 1940's. For several decades, manipulating the IAG-switch is performed across amphipods, isopods and decapods to better understand physiological aspects related to crustacean reproduction. In the giant freshwater prawn, *Macrobrachium rosenbergii*, recent studies involving transplantation of AG cells into WW prawns at early developmental stages yielded functional neo-males lacking the masculine Z chromosome. Those neo-males develop active AGs allowing them to reproduce as normal males and give rise to all-female progenies. The source of the transplanted AG cells are normal male donors bearing the ZZ genotype. Therefore, it was not clear whether the transplanted cells have a stem-cell-element causing them to proliferate and create a ZZ-genotyped AG within a WW-genotyped animal or whether the short-term secretion of IAG from those cells, following their transplantation, induces the proliferation of primordial cells leading to creation of a WW-genotyped AG. In the present study, AGs from ZZ males and WW neo-males were dissected, and their IAG-activity was tested in-situ via immunohistochemistry with Mr-IAG-specific antibodies. Using laser capture microdissection (LCM), cells from the AG of both ZZ and WW animals were dissected, gDNA was extracted and their genotype tested with W/Z-specific molecular markers. In addition, using fluorescence-activated cell sorting (FACS) AG cells were isolated from ZZ and WW males and the transcript levels of IAG in the cells were analyzed. AG cells in WW neo-males were found to bear the WW genotype and to actively express the IAG gene. The latter suggests that every young prawn is born with an array of primordial cells which, upon induction of the IAG-switch, may create an AG and develop into a reproductive male, even when masculine Z chromosomes are missing.

The IceDIVA post IceAGE, a project update focussing on peracarid crustaceans

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Biography:

Integrative taxonomy is the basis of biodiversity research.

The “Icelandic marine Animals meets Diversity along latitudinal gradients in the deep sea of the Atlantic Ocean” (IceDivA) project is flying under the Challenger 150 banner, focussing on abyssal plain communities east and west of the Mid-Atlantic Ridge. By sampling Northwest and Northeast Atlantic deep-sea basins, IceDivA aims to extend the previous Subarctic deep-sea program, IceAGE (Icelandic marine Animals: Genetics and Ecology), providing deep-sea samples to investigate topics regarding species richness, connectivity and evolution. Attention is drawn to the Marine Protected area NACES in the North Atlantic. Here we will present an overview of the IceDivA and IceAGE project, its participation in the UN Ocean Decade, ongoing research, preliminary results, and the outlook for the project with a focus on Amphipoda and Isopoda.

Modelling approaches for exploring patterns of crustacean biodiversity throughout NZ waters

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¹NIWA, Hamilton, New Zealand, ²University of Auckland, Auckland, New Zealand

Biography:

Tom is a marine ecologist and quantitative modeller at the National Institute of Water and Atmospheric Research in Dunedin. Tom has broad interests in marine biogeography, quantifying species-habitat relationships, stressor responses and spatial planning and an ecological background in marine megafauna and pelagic systems. Tom utilises spatial and population modelling approaches to understand variability in species and habitats to provide the best quality information for the management of marine ecosystems.

New Zealand's oceans include diverse crustacean species, which are often key members of seafloor community assemblages. Due to the breadth of the EEZ, there are limited data on benthic invertebrate biodiversity for some regions; predictive spatial modelling may fill such data gaps. We showcase efforts using species distribution modelling to quantify relationships between crustacean taxa and environmental drivers and predict their spatial distribution, resulting in national scale models for 43 crustacean genera. These models are underpinned by point records submitted to national and international biodiversity collections and databases such as OBIS, NIWA invertebrate, Te Papa, and Auckland Museum. Further modelling is in process to integrate cumulative stressors into spatial models, to account for their impacts on spatial distributions of benthic invertebrates including crustaceans. For example, a model of *Munida* spp. on the Chatham Rise highlights greater predictive accuracy when bottom fishing and sedimentation are included as predictors. Models and point records are regularly used by central and regional government agencies to inform management of seafloor ecosystems. For example, predicted distributions have been used to identify hotspots based on species richness, to design marine spatial planning to ensure representation of all aspects of seafloor biodiversity within conservation management approaches, and to inform designation of trawl corridors to minimise impacts on seafloor ecosystems.

Crustacean Futures: applying the IPBES Nature Futures Framework to develop positive future scenarios for crustaceans

Lundquist C¹

¹NIWA/University of Auckland, Hamilton, New Zealand

Biography:

Carolyn Lundquist is Principal Scientist of Marine Ecology at NIWA and Associate Professor in the School of Environment at the University of Auckland in Aotearoa New Zealand. She collaborates with ecologists, modelers, societal scientists, indigenous knowledge holders, industry, and government to inform decision-making from coasts and estuaries to the deep sea. She was recently elected to the IPBES Multidisciplinary Expert Panel, and is Co-Chair of the IPBES Task Force on Scenarios and Models which has developed the Nature Futures Framework, a new scenarios framework to chart different paths to desirable futures for nature and people.

IPBES (United Nations International Science-Policy Platform on Biodiversity and Ecosystem Services) has developed a new global biodiversity scenarios framework, building on previous approaches such as climate scenarios. This new framework is designed to catalyse the development of new and transformative biodiversity scenarios that identify management options and opportunities that can reverse the declines in biodiversity and ecosystem services. The Nature Futures Framework (NFF) is underpinned by the values that humans hold for nature, and recognises that different values often result in different priorities for managing landscapes and seascapes. These values can be envisioned in a triangular framework with three 'corners', each representing a different perspective on human relationships with nature: 1) instrumental or material benefits of nature (Nature for Society); 2) intrinsic values of nature, including the diversity of species, habitats, and ecosystems that form and sustain the natural world (Nature for Nature), and 3) relational values where humans are an integral part of natural systems, and societies, cultures, traditions and faiths are intricately intertwined with nature (Nature as Culture/One with Nature). For example, coastal or ocean scenarios based on sustaining commercial fisheries are likely to be quite different to local community group projects that aim to maximise coastal restoration or rewilding projects, even though both prioritise sustainable ocean futures. In particular, the NFF highlights the role of indigenous knowledge systems in biodiversity conservation and management, and the diversity of non-material benefits of natural systems that have been historically excluded from decision-making based on material values for nature. Crustacean scenarios using the NFF can highlight pathways toward sustainable management that bring together economic benefits from crustacean fisheries with nature conservation to ensure intact ocean ecosystems, underpinned by principles of whakapapa and kaitiakitanga to ensure positive futures for crustaceans, oceans and people.

The Amphipod Silk Road: Unravelling The Evolution of Amphipod Silk

McKim S¹

¹University of California, Santa Barbara, Santa Barbara, U.S.A.

Biography:

Siena McKim is an artist turned evolutionary biologist from San Diego California. Siena received her BFA at University of Michigan where she studied art and freshwater algae and discovered her first species. She is now a PhD student at UC California researching amphipod silk and amphipod evolution. Beyond her research for her PhD program, she spends time questing the origin of animals, biodiversity, and novel traits. With her research and outreach experience she hopes to become a museum curator. She spends her free time SCUBA diving, taking underwater photographs, rock climbing, illustrating, and playing with her pet snake Mochi.

Corophioid amphipods (Amphipoda: Corophiida) are a large group of crustacean silk producers which generate important structure for biofouling communities. Many corophioids are opportunistic suspension feeders which use novel marine silks to build protective tubes or unique feeding structures. Despite the crucial role of silks in amphipod ecology and the larger marine community, the origin of amphipod silk production and its impact on corophioid diversification remains unknown. Therefore, I am using next generation sequencing of transcriptomes and scanning electron microscopy to identify genetic and morphological silk-producing characters in corophioid amphipods. With my collaborator at the University of Florida (Brittany Cummings) we map silk characters on a new corophioid phylogeny and assess the evolutionary dynamics of silk production. This research will provide new transcriptomic data on a poorly explored amphipod group and reveal a unique evolutionary road to silk production in crustaceans.

Osmoregulation in nine species of fiddler crabs (Brachyura, Ocypodidae) from the Eastern Pacific coast of Ecuador

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⁵Universidad Autónoma de México, Ciudad del Carmen,, México

Biography:

Holds a B Sc degree in Biological Sciences. Currently, undertakes studies for a doctoral degree in Comparative Biology in the Department of Biology, FFCLRP, USP. Has experience in crustacean osmotic and ionic regulation, and interests in marine and freshwater biology.

The osmoregulatory ability of fiddler crabs from the Pacific coast of South America is entirely unknown. We examine hemolymph osmotic and chloride regulation in nine species of *Leptuca* (3), *Uca* (2) and *Minuca* (5), distributed along the coast of Ecuador between 1° 17' 35.2752" N and 3° 15' 58.086" S. Crabs were collected from habitats including vegetated river banks, muddy estuaries, mangroves and exposed sandy beaches. Mean salinities were 12.4-28.0 ‰ (372-839 mOsm/kg H₂O). Crabs were adjusted to laboratory conditions for 3 days prior to 5 days exposure to salinities ranging from distilled water (DW, 0 ‰, <3 mOsm/kg H₂O) to concentrated seawater (47.0 ‰, 1,400 mOsm/kg H₂O), corresponding to their approximate tolerance limits. Hemolymph osmolalities were hyper-regulated above ambient in all species and, at the lowest salinities (DW to 7 ‰), ranged from 392-699 mOsm/kg H₂O in *Leptuca*, 611-621 in *Uca* and 479-716 mOsm/kg H₂O in *Minuca*. At the highest salinities (28 to 47 ‰), osmolalities also were hyper-regulated above ambient, ranging from 1,111-1,684 mOsm/kg H₂O in *Leptuca*, 1,075-1,277 in *Uca* and 1,288-1,437 mOsm/kg H₂O in *Minuca*. Only *M. galapagensis* hypo-regulated (1,173 mOsm/kg H₂O). Hemolymph Cl⁻ was hyper/hypo-regulated in all species, except *M. argillicola*. Isochloride points ranged from 115-391 mM in *Leptuca*, 234-319 in *Uca* and 190-253 mM in *Minuca*. Cl⁻ hyper-regulatory capabilities ($\Delta\text{Cl-hemolymph}/\Delta\text{Cl-ambient}$) were 0.07-0.59 in *Leptuca*, -0.06-0.23 in *Uca* and -0.22-0.24 in *Minuca*; Cl⁻ hypo-regulatory indices were 0.4-0.98, -0.77-0.81 and 0.13-0.99, respectively. Comparative analyses (Bloomberg's K, PGLS) demonstrated lack of phylogenetic signal in all parameters, none of which correlated with habitat salinity or between parameter pairs. Fiddler crabs from the coast of Ecuador are strong hyper/hypo-chloride regulators but are modest hyper-osmoregulators, lacking hypo-regulatory ability. They are adapted mainly to dilute habitats into which they have radiated from a moderately saline environment inhabited by a slightly hypo-osmotic ancestor.

Evolutionary trade-offs in osmotic and ionic regulation and gill ion transporter gene expression in high latitude, cold climate Neotropical crabs from the 'end-of-the-world'

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Biography:

Professor of Evolutionary Physiology. Our research focuses on the physiological ecology of crustaceans from different habitats like the marine, intertidal, fresh water and semi-terrestrial biotopes. Investigations include osmotic and ionic regulation, gill ion transporter activity and localization, and transporter gene and protein expression, converging on testable mechanisms and models for ion transport in gill epithelia and cells, couched within a structural framework from the molecular to systemic levels of structural organization. These investigations include a strong evolutionary component, employing phylogenetic comparative methods and a multi-species approach to the phenomena studied.

Osmoregulatory investigations on crabs from high Neotropical latitudes are entirely lacking. Seeking to identify the consequences of evolution in cold climates, we examine osmotic and ionic regulation and gill ion transporter gene expression in two sub-Antarctic Eubrachyura from the Beagle Channel, Tierra del Fuego. Despite sharing the same osmotic niche, *Acanthocyclus albatrossis* tolerates a wider salinity range (2-65 ‰) than does *Halicarcinus planatus* (5-60 ‰); their respective lower and upper critical salinities are 4 and 12 ‰, and 63 and 50 ‰. *Acanthocyclus albatrossis* is a weak hyperosmotic regulator while *H. planatus* is a hyper-osmoconformer; isosmotic points are 1,380 and $\approx 1,340$ mOsm kg⁻¹ H₂O, respectively. Both crabs hyper/hypo-regulate [Cl⁻] well with iso-chloride points at 452 and 316 mmol L⁻¹ Cl⁻, respectively. Incongruously, [Na⁺] is hyper-regulated at high salinities. mRNA expression of the gill Na⁺/K⁺-ATPase α -subunit is salinity-sensitive in *A. albatrossis*, increasing ≈ 1.9 -fold at 5 compared to 30 ‰ (reference salinity), decreasing at 40 to 60 ‰. In contrast, expression in *H. planatus* is very low salinity-sensitive, increasing ≈ 4.7 -fold over 30 ‰, but decreasing at 50 ‰. V(H⁺)-ATPase B-subunit expression decreases in *A. albatrossis* at low and high salinities as seen in *H. planatus*. Na⁺-K⁺-2Cl⁻ symporter expression in *A. albatrossis* increases 2.6-fold at 5 ‰, but decreases at 60 ‰ compared to 30 ‰. Chloride uptake at low salinity may be mediated by increased Na⁺-K⁺-2Cl⁻ expression but Cl⁻ secretion is independent of symporter expression. These two unrelated eubrachyurans exhibit similar overall osmoregulatory characteristics and regulate better in dilute media; however, the gill transporter gene expressions underlying ion uptake and secretion show marked interspecific divergences. Cold climate crabs may limit osmoregulatory energy expenditure by allowing hemolymph Na⁺ to increase, hypo-regulating hemolymph [Cl⁻] alone, possibly apportioning resources for other energy-demanding processes like aerobic metabolism, growth, reproduction and seasonal molting.

New discoveries on geographical distribution of glacial relicts in the genus *Mysis* in southeast Norway.

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Biography:

Kenneth Meland is a mysid biosystematist from the University of Bergen, Norway. His research background lies in the field of biosystematics, combining morphological and molecular data for inference on evolutionary pathways of Mysida, Lophogastrida and Stygiomysida taxa and their relatedness to other higher Crustacea. For the past years, Meland has been working on mysid and peracarid fauna from anchialine caves. Meland is a subject editor in WORMS and Zootaxa, and his present research is focuses on completing a taxonomic monography on the Mysidacea of Norway.

A recent study of *Mysis* species distribution in south-eastern Norway has revealed that populations of both *Mysis salemaai* and *Mysis relicta* are found to inhabit high altitude lakes, up to 198 masl, which is close to the maximum postglacial marine limit. And the discovery of *M. salemaai* in Lake Lyseren (162 masl) is the highest situated population not only in Norway, but probably in its entire global distribution area.

A shared distribution of both species is observed in south and southwest Sweden. Where, until now *M. relicta* has been found to inhabit lakes and rivers further inland than *M. salemaai*, and also found widely distributed in eastern Norway. In contrast, *M. salemaai* has a more fragmented distribution and has been found to inhabit more coastal lakes, where the only known locality in Norway has been, not in the east Norway, but in a small lake, Stokkelandsvannet (only 22 masl), near Stavanger in southwest Norway.

Zoogeographical distribution of *M. salemaai* and *M. relicta* in Sweden combined with the new Norwegian data, suggests that both species have most likely migrated into Scandinavia from the Yoldia Sea as early as 11.000 cal yr BP.

Quo vadis Xanthoidea? Translating molecular phylogeny into practical taxonomy

Mendoza J¹

¹*Lee Kong Chian Natural History Museum, National University of Singapore, , Singapore*

Biography:

Jose Christopher E. Mendoza obtained his PhD from the National University of Singapore in 2011. He is currently the Curator of Crustacea at the Lee Kong Chian Natural History Museum, National University of Singapore, where he does research on the taxonomy and systematics of the brachyuran crabs of the Indo-West Pacific region. He also teaches modules on Invertebrate Zoology, and is currently the Editor-in-Chief of the Raffles Bulletin of Zoology, an open-access publication specializing on the zoology of Southeast Asia.

The brachyuran superfamily Xanthoidea MacLeay, 1838, is one of the largest and most ubiquitous groups of true crabs, with approximately 800 extant species and 170 genera distributed in shallow and deep marine habitats circumglobally. The taxonomy of this group has been the subject of revision over the past several decades, but much still remains unresolved. Our research on the molecular phylogenetics of Xanthoidea has shown it to be a derived, monophyletic heterotrematan superfamily, which emerged in the Eocene and diversified mostly during the Miocene and Oligocene epochs. Tree-inferred relationships within this group, however, question the stability of current family- and subfamily-level classification. Much of this classification system had been established using morphological characters. We explore the taxonomic implications of the latest molecular trees and attempt to provide useful morphological diagnoses for the clades identified, as well as highlight some contentious taxa and areas for further study.

Cumacea and Tanaidacea Type Catalogue at the Natural History Museum London

Merrin K², Hughes L¹

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Biography:

My career has two focuses, research into deep-sea isopods and teaching at undergraduate university level. Much of my research focuses on the taxonomy and systematics of deep-sea isopods, particularly of the sub-order Asellota from south-eastern Australia. From an education aspect, I teach biology to large undergraduate cohorts and am always trying to use examples from the crustacean and marine worlds in my teachings. I would love to talk to anyone who have developed novel approaches in teaching at undergraduate level, especially if they include crustaceans.

The Peracarid Crustaceans at the Natural History Museum have benefited from the dedicated study by local and international researchers. The cumacean collection represents the work of 180 years of peracarid scientists, most notably, Henry 'Harry' Duncan Spens Goodsir, Thomas Roscoe Rede Stebbing, Alfred Merle Norman, Georg Ossian Sars, William Thomas Calman, George Eric Howard Foxon, Norman Sumner Jones, John Bishop and Daniel Roccatagliata.

The earliest Cumacea type specimen is that of Goodsir from 1843, from the Frith of Forth, Scotland. The collection expanded greatly during the diligent works of Calman as the first museum-based cumacea researcher in the early 1900s, followed by Jones who publishing during the 1970s to 1980s. The type collection is global in scope, covering tropical to Antarctic waters with material from the UK, USA, Ghana, Senegal, South Africa, Thailand, New Zealand and Chile.

The tanaid collection, similar to the Cumacea, represents the work of several early peracarid scientists, namely Stebbing, Sars and Norman, in addition to more recent, leading tanaid workers Jürgen Sieg, Graham John Bird, David Malcolm Holdich, Roger Norman Bamber and Magdalena Błażewicz-Paszkowycz.

The earliest Tanaidacea type specimen is that of Lilljeborg from 1864 from Norway, a specimen that was donated to the museum by Georg Ossian Sars. The type collection is relatively modern with the majority of species described from the 1980s onward. The tanaid type collection is also global in scope with material from UK, Norway, Italy, Libya, Tanzania, South Africa, Brunei, Thailand, Hong Kong, Australia and Antarctica.

This project has successfully identified gaps in database records, validated publications against the physical collections and improved our knowledge of the type collection of these two important crustacean groups. This updated information will be available on the NHM data portal and WoRMS.

High mortality of horseshoe crabs *T. gigas* (Arthropoda, Merostomata, Tachypleinae) larvae and juveniles in lab-rearing facility

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Biography:

Faridah Mohamad earned her bachelor's degree in Zoology at the University of Malaya, a master's degree in Biological Sciences at Universiti Putra Malaysia and then a Doctor of Philosophy at Glasgow University, Scotland in the field of ecotoxicology. Her interest in horseshoe crab (HSC) ecology started after attending the IUCN Workshop on HSC in 2011. Since then, she has carried out studies and published articles related to horseshoe crabs in Malaysia. She is currently a member of the Horseshoe Crab Research Group UMT and the steering committee of IUCN HSC Specialist Group.

The population of horseshoe crab *Tachypleus gigas* in Malaysia is rapidly declining in the past few decades due to increased demand, either in the seafood market, or other purposes including pharmaceutical uses. To increase the populations, release of juveniles into the wild habitat is regarded as one of the best efforts. Therefore, successful rearing of juveniles for release is crucial. We successfully obtained horseshoe crab eggs from our artificial spawning ground. After hatching, the larvae are reared in 30 ppt artificial seawater in plastic containers (25 cm width x 30 cm length x 15 cm height) with a thin layer of fine sand at room temperature. However, survival is very low. From 24 containers of Instar 1, only 29% showed more than 50% survival indicated by moulting to Instar 2. Whereas 71% showed more than 50% mortality, with 25% showing 100% mortality at Instar 1 stage. Death occurs as early as on day 2 after hatching, and particularly high occurrence during week 1-3. Instar 1 which did not moult into Instar 2 (which normally happen between day 30-60) was observed to survive only until day-235. Again, mortality was high during week 1-3. Unfortunately, all 873 surviving Instar 2 only survived until day-140, with the first death occurring on day-67. As these instars are reared to be released, at this stage, releasing them into the wild as early as Instar 1 of less than 60 day old seems to be the best option in terms of cost, but releasing Instar 2 of less than 30 day old may be the best option for higher chance of survival in the wild. More detail study on the physical and biological parameters of rearing conditions need to be carried out in order to have a more successful rearing of juveniles for release.

On genome editing in embryos and cells of the freshwater prawn *Macrobrachium rosenbergii*

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Biography:

I started studying biology at Ben-Gurion University in the Negev, Israel. In the second year of the bachelor's degree, I became a research associate in Amir Sagi's lab and my interest in developmental biology and functional genomics grew. I started my master's in the lab and finished after one year, and started my doctorate research. After three years, I published two papers as first author and working on two more. I presented my results to professional and academic platforms in Israel and abroad.

The clustered regularly interspaced short palindromic repeats (CRISPR) technology provides the means for accurate genomic editing. It has been applied in many kinds of cells and animals for functional genomic studies and for precise selective breeding. To apply this method in one of the most important – and well studied – decapod crustacean species, the giant freshwater prawn *Macrobrachium rosenbergii* we established two CRISPR platforms for the species—the first through direct injection into early-stage embryos (entire organism genome editing) and the second by electroporation of a primary embryonic cell culture. Calibration and optimization of Cas9 concentrations, delivery methods and editing efficiencies were achieved. Editing patterns utilizing multiple guides were examined through next generation sequencing, with a wide range of editing efficiencies in embryos (up to 100%) and in primary embryonic cell cultures (maximum of 64%). In addition, there was a striking difference between the two platforms in terms of the pattern of deletions around the Cas9 cut site. A phenotypic proof of concept for successful editing was provided through the investigation of an early acting paired box protein 6 (Pax6) transcription factor, which showed clear effects on eye development in edited embryos and larvae. We intend to further lay the foundations for precise functional genomic research and applications of genome editing in *M. rosenbergii* for both aquaculture and sustainable biocontrol.

The effect of temperature on the feeding ecology of brown box crabs

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Biography:

Wave is a second year master's student in Dr. Jennifer Taylor's crustacean biomechanics lab at Scripps Institution of Oceanography. Her research focuses on the effects of temperature on brown box crab feeding ecology and how this impacts their experimental fishery. She is collaborating with local fishers and state natural resource agencies to disseminate the findings of her research to fisheries managers and conservation policy makers. Her long term research interests are the effects of climate and human stressors on fisheries species and how to use the findings of this research to inform management policies.

Fishing pressures for brown box crab, *Lopholithodes foraminatus*, are growing in Southern California, and sustainable populations depend on adequate nutrition. The temperature range that brown box crabs typically experience (8°C - 15°C) across their depth gradient (intertidal zone - 500 m) presents challenges for these ectothermic animals because the rates of their physiological processes vary with temperature. Here we examined how temperature affects the feeding behavior of brown box crabs. Adult crabs were exposed to one of three temperature treatments (N=10): 8°C (ambient), 15°C, and 20°C (representative of warm water events). Weekly throughout the exposure period, crabs were given two similar-sized prey items of different crushing strength (clam and mussel). Prey preference, time to consume prey, and claw pinch force were recorded prior to the start of the experiment and each week for the duration of the experiment. We hypothesized that crabs will prefer prey items that require less breaking force at the coldest temperature, consume prey faster at warmer temperatures, and have stronger pinch force at warmer temperatures. Our results confirm that pinch force is consistently greater at 15°C compared to 8°C. However, crabs at 8°C consumed more clams (higher strength) while those at 15°C consumed more mussels. Crabs at 8°C also consumed a greater total average number of prey items per week than crabs at 15°C. There was 100% mortality at 20°C within 1 week of exposure. These results show that brown box crab feeding behavior exhibits temperature thresholds, which can help fishery managers anticipate modifying catch limits to ensure populations remain stable when temperatures fluctuate seasonally or long-term due to climate change.

Monosex prawns and crayfish as biocontrol agents against pest snails

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Biography:

The presenter is a PhD candidate in the Department of Life Sciences in Ben Gurion University of the Negev. During her MSc, studying Ecology and Nature Conservation in Ben Gurion University of the Negev, she studied the freshwater snail community along water tracks in Emek HaMa'ayanot, Israel, on a freshwater-spring-to-fishpond gradient to understand the roots of pest snails in the local aquacultural industry. Her current work is aiming at further understanding the pest snail community dynamics and the disease transmitting patterns using the metapopulation framework, and how to implement prawn biocontrol on a regional level.

Snail-borne diseases (SBD) and freshwater snails themselves are presenting a global challenge: *Biomphalaria*, *Bulinus* and *Oncomelania* transmit human Schistosoma; Thiaridae transmit various fish-infecting trematodes and Pomacea apple snails harm rice crops. These are world-wide economic, health and veterinary issues.

The snails are often targeted by molluscicides, and lately the integration of more sustainable biocontrol agents was suggested. Here we present noninvasive monosex populations of prawns (*Macrobrachium rosenbergii*) and crayfish (*Cherax quadricarinatus*), that were generated using non-GMO methods to serve as biocontrol agents.

We examined the predation abilities of prawns on four species of aquacultural pest SBD transmitting snails found together in the field: *Melanoides tuberculata*, *Tarebia granifera*, *Thiara scabra* and *Pseudosuccinea columella*. The prawn was previously proven a successful size-selective predator of two of those species in the lab and field. In our following food-choice experiment, *M. rosenbergii* was successful in predated all four species, showing a preference for the soft-shelled snail first (*P. columella*) and the hard-shelled, stout snail the least (*T. scabra*). The prawn's ability for treating mixtures of snails, functional response, attack rate and handling times will be discussed for better biocontrol planning.

We subsequently examined the predation abilities of *C. quadricarinatus* against the hard-shelled species, and size-grade preferences by presenting small and medium snails. We found it a faster predator than the prawn, and very efficient with nearly 100% predation of the snails in both sizes.

We will discuss both predators as biocontrol agents in snail-struck areas and in agricultural polyculture, with the ability to choose the better suiting crustacean for the specific snail-control purpose. Furthermore, considering the requirements of biocontrol agents to be noninvasive themselves, we encourage strictly monosex crustacean populations as safely monitored biocontrol and an additive crop on their own as a win-win sustainable snail and SBD solution.

In silico analysis using the CrusTome database identifies molt-inhibiting hormone receptor candidates

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Biography:

Crustacean molting physiology and endocrinology.

Molt-inhibiting hormone (MIH) inhibits ecdysteroid molting hormone synthesis by a pair of molting glands or Y-organs (YOs). MIH is a member of the crustacean hyperglycemic hormone (CHH) neuropeptide superfamily, which includes CHH and insect ion transport peptide (ITP). The identity of the MIH receptor has eluded researchers for decades. As MIH signaling is mediated by cyclic nucleotide second messengers, it is hypothesized that the MIH receptor is a Class A (Rhodopsin-like) G protein-coupled receptor (GPCR). The YO of the blackback land crab, *Gecarcinus lateralis*, expresses 49 Class A GPCRs, three of which (GI-CHHR-A9, -A10, and -A12) were provisionally assigned as CHH-like receptors. CrusTome, a multi-species, multi-tissue, transcriptome database of 201 assembled mRNA transcriptomes from 189 crustaceans and 12 ecdysozoan outgroups, was used to deorphanize candidate MIH/CHH GPCRs in *G. lateralis*, relying on sequence homology to three functionally characterized ITP receptors (BNGR-A2, BNGR-A24, and BNGR-A34) in the silk moth, *Bombyx mori*. Phylogenetic analysis across species identified four additional putative MIH/CHH receptor sequences, for a total of seven candidates: one in the A2 clade, three in the A24 clade, and three in the A34 clade. The structures of MIH, CHH, and the candidate receptors were modeled to determine the best-fit ligand/receptor pairings. Simulations show that the extracellular loop 2 (ECL2) of two related GPCRs in the A34 clade (GI-CHHR-A9 and -A10) forms a pocket for binding GI-MIH but not GI-CHH. The ECL2 in GI-CHHR-A9 and -A10 has an additional beta sheet not found in human GPCRs or in the other five *G. lateralis* CHH GPCR candidates, suggesting that it can be used to identify these receptors in other crustacean species. Functional assays will determine which of the candidate GPCRs is the MIH receptor. Supported by NSF (IOS-1922701 and IOS-1922755).

Looking for *Jasus*: Challenges and implications of tracking rock lobster in a temperate marine reserve

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Biography:

*Hayley Nessia is a PhD candidate at the Institute of Marine Science at the University of Auckland. Her thesis is focused on spiny lobster (*Jasus edwardsii*) movement ecology, population status, and potential use as a tool for urchin barren control. She completed her Masters in 2018 investigating invasion biology of the Japanese mantis shrimp (*Oratosquilla oratoria*) in New Zealand). She has previously worked in terrestrial ecology, investigating impacts of invasive plant species, and also flies an Unmanned Aerial Vehicle (UAV) for the Maui63 charity to search for Maui dolphins.*

Rock lobster *Jasus edwardsii* are important predators on rocky reefs in northern New Zealand, but their populations within marine reserves have declined over the last two decades. It is thought to be due in part to lobster being caught on the offshore boundary when they move beyond reefs onto sandy habitats. To better understand the movement of rock lobster within and across reserve boundaries, an array of 47 passive acoustic receivers was installed within the Leigh marine reserve and 51 lobster were tracked over 1.5 years. Due to complex reef topography and low detection rates of lobster, positions were estimated using weighted positioning allowing broad-scale assessment of whether lobster were on reef, reef edge or sand, and rates of hourly detections were used to assess diurnal and seasonal activity. All but 3 tagged lobsters remained within 1 km of their tagged locations and lobster were predominantly found on reef or reef edge (87% of all detections). While there was evidence of some movement onto deeper sandflats, only one lobster was detected beyond the offshore boundary. These results contrast earlier studies which reported large offshore movements and may reflect the considerably smaller population size now present in the marine reserve. While the complexity of rocky reefs reduced signal transmissions and the resolution of movement data, the passive acoustic array still provided evidence of large-scale movement and activity patterns that can inform future management and design of marine reserves.

Speciation along depths gradient in species complex of deep-sea asellotes (genus *Ilyarachna*) around the Japan and the Kuril-Kamchatka Trench

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¹Atmosphere and Ocean Research Institute, The University Of Tokyo, Chiba, Japan

Biography:

Mizuki Ohta is a PhD Candidate, and will become a postdoctoral researcher of the Atmosphere and Ocean Research Institute, the University of Tokyo in April 2023. Her work focuses on the taxonomy of deep-sea isopods and their evolutions.

Recently, by molecular analyses, it has been revealed that the presence of species complexes is not uncommon in deep-sea organisms and is often reported along with the presence of cryptic species. Numerous reports showed that asellote isopods are no exception. The genus *Ilyarachna* is one of the most known genera in the family Munnopsidae Lilljeborg, 1864, which is known as a group of swimming asellotes and has a high abundance in the deep sea.

We are conducting to collect benthic organisms around the Japan Trench and the southern part of the Kuril-Kamchatka Trench and obtained many *Ilyarachna* specimens. Although most of them were identified as *Ilyarachna kussakini* based on morphology, molecular analysis of the mitochondrial COI gene revealed that they consist of three clades. Individuals of the first clade were collected from the bathyal zones (2,886–3,519 m) around the Japan Trench. Individuals of the second clade were collected from hadal depths (6,116–7,185 m) around the Erimo Seamount near the axis of the Kuril-Kamchatka Trench. An individual of the third clade is collected from the bathyal zone (3,340–3,519 m) around the Japan Trench. The genetic differences among the clades were large enough to classify them into separate species considering previous studies of other asellote species complexes. In addition, slight morphological differences of the pereonite 4 and mandibular palp article 1 were found among them.

To examine the environmental factors promoting genetic differentiation, the effects of the geographic and bathymetrical distance were analyzed by the IBD test and the multiple linear regression analysis. Although both distances were significantly correlated with genetic distance, the bathymetric distance was shown to be more effective in the accumulation of genetic deviations.

Molecular phylogeography of the benthic deep-sea family Neotanaidae reveals cases of relatively high dispersal abilities and wide depth ranges

Palacios Theil E¹, Błażewicz M¹

¹*Dept. of Invertebrate Zoology and Hydrobiology, Faculty of Biology and Environmental Protection, University of Lodz, Lodz, Poland*

Biography:

*Emma Palacios Theil has addressed ecology evolutionary questions using several models from aquatic environments, both freshwater and marine, such as pond water fleas (*Daphnia magna*), the marine urochordate *Oikopleura dioica*, the freshwater shrimp *Atyaephyra desmarestii* or symbiotic decapod crustaceans of the marine family *Pinnotheridae*. Her research includes studies of physiological and life history adaptations to food availability, analyses of genetic population structure or phylogenetic and taxonomical studies at different levels, from species to family. Her current research focuses on the ecology and taxonomy of deep-sea tanaids to further study the processes behind changes in biodiversity and its conservation.*

Neotanaidae offer a fantastic opportunity to study colonization and biogeography in benthic deep-sea habitats. The depth distributions of marine benthic invertebrates show patterns with two main transition zones: one between shelf and slope fauna and another at about 3000 m depth. This results mainly from the limitations imposed on distribution by the decreasing temperature and increasing pressure to which animals are exposed with the increase in depth. At the same time, 28 biogeographic provinces have been proposed for the lower bathyal and abyssal benthos based on temperature, salinity, and the influx of particulate organic matter.

Several of the 51 extant neotanaid species seem to challenge these vertical and horizontal proposed distribution patterns. Collection records include species with wide depth ranges, across both depth transition zones, some encompassing from the disphotic into the hadal zone. In addition, some have been reported from several biogeographic provinces, even different oceans, despite their (alleged) limited dispersal abilities. Therefore, it is easy to suspect that some might rather represent cryptic species complexes. In addition to solving this question, the resolution of their phylogenetic relationships, can contribute to our knowledge on the pathways of colonization of deep-sea environments and the connectivity among them.

Here we present the first phylogenetic analyses focusing on the study of the relationships among neotanaid species and their association with other deep-sea tanaids and some shallow-water relatives. Our molecular phylogenies, based on newly obtained fragments for COI, 16s and H3 genes, confirm high levels of connectivity between some fairly distant areas. Nevertheless, in some cases the potential for dispersal barriers in the horizontal plane is also detected.

In addition, we could confirm wide depth ranges for some neotanaid species, however none across the 3000 m threshold, as the spectrum of specimens available for molecular work did not yet allow for that.

Seasonal variation of the gut microbiota in the freshwater crab *Sinopotamon planum*

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Biography:

Da Pan is a Lecturer at the College of Life Sciences, Nanjing Normal University, China. His work mainly focuses on taxonomy, diversity, phylogeny, phylogeography, evolution, and conservation of freshwater crabs.

Gut microbiota is closely related to the health of the host and its adaptation to environmental changes. *Sinopotamon planum* is a species of freshwater crab that plays a key role as a benthic macroinvertebrate in freshwater ecosystems and is an important indicator of aquatic ecological health. In this study, we sequenced 60 gut microbial samples of *S. planum* and nine microbial samples from the surrounding environment in three seasons based on the 16S rRNA gene. The results showed that gut microbiota had the highest alpha diversity in summer, which may be related to the abundance of food resources in summer. Firmicutes, Proteobacteria, and Bacteroidota were the most dominant components of gut microbiota in all three seasons. Beta diversity analysis showed significant differences in gut microbial communities between seasons. Comparative analysis of gut microbes and surrounding environment microbes showed significant differences between these two groups. In conclusion, the community structure of gut microbiota in *S. planum* differed significantly between seasons, which probably was the result of self-regulation and changing in food resources.

The complexity of biosecurity in Aquaculture in New Zealand

Pande A¹

¹*Biosecurity New Zealand, MPI, Wellington, New Zealand*

Aquaculture is a growing industry in New Zealand, with a government strategy to reach aquaculture production of \$3 Billion by 2035. With such rapid expansion the industry needs good biosecurity to protect and enable this amount of growth. Aquaculture in New Zealand consists of many different sectors, land based, marine and freshwater as well as research facilities and grow out facilities for release for sport fishing. In each sector the risk profile is different depending on how the facility is linked to the environment and to other facilities. Therefore, different management practices are required to achieve best practice biosecurity for each sector and in fact each facility.

Government is working closely with industry partners, as well as representatives of other sectors and iwi to understand operational practices currently in play, how well and how widely biosecurity is understood and where the gaps are. Starting with the basic building block of farm level practices and working towards more cohesive, collaborative area based management, the aim is to work together to build and develop a pathway forward to be able to achieve industry wide practical, consistent and effective biosecurity.

Aquatic Disease Investigations: Tail Fan Necrosis -Still a mystery

Bestbier M¹, Pande A²

¹*Animal Health Laboratory, MPI, Wallaceville, , ,* ²*Biosecurity New Zealand, MPI, Wellington, ,*

Tail fan necrosis is a syndrome seen in the New Zealand Rock Lobster (*Jasus edwardsii*) since 1997, but the prevalence noticeably increased by 2000. Given that this condition affects the marketability of the lobster, efforts have been made to try and identify a causative agent in case this would elucidate ways to manage any potential spread or impact of this syndrome.

Identifying the cause of any condition causing ill health in aquatic organisms can be time consuming and complex. Traditional diagnostic methods can determine whether a known agent is at play, but is this the primary pathogen, or do other factors need to be present for the condition to manifest? Genomic methods can be applied to try and identify any heretofore unknown pathogenic agents, but with variable success. Epidemiological studies require large amounts of specific data that are often not easily obtainable when studying aquatic organisms.

Amphipods of Aotearoa: what is, and was, and is to come.

Peart R¹

¹NIWA, Wellington, New Zealand

Biography:

I am a marine Invertebrate Systematist at NIWA, in New Zealand. I mainly do research on amphipods - covering a number of aspects of their biology. Including their systematics, biogeography, phylogenetics, identifications and environmental interactions. I also dabble in other peracarid crustaceans, but my heart always sits with the amphipods.

Aotearoa's amphipod fauna punches above its weight in terms of proportion of species found here compared to other areas (approximately 600 species recorded from NZ EEZ – approximately 6% of the world's species). This is mainly due to the diverse habitat that exist here ranging from shallow soft sediment estuaries, rocky shores, many beaches, damp forests, continental slopes and marine basins, hydrothermal vents and one of the deepest trenches in the world. Species of amphipod in Aotearoa are intrinsic to managing our environment and building an understanding how humans can affect and be affected by the environment.

This presentation gives a state of the nation view of New Zealand's amphipod fauna, how it has changed over the years and what still needs to be done.

Drivers and impacts of brachyuran distribution in South African mangroves

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Biography:

Nasreen Peer holds a PhD in Zoology, specialising in the diversity and ecology of aquatic invertebrates in both coastal and freshwater habitats. Currently, her research involves understanding crustacean biodiversity and distribution in mangrove, seagrass, salt marsh, kelp and freshwater ecosystems; as well as community-based conservation in southern Africa, a project involving collaboration between community members and researchers. She is a lecturer at Stellenbosch University where she teaches botany, zoology, global change, and hopes to inspire students to question the way we relate to our environment and each other.

Mangroves, and their associated biota, exist within tropical, subtropical and warm temperate intertidal zones where they play a key role in shoreline protection, nutrient recycling, filtration of run off, and resource provision. In South Africa, mangroves are situated in estuarine habitats along the east coast where they occur at a southern latitudinal limit and are displaying a poleward shift, often encroaching significantly on saltmarsh habitat. Associated brachyurans seem to be experiencing a similar shift. Using species distribution models, we investigated the drivers of mangrove crab distribution. We found that biotic factors must be considered alongside abiotic factors when modelling current and potential distribution and that latitude is not a strong driver of presence or abundance of brachyurans within South African mangroves. Specifically, the diversity of mangrove macrofauna, plant morphology, and the presence of certain mangrove species all influence mangrove brachyuran presence and abundance. We outline current research efforts including the use of barcoding and metabarcoding approaches to monitor mangrove brachyuran distribution, the impacts of mangrove-associated brachyurans on newly invaded ecosystems, and the response of key species to global change impacts.

Small-scale population structuring results in differential susceptibility to pesticide exposure

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Biography:

I have recently finished my master's degree in Ecology and Evolution at Goethe University Frankfurt, Germany. During my time at university, I have mainly focused on the life-history and intraspecific diversity of freshwater amphipods. I am generally interested in the evolutionary and functional ecology of amphipods. In the near future I am aiming to do my PhD about the functional ecology of amphipods as well.

Rivers in central Europe are impacted by a wide range of anthropogenic stressors which force species with limited dispersal abilities to adapt or become locally extinct. Previous studies have shown that some invertebrates have pronounced population structuring throughout mountainous river networks, raising the question of whether this also translates into small-scale phenotypic differentiation and adaptation to local stressors. One such species is the European headwater crustacean *Gammarus fossarum* clade 11 (or lineage B), whose population structure was re-assessed four years after first assessment at the Long-Term Ecological Research (LTER) site of the Rhine-Main-Observatory (Kinzig catchment, Germany). The goal was to analyse the temporal stability/dynamics of the population structure and investigate whether a small-scale genetic structuring results in phenotypic differentiation and different susceptibility to the commonly applied pyrethroid insecticide deltamethrin. To this end, differences in life-history traits, as well as the difference in sensitivity towards the pyrethroid insecticide were examined. COI haplotype patterns were found to be stable over time and confirmed the small-scale population structuring within the catchment, with isolated headwater populations and connected downstream populations. While little life-history differentiation was observed, clear differences in susceptibility to the pyrethroid insecticide were found. Populations from pristine sites were significantly more tolerant than populations from anthropogenically impacted sites, indicating that prior exposure to a range of stressors does not automatically increase tolerance to a specific stressor. Thus, this study demonstrates that limited dispersal capacity is reflected not only in population structure, but also in small-scale variation in susceptibility to anthropogenic disturbance. These findings present important implications for the protection of riverine species and their intraspecific genetic variation.

Environmental DNA metabarcoding: Migrating research to management

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¹Natural History Museum Of Los Angeles County, Los Angeles, USA, ²National Oceanic and Atmospheric Administration, Pacific Marine Environmental Laboratories, Seattle, USA

Biography:

Dean spent the first part of his career on marine biomechanics, working with crustacea, corals, algae, fluid flow, and olfaction. Since the turn of the century, he has worked in marine invertebrate taxonomy and biodiversity. Currently, he manages the Diversity Initiative for the Southern California Ocean (DISCO), dedicated to bringing environmental DNA technology to the marine environment. He spends his spare time digitizing the marine invertebrate collection of the Natural History Museum of Los Angeles County.

Marine biodiversity is changing rapidly in response to climate change. Managing marine regions and resources requires us to detect and track those changes — to evaluate management we must measure its effect. The rapid pace and broad scale of change are challenging our ability to keep up. Environmental DNA metabarcoding has enormous promise as a critical tool in marine biodiversity monitoring — it is cheaper and faster than the conventional sampling methods that have informed resource management until now. But despite its effectiveness, eDNA has not yet been widely adopted by management and regulatory agencies because standardized protocols have not yet been developed and promoted. Therefore we are using our eDNA-based program, the “Diversity Initiative for the Southern California Ocean” (DISCO), to help bridge the gaps between academic eDNA research, specimen-based museum work, management organizations, and commercial biological consultants. By developing guidance, pilot studies, and proposing criteria for curated eDNA reference materials, we hope to accelerate management adoption of eDNA metabarcoding as a key tool for managing our response to climate change.

Large-scale connectivity of the deep-sea shrimp *Systellaspis debilis* (Decapoda, Caridea, Oplophoridae)

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Biography:

Pedro A. Peres is interested in using genomic approaches to answer questions in ecology and evolution. His current research involves investigating temporal and spatial genetic diversity components of marine populations, and also investigating deep-sea communities using environmental DNA.

The transition from genetics to genomics represents a huge step in our understanding of the natural world. Genomic approaches are revolutionizing our interpretation of population connectivity, genetic diversity, and speciation. By harnessing hundreds or thousands of markers across the genome, these methods can be used to investigate current and historical patterns and processes. Although deep-sea pelagic crustaceans represent some of the most abundant taxa in marine waters and inhabit the largest habitat on Earth, they are still underrepresented in genomic studies. Many midwater crustaceans are thought to represent a single panmictic population because they have distributions spanning oceanic basins. However, recent studies based on a limited number of molecular markers have revealed surprising levels of genetic structure among populations or even undetected speciation. Since studies that sample across global distributions are challenging and rare due to financial and logistical constraints, collaborative efforts are needed to investigate connectivity patterns in the deep sea. In this work, we investigate the large-scale connectivity of the deep-sea shrimp *Systellaspis debilis*, sampled across a great part of its distribution. This pelagic animal performs diel vertical migration (DVM), a predator avoidance behavior wherein an animal migrates to shallower waters to feed at night, migrating between 150m (night) and 4600m (day). We hypothesize that strong DVM, with access to fast-moving surface currents, will lead to low genetic structure even across vast spatial scales. We analyzed individuals from the Gulf of Mexico, Florida Straits, Bear Seamount, Bermuda, and Spain, using a reduced-representation genomic approach (double digest restriction-site associated DNA - ddRADseq). With this genomic dataset, we performed analyses of population structure, demography, and outlier detection. Our results contribute to this symposium by 1) showcasing one of the uses of genomic methods to study crustaceans; 2) discussing the potential effects of the DVM behavior in deep-sea species population connectivity.

Strangers of the deep: integrative taxonomy towards the unravelling of the decapodid stage of the deep-sea shrimp *Benthescycymus laciniatus* Rathbun, 1906

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¹Portuguese Institute for the Sea and Atmosphere (IPMA), Lisbon, Portugal, ²Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), , Portugal, ³Marine and Environmental Sciences Centre (MARE), Caparica, Portugal

Biography:

Rita F. T. Pires, PhD in Marine Sciences (Univ. of Lisbon), Master & Bachelor degrees in Marine Biology with specialization in Marine Ecology and Conservation (Univ. of Algarve 2007). Research assistant at the Portuguese Institute for Sea and Atmosphere (IPMA). She has been working on ecology and taxonomy of marine zooplankton, specializing in the identification of decapod crustacean and fish larvae, and jellyfish. Since 2016, she collaborates on the Portuguese citizen science program GelAvista, monitoring jellyfish. Her research interests also include biological oceanography, larval dispersal and connectivity processes, biophysical modelling and scientific dissemination.

Among the less understood decapod crustaceans, the deep-sea shrimps of the family Benthescycymidae emerge as some of the most interesting. Inhabiting depths of 500 to 2000 m, several aspects of the ecology (e.g., larval distribution and vertical migrations) and biology (e.g., reproduction and life history strategies) of these benthopelagic species are still eluding, and the literature references of both larvae and adults are rare. A recent phylogenetic study of several deep-sea dendrobranchiate genera, based on molecular and morphological characters, revealed the genus *Benthescycymus* as paraphyletic, now including only two species – *Benthescycymus crenatus* and *Benthescycymus laciniatus* – with the attribution of previously described species to new and distinct genera. Knowledge is lacking regarding this genus, particularly their unknown larval stages and the trophic impacts of their migrations in the water column. This work presents the first description of the decapodid stage of *B. laciniatus*, identified through integrative taxonomy (morphology and DNA barcode). The analysed specimens were collected in October 2022, during an oceanographic campaign in the Lion seamount (Madeira-Tore geological complex, north-eastern Atlantic), with a Manta trawl net, in the neuston layer after sunset (at dusk). Several morphological characters distinguished the individuals from close taxa described in the literature, some of the most conspicuous being: carapace with a rounded prolongation in the latero-frontal region and a well-marked cervical groove; a long rostrum overreaching the antennal scale with one large spine and several minute dorsal spines; one strong posteromedial spine on the second to sixth somites and one pair of minute posterolateral spines on the third to fifth somites; and a triangular-bifurcated telson. The morphology of the decapodid stage is discussed according to the available knowledge for dendrobranchiate shrimps. A glimpse on the larval ecology of the species is presented.

Axius is not an "axiid" – new insights into the phylogeny and classification of axiidean shrimps

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¹*Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China,* ²*Institute of Marine Biology, National Taiwan Ocean University, Keelung, Taiwan,* ³*Museums Victoria, Melbourne, Australia*

Biography:

*Gary Poore is Curator Emeritus at Museums Victoria where he was Curator of Crustacea between 1979 and 2009. He continues research on the systematics of several crustacean taxa and maintains international collaborations, particularly on decapods (lobsters, crabs etc) and isopods. His book with Shane Ahyong, *Marine Decapod Crustacea A Guide to Families and Genera of the World*, was published in January 2023.*

The infraorder Axiidea is a group of cryptic, marine burrowing decapod crustaceans with high morphological and ecological diversity. Although axiidean systematics have received considerable study, the higher level classification remains in flux. The monophyly and relationships of some of the major lineages are still undecided because of limited taxon sampling and molecular data. In this study, we reconstruct the most comprehensive phylogeny of Axiidea to date using three types of sequencing data (Sanger, genome skimming and ultra-conserved element [UCE]) from 125 species belonging to 56 genera and seven families. The UCE tree supports a monophyletic Axiidea sister to a clade containing Anomura and Gebiidea. Within Axiidea, the monophyly of Callianideidae and Micheleidae is recovered, while Axiidae and Strahlaxiidae are shown to be non-monophyletic in all analyses. The family Axiidae is now restricted to *Axius*, *Australocaris*, *Neaxius* and *Neaxiopsis* the last two previously in Strahlaxiidae. Strahlaxiidae is restricted to only *Strahlaxius*. All remaining 52 of the 54 genera previously included in Axiidae s.l. are transferred to Calocarididae, a name previously synonymised. Relationships revealed by these molecular analyses do have morphological support from overlooked character traits of the pereopods. Our findings provide new insights into taxonomy and evolution of this group, and the newly designed UCE probe sets are expected to play a greater role in future phylogenomic studies of decapod crustaceans.

Improving ovarian maturation and spawning in the white shrimp, *Litopenaeus vannamei*, using serotonin and spiperone; a step toward the detection of ovarian inducing pheromones

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Biography:

Undergraduate student of Marine Biology at the National University of Costa Rica. Currently finishing my degree in Freshwater and Marine Resource Management. Laboratory assistant student at Oceanography and Coastal Management Laboratory (LAOCOS-Universidad Nacional, Costa Rica) from 2018 to 2020. Pro bono assistant Laboratory of Systematics, Genetics and Evolution (LabSGE-Universidad Nacional, Costa Rica) from 2018 to 2020

The pacific white shrimp, *Litopenaeus vannamei*, is the most consumed and cultured crustacean species in the world. Researching for alternative reproduction techniques to eyestalk ablation, Alfaro et al. (2004) demonstrated the stimulatory effect of the combined application of serotonin and the dopamine antagonist, spiperone, and the possible existence of ovarian maturation inducing pheromones. The present contribution was designed to validate and to optimize this new technique and reinforce the hypothesis about the existence of maturation and spawning inducing pheromones in *L. vannamei*. Three tanks of 18 m² were cultured with female (40.5 ± 5.1 g) and male (33.4 ± 4.3 g) broodstock. Each tank was seeded with 70 animals: 20 treated females, 20 control females and 30 males to evaluate reproductive activity. In tanks 1 and 2, 50% of females (treated females) were injected with serotonin and spiperone at two different concentrations, and tank 3 presented eyestalk ablated females. Control females were used to observe the indirect effect of the three treatments over ovarian maturation. As comparative parameters, stages of ovarian maturation were measured weekly, and the maturation index was calculated. The rate of mating and the quality of spawning, estimating total number of eggs, nauplii and hatching rate, were evaluated. Ovarian maturation was induced in the three treatments and control females. Average maturation indexes of treated females and control females of tanks 2 and 3 were statistically different (p-value <0.05). The maturation index of control females of tanks 2 and 3 were also statistically different (p-value <0.05), suggesting the presence of reproduction stimulating compounds in the water with injected females (tanks 1 and 2). This study demonstrated the effectivity of sexual maturation of non-treated females, reenforcing the hypothesis of reproductive pheromone released by serotonin plus spiperone maturing females of this crustacean species.

Phylogeographic patterns of cosmopolitan species versus vicariant species in abyssal squat lobsters with insights into speciation and dispersal in the deep sea

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¹Harvard University, Cambridge, United States

Biography:

Biodiversity postdoctoral fellow at the Museum of Comparative Zoology, Harvard University. My research is focused on different aspects of the evolution, biogeography, and systematics of crustaceans and other arthropod. I am extremely interested in characterizing major patterns of biodiversity within crustaceans as a critical step toward understanding ecological and evolutionary processes promoting speciation in marine environments. I am currently investigating speciation patterns among shallow-water and deep-sea taxa, to place deep-sea main events of colonization, determine and compare rates of diversification-extinction in both environments, and elucidate phylogeographic and genomic patterns using Ultraconserved elements (UCEs).

The enigmatic but still mostly unknown deep ocean occupies more than 70% of our planet and has often been perceived as a homogenous habitat lacking horizontal barriers to dispersal. The discovery that many widespread species in abyssal depths are in fact species complexes has however challenged this traditional view of general cosmopolitanisms in abyssal taxa. Squat lobsters in the family Munidopsidae are nearly exclusive deep-sea dwellers and are amongst the few groups of decapods inhabiting abyssal depths (> 2,000 m). The family includes numerous species that are widely distributed in all the oceans and latitudes, and, at the same time, many sister species show vicariant distributions. We analyze mitochondrial and genomic data (COI and UCEs: Ultra Conserved elements) in 30 squat lobster species. Our aims are 1) to unveil biogeographic patterns of diversity in globally distributed taxa and 2) to estimate genetic divergences between sister species across neighboring oceanic regions, and 3) to discover the potential existence of species complexes among these putative cosmopolitan squat lobsters. Our results can help to understand the drivers of biodiversity and speciation in the deep ocean in an era where it has become a target of economic interests as a source of multiple natural resources.

Intro to crustacean sexual plasticity symposium – the case of the IAG gender switch

Sagi A¹, Levy T²

¹Ben Gurion University, Beer Sheva, Israel, ²Stanford University, Stanford, USA

Biography:

We specialize in the molecular background behind crustacean growth and reproductive physiology please see at:

<https://lifewp.bgu.ac.il/wp/sagia/>

Among other factors, maleness in crustaceans is induced by the presence of the androgenic gland— a unique crustacean endocrine organ that secretes the insulin-like androgenic gland (IAG) hormone. On the other hand, absence of the gland or deficiency in IAG expression results in feminization. Therefore, by virtue of its universal role as a master regulator of crustacean sexual development, the IAG hormone may be regarded as the sexual 'IAG-switch'. In recent years, IAG hormones have been found – and sequenced – in dozens of decapod crustacean species, including crabs, prawns, crayfish and shrimps, bearing different types of reproductive strategies—from gonochorism, through hermaphroditism and intersexuality, to parthenogenesis. Recent completion of a wide scale IAG-switch manipulation study in the prawn *Macrobrachium rosenbergii* demonstrates the vast plasticity of sex developmental processes in crustaceans. This wide study resulted with individuals from all possible sexual genotypes (from ZZ to WW) bearing both complete and functional male or female phenotypes. As an introduction to the crustacean sexual plasticity symposium, we will describe the IAG-switch and the immense phenotypic outcomes of its management without any genomic alterations.

Twenty years on: updating the inventory of New Zealand Crustacea

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¹NIWA, Wellington, New Zealand, ²RMIT University, Melbourne, Australia, ³Western Australian Museum, Welshpool, Australia, ⁴retired, , New Zealand, ⁵University of Alaska, Anchorage, USA

Biography:

Deep-sea taxonomist, decapod specialist, New Zealand based

New Zealand was the first country to catalogue its entire known living and fossil life in a comprehensive three-volume inventory completed in 2012. Based on the Species 2000 Catalogue of Life initiative, it documented New Zealand's unique fauna and flora that is characterized by high levels of endemism in many groups. Here, we present an update on the recent taxonomic and systematic research of New Zealand's marine crustacean biota. Over 3300 species are now recorded, with 740 taxa added to the New Zealand marine Crustacea in the last twenty years. The overall level of endemism is currently at 37%, however, this masks an extreme range from <10% (e.g. pelagic euphausiid shrimp and copepods) to 93% in the small epibenthic peracarid Cumacea (comma shrimp). Considering that a significant portion of the nearly 730 species of known undescribed and undetermined species are likely to be endemic, the level of endemism will only increase in the future. Despite the incredible progress made in the last decade, the potential for new species discoveries remains extremely high with little indication of our species richness curve reaching a plateau and (conservative) estimates of twice as many species remaining to be described or discovered. We highlight some exciting discoveries of the last twenty years, our ongoing challenges in discovering and documenting our fauna and place the New Zealand fauna in a global context.

Both local environment and global biogeography affect a local amphipod community structure in Akkeshi Bay, northeastern Japan

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¹Hokkaido University, Akkeshi, Japan

Biography:

I am a graduate student in Akkeshi Marine Station, Hokkaido University. My study focuses on taxonomy and ecology of amphipod crustaceans. I enjoy conducting field surveys using methods such as net trawling, snorkeling, SCUBA diving, and canoeing. Recently I have also been extending my research to incorporate broad-scale processes, such as biogeography and ocean current dynamics.

The decline of biodiversity in cold regions is a concern due to global warming. However, information of distribution and ecology of Gammaridean amphipods is still limited in Asian cold regions. Recent studies suggests that local community structure is affected both by local environmental factors and by macroecological processes. Although many studies focused on the biogeography of amphipods, the effect of biogeography on local community structures has been less examined. The present study aimed to clarify the species composition and community structure of benthic amphipods in the subtidal bottoms (5-32 m deep) of Akkeshi Bay, eastern Hokkaido, Japan, and to discuss its spatial variability in relation to environmental gradients and biogeographic affinities of the component species. Collection of amphipods was conducted at 9 sites in 2020. Amphipod species were identified to 21 families and 40 species. The biogeographic affinities of the 15 identified species were categorized into the two groups: "Arctic and surroundings" and "Northwestern Pacific". Similarity analyses revealed that the amphipod community differed among the three habitats: (1) the marine soft bottoms, (2) the soft bottom of the estuarine and (3) the marine hard bottom. The marine soft-bottom community was subdivided into three subgroups, which were partly explained by the variation in depth. The variation in species composition was also related to the biogeographical affinities of the component species, with Arctic and surrounding species occurring in deeper sites than Northwestern Pacific species. The observed variation in community structures along the depth gradient seems to reflect both variations in environmental factors, such as temperature, and in suitable temperature range of species that are determined by biogeographical histories. The present study highlights the importance of considering both environmental gradients and macroecological features of component species in interpreting variation in amphipod community structures in a local area.

The carbon reduction through huge and complex burrow system of thalassinidean mud shrimp *Laomedia* nov. sp. (Crustacea: Laomediidae) from Korean intertidal

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Biography:

Post doctoral scientist

Thalassinidean mud shrimp *Laomedia* nov. sp. is one of the most abundant species in the upper tidal flats of the west coast of Korea. The genus *Laomedia* is represented by four species; *L. astacina*, *L. paucispinosa*, *L. healyi* and *L. barronensis*. The burrows inhabited by *Laomedia* nov. sp. are huge and structurally complex and their size, structure, and morphology are distinctly different from those reported for other *Laomedia* species, so this species is presumed to be a new *Laomedia* species. *Laomedia* nov. sp. burrows have the structural characteristics of being divided into three parts. The upper part consists of a horizontal gallery and a vertical shaft connected to the surface and the lower parts of several horizontal passages are connected to the main gallery to form the middle part of the burrow. The main gallery is inclined, spirally twisted, and extended downwards, and the direction of the twist is periodically reversed in the middle part. In the lower part, the main gallery is extended almost vertically and connected to a horizontally extended chamber at a certain interval of depth. The sediment-water interface by the burrow of *Laomedia* nov. sp. was increased by up to 1,511%, which is believed to highest value among marine invertebrates. However, little is known of the ecological characteristics and functions of this unique burrow system. The carbon dynamics in the intertidal sediments are influenced by an array of biotic and abiotic factors among which thalassinidean mud shrimps play an important role. We introduce the carbon reduction through unique burrow system of *Laomedia* nov. sp. by quantifying carbon inflow and outflow via irrigation and sediment reworking of this species.

Crayfish exoskeletal phosphate transporters - structural conservation from bacteria and pancrustaceans to mammals with different roles

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Biography:

Shai Avraham Shaked is a Ph.D. student in the Life Sciences department, at the Ben-Gurion University of the Negev. He graduated from a master's program at BGU in 2021 written a thesis titled 'The molecular background of building and hardening the exoskeleton in crayfish'. Shai has a B.Sc. in marine biotechnology from Ruppin Academic Center, Israel. His Ph.D. research deals with selected key functional proteins involved in exoskeleton formation and mineralization. Characterization of such proteins opens exciting opportunities for bio-mimesis of exoskeleton-building processes in vast industrial, biomedical, and engineering processes.

In vertebrates, many mechanisms involve the transport of phosphate ions by SLC20 Na⁺-coupled phosphate cotransporters, including the biomineralization of their skeletons with calcium-phosphate minerals. Contrary, crustaceans mineralize their exoskeletons primarily with calcium carbonate and only the stabilization of its amorphous phase is thought to be controlled by phosphate ions. In this study, we investigated the existence of SLC20A2 orthologs in crustaceans. A molt-related transcriptomic library and a novel binary patterning approach were exploited to reveal a SLC20A2 transport protein-encoding gene in the crayfish *Cherax quadricarinatus*. Functional genomics experiments via Cq-SLC20A2 RNAi demonstrated increased crystallinity of ACC at the gastroliths (exoskeletal transient calcium storage organs). Evolutionarily, the putative *C. quadricarinatus* SLC20A2 showed high structural similarity to phosphate transporters from the bacteria *Thermatoga maritima* and *Homo sapiens*. Other than the functional supporting evidence suggested by our RNAi experiment, being structurally highly similar to the crystalized solved structure of a bacterial transporter on one hand, and to a human transporter with known function on the other hand, further support the notion that Cq-SLC20A2 is a phosphate transporter in the exoskeletal system of a crustacean. This first discovery of the involvement of a conserved Cq-SLC20A2 in crustacean exoskeletal mineralization through active phosphate transport represents an important link in the evolutionary history of ion transport. The conserved structure of phosphate transporters across phyla suggests function maintenance, although serving different roles in different organisms.

A Crystalline Photonic Device Enabling Crustaceans to See But Not be Seen

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Biography:

I completed my BSc in chemistry at BGU in the biophysics track, as part of programs for excellent students. During my undergraduate studies I worked in Dr. Palmer's and Prof. Amir Sagi's labs and I am now finishing my MSc. My research focuses on isoxanthopterin in the eyes of crustaceans. This material has exceptional optical properties. These biogenic crystals function in crustaceans as: (i) a camouflage device enables them to remain inconspicuous against the background in the larva stage, (ii) vision device.

High refractive index molecular crystals are used as reflective materials in animal coloration and vision. Here we report the discovery of an 'ingenious' camouflage device in the eyes of larval crustaceans constructed from crystalline isoxanthopterin. Many aquatic animals, including larval crustaceans, use transparency to avoid being seen. However, absorbing eye pigments necessary for vision are highly conspicuous and increase the risk of detection by predators. To mitigate against this, larval crustaceans have evolved a reflective device – the 'eyeshine reflector' which deflects light away from, and conceals, the conspicuous eye pigment. Using cryo-SEM and TEM we show that the eyeshine of larval shrimp is produced by light-scattering from dense arrays of high refractive index, core-shell nanoparticles made of crystalline isoxanthopterin. The same nanoparticles were found previously in a different optical device in the eyes of adult crustaceans. The reflectivity and scattering of the particles are enhanced by their birefringence, which results from the anisotropic arrangement of refractive indexes within the particle shell. These particles are located in specialized cells overlaying the pigment. Reflectance measurements performed on larval shrimp from the Gulf of Aqaba and on other model specimens show that a spectrum of eyeshine colors are generated by this device, ranging from deep blue to yellow. Optical modeling demonstrates that the color of the scattering is determined by the size of the particles and their short-range ordering. The eyeshine color of the shrimp is spectrally-matched to the water color in their native habitat and also changes upon light-dark adaptation. This enables them to remain inconspicuous against the background. Our characterization of this unique optical device provides inspiration for the design of new synthetic pigments constructed from crystalline spherulites, where color can be tuned by controlling particle size and order.

Complex biogeographical history, introgression, and cryptic diversity of the three Chinese endemic freshwater crabs (Brachyura, Potamidae)

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Biography:

Dr. Boyang Shi graduated from Nanjing Normal University, and mainly studied the biogeography, diversification, and evolutionary history of Chinese freshwater crabs.

The paleoclimate regimes altered species biogeographic history through effect migration, adaptation, introgression, and speciation. Three congeneric *Sinopotamon* crabs found on both sides of the Qinling Mountains–Huaihe River Line (QHL), a critical ecological boundary in eastern China, provide a natural laboratory to understand how paleoclimatic oscillations determine the species biogeographical history and the maintenance or loss of species barriers. A total of 642 individuals were collected throughout their entire distributional ranges. We used time-calibrated multilocus phylogenies based on 2 mtDNA sequences, 4 nuclear-intron genes, and 9 microsatellite loci, combine with morphological variation and fine-tuned ecological niche modeling (ENM) to explore the biogeographical history of independently evolving lineages. Phylogenetic analyses consistently generated two well-supported clades, and recover three *Sinopotamon* species as polyphyletic: lineage A, *S. yangtsekiense* s. l.; lineage B, three species. The divergence time between the two lineages was broadly consistent with the timing of the critical paleoclimate transition event (monsoon intensity) in the mid-Pleistocene (95% HPD, 0.48–1.06 Ma). Genetic structures indicate that gene introgression occurred within lineage B. Bayesian skyline plot and ENM indicated a moderate demographic expansion after the Last Glacial Maximum (~15 kya). A putative dispersal corridor was detected along QHL, with unidirectional gene flow from north to south. In summary, the results warrant morphological and phylogenetic studies to disentangle cryptic diversity within three species, and the two main drivers of cryptic divergence were (a) differences in the intensity of the monsoons on each side of the QHL boundary during the mid-Pleistocene, and (2) isolation of different populations in a number of separate refuges during the LGM. Additionally, population genetic connectivity was strongly associated with stable climatic habitats shaped by complex topography and glacial refuges, and followed by phases of dispersal and occasional overlap of ranges leading to secondary contact and gene introgression.

Trophic ecology of freshwater decapods in the last freshwater swamp forest in Singapore.

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Biography:

Soh Bryan will be graduating with a Bachelor of Environmental Studies degree in Biology. An undergraduate of National University of Singapore, Bryan developed his interest in decapod crustaceans through assisting with freshwater crab fieldwork as a student helper in the Freshwater and Invasion Biology Laboratory and through his internship at National Parks Board. Bryan also furthered his love of wildlife by volunteering at animal shelters and assisting in citizen science surveys. After graduation, Bryan plans to pursue a Masters of Science degree in Life Sciences on endemic freshwater decapods, further contributing to conservation and understanding of these species in Singapore.

Singapore's last remaining freshwater swamp forest, Nee Soon Swamp Forest (NSSF), harbours unique flora and fauna in its relatively acidic waters (pH 4.6 to 5.5), including the endemic and/or threatened decapod crustaceans, Johnson's freshwater crab *Irmengardia johnsoni*, reticulated swamp crab *Parathelphusa reticulata*, and flat-clawed river prawn *Marobrachium platycheles*. Freshwater decapods perform key roles in freshwater ecosystems, from ecosystem engineers, to providing top-down or bottom-down regulation in food webs, to nutrient cycling. Given their likely crucial but understudied ecological role in the freshwater swamp ecosystems, we set out to investigate the trophic status of the freshwater decapods among Nee Soon Swamp Forest fauna using $\delta^{13}\text{C}$: $\delta^{15}\text{N}$ ratios. Carbon and nitrogen stable isotopic analysis was performed on various taxa and/or functional groups (including fishes, macroinvertebrates, and plants) to understand the trophic relationships in two different parts of NSSF (forest core vs forest edge); specifically, we compared assemblages, trophic status, and food webs, and discuss the ecological and conservation implications of the results—highlighting the roles of freshwater decapods within this rare habitat of high conservation significance within Singapore.

Ocean warming and acidification alter metabolic physiology and carbonic acid gene expression in juvenile Northern spot shrimp (*Pandalus platyceros*): Implications for resilience to climate change

Tamone S¹, Musbach J², Levy T³

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Biography:

Dr. Sherry Tamone is a Professor Emerita of Biology at the University of Alaska Southeast (UAS). She received her PhD in Endocrinology in 1993 from UC Davis Bodega Marine Laboratory and has conducted research concerning crustacean growth, reproduction and metabolism for over thirty years. Dr. Tamone has been an active member of The Crustacean Society since 1993. In 1999, Dr. Tamone became an Assistant Professor at UAS and over the next decades collaborated with faculty all over the world. She earned a Fulbright Research Scholarship to Israel to collaborate on projects involving sexual differentiation in protandric shrimp

Northern spot shrimp (*Pandalus platyceros*) range from southern California to Alaska and are commercially important throughout their northern range, particularly to small communities in Southeast Alaska. Climate change is currently impacting coastal communities of Alaska, and there has been increased efforts to understand potential impacts of ocean warming and acidification on important fisheries. We were interested in how temperature and pH changed the metabolic rate and the expression of target genes in stages of shrimp that were likely susceptible to environmental perturbations. To this end, we built a low-cost CO₂ dosing system and exposed post-larval juveniles to ambient seawater (4°C, pH ~7.9), increased temperature (9°C), decreased pH (7.5), or a combination of treatments in a multifactorial design. We were interested in the impacts of treatments on metabolic rates and the expression of carbonic anhydrase (CA) and heat shock protein 70 (HSP70) in juvenile shrimp. Larvae were hatched in the UAS Marine Laboratory and raised on live *Artemia* through larval settlement. Post settled juveniles were acclimated and transferred to treatment tanks for two weeks. Metabolic rates were measured on shrimp (n=6) removed after 1, 3, 7, and 14 days. Expression of CA and HSPs genes were measured from shrimp removed after 4, 24, and 72 hours and after one week. Metabolic rates were variable between individuals and between treatments, but metabolic suppression was evident after 24 hours. The most notable result was that of CA gene expression. Carbonic anhydrase gene expression significantly increased after 3 days of exposure to decreased environmental pH. Expression of HSP70 gene demonstrated an increased trend after 4 hours and 3 days of exposure. All shrimp survived the experiment and were returned to the communal tank. These results implicate changes in physiology that may serve to enhance resilience to this species as climate changes.

Indochinese freshwater crabs of the genus *Badistemon*: a brief “walk-through” of their taxonomy, with descriptions of new species from Thailand

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Biography:

Graduated from the National University of Singapore with a bachelors degree in Environmental Studies (Biology). Currently holding a research assistant post at the Lee Kong Chian Natural History Museum, National University of Singapore, and as a lab associate to the Freshwater and Invasion Biology Laboratory, Department of Biology, National University of Singapore. My research interest and work revolves around the taxonomy and systematics of freshwater crabs (Potamidae, Gecarcinucidae), with special emphasis on the poorly studied Indochina region. My work mainly focuses on morphological analysis with molecular backing, to revise genera, better understand the intergeneric relationships and uncover new species.

The genus *Badistemon* was established for a single species, *B. turgidulum*, from the Tenasserim Range in eastern Myanmar, bordering Thailand. Species of *Badistemon* can be distinguished by their unique suite of characters, being relatively small crabs with a squarish carapace, distinctly long ambulatory legs, and a male first gonopod terminal segment that is relatively short, conical, and lacking a dorsal flap. Three other species are currently included in the genus, viz., *B. pealianus* (Wood-Mason, 1871) and *B. fulvum* Mitra, Monica & Waikhom, 2020 from eastern India, and *B. nanensis* Rogers, Sanomuang & Sanomuang, 2021, from northern Thailand. Here, we detail two new species of *Badistemon* from northern Thailand, *B. fongkaewi* n. sp. and *B. chinnaphai* n. sp., bringing the total tally of *Badistemon* species to six. The two new species are distinguished from their congeners primarily by differences in the male first gonopod, external orbital tooth and third maxillipeds. Finally, analysis of the distribution pattern and species richness of *Badistemon*, revealed that it is not uniform. Rather, there are areas with higher species richness and conversely, large geographical gaps devoid of any species. This suggests that the species diversity of *Badistemon* is most likely under-represented, thus providing impetus for future research involving more comprehensive surveys and molecular phylogenetic analyses.

Assessing the diversity of amphipods associated with non-crustacean zooplankton in Norway: the ParaZoo project

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Biography:

Anne Helene S. Tandberg is a researcher at the University Museum of Bergen, Norway where she focuses on taxonomic research on peracarids from cold and deep seas as well as hydrothermal vents. She has accumulated a little over 4 years of marine expedition time, most of this in polar or cold regions, and teaches regularly arctic benthos at the University Studies at Svalbard, Norway. She is the curator of the marine exhibits at the University Museum in Bergen, and leads the Norwegian committee for IUCN-evaluation of crustacea. She is currently the European governor for TCS.

It is well known that amphipods associate with jellyfish, but these interactions remain underreported in scientific literature even for relatively well-studied regions such as the North-East Atlantic and Atlanto-Arctic Oceans. The extent and exact nature of these interactions are still not fully understood, due in part to difficulties in the identification of all symbionts involved. Project ParaZoo, funded by the Norwegian Taxonomy Initiative, is mapping the biodiversity of amphipods associated with the non-crustacean zooplankton in Norwegian waters.

Live specimens of jellyfish and amphipods are collected from different locations, both near-shore and off-shore. Diverse sampling methods are employed to maximize the representation of the planktonic hosts, including manual collection, scuba diving, and the use of different plankton and hyperbenthic nets. Identification of the specimens follows an integrative approach, combining morphological and ecological observations with DNA barcoding (mtCOI), with the aim of producing a detailed inventory of the species involved.

Preliminary results show that the identity of the species involved differs significantly between published occurrences and other sources of information (e.g. grey literature, citizen science). This suggests that the apparently low diversity of gelatinous hosts involved is an artifact. In addition to the well-known scyphomedusae associations we provide the first reliable records of siphonophores, ctenophores, and hydromedusae associated with amphipods in Norway.

Mysteries and myths about distribution, abundance and diversity of Peracarida

Tandberg A¹

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Biography:

Anne Helene S. Tandberg works mainly with Amphipoda. Her focus is taxonomy and phylogeny, with a strong sideinterest in biogeography and ecology. She has focused on deep and cold waters, as well as reduced habitats. She teaches Arctic field-courses in marine benthology and works with producing museum-exhibits about life in the ocean.

The Peracarida is one of the crustacea-groups that is still open for a lot of basic discoveries. Since 2000, an average of 330 taxa have yearly been described within the superorder; Amphipoda, Isopoda and Tanaidacea unsurprisingly being the orders with most new taxa.

We think we know a little about the distribution, abundance and diversity of the Peracarida, but how much is the “true” picture and how much is influenced by where we have sampled, who has sampled at the places we have been at, and how we have sampled? This presentation is not meant to give any answers, but to be an introduction to a discussion within the frames of the symposium dedicated to the Peracarida.

Development of a novel methylation-based ageing method for European lobsters (*Homarus gammarus*)

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¹University Of East Anglia, Norwich, United Kingdom, ²National Lobster Hatchery, Padstow, United Kingdom

Biography:

Dr Martin Taylor is an associate professor at the University of East Anglia in the UK. He focusses on applying molecular tools to better understand the evolution and exploitation of aquatic organisms. He has interests which span whole genome duplication, mimicry, speciation, population structure, food traceability and more recently using DNA methods to estimate chronological age.

Crustaceans are notoriously difficult to age because of highly variable growth rates, moulting of their exoskeleton throughout life and associated lack of age-related growth marks. The poor knowledge of age structure in crustaceans therefore hampers accurate assessment of population dynamics and consequently sustainable fisheries management. Quantification of DNA methylation may allow for age prediction across diverse species. Here, we report the development of a methylation based ageing methodology for the economically important European lobster (*Homarus gammarus*). Across known age cohorts of lobsters, there was a highly significant relationship between age and percentage methylation and an Elastic Net regression model allowed the accurate and precise age estimation of known-age individuals. Applying this ageing model to wild lobsters of unknown age gave predicted ages concordant with minimum size at age estimates from mark-recapture studies. We also investigated the role of environment and tissue type on age estimates. Epigenetic clocks show strong potential as a nonlethal ageing technique for European lobsters.

Diversity and distribution of chirostyloid and galatheid squat lobsters in the Indian waters, with a note on their parasites

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¹Centre for Marine Living Resources and Ecology, Kochi, India

Biography:

Shivam Tiwari is a doctoral student at the Centre for Marine Living Resources and Ecology, Cochin, working on the diversity and distribution of chirostyloid, galatheid and lithodid anomurans in the Indian waters. For the last three years, he has been working with samples collected on-board the Fishery Oceanographic Research Vessel Sagar Sampada from the continental slopes and coastal waters of the Indian EEZ. His primary focus is to identify anomuran crustaceans using an integrated approach combining conventional morphology, DNA barcoding and Micro-CT scanning techniques. Until now, he has identified more than 10 new species, and published 5 lead author papers.

Abstract: Crustaceans of the anomuran superfamilies Chirostyloidea and Galattheoidea (except the family Porcellanidae), and prevalence of their parasites are inadequately documented in the Indian waters. Published literature was restricted to surveys in a few coastal regions and those of the RIMSS Investigator, Valdivia, Galathea, the International Indian Ocean Expedition, the FORV Sagar Sampada and ORV Sagar Kanya. The present work summarizes data from literature (67 sampling sites) and observations from the FORVSS surveys (64 stations). The consolidated data revealed a total of 84 species, including 14 chirostyloids in five genera of three families, and 70 galatheids in 19 genera of three families. These include nine new species and four first geographical records for India. *Munidopsis* Whiteaves, 1874 was the most speciose genus (29 species), followed by *Galathea* Fabricius, 1793 (10) and *Uroptychus* Henderson, 1888 (8). Squat lobster diversity was the highest in the Arabian Sea region (28 species), followed by 26 and 13 in the Andaman & Nicobar waters and Bay of Bengal, respectively; only five species were recorded in all the three regions, and 12 species were recorded in two regions. Exclusively deep-water species (> 200 metres depth) accounted for 70% of the total diversity, followed by shallow water species (< 200 metres depth; 26%); only 4% were recorded from a wide range of depths. Out of the 378 specimens examined, 40 were observed to be infected with rhizocephalan barnacles (67.5%) and bopyrid isopods (32.5%), and the hosts belonged to three genera namely *Munidopsis*, *Gonionida* Macpherson & Baba, 2022 and *Trapezionida* Macpherson & Baba, 2022. Despite their vast geographical extent, the Indian waters are scantily surveyed, thereby necessitating extensive systematic surveys to unravel the squat lobster diversity and prevalence of parasites across this region.

A draft male genome and a refined pathway for sexual manipulation of the ornate spiny lobster *Panulirus ornatus*

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Biography:

Hang Tran has vast knowledge and experience with animal husbandry and molecular techniques. During her training in Vietnam, Hang successfully developed mono-sex technology in freshwater prawns through androgenic gland micro-surgery and gene silencing. Hang will attempt to develop mono-sex technology in spiny lobsters by inducing sex change through gene silencing or chemical/thermal manipulation of the eggs. Hang will expand the scientific knowledge of sexual development pathways in decapods by exploring the sex determining gene iDMY in the ornate spiny lobster male genome and investigate how it regulates key sexual development genes like IAG and vitellogenin.

The ornate spiny lobster *Panulirus ornatus* is reared in captivity in Australia to alleviate pressure on wild stocks, enabling monosex culture (either all male or all female populations) of this species which is a desirable practice to increase farmers' yield and profits. The *P. ornatus* male genome was assembled through Chromium 10X Genomic libraries (Illumina), Pacific BioSciences library (PacBio) and RNA-Seq data (2.4 Gbp; 201,695 scaffolds; scaffold N50 = 76,252; and 84.3% BUSCO). The male-specific DNA marker Po-iDMY was mapped within the male genome sequence. This genetic marker enables reliable determination of *P. ornatus* genetic background following sexual manipulation, a key component for monosex culture. In addition, the key masculinizing hormone – the insulin-like androgenic gland hormone (IAG) – was found to express at the first juvenile stage (J1), prior to the development of sexual characteristics. This finding is different from previous study in the eastern spiny lobster (*Sagmariasus verreauxi*) where IAG expression commences after the appearance of gonophores. This is indicating there are many factors at play with species-specific intricacies which require close examination when addressing monosex trials. Nevertheless, this is also opening an exciting opportunity to further investigate the pathway to successful manipulations across spiny lobsters.

Fifteen years of the World Register of Marine Species (WoRMS): where are we, and what will the next decade bring?

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¹Flanders Marine Institute (vliz), Oostende, Belgium

Biography:

Trained as a marine biologist at the University of Ghent (Belgium). Leen is a project manager at the Data Centre division of the Flanders Marine Institute (VLIZ) (Belgium), running the MarineLife+ programme. Leen coordinates the Aphia database infrastructure (which includes the World Register of Marine Species (WoRMS)), the European Ocean Biodiversity Information System (EurOBIS), the Interim Register of Marine and Non-Marine Genera (IRMNG) and the LifeWatch Species Information Backbone. Also involved in the EMODnet Biology project, as lead of the work package on data management and current chair of the Global Team of Catalogue of Life (CoL).

The World Register of Marine Species is an authoritative classification and comprehensive catalogue of marine taxon names. Its content is controlled by a global network of more than 280 taxonomic and thematic experts, thereby ensuring almost 24/7 activity to keep the Register up to date on the level of taxonomy, and expand its content with e.g. distribution information and attributes. By providing easy and free access to its expert-validated content, WoRMS aims to improve the general quality in the usage of marine taxon names, and to expand its potential as a high quality and trustworthy source, not only in biodiversity research and management but also for policy makers and the public at large.

In 2022, WoRMS celebrated its fifteenth anniversary. Over the past 15 years, the content of WoRMS has grown tremendously, as well as its network of volunteer experts and its connection to regional and global initiatives. In 2021, WoRMS was endorsed as a UN Ocean Decade project. During the full span of the Ocean Decade, WoRMS will continue its endeavours to be able to provide a full taxonomic overview of all marine life, thereby not only supporting scientists, but everyone who makes use of species names, including policy makers, industry and the public at large. Several taxonomic gaps still need to be addressed, as well as exploring new challenges in the field of taxonomy, such as temporary names.

The usage of WoRMS is very diverse: scientists consult its content directly online through the search interface, or by making use of the available range of web tools and services. Its intensive consultation is also reflected in citations of WoRMS. In addition, many initiatives – e.g. lifeWatch, OBIS, EMODnet Biology, GBIF, EoL, COL, ... - are deploying WoRMS as the taxonomic backbone for their own work.

Closing gaps in reproduction and development of decapods using integrated omics approaches

Ventura T^{1,2}

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Biography:

Associate Professor Tomer Ventura pioneered the application of single gene silencing to induce fully functional sex change in crustaceans. This has wide application for practicing Monosex Population Culture (all-male or all-female), which has tremendous value for the entire aquaculture industry. This is the first application of gene silencing in aquaculture. Associate Professor Ventura's molecular expertise is vital in translating novel basic scientific results into applicable biotechnologies. He is leading a group dedicated to better understand the molecular mechanism underlying crustacean reproduction and development.

Over the past decade, the use of RNA sequencing (RNA-Seq) grew exponentially, enabling the identification of previously hard to find key factors which regulate reproduction and development, including hormones, receptors, enzymes, transcription factors and structural proteins. These known targets are surmounted by many unidentified genes of unknown function. To better resolve the function of these unknown genes, an RNA-Seq based approach can be taken, using sequencing of multiple replicates per sample type, including tissues, life stages or treatments. With this approach, we generated large datasets that pile up at a much higher pace than our capacity to resolve function of newly identified genes. For one species as an example, which has been the focus of a new aquaculture in decapods, the ornate spiny lobster *Panulirus ornatus*, we produced replicate RNA-Seq libraries of eleven embryo stages, twelve metamorphic stages and 20 different tissues from juvenile and mature males and females. In total, we have generated more than 200 files of at least six gigabyte each, and we expect to double this amount, just for this species. In order for us to be able to deduce functions, one first step, following phylogenetic analysis, is to follow the expression pattern across these multiple datasets and compare with other species. While the data is all publicly available, looking up the expression patterns is a dedicated task requiring many excel files that are kept by many researchers for many different datasets. To streamline this process, we generated CrustyBase.org, a repository where databases can be shared to enable rapid detection of new genes and assessing their expression pattern. The proof of function can rely on gene silencing, or other omics approaches, like proteomics and metabolomics. A few key examples of deduced function will be shared in the context of the molt regulation.

Male sexually biased expression of W- and Z-associated cytochrome P450-like gene in early sexual differentiation of the prawn *Macrobrachium rosenbergii*

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Biography:

*Melody Wahl is a third-year Ph.D. student at the Amir Sagi lab in the Ben-Gurion University of the Negev. Her doctoral work explores the sexual differentiation and sex determination mechanisms in the giant freshwater prawn *Macrobrachium rosenbergii*. Using state-of-the-art NGS genomic and transcriptomic platforms, bioinformatics, molecular tools, and functional genomics, she aims to shed new light on the molecular bridge between sex determination and sexual differentiation in decapod crustaceans with the WZ/ZZ system of sexual heritability.*

The insulin-like androgenic gland (IAG) hormone is a universal master switch in crustacean sex differentiation, in which IAG expression induces masculinization and the absence of IAG expression results in feminization, thus termed the “IAG-switch”. Through manipulations of the IAG-switch, a high degree of sexual plasticity in the freshwater prawn *Macrobrachium rosenbergii*, a gonochoristic species known to bear the WZ/ZZ system, has been recently demonstrated. The manipulations afforded functional WZ males, ZZ females, and, surprisingly, even WW males and females. To uncover the molecular bridge between sex determination and sexual differentiation in crustaceans through the study of individuals lacking either the Z or the W chromosome, we constructed RNA library of early-stages (embryo, larva and post-larva) WW females and ZZ males. Differential expression analysis between sexes in each stage, yielded a total number of 764 differential expressed genes (DEGs) located on W- and Z- associated scaffolds. Following clustering analysis, one of the W and Z-associated DEG was identified as a homolog to a family of cytochrome P450 proteins, with minor genomic sequence differences between W and Z while being significantly male-biased at the expression level. The cytochrome P450 family proteins are known from the literature in many taxa to be related to reproduction, with some cases of masculine related expression in crustaceans. The possible role of a male sexually biased cytochrome P450 gene in prawns at an early sexual differentiation period will be discussed with the aim of attending the molecular toolkit upstream of the IAG-switch which presumably lies under the direct control of sex chromosome elements.

Rediscovery of the enigmatic worm-parasite barnacle *Rhizolepas* reveals its surprising phylogenetic position in Poecilasmataidae (superfamily Lepadoidea)

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Biography:

Hiroshi Watanabe is a marine ecologist who is working for larval dispersal, phylogeography and biogeography of deep-sea hydrothermal vent animals of invertebrates, especially barnacles, in Japan Agency for Marine-Earth Science and Technology (JAMSTEC).

Understanding how parasitic animals evolve is key to unravelling how biodiversity is generated as a whole, as parasites could account for half of the species richness in the world. Barnacles include some of the most astonishingly adapted parasites with the adult body reduced to just a network of tubes and a reproductive organ, but how it got there from a sessile, filter-feeding common ancestor is still a mystery. The exceedingly rare scale-worm parasite barnacle *Rhizolepas* has reduced feeding organs in the main body (capitulum and stalk) but extends a “root” system from the end of stalk into the host body, convergent with rhizocephalans. Here, we rediscovered this genus and present its first molecular data showing a surprising phylogenetic position nested within genus *Octolasmis* in Poecilasmataidae (superfamily Lepadoidea). Our results imply that species in this genus-level clade use at least six different phyla of host animals and display a wide array of stages from free-living towards parasitism in terms of plate reduction and host-parasite intimacy. This exemplify that the exploration of heterogeneous hosts by repeated host-switching may increase the chance for true parasitism to evolve, followed by rapid modification of anatomy as seen in *Rhizolepas* – providing an analogue to how the network-like body plan of rhizocephalans may have evolved.

CRISPR editing analysis in *Macrobrachium rosenbergii* genome: characterizing single nucleotide polymorphism and repetitive sequences

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Biography:

Hanin Wattad is an MSc student supervised by Prof. Amir Sagi in the department of Life Sciences at Ben-Gurion University of the Negev. She received her BSc in Marine Biology and Biotechnology from Ben-Gurion University in Eilat. During her BSc, Hanin was involved in developing an in-vitro artificial intestine system in the "Fish-AI" research project, funded by the European Union's Horizon 2020. After receiving her BSc degree, she worked for 18 months in the framework of the CRISPRIL consortium as a research assistant at Prof. Amir Sagi's laboratory, where her research focused on CRISPR-Cas genome-editing in *Macrobrachium rosenbergii*.

The CRISPR-Cas genome-editing tool enables induction of targeted mutagenesis to determine the role of particular genes. Recently, a CRISPR platform for the prawn *Macrobrachium rosenbergii* embryonic primary cell culture was established in our laboratory, allowing the performance of genome editing in this crustacean. In this prawn the study of differential features from paternal and maternal origin is possible using a high-quality phased genome that enables partial identification of sex chromosomes sequences. Also, this genome exhibits a high frequency of repetitive sequences and single nucleotide polymorphisms (SNPs). When comparing NGS results from different editing experiments, these elements impact the accuracy of editing analyses. Several guides for more than 55 different genes were studied in *M. rosenbergii* embryonic primary cells upon knock-out via electroporation showing a range of editing efficiencies for different guides. When looking at sequences of edited cells either at a narrow analysis window of nucleotides (2bp) or wide window of nucleotides (20bp) around the expected cut-site, some of the guides showed significant differences between the two. Cases of editing patterns that exhibited low editing efficiency in the narrow perspective, simultaneously with critically higher scores in the wide perspective, led us to re-examine the reliability of these results. NGS analyses demonstrated high frequency of SNPs and repetitive sequences, both in genes located on the autosomal chromosomes or on sex chromosomes. This may stem from genetic differences between individuals, or from differences between sex-linked genes on sex chromosomes. In order to enable future applications based on the CRISPR tool in *M. rosenbergii*, we also verified the reliability of editing efficiencies and tracked off-target frequencies for some guides through GUIDE-Seq showing variable cases of off-target to be further discussed. These insights enable the selection of optimal guides for genomic editing, contributing to both research and practical applications.

To eat and to be eaten: the role of freshwater crabs in aquatic food webs

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Biography:

Ingo Wehrtmann is working at the Universidad de Costa Rica, where he is teaching at the Escuela de Biología and is associated researcher at the Centro de Investigación en Ciencias Marinas y Limnología (CIMAR) and the Centro de Investigación en Biodiversidad y Ecología Tropical (CIBET). His research interests include decapod ecology from marine and freshwater habitats, working on reproduction of decapods, fishery-biology of commercially important shrimp species as well as introduced and invasive species such as crayfish in Costa Rica. He is also involved in several projects regarding microplastics in aquatic invertebrates and is very much interested in international collaborations.

All freshwater crabs complete their life cycle in aquatic systems and obtain energy and macro- and micronutrients from their environments. Crabs are crucial players in aquatic food webs, and their biomass often dominates other benthic macroinvertebrates. Moreover, many freshwater crab species have an amphibious lifestyle, thus linking terrestrial and aquatic energy flows. Their trophic ecology, however, is widely unknown, partly because they are primarily active at night, thus limiting the possibility of observing predator-prey interactions during the day. Here we summarize the available literature with records of freshwater crabs preying or being preyed upon by other organisms in the field and complement these observations with a summary of published information about their feeding habits using data from stomach content analyses. The literature review revealed numerous observations of freshwater crabs preying on frogs and toads. Crabs also prey on lizards and snakes, and there are numerous reports of predation on mollusks, insect larvae and other invertebrates. Crabs are also consumed by a wide range of animals. Most frequent are reports of different species of otters and birds preying on freshwater crabs. There are also observations of monkeys from Brazil and West Africa eating freshwater crabs. Small juvenile crabs can also be prey items for larger predatory stream macroinvertebrates. Results from studies that have analyzed this group's stomach contents indicate that freshwater crabs are generally opportunistic omnivores that can ingest plants and animals. Although the food spectra include predominately aquatic organisms, there are also reports of the presence of terrestrial animals such as ants. Overall, we are still far from fully understanding the role of freshwater crabs in aquatic food webs.

The hadal zone is a series of inverted islands: Evidence from global population genomics of a cosmopolitan amphipod

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Biography:

Johanna Weston is an ecologist with a passion for using scavenging amphipods to understand the drivers of biodiversity across the hadal zone. Her doctoral research at Newcastle University led to three contributions, (1) description of four new species and a new genus; (2) ecology of a non-subduction hadal feature; and (3) assessment of global phylogeography between disjunct populations. Currently, as Postdoctoral Scholar at WHOI, she is focused on the timing of hadal colonization and the natural history of other hadal-dwelling crustaceans. She looks forward to the Crustacean Congress to highlight hadal peracarids and leave inspired by the latest crustacean science.

The deepest marine ecosystem, the hadal zone (depths >6 km), hosts endemic biodiversity resulting from long-term geographic isolation and environmental selection pressures. However, the degree to which hadal features act as isolated island habitats to promote, first, reproductive isolation and second, speciation, is largely untested due to substantive technological and logistical challenges. Scavenging amphipods, with relative ease in recovery, represent a model group to test eco-evolutionary patterns across the hadal zone. Here, we analyzed genome-wide single-nucleotide polymorphism markers (2,933 SNPs) and two mitochondrial regions (16S and COI) for 12 populations of *Bathycallisoma schellenbergi* across the Pacific, Atlantic, Indian, and Southern oceans. Despite a cosmopolitan distribution, populations were highly restricted to individual features with only limited gene flow between topographically connected features, like the Kermadec and Tonga trenches. This lack of connectivity suggests that populations are on separate evolutionary trajectories, with evidence of potential cryptic speciation at the Atacama Trench. Together, this global study demonstrates that the shallower ocean floor separating hadal features poses strong barriers to dispersal, driving genetic isolation and creating pockets of diversity to conserve. Further work now seeks to resolve the timing of the descent of *Bathycallisoma schellenbergi* or the ancestral lineage into the hadal zone.

Where's my extended specimen? Building towards a globally connected biodiversity science.

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Biography:

Regina was introduced to marine field work in the Sea of Cortez as an undergraduate and fell in love with both invertebrates and exotic places. Her interests range from descriptive taxonomy of isopods and building molecular phylogenies, making museum collections visible, to building barcode libraries to interpret eDNA.

Many of us have written species descriptions and compiled monographs. Some of us have created DNA barcodes and generated both morphological and molecular phylogenies. A few of us are funded to digitize our vast marine invertebrate holdings, making biological specimens that have been invisible for centuries surface on the web. Aggregators exist to collect some of this disparate data, including the Integrated Digitized Biocollections (iDigBio.org) and Global Biodiversity Information Facility (GBIF), genetic sequence databases such as (GenBank) and the Barcode of Life Data Systems (BOLD), and specimen data portals such as InvertEBase <https://invertebase.org/portal/> (based on Symbiota, open-source software for managing and mobilizing biodiversity data). But despite all this effort, we still lack the ability to seamlessly follow the connections between all these elements of a complete, specimen-based understanding of organisms — the ideals expressed in the emerging “Extended Specimen” concept. In this view, specimens (e.g., type specimens) stand at the center of an interlinked cloud of digitally accessible information, and resolving and refining our taxonomic understanding of biodiversity depends on combining local and non-local specimen-based data. Therefore, launched from the seemingly simple goal of creating a compilation of all marine isopod species living in Southern California (ms. in review), we are exploring the opportunities and challenges of creating an entry point to specimen-based data that will be immediately relevant to the region's taxonomy and biogeography, yet also interwoven with the entire global mesh of biodiversity data.

Recognition of a novel epicaridium larval external yolk sac in primitive bopyrids (Isopoda: Bopyridae) parasitizing deep water squat lobsters

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Biography:

I am a Full Professor (Donald E. Axinn Distinguished Professorship) in the Department of Biology at Hofstra University. My research focuses on the associations between crustacean hosts and their symbionts, particularly parasitic isopods. I have published over 85 peer-reviewed papers on these crustaceans and other marine groups. My work has been funded by the National Science Foundation, the National Oceanic and Atmospheric Administration, the Sigma-Xi Scientific Society, and the Lerner-Gray Fund for Marine Research. Since 2014 I have served as the Treasurer for The Crustacean Society.

The presence of external yolk sacs in invertebrate is rare (e.g., known from some cephalopods), with all reported cases exhibiting yolk that is taken up through connection with the anterior alimentary canal. Herein, we report a larval bopyrid isopod type with a novel yolk sac connected to the posterior end of the alimentary canal. Members of the putatively primitive genera *Parapleurocryptella* and *Pleurocryptella* are ectoparasites of the squat lobsters, occupying their branchial chambers and feeding on their hemolymph. Females of these species produce broods of eggs that develop into epicaridium larvae. In contrast to nearly all epicaridium larvae known from epicarideans (exclusively parasites of other crustaceans as larvae and adults), the broods of the presently studied species had epicaridium larvae with a posterior, external cuticularized yolk sac. This structure has been noted in a few prior descriptions of epicaridium larvae of parasitic isopods; however, it was not recognized as containing the yolk which is utilized by the developing larvae. Among the samples, multiple broods were studied with SEM, including those with the second stage (microniscus) larvae exhibiting reduced sacs, consistent with the hypothesis of that the yolk is depleted during development. The findings suggest species in these two genera may exhibit an abbreviated life cycle where calanoid copepods are not involved as intermediate hosts and the isopods are released at the cryptoniscus stage, ready to settle on definitive hosts. Such a life cycle has only been documented in one species of epicaridean but without a yolk sac. Future research should examine the larval morphology and life histories of a wider range of species of *Pleurocryptella* and related genera, ideally with molecular analyses to confirm their relatedness and basal position among the bopyrids.

Phreatoicidean isopods: hidden diversity from the early Mesozoic

Wilson G

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Biography:

George D.F. (Buz) Wilson began studying deep-sea isopods (Asellota) in 1969 at the Scripps Institution of Oceanography, as well as participating to cruises to the Pacific Ocean at all depths ranging from the Philippine Trench to the San Diego Trough. In 1991, he took a job at the Australian Museum, with one aim being to study phreatoicidean isopods that were incompletely understood. This research program took him to remote locations throughout Australia and New Zealand where many new taxa were discovered and described. After retirement in 2014, he continues research in his lab in Michigan USA.

The phreatoicidean isopods are the epitome of hidden diversity in Eastern Gondwanan continents. They are survivors of multiple "great extinctions" that have reset the global biosphere. Their classification includes three diverse families: Phreatoicidae, Amphisopidae and Hypsimetopidae. Smaller groups of species are found in Phreatoicopsidae, Ponderellidae and Mesamphisopidae as well as in a few genera that are not well classified, like *Crenoicus*. The hotspot of generic diversity lies in Tasmania, with 8 described and several undescribed genera. Phreatoicidean habits and biology tends to generate flocks of similar species; *Eophreatoicus*, *Colubotelson* and *Notamphisopus* are the best described examples. Current understanding of their evolution suggests that they probably arose from isopod ancestors during the Devonian malacostracan radiation but are highly modified from the basic malacostracan body plan. Although phreatoicideans are isopods, they are not really "like-footed" because their limbs are specialized for locomotion or reproduction. Their general lifestyle, a preference for detritovory and decaying plant matter, possibly played a role in their longevity. They prefer cryptic habitats, such as living among aquatic mosses and plants, burrowing in moist stream sides or in burrows of other crustaceans, hiding under rocks and living in caves and aquifers. These habitats may have provided protection from great environmental disruptions caused by the terminal Cretaceous event. Phreatoicidean ancestors predate the breakup of Pangea, shown by their presence in Australian and Antarctic freshwater during the Early Triassic. Modern biogeography finds them living on continents of Eastern Gondwana but not Laurasia. Their distribution in Gondwana helps specify the timing of their evolutionary pattern assuming their freshwater adaptation and low vagility. Phylogenetically distinct lineages of Hypsimetopidae in India are recently discovered evidence for two separate migrations to that continent and for an early Mesozoic evolutionary radiation in the fresh waters of Antarctica and adjacent cratons.

Better Living Through Data Standards

Windsor A¹

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Biography:

I currently am engaged in research on various food-related metagenomics projects, including seafoods. I am keenly interested sample metadata curation to increase data utility to other researchers through use of ontologies and standardized metadata. Outside of my day job, I continue to collaborate with several colleagues on crustacean systematics, particularly issues within the superfamily Majoidea and commercially important species.

Increased accessibility to and affordability of nucleic acid sequencing has enabled its widespread use in crustacean studies in population studies, environmental metagenomics, phylogenomics and everything in between. The accumulation of such a quantity and variability of data from these studies makes the often-overlooked use of rich metadata and good data management a critical aspect of research. Neglecting these impacts both short term and long-term goals by research teams and other future researchers. Fortunately, there are some best practices for using rich metadata to ensure data are findable, accessible, interoperable, and reusable (FAIR). For one, metadata standards provide controlled vocabularies and ontologies to improve the description, effective re-use, and analysis of information from within and across studies, thus allowing for interoperability across unrelated datasets. Metadata templates, such as the National Center for Biotechnology Information (NCBI) Invertebrate Biosample template, apply generalized data standard fields in a way that is broadly applicable and adaptable across investigation types. An advantage of using a standardized template is that there is an explicit definition for each field. However, these fields often require precise ontological terms to populate correctly. Ontologies can be confusing to the uninitiated and lead to frustration when submitting to a data repository. Here, I aim to introduce relevant ontologies and decode some of these template fields with crustacean sequencing projects in mind.

Ecology of coral associated gall and pits crabs (Decapoda: Cryptochiridae): biodiversity and host usage in Hong Kong

Wong K¹

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Biography:

Kingsley Wong is currently a Phd student at the University of Taiwan, based Taipei. Previously based Hong Kong, he is interested in species diversity and taxonomy of decapod crustaceans, particularly brachyuran crabs. Now he is investigating coral-associated gall crabs (Cryptochiridae) from seas of Taiwan and nearby.

Cryptochirid crabs (gall and pit crabs), a highly specialized group under the Thoracotremata, are obligate symbionts of scleractinian corals in tropical and subtropical seas. With pronounced sexual dimorphism, females are nearly sedentary, sacrificing mobility for protection within respective hosts and reproductive success. Given its concealed habitus, the group has remained poorly sampled, and relevant taxonomic understanding remaining obscure. Based on recent sampling, using a combined approach in considering morphological characters, genetic evidences and host records, we reported on five species (of six OTUs) from shallow-water coral communities of Hong Kong, including description of two new species. Significant aspects pending further investigation include: (1) discrepancy between inventory of scleractinian and coral-associated fauna (cryptochirids); (2) current regional inventory based on morphology-based taxonomy being a crude underestimate, especially in terms of specific diversity otherwise revealed by genetic data ; (3) phylogenetic relationships among cryptochirid lineages pending resolution; (4) substantial range of "external" morphological features as result of interaction with host, and urgent in need of further characters for precise species delimitation; and (5) records and patterns of host usage obscured by poor taxonomic resolution.

The National Marine High Risk Site Surveillance programme: detecting incursions and range extensions of non-indigenous crustaceans in Aotearoa New Zealand

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Biography:

Chris Woods is a Marine Ecologist specializing in marine aquaculture and invasion science. Graduating from Victoria University of Wellington with a PhD on seahorse aquaculture, he has worked for NIWA since 1995. He has had long-term involvement in NIWA's research on bivalve, finfish, crustacean and echinoderm culture/ecology, as well as national marine port baseline surveys and targeted marine pest surveillance projects. His present specialties include marine biofouling and the detection and control of non-indigenous species, and he manages the delivery of the National Marine High Risk Site Surveillance programme for the Ministry for Primary Industries.

An effective surveillance system is a vital component of any biosecurity system. Biosecurity New Zealand (a Business Unit within the Ministry for Primary Industries) in partnership with the National Institute of Water and Atmospheric Research conceived, developed, and implemented the National Marine High Risk Site Surveillance (NMHRSS) programme, which celebrated its 20th anniversary in 2022. The NMHRSS programme delivers active biosecurity surveillance at 12 of Aotearoa New Zealand's ports and marinas deemed to be high-risk for the introduction and establishment of marine non-indigenous species (NIS). The NMHRSS programme is designed to detect the presence of a group of five primary target non-indigenous and potentially invasive marine animals and plants that Biosecurity New Zealand has identified as presenting a significant risk of arriving and establishing in New Zealand. The NMHRSS programme has two secondary objectives which are: 1) to detect incursions of marine NIS not previously recorded in New Zealand; and 2) to detect range extensions by marine NIS that are already established in New Zealand waters (including four secondary target species). Here, we discuss this flagship biosecurity surveillance programme, the target crustacean NIS the NMHRSS programme surveils for, provide examples of incursions of new-to-New Zealand crustacean species detected by the programme, and provide examples of detected range extensions of established non-indigenous crustaceans at survey sites.

Remoteness revealed: Anambas and Natuna Islands—a microcosm of Southeast Asian freshwater crab diversity

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Biography:

Darren CJ Yeo is an Associate Professor at the Department of Biological Sciences, National University of Singapore (NUS), where he leads the Freshwater and Invasion Biology Lab; he is also Head of the Lee Kong Chian Natural History Museum, NUS. His research interests include freshwater decapod crustaceans, aquatic invasions, and freshwater ecology and biodiversity, which the lab investigates through studies of inland waters in Singapore and other parts of tropical Asia.

Anambas and Natuna are relatively isolated archipelagos in the southern part of the South China Sea. Explorations by European naturalists in the late 1800s yielded in 1918 the first crab record from inland habitats of these islands, and in 1986 two more such species, all three being secondary freshwater species belonging to the semi-terrestrial genus *Geosesarma* (Sesarmidae). The first primary freshwater crab species recorded from the islands, *Balssiathelphusa natunaensis* (Gecarcinucidae), was described in 1970, based on the same historical material. Yet one more Asian primary freshwater crab family was not known from these islands until a 2002 biodiversity expedition to the archipelagos by a multinational team of South China Sea rim researchers, formed as a confidence building mechanism under the Indonesian Ministry of Foreign Affairs, discovered a new genus as well as new species of the family Potamidae. These and other material collected have since contributed significantly to phylogeographic studies of Asian freshwater crabs while remaining undescribed and unreported taxonomically. This presentation treats the taxonomy and reveals the diversity of the primary and secondary freshwater crabs in the families Potamidae, Gecarcinucidae and Sesarmidae from Anambas and Natuna—that though isolated nevertheless reflect a microcosm of Southeast Asian freshwater crab diversity.

A new insight into the evolutionary trend of the family Lernaepodidae (Copepoda: Siphonostomatoida) based on molecular data

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Biography:

Nanami Yumura is a PhD student at the University of Tokyo. She received her MSc from Hiroshima University in the area of the taxonomy of parasitic copepods.

The copepod family Lernaepodidae is a fish ectoparasite of highly modified morphological features. Such as elongated or expanded bodies of adult females without legs, attachment organs called 'bullae' held by transformed arm-like maxillae, and the presence of 'dwarf' males. The taxonomy and phylogeny of this family have not been conclusively determined because of their simple body plan. Kabata (1979), relying on morphology, proposed a sister relationship between species parasitizing freshwater hosts and seawater hosts including elasmobranchs, but his hypothesis had not yet been genetically verified. Castro Romero & Baeza Kuroki (1987) defined three morphological groups of *Parabrachiella* based on synapomorphy, which is the number of posterior processes of the adult female, but their hypothesis is questioned. The present study aims to clarify molecular phylogenetic relationships among eight genera and 23 species of lernaepodids using nuclear and mitochondrial gene sequences.

We detected two highly supported clades consisting of parasites on elasmobranch and freshwater teleost hosts (*Pseudocharapinus*, *Salmincola* and *Lernaepoda*) and those on seawater teleost hosts (*Clavellotis*, *Clavellopsis*, *Clavella* and *Alella*), and paraphyletic *Parabrachiella*. Our results do not support the Kabata's group comprising freshwater taxa but implied host switching from elasmobranchs to freshwater teleost fish. The *Clavella*-branch proposed by Kabata (1979) based on the morphology of males and cephalothoraxes and appendages of adult females was clearly supported. The synapomorphy proposed by Castro Romero & Baeza Kuroki (1987) was suggested to be convergent. Homological tracing of characters of *Parabrachiella* species is absolutely needed to resolve the chaotic taxonomy of the genus. Our results based on molecular sequences formulated a new insight of the evolution of the Lernaepodidae.

Castro Romero R & Baeza Kuroki H, 1987, Estudios Oceanológicos, 6, 1-24.

Kabata Z, Ray Society, London, 1979. 152: 468 pp.

Toxicogenetic effects of biodegradable polymers on two crustaceans: *Hippolyte inermis* and *Idotea baltica basteri*

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Biography:

Research interests are in the areas of molecular biology, ecology, development and evolutionary genomics. Major aims concern in i. studying the molecular basis of cellular mechanisms that underlie the responses of benthic organisms to environmental stress; ii. secondary metabolites from marine organisms as source of stress and biologically active compounds

Crustaceans as most marine invertebrates represent very fascinating organisms for their diversity, adaptations, and functions in a variety of ecosystems, and response to environmental pollutions. Plastics are ubiquitous materials in our lives and their durability represents a major environmental issue. Several studies reported the occurrence of plastic litter in different environments and are focused on improving environmentally-friendly solutions. In recent years, biodegradable plastics are proposed as an alternative to conventional plastics, with the aim of reducing environmental impacts. Even though studies are ongoing to enhance biodegradable productions, a few data reported about their behavior and toxicity in sea water and their effects on the physiology of marine invertebrates, once they are grazed or filtered. In this work, five biodegradable polymers (Polybutylene succinate (PBS), Poly(butylene succinate-co-butylene adipate (PBSA), Polycaprolactone (PCL), Poly- β -hydroxybutyrate (PHB) and Polylactic acid (PLA) were tested at two different concentrations on two marine crustacean models: the decapod *Hippolyte inermis* and the isopod *Idotea baltica basteri*. Our findings revealed drastically different effects in the two crustaceans. In fact, in the case of *I. baltica basteri* the effect was tested on growth and mortality of the individuals but biodegradable plastics did not show impacts on survival rates. In contrast, negative effects were observed on the mortality of *H. inermis*, mainly when they were exposed to PBS and PBSA. This negative effect was confirmed by molecular investigations, following the variation of expression levels of several genes involved in the physiological response to stress. These findings open new perspectives on the role of crustaceans as model organisms useful in providing insights into molecular mechanisms ruling the response to xenobiotics in marine environments.

The sexual biology of the hermaphroditic shrimp *Hippolyte inermis* Leach – a transcriptomic approach following seasonal physiological changes

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Biography:

Senior Researcher at the Stazione Zoologica Anton Dohrn and Contract Professor at the University Federico II of Naples is interested in marine ecology and food webs. Performs investigations on invertebrate physiology and sexual biology with particular attention to chemical ecology relationships, ecophysiology and biotechnological applications for aquaculture and medicine. Is presently President of the International Society for Invertebrate Reproduction and Development.

Decapod crustaceans are convenient models for sexual endocrinology studies, because of the functions of their androgenic gland (AG), producing an insulin-like androgenic hormone (IAG) that acts as a sexual switch (the IAG-switch). *Hippolyte inermis*, in particular, is a protandric shrimp exhibiting a peculiar mechanism of sex reversal triggered by the presence of diatoms in the diet available in spring. It shows two distinct reproductive strategies in spring and fall. In spring, the shrimp appears as a gonochoristic species, due to an early sex reversal triggered by diatoms. In fall the shrimp acts as a protandric species, producing an all-male population shifting to the female sex after about one year. We have collected shrimps at various size and physiological stages, both in spring and in fall, and obtained transcriptomic data of each pool, to detect physiological and hormonal shifts triggered by the diatom food. In addition, we have cultured shrimp females and obtained their larvae. After the settlement, we have raised larvae providing two different diets: a) including diatoms and b) without diatoms. Their transcriptomic profiles were obtained and compared to those of shrimps collected in the field during the two seasons. The results demonstrate that the sexual shift induced by diatoms is quite rapid and is concluded in a few days. The above suggests this Mediterranean shrimp as a unique organism for the study of the role of the IAG-switch under various environmental triggers and non-gonochoristic scenarios. In addition, the cellular mechanisms herein identified, triggered by benthic diatom borne chemicals, might facilitate potential development of biotechnologies in the field of cell death to be applied in medicine and aquaculture.

Poster Presentations

Spatial distribution of amphipod assemblages in Marine Protected Areas of the German Bight (North Sea)

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Biography:

Started working with amphipod crustaceans (ecology and taxonomy) in 2007;

PhD in Zoology from Free University of Berlin (Germany) in 2013;

Researcher at AWI Bremerhaven (Germany) in different benthos monitoring projects since 2015

Marine Protected Areas (MPAs) are a major tool for nature conservation management. Their continuous monitoring is necessary in order to assess the status of marine communities and, if applicable, the success of management measures such as fisheries exclusion. Three MPAs have been designated in the German Exclusive Economic Zone of the North Sea: the Dogger Bank, the Borkum Reef Ground and the Sylt Outer Reef. All of them are subject of a long-term monitoring of benthic communities that was initiated in 2011. The collected data allow for valuable insights into spatio-temporal dynamics of benthic crustaceans in the southern North Sea. Here, we focused on the diverse group of Amphipoda. Members of this group were consistently recorded exhibiting a high species richness throughout all three MPAs. Their respective species composition, however, was clearly differentiated between the distinct areas. The occurrence of some taxa such as several species of the genera *Cheirocratus*, *Gammaropsis* and *Ampelisca* was restricted to certain MPAs, thereby contributing to the observed differentiation among MPAs. This seemed to be related to particular habitat types within these areas such as coarse sediments and the vicinity to reef structures. Our findings underline the important role of MPAs for the preservation of crustacean biodiversity in the North Sea.

Morphological vs molecular approaches in conception of the genus *Parathranites* (Crustacea, Decapoda, Portunoidea, Carcinidae)

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¹University Of Ostrava, Ostrava, Czech Republic

Biography:

Anna Bližňáková is PhD student studying at the University of Ostrava. In her research, she focuses on the taxonomy, ecology, and biodiversity of the crabs superfamily Portunoidea commonly known as swimming crabs. Most of the study focused on the commercially important genus *Charybdis* and related genera occurring predominantly in the Indo-West Pacific region. Currently, she focuses on the deep-sea genus *Parathranites* (Carcinidae), whose distribution extends from the Indo-Pacific region to French Polynesia.

Superfamily Portunoidea Rafinesque, 1815 is a diverse group of ecologically and economically important marine crabs with the last segment of the pereopods (dactylus) changed into a shape resembling a paddle, as an adaptation to free movement in the water column. The genus *Parathranites* is the only genus in the subfamily Parathranitiinae Spiridonov, 2020 within the family Carcinidae MacLeay, 1838. Alain Crosnier provided a revision of the genus *Parathranites* based on the morphology in 2002, and added six new species to the two already existing – *P. hexagonus* Rathbun, 1906 and *P. orientalis* (Miers, 1886). Examining the material of crabs from New Caledonia and Madagascar, we performed a morphological and molecular comparison of forms of *P. orientalis* mentioned already by Crosnier. The result of the analyses revealed *P. orientalis* as a species complex, with at least three genetic lineages distinguishable by molecular data, and supported also by morphological proofs. The constructed tree for the genus, based on newly amplified sequences and those obtained from the Bold and GenBank databases, highlighted the need for taxonomic rearrangement of the genus and pointed to intraspecific variability of some species. Splitting of the genus into at least two separate taxa is indicated. Remarkable is also a geographic separation of the central Pacific *P. hexagonus* (Hawaii) and *P. parahexagonus* (Tuamotu) from other congeners, with *P. orientalis* being the most common and widespread in the remaining part of the Indo-West Pacific (IWP), while, and the others rare, known from limited discrete localities in the Indian Oceans and the western part of the Pacific. The morphological differences are most distinctive in the two central Pacific species.

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Integrating the Geometric Morphometrics Toolkit into the Taxonomy of Deep-Sea Macrostylid Isopods

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¹Senckenberg Naturmuseum, Frankfurt am Main, Germany

Biography:

Anchita Casaubon graduated from Ronald Reagan Doral Senior High School in Miami, FL, in 2011. She attended the University of Miami and received a B.S. in Biomedical Engineering in 2015, earned a second B.S. in Marine Biology from the Florida International University in 2019. She started graduate school at Tennessee Technological University in January 2020 and received her Master of Science degree in Biology in December 2022. She is currently a PhD candidate at the Senckenberg Naturmuseum and will receive her PhD in 2026.

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

Eye movement reflexes establish the home direction in path integrating fiddler crabs, *Uca pugilator*

Chatterji R¹, Layne J¹

¹University of Cincinnati, Cincinnati, United States

Biography:

Ruma Chatterji is a doctoral candidate in the Department of Biological Sciences at the University of Cincinnati. Upon graduating with her master's in biology from Texas A&M University- Corpus Christi, where she investigated memory mechanisms in Aplysia, her fascination with examining the role of memory in animal behavior propelled her to pursuing related research for her PhD. She is currently studying navigation mechanisms in fiddler crabs (Uca pugilator) and is investigating aspects of home vector memory subserving path integration, such as how it is stored and its duration. She looks forward to contributing to the field of crustacean behavioral ecology.

As animals execute essential behaviors like foraging, they must orient with respect to the space around them. That is, they must have some neural/behavioral mechanism for spatial navigation. One such navigation mechanism is path integration, whereby animals recall their starting point by continuously measuring distances and directions of their movements, summing these to form a single memory-stored vector. This is referred to as the home vector, and it must be stored using some form of coordinates. Coordinates establish a frame of reference for the vector and, therefore, the animal, which is either geocentric or egocentric. Examples of the former have been well-studied, but it remains unclear what really constitutes an egocentric frame of reference. Fiddler crabs make an excellent model to investigate the nature of this frame of reference because they tend to align the transverse axis of their body with the direction of home, and it has been speculated that their home vector is identical with the body axis. However, this cannot be correct since body axis is often not well-aligned with home, but the crab's concept of its home direction is. The body axis may still form the basis for the coordinate system if the crab adjusts its vector to account for bodily deviations from the home direction. Notably, due to ocular reflexes that stabilize the eyes against body rotation, this deviation of body axis from home is closely mirrored by the angle between eye and body, if there is good ocular stabilization. Indeed, we hypothesized that the body-home deviation angle – and thus the home vector itself – is embodied in the eye-body angle. This was confirmed: crabs with good eye stability had more accurate home vectors than those with poor eye stability, and the quantitative degree of stability accurately predicted the crabs' perception of home direction.

Early stage in the life history of shrimps of the genus *Alpheus*: description of larval morphology as the first step to meroplankton studies

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Biography:

I obtained my PhD in 2022 in the area of biodiversity and ecology of marine shrimp populations. Since then, in my research laboratory, we have been working on these areas of knowledge. We have recently started research on post-embryonic development in marine shrimp with a focus on taxonomy and larval morphology

Considering the importance of studies on larval morphology for the taxonomy and in the identification of the larvae of species in the plankton, the aim of this study was to describe the first larval stage (Zoea I) in alpheid shrimps, belonging to four species of *Alpheus* (1. *Alpheus brasileiro*, 2. *A. buckupi*, 3. *A. petronioi* and 4. *A. packardii*). Ovigerous females were collected in the southeastern coast of Brazil. The results allowed the identification of a combination of morphological characters of the species: (1) *A. brasileiro* - antennal scale 5-segmented with 11 plumose setae and 2 simple setae; coxal endite of maxillule with 3 simple and 2 sparsely plumose setae; and coxal endite of maxilla with 1 simple and 1 sparsely plumose setae; (2) *A. buckupi* - basal endite of maxillule with 2 stout spines and 2 small plumose setae; basal endite of maxilla bilobed, with 3 and 4 simple setae on proximal and distal lobe, and five simple setae on the basis of the first maxilliped; (3) *A. petronioi* - basal endite of maxillule with 2 stout spines, and 2 small plumose setae; endopod of maxillule with 1 terminal denticulate seta, 1 short terminal simple seta and 1 subterminal spine; basal endite of maxilla bilobed, with 4 and 5 simple setae on proximal and distal lobe, respectively and basis of second maxilliped with 5 simple setae; (4) *A. packardii* - maxilla with 1 simple and 1 sparsely plumose setae on the coxal endite, basal endite bilobed with 3 simple, 1 sparsely plumose setae on the proximal lobe, 2 simple and 1 sparsely plumose setae in the distal lobe. The information presented here is essential for understanding the life history of these species, as well as being the first step towards identifying the larvae in the plankton.

Microplastic ingestion by rafting Gooseneck barnacles in the South Pacific Ocean

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Biography:

*I am a Marine Biology Masters student at Victoria university. I have always been interested in the strangest and most unique sea life, and that interest has led me to studying marine biology. Outside of study I spend most of my time diving the coasts around Wellington and doing underwater photography. Although I'm no expert when it comes to crustaceans, the rafting communities of the open ocean are of great interest to me so to work on *Lepas* barnacles for my project is very exciting.*

Pelagic gooseneck barnacles (*Lepas* spp.) are remarkably complex both in their taxonomy and their ecology. It is their unique feeding behaviour which makes them especially susceptible to a more recent type of threat, microplastics. Microplastic pollution is an area of growing concern for all life in the open ocean. They have been found in even the most isolated parts of the sea. In high quantities, microplastic has the potential to cause damage, starvation and even carry toxic chemicals. Previous research has shown that *Lepas* barnacles consume microplastic in incredible amounts. This might make them especially susceptible to negative effects and may also provide the potential for them to be an open ocean microplastic bioindicator. My research aims to expand our understanding of microplastic ingestion by these barnacles. I will investigate to what extent the *Lepas* barnacles from around the south Pacific Ocean ingest microplastics. These barnacles are collected from floating tsunami detection buoys out in the open ocean. I will dissect them to reveal the levels of plastic they have ingested. This plastic will be analysed in detail and along with other variables such as morphological attributes and species, interesting patterns may arise. To assist with this research I have done some preliminary work on understanding *Lepas* species distributions across a latitudinal gradient in the South Pacific Ocean. This work used varying levels of identification complexity with external, internal and genetic, to identify which species were present, and to uncover potential areas of taxonomic uncertainty. The results from this work have shown a noticeable gradient in species compositions with latitude. This research of barnacle species and their microplastic ingestion in the South Pacific Ocean will greatly help us understand the evermore important issue of microplastics and their effects on life in the ocean.

Molecular taxonomy of the Mediterranean–eastern Atlantic *Periclimenes* species: how many species does the group truly count?

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Biography:

Karolína Fišarová is a PhD student in the crustacean team of prof. Zdenek Ďuriš at the University of Ostrava, Czech Republic. She holds a master's degree in zoology. Her doctoral research focuses on biodiversity, ecology and phylogeny of symbiotic shrimps of the family Palaemonidae, specifically the genus *Periclimenes*. In addition to shrimp research, her interests include a wide range of marine organisms, and she is also interested in ornithology and environmental protection. In her free time she enjoys diving, swimming, traveling, reading and music.

The genus *Periclimenes* Costa, 1844 is the most numerous genus of the Palaemonidae family with about 160 valid species. However, in the last two centuries, the species richness of the genus reached up to 300 species. Since then, many shrimps have split into the separate genera. The recent molecular studies have identified the genus *Periclimenes* as a polyphyletic one with a single monophyletic group of anemone species from the Mediterranean and the eastern Atlantic. This group, so-called true *Periclimenes*, is made up of four species: *P. aegylios*, *P. sagittifer*, *P. scriptus*, *P. amethysteus*. These species form an isolated genetic lineage separated from the rest of the Atlantic and Indo-Pacific species of the genus. Nevertheless, the systematic relationships within the group, especially between the species *P. aegylios* and *P. sagittifer*, still remains unclear. Our molecular study includes, in addition to current species, a potentially new species from the waters of West Africa. Phylogenetic trees have been generated on a concatenated dataset of a nuclear (H3) and of four mitochondrial (12S, 16S, 18S COI) genes, using Maximum likelihood (ML) and Bayesian inference (BI) models. The species *P. aegylios* and *P. sagittifer* appear to be conspecific. These species are well distinguished from each other by the coloration and distribution (the Mediterranean, the East Atlantic), but genetically they are nearly identical. It is in the concordance with the previously published subspecies status of both species (Grippa & d'Udekem d'Acoz 1996). The differentiation of other species, including not undescribed representative of the group, is well supported within the true *Periclimenes* lineage. The number of species of the "true *Periclimenes* group" will probably remain on four species, but there shall be significant shifts in the taxonomic structure in the future.

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Phylogeny and adaptative evolution to chemosynthetic habitat in barnacle (Cirripedia: Thoracica) revealed by mitogenomes

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Biography:

Zhibin Gan, associate professor, Institute of Oceanology, Chinese Academy of Sciences. Interested in biodiversity, taxonomy & evolution of crustacean.

Thoracican barnacles represent a unique group that has evolved in parallel identical ecotypes (sessile, stalked and asymmetric) in both normal and chemosynthetic environments. Hydrothermal vents and methane seeps are typical extreme deep-sea chemosynthetic habitats for marine macrobenthos. Characterizing the evolutionary history and adaptive strategy of barnacles is fundamentally important for understanding their origin, speciation, and diversification. Herein, we performed a series of evolutionary analyses focusing on the mitochondrial genomes of the main extant barnacle lineages. Phylogenetic inferences and topology tests contradict the traditional view of the sister relationship between verrucomorphs and balanomorphs, instead revealing that pollicipedids, calanticids and balanomorphs share common ancestor. Selective pressure analyses indicate that the two barnacle lineages of chemosynthetic ecosystems exhibit similar patterns in their evolution of adaptive characters, but have diverse and specific positive substitution sites of mitogenomes. Divergence times suggest that chemosynthetic barnacles originated in the Cenozoic, coinciding with the origins of other metazoan animals in chemosynthetic habitats as well as the Paleogene mass extinction and oceanic anoxic events. It is reasonable to suppose that ecological niche vacancy, sitotaxis, gene specificity in adaptive stress responses, and the subdivision of the ecological niche contributed to the origin and diversification of barnacle in chemosynthetic ecosystems.

For the shallows and the depths – A first probe set to target ultraconserved elements (UCEs) for Malacostraca

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Biography:

Jonas studied biology in Tübingen and Kiel with majors in ecology and biodiversity. He received his PhD at Kiel University in 2018 with a thesis on establishment and dispersal of non-native crabs along the coasts of Germany. Since 2019, he is affiliated with the Mangrove Ecology working group at the Leibniz Centre for Tropical Marine Research in Bremen, Germany. In 2021/2022, he joined the Museum of Comparative Zoology at Harvard University as a postdoctoral fellow for a collection-based research project on range-shifting mangrove crabs. His main interests are (molecular) ecology and genetic diversity of marine invertebrates under global change.

Since its introduction about 10 years ago, target enrichment sequencing of ultraconserved genomic elements (UCEs) has proven to be an invaluable tool for studies across temporal and evolutionary scales, and thus employed from population genetics, to historical biogeography and deep phylogenetics. UCE probe sets are available for an increasing range of major taxonomic groups, including vertebrates, terrestrial arthropods, and mollusks. Here, we present the first probe set targeting UCEs in crustaceans, specifically in decapods and other malacostracan lineages. Probes were designed using published genomes of nine decapod and one peracarid species, as well as raw Nanopore long reads of one additional brachyuran species. The final probe set consists of about 20,000 probes, targeting 1,348 unique UCE loci. Preliminary analyses of UCE data obtained from an intertidal mangrove crab, and from deep-sea squat lobsters indicate high UCE recovery rates (regularly about 1,000 loci per sample) in taxonomically shallow datasets. To test the probe set on deeper taxonomic levels, we additionally compiled a dataset across the entire Malacostraca (including representatives of the Decapoda, Peracarida, Euphausiacea, Stomatopoda, and Phyllocarida), and were able to recover dozens to hundreds of UCEs for the non-decapod species. Additionally, we recovered similar numbers of UCEs from historical museum specimens up to >100 years old, that were included in all three datasets. Overall, our results highlight the versatility of this UCE probe set and its high potential for crustacean studies.

Where no man has gone before - the first insight into the mitogenomes of deep-sea crustaceans of the family Pseudotanaidae (Tanaidacea, Peracarida).

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Biography:

I completed my doctoral thesis in 2020 with the title Diversity and distribution of deep-sea Pseudotanaidae. (Tanaidacea, Peracarida). In my dissertation, I described one genus and 23 species of crustaceans belonging to the family Pseudotanaidae. I am currently a postdoc at the Department of Genetics and Marine Biotechnology, Institute of Oceanology Polish Academy of Sciences where I continue to study the diversity of the Pseudotanaidae fauna, using an integrative taxonomy approach, combining morphological, genetic and ecological analyses.

Pseudotanaidae is a cosmopolitan family of animals occupying marine ecosystems in a full latitudinal gradient. Until now, more than 90 species have been described and classified into five genera (*Akanthiotanais*, *Beksitanais*, *Mystricentrus*, *Parapseudotanaeis*, and *Pseudotanaeis*). This group of organisms has no planktonic larval stage and females carrying eggs into the brood pouch. They are considered to have limited dispersal capabilities and narrow taxa zoogeographic ranges. Therefore, pseudotanaids may become a promising indicator for environmental impact assessment.

To date, the diversity of Pseudotanaidae has been evaluated mainly based on morphology, and only recently genetic analyses have started to gain some real traction (Sanger sequencing). Here, we present the first four mitogenomes from the Pseudotanaidae family. All analyzed mitogenomes belong to the individuals collected in the North Atlantic and have been morphologically and genetically classified into the *affinis+longsetosus* morphogroup of the *Pseudotanaeis* genus. The assembled mitogenomes are characterized by conserved gene order, and significant, sequence divergence between species reaching from 16.5% up to 22%. We have also observed an unusual change in their mitochondrial genetic code, where the typical termination codon TAA, codes for the amino acid tyrosine (Y) in *Pseudotanaeis*.

Convergent Evolution of Carcinization Using 3D Morphometrics

Julius J¹, Keiler J, Rodriguez-Flores P, Luque J, Hopkins M, Ortega-Hernández J, Ballou L, Bracken-Grissom H, Wolfe J

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Biography:

Joy Julius is a post-baccalaureate student at Harvard University.

A fundamental question in evolutionary biology is whether we can predict phenotypes. At least five cases of convergent evolution of the crab-like body plan are known in meirans (anomurans and brachyurans) and this phenomenon is known as carcinization. Here, we present the methods used in our journey to statistically quantify carcinization. For this objective, we have used micro-computed tomography (micro-CT) to build 3D models of meiran taxa that span the body shape differences of the clade, using ImageJ and 3D Slicer software. Together, these methods allow for the easy 3D visualization of morphology that was previously inaccessible. We synthesize data from landmarks and semilandmarks applied to the carapace and pleon, and use these to calculate a morphospace. We will create a database for 3D specimens that is accessible to the public, including representative species from Harvard's Museum of Comparative Zoology.

Annual and lunar breeding rhythmicity in the acorn barnacle, *Tetraclita kuroshioensis* Chan, Tsang & Chu, 2007 in Okinawa, Japan

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Biography:

2021 - Graduate School of Science and Engineering, University of the Ryukyus, Master's Program

2021 - 2022 Teaching Assistant, University of the Ryukyus

2017 - 2021 - Department of Chemistry, Biology and Marine Science, Faculty of Science, University of the Ryukyus

Barnacles are a group of crustaceans and many are hermaphroditic. We investigated the breeding season of *Tetraclita kuroshioensis*, which is a common species on the coast of Okinawa Island, Japan. We studied the development of the gonads and retention of the egg mass and larvae at attachment sites on a vertically distributed area to estimate the involvement of environmental factors in cueing reproductive rhythmicity in the barnacle. *T. kuroshioensis* specimens were collected at Agari Tida Park on the southeastern coast of Okinawa Island. Samples (20 individuals/month) were collected monthly around the full moon from September 2019 to October 2020. Gonadal development was histologically observed. Additional samples (30 individuals/month) were collected in April, August, and October 2021 (8 times/month). The sample collection locations were set at 120–150 cm (upper), 100–120 cm (middle), and ≤100 cm (lower) above the tidal reference plane. The presence of ovaries and eggs/larvae was checked under a stereomicroscope. Histological observations revealed that the ovaries collected from March to September had oocytes at several developmental stages, while those collected from October to February had immature oocytes. In contrast, fully mature testes were obtained from April to October but not from November to March. Peak ovarian development and retention of the egg mass and larvae were observed in the upper collection location around high tide. The peaks in the middle collection location occurred in August and around the new moon and waxing moon in October, while those in the lower collection location occurred around the new moon in August and October. These results suggest that the reproductive activity of this species during the breeding season depends on their habitat under the influence of the lunar/tidal cycle.

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

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¹Department of Marine Zoology, Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany, ²Department of Biological Sciences, Institute of Ecology, Evolution and Diversity, Johann Wolfgang Goethe University, Frankfurt am Main, Germany

Biography:

Henry Knauber is a crustacean taxonomist and PhD candidate in deep-sea biology working at the Senckenberg Research Institute Frankfurt, Germany. He is enrolled as a PhD-student under a PhD-scholarship at the Goethe-University Frankfurt, where he started his scientific work on deep-sea isopods back during his bachelor thesis and since then gradually extended in terms of scope and aims. Currently, Henry investigates deep-sea isopod families with different dispersal abilities using integrative taxonomy to find out how depth, distance and geomorphological features impact benthic speciation processes. Henry also works for the Senckenberg Ocean Species Alliance (SOSA) testing out new approaches to taxonomy.

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

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

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

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

Re-discovering *Cancellus macrothrix* Stebbing, 1924 in the Great African Seaforest: Taxonomic re-description and biological notes

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Biography:

With a particular interest in hermit crabs and crustaceans of South Africa I work at the interface of marine research and documentary storytelling. For many years I have been providing the scientific foundation for the 'Sea Change Project', our most successful story being the Academy Award winning "My Octopus Teacher". As trained taxonomist I have a broad interest and skills in ecology. Combining my diversity research with 'tracking' organisms in the water informs our daily dives in the 'Great African Seaforest', a monumental ecosystem we aim to protect.

Species in the genus *Cancellus* are highly specialized hermit crabs that usually live in pieces of rock, coral, wood or sponges. Globally 17 extant species are known, many of which from very few specimens. The South African species, *Cancellus macrothrix* Stebbing, 1924, previously only known from three specimens that were all collected over a century ago, is the only known species in the genus to occupy gastropod shells. This, and the combination of historically poor descriptions with the absence of material to examine, has led to the understanding that *C. macrothrix* was an aberrant species. Local diving knowledge was used to track and observe *C. macrothrix* in the kelp forest rocky reefs of False Bay, South Africa, where it was found not to be rare. From new material collected and from two of the three historical specimens *C. macrothrix* is re-described following modern taxonomy, including the use of microCT scans and molecular CO1 genetic barcodes. Uncertainties of this species belonging to the genus are addressed and the knowledge of the unique reproduction of brooding of its young on the hind body inside the shell is being expanded. Furthermore, in the tank *C. macrothrix* was observed preying on urchins by clipping off the urchin's spines and tube feed using its specialized claws, indicating that it could help control urchin populations in the wild.

Phylogenetic and Phylogenomic Analyses Reveal Surprises and New Insights into Taxonomy and Evolution of Axiidea (Crustacea: Decapoda)

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Biography:

Dr. Xinzheng Li, the president of the Chinese Crustacean Society and professor of the Institute of Oceanology, Chinese Academy of Sciences. He works on the taxonomy, zoogeography, phylogeny and biodiversity of decapod crustaceans, has publishes 5 monographs on crustacean and marine macrobenthic fields.

The infraorder Axiidea de Saint Laurent, 1979 is a group of cryptic, marine burrowing decapod crustaceans with surprisingly high morphological and ecological diversity. Although axiidean systematics have received considerable study, the higher level classification remains in flux. The monophyly and relationships of some of the major lineages are still undecided because of limited taxon sampling and molecular data. In this study, we reconstruct the most comprehensive phylogeny of Axiidea to date using three types of sequencing data (Sanger, genome skimming and ultra-conserved element [UCE]) from 125 species belonging to 56 genera and seven families. The UCE tree supports a monophyletic Axiidea sister to a clade containing 'Brachyura + Anomura' and Gebiidea. Within Axiidea, the monophyly of Callianideidae and Micheleidae is recovered, while Axiidae and Strahlaxiidae are shown to be non-monophyletic in all analyses, indicating the necessity for further taxonomic revisions of both families. Axiidae Huxley, 1879 is now restricted to *Axius*, *Australocaris*, *Neaxius* and *Neaxiopsis* and Strahlaxiidae Poore, 1984 to *Strahlaxius* Sakai & de Saint Laurent, 1989. All remaining genera previously included in Axiidae s.l. are transferred to Calocarididae Ortmann, 1891. Ancestral state reconstruction analyses reveal that some morphological traits widely used as diagnostic characters in previous taxonomic studies are actually consequences of convergent evolution, while others are informative synapomorphies. The divergence time estimation analysis shows that axiidean shrimps originated in the Late Devonian and some major lineages diverged earlier than expected. We hypothesize that adaptations to burrowing lifestyle and multiple deep-sea colonization helped axiidean shrimps survive a sequence of crises during the Mesozoic and diversify since their emergence. Our findings provide new insights into taxonomy and evolution of this group, and the newly designed UCE probe sets are expected to play a greater role in future phylogenomic studies of decapod crustaceans.

Study on the taxonomy and phylogeny of the Anomura from the South China sea coast

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Biography:

Dr. Xinming Liu Associate Research Fellow, Institutes of Marine Drugs, Guangxi University of Chinese Medicine, Nanning.

Research Interests: Taxonomy and systematic of Anomura (squat lobsters and hermit crabs), Nudibranchia, Biodiversity of coral reefs.

More than 2000 species of Anomura were collected around South China sea coast including 5 countries 23 areas 76 stations since 2017. The present study revealed that 92 species of 26 genera 7 families 3 supfamilies from Anomura were identified, photography showed the fresh coloration and dominant morphology structure were taken at the same time, underwater photograph shows the habitation of anomura were also taken under water. 84 species of anomura which have been recorded already were redescribed in detail, 8 species including *Paguristes runyanae* Haig & Ball, 1988, *Paguristes gonagrus* H. Milne Edwards, 1836, *Paguristes macrops* Rahayu & Forest, 2009, *Dardanus brachyops* Forest 1962, *Pagurus hedleyi* Grant & McCulloch, 1906, *Paguropsis confusa* Lemaitre, Rahayu & Komai, 2018, *Pagurixus nomurai* Komai & Asakura, 1995, *Lauriea punctata* Macpherson & Robainas-Barcia, 2013 were first records from Chinese waters. The information of the sexual dimorphism, color in life and the distribution have been updated, the importance of fresh color in the taxonomy was also discussed with the example from genus *Dardanus*. Phylogeny of the family Porcellanidae, supfamily Paguridea and suborder Anomura were reconstructed based on the mitochondrial genes of 16S rRNA, the “ Hermit to King” hypothesis was supported by this research, Carcinization trend posited in two forms: one from symmetrical hermit crab through squat lobster to crab-like form, the other from symmetrical hermit crab through asymmetrical hermit crab to crab-like form.

Integrative analyses to resolve the taxonomic identity of cryptic species: the case of mole crabs of the genus *Emerita* (Anomura) from the Western Atlantic

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Biography:

FLM: Biologist and Ph.D. in Zoology (UNESP); postdoctoral Associate at the University of Louisiana, Lafayette, USA. Full Professor at the University of São Paulo (Ribeirão Preto, Brazil) since 1993. He has experience in Zoology, Ecology and Marine Biology, with an emphasis on Morphology, Systematics and Ecology of marine and freshwater decapod crustaceans.

Based on recent molecular phylogenetic studies, many species of decapod crustaceans have been shown to contain complex of species, many of which are cryptic based on convergent morphological characters. Biogeographical coexistent distribution of some species of the genus *Emerita* from the Western Atlantic lead us to examine thoroughly the subtle morphological differences between *E. brasiliensis* and *E. portoricensis* along the Brazilian coast and compare them using Maximum Likelihood trees of two mitochondrial genetic markers (16S rRNA and COI) and morphology to corroborate the molecular data. Our molecular-based phylogeny, combined with a detailed morphological analysis, showed that in fact the Brazilian population was considered as a cryptic species. Once described, the number of species in the genus *Emerita* will be raised to 12, with five of them occurring in the Western Atlantic.

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Molecular systematics revealing species complexes in neotropical freshwater crabs: a case study with *Dilocarcinus* H. Milne Edwards, 1853

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Biography:

FLM: Biologist and Ph.D. in Zoology (UNESP); postdoctoral Associate at the University of Louisiana, Lafayette, USA. Full Professor at the University of São Paulo (Ribeirão Preto, Brazil) since 1993. He has experience in Zoology, Ecology and Marine Biology, with an emphasis on Morphology, Systematics and Ecology of marine and freshwater decapod crustaceans.

Although not as diverse as the Pseudothelphusidae, Neotropical crabs of the Trichodactylidae family are distributed throughout most of South America. Despite the relatively low number of species and wide distribution, a number of taxonomic issues involving many of its genera and species still need to be better understood. In this context, molecular systematics emerges as an essential tool in elucidating such questions, since some groups currently under a single denomination could potentially constitute species complexes. We obtained samples from different areas where *Dilocarcinus pagei* Stimpson, 1861 is known to occur and employed two mtDNA markers (CO1 and 16rRNA) to build a phylogenetic scenario using maximum likelihood (ML) and Bayesian inference (BI). The concatenated topology obtained, which is supported by both approaches, highlighted the existence of a complex of at least two species under the name of *D. pagei*. The present study reveals an underestimated diversity behind a species with one of the widest geographic distributions among the trichodactylids. This result clearly shows the need to increase and update the taxonomic studies on the highly diverse Neotropical freshwater crab fauna, as well as to increase the biological knowledge about the different lineages.

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Delimitation of *Ptilohyale littoralis* stimpson, 1853 (amphipoda, hyalidae)

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Biography:

Silvana G. L. Siqueira is currently a collaborating researcher at the Department of Animal Biology (IB/ UNICAMP) and a volunteer coordinator of the popular STU pre-university course. She received a graduate degree in Biological Sciences from the Federal University of Goiás in 2001, Master's and Ph.D. degrees in Ecology from the State University of Campinas (Unicamp) in 2007 and 2012 respectively, and a Postdoctoral fellow in Systematics of amphipods from the UFRJ National Museum in 2017. Her interests and experience include the ecology of marine benthic environments, the taxonomy of Amphipoda, ecotoxicology, scientific dissemination, and others.

Recently, *Ptilohyale littoralis* (Stimpson, 1853) was recorded in the “Bostrychietum” community on the rocky shores of the northern coast of São Paulo, a species that had not yet been described from the Brazilian coast. Its distribution was limited to the Atlantic coast of North America and it has recently been declared an exotic species in part of the European Atlantic. Its abundance and distribution in Brazil were investigated and they are in large numbers and occupying regions previously dominated by other species. It is expected that invasive species have greater reproductive potential and flexibility to adapt to different environments and they have been considered as the second cause of biodiversity loss in the world. Although morphological analyses are of great value in identifying and recording invasive species, tools such as molecular data can help this process. There is still no sequencing record for *P. littoralis* in worldwide databases. It is necessary to investigate whether *P. littoralis* is a distinct species from other Hyalidae species that occur in the region or whether there are factors such as phenotypic plasticity or speciation. In addition to all available COI sequences of the Hyalidae family rooted in the amphipod *Hyaella* sp. (Hyalellidae) for comparative characterization of the species sampled in this work, individuals of *P. littoralis*, *Hyale macrodactyla*, *Serejohyale youngi*, *Apohyale media*, *Hyale niger* and *Parhyale hawaiiensis* from Brazilian waters were sequenced. The phylogenetic reconstruction by Maximum Likelihood confirms that *P. littoralis* is a distinct species from all other Hyalidae in the region even distant from *Parhyale plumicornis*, in which it was once considered a synonym. The addition of new specimens from Europe and North America might confirm the recent introduction of *P. littoralis* in the southwestern Atlantic.

Population dynamics of a potentially invasive hyalid (*Ptilohyale littoralis* Stimpson, 1853) compared to a local dominant species (*Parhyale hawaiiensis*, Dana, 1853)

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Biography:

Silvana G. L. Siqueira is currently a collaborating researcher at the Department of Animal Biology (IB/UNICAMP) and a volunteer coordinator of the popular STU pre-university course. She received a graduate degree in Biological Sciences from the Federal University of Goiás in 2001, Master's and Ph.D. degrees in Ecology from the State University of Campinas (Unicamp) in 2007 and 2012 respectively, and a Postdoctoral fellow in Systematics of amphipods from the UFRJ National Museum in 2017. Her interests and experience include the ecology of marine benthic environments, the taxonomy of Amphipoda, ecotoxicology, scientific dissemination, and others.

The Hyalidae family (Amphipoda) is identified as one of the most abundant and diverse that live in macroalgae in the mesolitoral of rocky shores, with species such as *Parhyale hawaiiensis* (Dana 1853), *Aphohyale media* (Dana 1853) and, more recently, on the north coast of São Paulo, Brazil, *Ptilohyale littoralis* (Stimpson, 1853), a species native to the Atlantic Northwest. Recent studies have shown that *P. littoralis* is occupying regions previously dominated by *P. hawaiiensis*, suggesting that it is a better competitor and a potentially invasive. In these cases, to estimate their growth/extinction, populations have been analyzed by demographic parameters. Monthly (February 2021/January 2022) 4 squares of 100 cm² of the macroalgae *Bostrychia* sp. were sampled on two rocky shores at Praia das Cigarras. The samples were fixed in 70% alcohol and the species were photographed, measured and grouped into sexual and size classes. The dynamics of *P. littoralis* and *P. hawaiiensis* were evaluated to compare their potential/reproductive strategy. Corroborating previous studies, they were the most abundant of the associated fauna. Compared to *P. hawaiiensis*, *P. littoralis* has a lower average of eggs, but it has a higher number of ovate females (fo) in percentage relative to the total population. The smallest *P. littoralis* fo has 3.388mm and the largest 7.837mm, *P. hawaiiensis* range of fo was 5.165mm to 8.203mm. Unlike *P. hawaiiensis*, *P. littoralis* has not a positive correlation between the size of fo and the number of eggs. In both species males have larger sizes, however females are more frequent. All classes of *P. littoralis* showed differences between months, with the exception of females that just showed differences to the sampling point (ANOVA, $p < 0.001$) possibly indicating a greater tolerance for sites with high hydrodynamics. Furthermore, it was possible to observe an alternation of dominance between these species throughout the year.

Species Diversity and Biogeography of Deep-sea Cumaceans in the Northwest Pacific.

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Biography:

Kai Okamoto is currently a student in a master's course at the Graduate School of Science, University of Tokyo. He earned his bachelor of Faculty of Science, Kumamoto University in March 2022.

Deep sea (≥ 200 m depth) is the extensive habitat that covers about 65% of the earth surface. The biodiversity in the deep sea is comparable to that of tropical forests (Grassle, 1989), but large knowledge gaps exist in biodiversity and spatial distribution patterns of deep-sea benthos among regions and taxonomic groups. We focused on the small crustacean taxon Cumacea (Malacostraca, Peracarida), which has the highest species diversity in the abyssal depth (Rex, 1981). The dispersal capability of cumaceans is not considered to be high because they do not have a planktonic larval stage. Studies of deep-sea cumaceans are delayed as compared to those of other deep-sea animals, with only a few examples using molecular methods.

This study provides the first systematic knowledge on the species diversity and biogeography of deep-sea cumaceans in the Northwest Pacific off Japan. Specimens were collected from 42 sites between the depths of 237 and 7,185 m during numerous cruises. These collections allow us to compare the bathymetric distribution patterns associated with bathymetrical environmental changes.

We recognized 20 genera in 5 families morphologically and identified species in some genera by using morphological and molecular methods. The bathymetric distribution ranges of studied species tended to increase with the depth. This trend may reflect drastic bathymetrical environmental changes promoting speciation in the upper bathyal zone (≥ 800 m). Previous studies suggested that geographical barriers play an important role in distribution-pattern formation (e.g. Uhlir et al., 2021). Interestingly, we detected no genetic deviation between the Japan Sea and Pacific populations, which are separated by a shallow strait at 130 m, for a single species. The life cycle of deep-sea cumaceans is unknown, but some cumaceans might migrate to such shallow layers. Further studies are expected to better understand biodiversity, biogeography, and evolutionary processes in the deep sea.

Paternity patterns associated with sperm receptive structures in decapods

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Biography:

Luis Miguel Pardo, PhD in Biology and marine biologist, titular professor in the Universidad Austral de Chile, Valdivia, Chile. Specialist in benthic invertebrate ecology with emphasis on taxonomy and reproductive biology of marine decapods. In the last 15 years, I have had a special interest in establishing the biological basis for sustainable marine decapod fisheries.

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In crustacean Decapoda, polyandry is ubiquitous in most species and multiple paternity is associated to mating strategies and reproductive structures. Putative benefits of multiple paternity are associated to maintain genetic variability of the descendance, which should be highly valuable in an environmental changing scenario. However, multiple paternity does not occur in all decapod groups. In this review, the paternity pattern has been analyzed focusing on the ejaculate reception structure. Species with external fertilization and simple or without structure to deposit sperm masses such as Caridean shrimps, chelated lobster (Astacidea) and Anomuran shown high incidence of multiple paternity, 100% (n= 5 spp), 100% (n=7), 75% (n=4) respectively. On the other hand, species with internal fertilization with specialized seminal receptacles like Eubrachyura, single paternity seems to increase drastically, and when multiple paternity occurs, the disproportion between the males involved in fertilization is high (67% of species with highly skewed paternity (>90%) in favor of a single male, n=9). Whereas males' strategies to assure paternity could be more effective in species with internal fertilization, female cryptic choice could be more effective in species with external fertilization. Few or no reports of paternity patterns for other groups like Penaeoidea, Axiidae, Achelata are available (0,0 and 1 studies respectively) which are necessary for a complete understanding of the importance of multiple paternity in the mating strategy evolution.

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Crustaceans on the move: the continuing story of biofouling communities on tsunami detection buoys

Peart R¹

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Biography:

I am a Marine Invertebrate Systematist at NIWA in Aotearoa New Zealand. I research primarily on amphipod biology - their systematics, phylogenetics, distributions and interactions with the environment. I have also been known to dabble in other peracarid crustacean groups, but my heart is always with the amphipods

The DART buoy network around the Pacific Rim provides a high-speed early warning of tsunami activity in our region, triggering alert systems for vulnerable coastal communities. This network also can measure and detect changes in the complex pelagic biota of the Pacific Ocean and how they may influence the marine biota landscape of Aotearoa, New Zealand.

NIWA maintains 12 tsunami detection buoys in the waters off New Zealand and further north. As with most solid structures in the aquatic environment, these buoys attract a large biofouling community. The placement of the buoys in NZ's EEZ is a special opportunity to examine the composition and presence of an unknown marine biota (pelagic) and the influences to NZ's marine biota. Previous studies in other parts of the world documenting artificial ecosystems shows this community is often comprised of 'new to science' fauna, nursery fauna (vertebrates and invertebrates), naturally pelagic fauna, and may have a large component of adventive/invasive fauna. Despite this research there are no records of this being done on the Tsunami detection buoys around the Pacific Rim.

There are considerable gaps in our knowledge of what species occur in NZ's EEZ and how they influence our inshore biota and fisheries. As climatic and environmental conditions change due to anthropogenic influences, species ranges will change. Having a detailed latitudinal time series, this project observes and documents these changes and provides strong connections to NZ's biosecurity landscape. It is vital to understand the pathways of adventive organisms and other vectors which may contribute to the translocation of non-indigenous organisms, such as rafting, not just hull and ballast-water. These DART buoys provide spatial and temporal information as 'floating reefs' in the deep oceanic water as refuges for a variety of organisms in the area.

The influence of environmental and ocean-climatic drivers in the abundance of shrimps in a shallow marine area

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Biography:

PhD candidate at the São Paulo State University's Biosciences Institute (UNESP). My research focuses on decapod crustacean biodiversity and ecology in tropical and subtropical shallow marine environments.

Different life cycles lead to differences in species niche and ecological requirements. In this study, we assessed spatial and temporal variance in the abundance of eight shrimp species by analyzing a dataset spanning 27 years in a southeastern Brazilian tropical bay. We also examined the influence of ocean climatic and environmental factors on the abundance of these species. Periods of neutrality in El Niño Southern Oscillation favored increases in abundance of *Artemesia longinaris*, *Pleoticus muelleri*, *Rimapenaeus constrictus*, *Sicyonia dorsalis*, and *Nematopalaemon schmitti*. The shrimps *P. muelleri* and *S. dorsalis* also had higher abundances in La Niña periods. During La Niña and neutral periods, there is a shift in the atmospheric pressure gradient favoring Northeast winds, which increases SACW intrusion and weakens the Coastal Water. Thus, species that respond negatively to elevated temperatures, such as *P. muelleri* and *S. dorsalis*, migrate to deeper areas during El Niño, which were not sampled in this study. El Niño events favored the abundance of *Litopenaeus schmitti* and *R. constrictus*. El Niño is known to increase water surface temperature in southeastern Brazil; thus, the temperature increase benefits these species, whose abundance increases with elevated temperatures. All species showed a preference for sediments composed of silt and clay. Long-term monitoring of communities captured as species of commercial interest or incidentally is essential for establishing standards and measures to protect ecosystems.

Characterization of mole crabs (crustacea, anomura, hippoidea) from the Pacific and Caribbean coasts of Costa Rica

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Biography:

My name is Sandra López Díaz, a recent MSc from Spain. I discovered the world of scientific research thanks to my MSc studies. During our fieldwork in Costa Rica, I was able to find the Superfamily Hippoidea. I focused my thesis on the study of these beautiful animals, sampling them in the field, followed by identification and lab work which led me to get acquainted with them. All these factors and all the process to get to know more about Hippoidea, gave me the key to try to open locks studying these poorly understood and ecologically complex species

Mole crabs (superfamily Hippoidea) were collected from Costa Rican shores, the Pacific (on two beaches), and the Caribbean (on one beach). An intense sampling was performed during low and medium tide to obtain data on the species interactions, body size, abundance, and associated community. Additionally, phylogenetic analyses based on two mitochondrial genes (COI and 16S) were performed to explore phylogeographic patterns and phylogenetic placement of the species from Costa Rica. Five species were found on each coast: *Emerita rathbunae*, *Hippa strigillata*, *Lepidopa deamae*, *Lepidopa* cf. *mearnsi* and *Albunea* cf. *lucasia* in the Pacific, and *Emerita portoricensis*, *Hippa* cf. *testudinaria*, *Lepidopa richmondi*, *Lepidopa dexterdae* and *Albunea paretii* in the Caribbean. *Hippa* cf. *testudinaria* and *Lepidopa dexterdae* are recorded for the first time in Costa Rica. We discuss the discovery of a possible new species, previously identified as *Emerita portoricensis*.

In the Pacific (Cabuyal beach), regarding the ecological results, we did not find a relationship between body size and tide phase (low or medium) for *Emerita rathbunae* but occurs one between the tide phase and the abundance. The case of *Hippa strigillata* shows a relationship between tide phase and body size, although there is no relationship between tide phase and abundance. Surprisingly, the Caribbean populations of *Hippa* and *Emerita* (*E. portoricensis* and *H. cf. testudinaria*) show the opposite patterns observed for their Pacific sister species. We also analyzed the relationships between tide and the presence of ovigerous females and associated gastropod communities.

Additional fieldwork would be required to better understand the natural history of mole crabs in these areas; for instance, to explain if their abundance and sex ratio are season-dependent and why the Caribbean and the Pacific mole crab communities show different overall ecological patterns.

Historical biogeography of squat lobsters in the family Eumunididae (Chirostyloidea) helps to unveil the role of marine hotspots and geographic barriers in deep-sea diversification

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Biography:

Biodiversity postdoctoral fellow at the Museum of Comparative Zoology, Harvard University. My research is focused on different aspects of the evolution, biogeography, and systematics of crustaceans and other arthropod. I am extremely interested in characterizing major patterns of biodiversity within crustaceans as a critical step toward understanding ecological and evolutionary processes promoting speciation in marine environments. I am currently investigating speciation patterns among shallow-water and deep-sea taxa, to place deep-sea main events of colonization, determine and compare rates of diversification-extinction in both environments, and elucidate phylogeographic and genomic patterns using Ultraconserved elements (UCEs).

The family Eumunididae is an idoneous system to study deep-sea diversification processes. It includes 34 species present on continental shelves and slopes with a circumtropical distribution. The peak of species richness, as in so many marine groups including other squat lobsters, is in the Southwestern Pacific. However, most research on biogeography and diversification patterns has been focused on shallow-water species. Here, we pursue to answer two questions: i) What was the role of the closure of both the Isthmus of Panama and the Tethys Seaway in eumunidids' evolutionary history? ii) Is there any variation in the diversification rates (speciation and extinction rates) among different geographic areas? To answer these questions, we reconstruct a time-calibrated phylogeny with more than 80% of the known species within Eumunididae using genomic data (Ultra Conserved Elements, UCEs), for more than 1,000 loci. We identify the ancestral areas of diversification and use the Dispersal-Extinction Cladogenesis (DEC) and Geological State Speciation and Extinction (GeoSSE) models to estimate the geographic variation in the diversification rates. Our results highlight that combining dense taxonomic sampling with the analysis of genomic data fundamentally improves our understanding of the evolutionary history and current patterns of diversity in a deep-sea biogeographic framework.

Comparison of the the mitochondrial genome of four *Ligia* isopods assembled using genome skimming approaches

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Biography:

Santamaria's primary research interests are on cryptic biodiversity and phylogeography of coastal isopod, particularly Ligia isopods and those from highly biodiverse and geologically active regions. As a Hispanic, he is aware of the difficulties that under-represented students face in higher education and when pursuing careers in the biological sciences. Thus, he is dedicated to increasing their participation in the sciences.

The mitochondrial genomes of isopods are known to exhibit unique gene patterns and gene rearrangements that differ from the pan-crustacean ground gene arrangement. Distantly related isopod genera have been shown to differ in their mitochondrial gene patterns, with rearrangements such as the translocation of genes such as NAD1 and the 12S rDNA gene, and the loss of tRNA genes being common. To our knowledge, previous work been limited to comparisons of the mitochondrial genomes of species across genera and families, leaving unclear whether mitochondrial gene rearrangements occur amongst closely related species. In this study, we compare the mitochondrial genomes of four *Ligia* isopod species assembled using genome skimming approaches from Illumina sequencing read data. We assembled complete mitochondrial genomes for two *Ligia* species from Asia (*L. exotica* and *L. taiwanensis*), one from South Africa (*L. natalensis*), and one from Australia (*L. australensis*). The former two species appear to share a mitochondrial gene arrangement that differs from the latter, indicating that gene rearrangements have occurred amongst *Ligia* species.

These fronds are made for raftin': comparative phylogeography of Peracarida associated with brown algae in the Western Atlantic

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Biography:

Master in Zoology and PhD candidate in Animal Biology. I am interested in biodiversity, phylogenetics and biogeography of peracarids associated with several living organisms, including algae, whales and sea turtles.

Peracarids are characterized by the lack of larval phase and, consequently, they usually present low dispersion rates that lead to high endemism rates. Despite their low dispersion rate, peracarids associated to macroalgae can use surface currents to disperse by rafting of detached seaweeds, connecting some populations and isolating others. Phylogeographic studies on Peracarida in Brazil are yet scarce and mostly absent in continental and oceanic islands. In this study, we used the species *Ampithoe marcuzzii* (Amphipoda: Ampithoidae) and *Chondrochelia dubia* (Tanaidacea: Leptocheliidae) as models to understand the oceanic barriers and environmental variables that structure the populations over 5,000 km of their distribution. Based on mitochondrial, nuclear markers and single nuclear polymorphisms, the specific evolutionary histories suggest two species complexes, with partial congruence between them. The *A. marcuzzii* complex presented a continent-island separation shaped by abiotic variables, with connection of Brazilian oceanic islands with the Caribbean, whereas the continent lineage was characterized by strong latitudinal population structure, with evidences of isolation-by-distance and isolation-by-environment. In contrast, the *C. dubia* complex showed connectivity among oceanic islands, Caribbean and the northeastern Brazilian coast, while separated from the southeastern lineage with a geographic boundary at the Paraguaçu river mouth, suggesting independent evolution of both lineages. Estimated divergence times for both complexes suggest that the same events isolated the populations of *C. dubia* and *A. marcuzzii* in the Miocene. Therefore, despite co-occurring in seaweeds along the western Atlantic, population structure patterns are partially congruent and might have been driven by different environmental conditions.

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Like two peas in a pod: unexpected low genetic diversity of commensal amphipods on western Atlantic Sea turtles

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Biography:

Master in Zoology and PhD candidate in Animal Biology. I am interested in biodiversity, phylogenetics and biogeography of peracarids associated with several living organisms, including algae, whales and sea turtles.

Obligate commensalism in the marine environment and its evolutionary role are still poorly investigated. Within marine turtles, crustaceans represent one of the most diverse group of epibionts, and amphipods show a great variety of ecological adaptations. Several species of amphipods are known as facultative commensals but only two species are known as obligate commensals of sea turtles: *Hyachelia tortugae* and *H. lowryi*. Here, we studied the phylogenetic position of *Hyachelia* within Hyalidae and the comparative phylogeography of these two species in the southwestern Atlantic Ocean. Specimens were sampled in feeding areas of green and hawksbill turtles, as well as in nesting areas of loggerhead turtles along the Brazilian coast. Mitochondrial and nuclear markers [cytochrome c oxidase I (COI) and 18SrRNA] were used to infer the phylogeny, whereas the mitochondrial markers COI and 16SrRNA were used for phylogeographic purposes. We recovered an early branch of the genus *Hyachelia* as the sister clade of remaining Hyalidae, showing that morphological differences that separated *Hyachelia* in the subfamily Hyacheliinae are supported by molecular analyses, originating about 120 Mya. Preliminary genetic diversity assessment of *H. tortugae* shows greater diversity when compared to *H. lowryi*, despite *H. lowryi* being reported in three sea turtle hosts while *H. tortugae* is only found on green turtles. Low genetic diversity results among and between hosts, and the incipient population structure are unexpected for organisms with such poor dispersion capacity, showing that few maternal lineages are contributing to population demographic structure. Other markers and new analyses are being added to further clarify which factors might influence their population dynamics.

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Amphipods from the island where the bubbles sink: first assessment of macroalgae associated fauna in Saint Peter and Saint Paul Archipelago

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Biography:

Silvana G. L. Siqueira is currently a collaborating researcher at the Department of Animal Biology (IB/ UNICAMP) and a volunteer coordinator of the popular STU pre-university course. She received a graduate degree in Biological Sciences from the Federal University of Goiás in 2001, Master's and Ph.D. degrees in Ecology from the State University of Campinas (Unicamp) in 2007 and 2012 respectively, and a Postdoctoral fellow in Systematics of amphipods from the UFRJ National Museum in 2017. Her interests and experience include the ecology of marine benthic environments, the taxonomy of Amphipoda, ecotoxicology, scientific dissemination, and others.

With the increase in climate change and anthropogenic pressures, biodiversity knowledge represents a key factor for monitoring marine ecosystems, especially in tropical regions where information is scarce. In this way, studies that describe species richness in different marine environments such as oceanic islands become important for conservation. Saint Peter and Saint Paul Archipelago (SPSPA) is one of the smallest and most isolated oceanic islands in the world. SPSPA is a group of 14 islets, with surrounding depths of 5,000 m, located near the Mid-Atlantic ridge, around 1,000km from the Brazilian coast and 1,890 km from Senegal. It belongs to the Brazilian Exclusive Economic Zone and it is maintained by the Brazilian Navy as a scientific base. Despite the great economic, scientific and strategic importance of this environment for Brazil, the biological communities of marine invertebrates are not well known. Within this context, this work aims to describe the richness of amphipods associated with macroalgae in the SPSPA, as a means of subsidizing monitoring programs in the region. Samplings were performed on the Belmonte island's cove by manual removal of macroalgae, which was washed for associated fauna retention. Specimens were fixed and preserved in ethanol and taken to the mainland for morphological identification. The 1237 specimens were collected, and identified in eight families: Ampithoidae, Caprellidae, Colomastigidae, Hyalidae, Ischyroceridae, Leucothoidae, Maeridae, and Stenothoidae. From a total of eleven species collected and identified, five are new. The new ones are from the genus *Ampithoe*, *Cymadusa*, *Caprella*, *Colomatix*, and *Leucothoe*. These results suggest a high rate of amphipod endemism in Saint Peter and Saint Paul Archipelago as observed in previous studies with fish and other invertebrates.

Analysis of embryonic prawn primary cell culture by metabolic activity, cell cycle analysis and lipid metabolomics.

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Biography:

Since the first time I was taught about the structure of DNA, I was always curious about biology in school. It has always been fascinating to learn more about it. It was the reason why I studied biology in high school. In college, I choose to study Biotechnology to learn the applications of biology in human lifestyle. My master's project was based on cancer biology, but I didn't wish to continue with it, this led me into the world of crustacean physiology, and I am currently working on the immortalization of crustacean cell lines for the application in cellular agriculture.

Despite extensive research efforts, no crustacean cell line is available. We explored the culture of embryonic primary cells isolated from the prawn *Macrobrachium rosenbergii* with three different commercial media, assuming embryo to be highly proliferative. The cultures were monitored at five-time point regimens, for cell metabolic activity using CCK-8, cell cycle analyses by FACS, and metabolomics and lipidomics by LC/MS. The results showed that all used media in the cultures allowed increment in metabolic activity of cells with a peak at day 4 using DMEM high glucose or Optimem. In the first seven days 8% proliferation of culture was observed in Optimem, making this media appropriate for short-term in vitro experiments. Differently, DMEM: F12 did not sustain cell proliferation potentials up to day four, but augmented gradually thereafter up to 14 days. The DMEM high glucose, at day 14 had twice the events of cells in S phase compared to day 4 probably based on metabolite accumulation in the media. All the above suggest that cell cycle progress and proliferation were triggered by specific metabolites present or absent in specific media. Lipidomics analysis of the media's metabolites of Optimem grown cells throughout culture showed significantly higher concentrations of 29 annotated lipids, out of which specific phosphatidylcholine and phosphatidylserine were found to be the most secreted by the cultured cells from day 4 to day 14. Contrary, one specific fatty acid that was lowered significantly in the media suggested its utilization from day 4. Further advanced MS metabolite validation and pathways, could reveal essential additives inducing sustainable growth and proliferation, impeding cells from becoming senescence. These promising metabolites, adjusted to our culture, could be a master key in a future qualified growth media toward the development of crustacean immortal cell lines.

All is not lost: ex-situ and in-situ studies reveal resilience to drought stress in the critically endangered Singapore freshwater crab *Johora singaporensis*

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Biography:

Elysia Toh (MSc) is a PhD candidate at the University of Sunshine Coast. A researcher and lover of freshwater decapods, she spent her undergraduate understanding how behaviour of non-native Oriental river prawn varied across an invasion gradient, her MSc. research focused on conservation biology of the critically endangered Singapore freshwater crab; while her PhD research focuses on biology of tropical and sub-tropical peat swamps. Besides decapod crustaceans, her research interests include freshwater ecology, invasion biology and behavioural biology. Elysia also involves herself in Singapore's conservation scene, working closely with conservation organisations and government agencies to inform conservation management.

Freshwater ecosystems are highly vulnerable to variations in climate. Increased frequency and intensity of drought events, known to affect freshwater organisms, need to be understood in order to drive effective conservation. In Singapore, the endemic and critically endangered Singapore freshwater crab *Johora singaporensis* (Ng, 1986) is only found in hill stream habitats that are highly susceptible to drying up during periods of low or no rainfall, which may be exacerbated by climate change. While disappearances of the species have been noted at sections of the streams that have previously dried up temporarily, no study so far has investigated the impacts of drought stress on this species. Here, we elucidated the effects of drought on in-situ environmental parameters and *J. singaporensis* condition factor across one year as well as its ex-situ behavioural responses. Bayesian modelling showed that seasonality significantly affected hill streams parameters and in-situ condition factor but may have been confounded by locality-specific differences. Significant differences in condition factor, for example, was observed between localities during the Southwest monsoon, but not during other seasons. Ex-situ behavioural studies further showed that the semi-terrestrial *J. singaporensis* will burrow under drought stress conditions, potentially shielding them from short-term adverse impacts of drying events. In comparison, the syntopic and fully aquatic lowland freshwater crab *Parathelphusa maculata* had a lower tendency to burrow under drought conditions as well as across various substrates. Our findings show that while hill streams and condition factor of the species can be susceptible to drying events, *J. singaporensis* may nevertheless mitigate the impacts through behavioural responses.

Cumacean biodiversity of the circum-Antarctic: the unsung crustacean buffet

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Biography:

Victoria is a master's student at the University of Alaska Anchorage. Initially drawn to gelatinous invertebrates in middle school, she became a cumacean enthusiast after learning about Dr. Sarah Gerken's research as an undergraduate student, and completing a research project to determine if cumaceans contain gut microbes (spoiler: they do!). She is excited to continue her studies in Antarctica, where she hopes to document cumacean biodiversity in the circum-Antarctic!

Outside of academia, Victoria is a ship captain and wilderness guide in Prince William Sound, Alaska. She loves teaching guests about the rich natural history and wildlife in the Sound.

Peracarids are the dominant crustaceans in the stenothermic waters of Antarctica. Cumaceans (Crustacea: Peracarida) are understudied despite their high abundance (up to 31,548/m² in McMurdo Sound) and diversity in Antarctic marine sediment, with 89-91% of species endemic to the region. Antarctica has experienced rapid warming for the last 50 years, with various rates of warming around the continent. Cumaceans play important roles in benthic ecology, including remobilizing carbon from the sediment back into the food web and prey for larger fauna. Cumaceans are weak swimmers and thus are most commonly found where mild currents supply nutrients due to their poor dispersal capabilities. They bury themselves in the surface layer of soft mud and sand, frequently at water depths less than 200 meters.

The main objective of this research is to determine baseline biodiversity of cumaceans in three regions of Antarctica: West Antarctic Peninsula (WAP/ Weddell Sea), East Antarctic, and the Ross Sea. Due to environmental variation in the circum-Antarctic, we expect different species to exhibit varying distributional patterns across the three Antarctic sites. We also expect cryptic speciation to be present and detectable using DNA barcoding to determine unique species in each region. We will use DNA barcoding to determine species distributions and species boundaries, and a sequence alignment and statistical significance score will be assigned based on percent homology.

Due to cumaceans' poor dispersal capabilities, it is expected that DNA sequences will vary among the three sites. However, if cumaceans in the Antarctic region are spreading with the Antarctic Circumpolar Current, we would expect to see less sequence divergence between the sites. This information will be useful for monitoring efforts in future research as the Antarctic region changes, as well as illuminating diversity of an under-appreciated order of crustaceans.

Transcriptomic Analysis and Time to Hatch Visual Prediction of Embryo Development in the Ornate Spiny Lobster (*Panulirus ornatus*)

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Biography:

Associate Professor Tomer Ventura pioneered the application of single gene silencing to induce fully functional sex change in crustaceans. This has wide application for practicing Monosex Population Culture (all-male or all-female), which has tremendous value for the entire aquaculture industry. This is the first application of gene silencing in aquaculture.

Associate Professor Ventura's molecular expertise is vital in translating novel basic scientific results into applicable biotechnologies. He is leading a group dedicated to better understand the molecular mechanism underlying crustacean development and reproduction.

The closed life-cycle culture of tropical spiny lobster, *Panulirus ornatus* conducted at the Institute for Marine and Antarctic studies provides a unique opportunity to study specific developmental stages across embryogenesis. This production provides access to embryos at defined time points, however physical staging is a challenge due to their small size and the environmental factors impacting their development. A transcriptome detailing 11 distinct stages across the 30-day embryonal development period of *P. ornatus* was established as the most in-depth transcriptomic library of embryogenesis in decapods. Key genes were characterised across the 11 stages of embryogenesis. The gastrula-specific genes, nanos and brachyury, presented an expression profile indicating gastrulation occurs in early embryogenesis. The expression of neuropeptides was reported across *P. ornatus* embryos, suggesting they are primarily active during the later stages of embryogenesis as the nervous system develops and the animal prepares to hatch. In addition to the molecular tools used to characterise embryo development, developmental characteristics, such as eye spot development, provide a measurable visual indicator. Hatch prediction models based on visual characteristics were shown to be an accurate prediction method for timing hatch for *P. ornatus* embryos kept at 26°C.

Developing mono-sex technology in red claw crayfish *Cherax quadricarinatus*

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Biography:

Associate Professor Tomer Ventura pioneered the application of single gene silencing to induce fully functional sex change in crustaceans. This has wide application for practicing Monosex Population Culture (all-male or all-female), which has tremendous value for the entire aquaculture industry. This is the first application of gene silencing in aquaculture.

Associate Professor Ventura's molecular expertise is vital in translating novel basic scientific results into applicable biotechnologies. He is leading a group dedicated to better understand the molecular mechanism underlying crustacean development and reproduction.

The Australian red claw crayfish *Cherax quadricarinatus*, an emerging species within the freshwater aquaculture trade, is not only an ideal species for commercial production due to its high fecundity, fast growth, and physiological robustness, but also notoriously invasive. Investigating the reproductive axis of this species has been of great interest to farmers, geneticists and conservationists alike for many decades, however aside from the characterisation of the key masculinising insulin-like androgenic gland hormone (IAG) produced by the male specific androgenic gland (AG), little remains known about this system and the downstream signalling cascade involved. This investigation used RNA interference to silence IAG in adult intersex *C. quadricarinatus* (Cq-IAG), known to be functionally male but genotypically female, successfully inducing sexual redifferentiation in all individuals. To investigate the downstream effects of Cq-IAG knockdown, a comprehensive transcriptomic library was constructed, comprised of three tissues within the male reproductive axis. Several factors known to be involved in the IAG signal transduction pathway, including a receptor, binding factor and additional insulin-like peptide, were found to not be differentially expressed in response to Cq-IAG silencing, suggesting that the phenotypic changes observed may have occurred through post-transcriptional modifications. Many downstream factors displayed differential expression on a transcriptomic level, most notably related to stress, cell repair, apoptosis and cell proliferation. These results suggest that IAG is required for sperm maturation, with necrosis of arrested tissue occurring in its absence. These results and the construction of a transcriptomic library for this species will inform future re-search involving reproductive pathways as well as biotechnological developments in this commercially and ecologically significant species.

From description to transcriptome: The journey of *Eurythenes atacamensis* (Amphipoda) to improve understanding of eco-evolutionary dynamics in the hadal zone

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Biography:

Johanna Weston is an ecologist with a passion for using scavenging amphipods to understand the drivers of biodiversity across the hadal zone. Her doctoral research at Newcastle University led to three contributions, (1) description of four new species and a new genus; (2) ecology of a non-subduction hadal feature; and (3) assessment of global phylogeography between disjunct populations. Currently, as Postdoctoral Scholar at WHOI, she is focused on the timing of hadal colonization and the natural history of other hadal-dwelling crustaceans. She looks forward to the Crustacean Congress to highlight hadal peracarids and leave inspired by the latest crustacean science.

The hadal zone represents hotspots for endemic and undiscovered biodiversity resulting from geographic isolation and environmental selection pressures. The 47 features with depths >6,000 m are shaped by a suite of extrinsic and intrinsic factors making the environment, carbon flux, seismicity, and geomorphology of each feature unique. Among these, the Atacama Trench, paralleling the coastlines of Peru and Chile, is particularly distinctive with eutrophic conditions and relatively geologically recent formation. Multiple sampling efforts of the Atacama Trench between 2009 – 2022 with baited free-fall lander has led to the description of multiple new species, including a snailfish (*Paraliparis selti*), three small *Hirondellea* amphipod species, and a large, visually distinctive *Eurythenes* amphipod. Here, we present the integrative description of *Eurythenes atacamensis* Weston & Espinos-Leal 2021, which paired morphological taxonomy with DNA barcoding to robustly delineate this species. Further, we present a replicated pattern of ontogenetic vertical stratification over its bathymetric range, spanning from 4,974 to 8,081 m and a latitudinal extent of ~500 km. Across the trench axis, only juveniles were present at abyssal depths, and the size of females was unrelated to depth, whereas juveniles followed a sigmoidal relationship with a step-up in size at depths >7,200 m. Finally, we showcase in-progress efforts to apply RNA-seq to compare the transcriptome of *E. atacamensis* with shallow-water relatives to investigate the genetic changes associated with adaptation to the hadal environment. Together, in a short period, *E. atacamensis* has become a model species for hadal science and continues to improve our understanding of the eco-evolutionary dynamics across the deepest marine ecosystem.

Unraveling the social and genetic structure of *Paracerceis* sp., a Puerto Rican sphaeromatid isopod associated with the giant barrel sponge *Xestospongia muta*

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Biography:

Regina was introduced to marine field work in the Sea of Cortez as an undergraduate and fell in love with both invertebrates and exotic places. Her interests range from descriptive taxonomy of isopods and building molecular phylogenies, making museum collections visible, to building barcode libraries to interpret eDNA.

Isopods are morphologically diverse peracarids, comprising 40% of the suborder. They inhabit a diversity of habitats, including coral reefs, forests, caves, deserts, and the deep sea. Most are free-living, others are commensals, and some are endo- or ectoparasites on other invertebrates and fishes. Sphaeromatidae are primarily marine, primarily in shallow water, with about 100 genera and 1,000 described species. In some sphaeromatid genera, males and females are of similar size and morphology, while some exhibit extreme dimorphic morphologies with highly ornamented males. At least six of the thirteen extant species of the genus *Paracerceis* are known natives to the Atlantic-Caribbean region (*P. caudata*, *P. cohenae*, *P. edithae*, *P. glynni*, *P. nuttingi*, and *P. tomentosa*). We provide molecular and behavioral data on what may be a new species of *Paracerceis* associated with the long-lived, charismatic giant barrel sponge, *Xestospongia muta*. Recently generated molecular sequences will be used to infer the phylogenetic relationships between *Paracerceis* sp. and congeners. The sponge *X. muta* provides valuable habitat and key ecological resources for smaller organisms, making it a good candidate for studying the evolution of social behavior. In-situ observations of the *Paracerceis* sp.–*X. muta* social system reveal fascinating behaviors. *Paracerceis* sp. displays ecological and behavioral similarities and differences relative to its congener from the U.S. Pacific coast, *P. sculpta*. We provide preliminary evidence for parental care and overlapping of generations, absent in *P. sculpta*. *Paracerceis* sp. inhabits the external surface (exopinacoderm) of *X. muta*, whereas *P. sculpta* solely uses the spongocoel of the calcarean sponge *Leucandra losangelensis*. We also report on a peculiar inter-specific interaction with ophiuroids. The novel social behavior in this isopod system combined with morphological and genetic data reveals insights into the complex mating system of these sphaeromatid isopods.

The assemblages of deep-sea amphipods off the northeastern coast of Japan, Northwest Pacific Ocean

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Biography:

Daiki Yamamoto is a first-year doctoral student at the University of Tokyo, Graduate School of Frontier Sciences Natural Environmental Studies. He received an integrated Master's degree in MSci Marine Biology, at the University of Southampton, in August 2021. His current research interest includes the deep-sea crustacean, Amphipoda in particular, and their distributions and speciation mechanism in the deep sea.

The deep sea is one of the most biodiverse on earth, but our understanding of the mechanisms responsible for this high diversity, coupled with a lack of taxonomic knowledge (including molecular data), is incomplete. Amphipoda, belonging to the superorder Peracarida, is one of the most abundant taxa in the deep sea. However, studies of accurate bathymetric distribution and compositions exclusive to deep-sea amphipods are still limited, with efforts biased towards necrophagous taxa (e.g., Lysianassoidea).

Understanding the bathymetric distribution of benthic deep-sea amphipods, which often exhibit higher habitat specificity and more limited dispersion than benthopelagic necrophagous amphipods, enables the testing of hypotheses to explain mechanisms producing high biodiversity in this ecosystem. The present study provides a preliminary insight into deep-sea amphipod assemblages off northeastern Japan, covering bathyal to hadal depths. The assemblage data are complemented with phylogenetic analyses, attempting to explore the speciation in the deep sea.

Since 2012, around the landward slope of the Japan Trench, intense sampling has been conducted in the depth range of 237 m to 7,653 m. Across 40 stations, over 6,000 specimens were collected using a beam trawl equipped with a plankton net. Specimens were classified using morphological features, with the aid of DNA barcoding. 33 families have been identified so far, dominated by not only the groups of superfamily Lysianassoidea and families Ampeliscidae and Phoxocephalidae, which together constitute 60% of the collected samples. Amphipods exhibiting both epibenthic and benthopelagic lifestyles (e.g., Oedicerotidae, Eusiridae, and Synopiidae) were also recorded but not as common as endobenthic taxa. Our study also shows a change in the dominant families with depth. Furthermore, we look to discuss the result of phylogenetic analyses, to deepen our understanding of bathymetric distribution and speciation patterns in benthic crustaceans.

Mapping of morphological characters of spermatophores and spermatozoa of spider crabs *Libinia* Leach, 1815 (Majoidea, Epialtidae) in a phylogenetic context

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Biography:

Ahead of the Invertebrate Morphology Laboratory and Electron microscopy laboratory of UNESP, Jaboticabal. My interest is in decapod reproductive system morphology and evolution, focusing on spermatozoa ultrastructure, sperm transfer, sperm competition and ovarian development.

Libinia is a monophyletic genus that belongs to family Epialtidae and subfamily Pisinae; it composed by 10 valid species, distributed in both Eastern Pacific and Western Atlantic. Spermatophores and spermatozoa ultrastructure have been successful used in solve decapod decapods' taxonomic and phylogenetic hypotheses. There are few studies with epialtid crabs that described the morphology of spermatophores and sperm, which do not allow deeper speculation about the phylogenetic relationships among species using these reproductive characters. We proposed a comparative approach of the ultrastructural morphology of spermatophores and sperm of some representatives of *Libinia* and other epialtid crabs. Phylogenetic trees obtained through the Maximum Likelihood from multi DNA sequences (16S rDNA, 12S rRNA and COI) concatenated suggested that *Libinia* is monophyletic. Spermatophore morphology among *Libinia* species and congeners was similar, being rounded or elliptical with thick walls of granular appearance, they store a variable number of spermatozoa. The ultrastructural characteristics of the spermatozoa followed the pattern found for Majoidea, but with many particularities in comparison with other congeners. The spermatophore morphology, albeit with subtle differences, was not informative to use as taxonomic characters; while the perforatorial chamber and the acrosome vesicle were variable and showed differences between species. Thus, the spermiotaxonomy of *Libinia dubia*, *L. emarginata*, *L. ferreirae*, *L. spinosa*, *Stenocionops spinosissimus* and *Macrocoeloma trispinosum*, corroborated previous morphological and molecular evidence.

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Comparative spermatophore and spermatozoa ultrastructure in an Heterotremata clade (Brachyura): The evolution of characters and their phylogenetic placement

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Biography:

Ahead of the Invertebrate Morphology Laboratory and Electron microscopy laboratory of UNESP, Jaboticabal. My interest is in decapod reproductive system morphology and evolution, focusing on spermatozoa ultrastructure, sperm transfer, sperm competition and ovarian development.

Recent phylogenetic studies revealed close relationships between several families of heterotrem crabs. In this context, we describe the ultrastructure of spermatozoa of species of the Aethridae, Menippidae, Calappidae, Parthenopidae, Cancridae and, Leucosiidae to elucidate the phylogenetic placement among taxa and the evolution of spermatozoa's characters. The vasa deferentia were submitted to routine protocols for transmission electron microscopy. The spermatophore in all Heterotremata studied here have a clear wall or pellicle and are basically round shaped. Our spermatozoa results showed that the presence of acrosome ray zone as a honey-comb structure appear to be a synapomorphy to these closely related families and parallel rays is a homoplasy occurring in Portunidae and the rest of the paraphyletic Heterotremata clade. The striation of the subopercular material is also a synapomorphic character for these families while the absence is a homoplastic trait and apomorphic to Parthenopidae and Cancridae. Moreover, our results indicate a sharing of certain traits with Aethridae and Portunidae in the spermatozoa morphology of Menippe nodifrons. In Cancridae and Parthenopidae, the perforated operculum is a homoplastic character while the perforatorial chamber crossing the operculum is the main synapomorphy of Cancridae. In Calappidae and Portunidae, the absence of the inner acrosome layer is an apomorphy. The presence of a thin, two-layered, broad operculum filled with a granular matrix is a synapomorphy of the Parthenopidae. Finally, in Leucosiidae, the inner layer positioned at the equator of the acrosome vesicle and the presence of a particular type of periopercular rim are a synapomorphy of the group. Overall, our results corroborate with recent and more complete phylogenetic analyses carried out with this Heterotremata clade and demonstrate that spermatozoa ultrastructure is a powerful tool to be used in phylogenetic studies.

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Spermatozoa ultrastructure in Varunidae crabs (Thoracotremata)

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Biography:

Ahead of the Invertebrate Morphology Laboratory and Electron Microscopy Laboratory of UNESP, Jaboticabal. My interest is in decapod reproductive system morphology and evolution, focusing on spermatozoa ultrastructure, sperm transfer, sperm competition, and ovarian development.

Here we described the spermatozoa ultrastructure of the Brazilian Varunidae crabs *Cyclograpsus integer*, *Cyrtograpsus angulatus*, and *Neohelice granulata*, compared to other varunids from literature focusing on the family apomorphies. The vasa deferentia were fixed and processed to transmission electron microscopy. Varunidae spermatozoa are characterized by a spherical acrosome, showing three concentric zones: inner, outer, and peripheral. All species share the absence of the apical button, periopercular rim, accessory opercular ring and xanthid ring. All varunids also show the thickened ring. The perforatorial chamber is deltoid for all species, being narrow to *C. integer* and *C. angulatus* and very deeply deltoid in *N. granulata*. The apex of the perforatorial chamber is a variable characteristic among the species, with *C. integer* showing a pointed and rounded apex protruding from the perforated operculum. In *C. angulatus* and *N. granulata*, the perforatorial chamber apex is round and wide and only reaches the operculum. The peripheral margin of the operculum is thick in *C. integer* and *N. granulata* and thin in *C. angulatus*. The specific differences compared with other varunids from the literature were the margin of the operculum that is thin and curved in *Eriocheir japonicus* and *Varuna literata*. In contrast to *V. literata*, the inner acrosome zone is straight instead of rounded. The spermatozoal ultrastructure supports the Thoracotremata grouping and the phylogenetical position of Varunidae, demonstrating that spermatozoa ultrastructure or spermiotaxonomy reflects the molecular phylogenies. In conclusion, the main characteristic found in Varunidae is the absence of an apical button on the perforated operculum. The apical button is considered a plesiomorphic character to all Thoracotremata and seems lost in Varunidae.

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