ICC IX

WASHINGTON, DC, USA

MAY 22-25, 2018

9th International Crustacean Congress

ABSTRACT BOOK

Unraveling Unresloved Taxonomy in a World of Invaders: Delimiting the Lysmata Vittata Species Complex in Light of a Recent North American Introduction

Aguilar R, Baeza JAlop0, Sanjeevi P, MacDonald KS, Driskell AC, Almeida AO, Cunha A, Leray M, Ogburn MB, Hines AH
Smithsonian Environmental Research Center, Clemson University, NMNH, Federal University of Pernambuco, Naos Island Laboratories

Invasive species pose a significant threat to global biodiversity, ecosystem function, economic stability, and human health. Predicting and mitigating their potential ecological and economic impacts is often complicated by uncertainly surrounding the systematics and ecology of many introduced and native marine taxa. DNA barcoding, especially when incorporated in an integrative taxonomic framework (e.g., also including morphological, ecological, or other data) is an extremely powerful tool in delineating phenotypically similar species. In 2013, an unknown peppermint shrimp, tentatively identified as Lysmata vittata Stimpson 1860, native to the Indo-West Pacific, appeared in Chesapeake Bay and surrounding coastal areas. However, preliminary analyses indicated that L. vittata is a species complex, with the status of the junior synonym L. rauli Laubenheimer and Rhyne 2010, described from Brazil (but native to the Indo-West pacific), in question. These taxonomic uncertainties were further complicated by the destruction of Stimpon's L. vittata type material and brief species description. In the present study, we employed an integrative taxonomic approach to delimit the putative L. vittata species complex, incorporating US L. vittata, Brazilian L. rauli, Indo-Pacific museum specimens, and publicly available genetic data. After designating a neotype for L. vittata, we posit that US individuals represent L. vittata sensu stricto and L. rauli should be elevated to full species status, with evidence that L. rauli may represent a complex of sibling species.

First Report of Morphological Anomaly in Deep-Sea Shrimps of the Genus Glyphocrangon a. Milne-Edwards For the Atlantic Ocean

Alves-Junior FA, Araujo MSLC, Souza-Filho JF*
Universidade Federal de Pernambuco

Morphological malformation is a type of anomaly resulting from an abnormal development in animal ontogeny. In marine environmental, especially in crustaceans, these anomalies are related primarily to genetic factors, predation or due to pollution, but these changes have not been previously reported for carideans shrimps of the genus Glyphocrangon A. Milne-Edwards, 1881. In this paper, we report morphological abnormality for deep-sea shrimps of the species Glyphocrangon aculeata Milne Edwards, 1881. The samplings were carried out in Potiguar Basin between the States of Rio Grande do Norte e Ceará, both located in the Northeast of Brazil, aboard R/V Luke Thomas and R/V Seward Johnson in 2009 and 2011 respectively, through of bottom trawls of an approximately 30 minutes duration were conducted on the continental slope along the isobaths of 400 m, 1.000 m and 2.000 m, using a semi-balloon otter trawl with 50 mm mesh size and 18 m opening. Only one ovigerous female collected at 1074 m of depth was registered with abnormalities in some regions of the carapace as: rostrum reaching only 2/3 of the scaphocerite length, absence of antennal spine; abdomen with carinae less pronounced and telson short, strongly recurved and not exceeding uropods tip. Those characteristics indicates that, besides possible physical damage on the animal's body, genetics alterations or nutritional deficiencies indicators, might be associated with these morphological variations observed in the anomalous exemplary.

First Report of the Ectoparasitic Isopod, Holophryxus acanthephyrae Stephensen, 1912 (Cymothoida: Dajidae) in the South Atlantic, from a New Host, the Deep-Sea Shrimp, Acanthephyra acanthitelsonis Spence Bate, 1888

Alves-Junior FA, Bertrand A, Araujo MSLC, Paiva RJC, Souza-Filho JF*
Universidade Federal de Pernambuco

The crustacean family of isopods, Dajidae, comprises 18 genera containing 54 species with widespread distribution. The species of this family are ectoparasites, especially on euphausiids, mysids and shrimps. The species of Holophryxus acanthephyrae has a life cycle involving a first intermediate host (copepod) and a definitive host (shrimp), and adheres particularly on deep-sea shrimps of genus Acanthephyra. Here, we make the first report of dajid isopod Holophryxus acanthephyrae from Brazilian waters (South Atlantic) and the first occurrence as parasite on deep-sea shrimp Acanthephyra acanthitelsonis. The specimen was collected under the framework of the project "ABRACOS 2" (Acoustic along the BRazilian COast), on board of R/V Antea in April 2017, using a micronekton net (mesh size of 10 mm) in Rocas Atoll, with stations between 40–1660 m depth. The specimen female of H. acanthephyrae was found in pelagic zone in Rocas Atoll, at 630 m depth, at water mass South Atlantic Central Water (SACW) with temperature of 4.8 °C, adhered on postero-dorsal margin of the carapace of the deep-sea shrimp A. acanthitelsonis. Thus, this work updates the record of H. acanthephyrae with the first observation in Brazilian waters. Also we provide the first observation of parasitism on A. acanthitelsonis, raising the knowledge on Dajidae family, their host range, and on deeper waters studies in Brazil.

Preservation of Cuticle of Protaxius isochela Woodward (Axiidea, Axiidae) from the Agrio Formation (Lower Cretaceous), Neuquén Basin, West-Central Argentina

Andrada AM, Lazo DG, Bressan GS
Universidad de Buenos Aires, Instituto de Estudios inos "Don Pablo Groeber" (IDEAN, UBA-CONICET)

The cuticle of four specimens of Protaxius isochela Woodward (Axiidea, Axiidae) contained in ellipsoidal carbonate concretions was studied with the objective of knowing its composition and ultrastructure. They come from a thin interval of fine sandstones of the marine mixed platform of the Agrio Formation (early Hauterivian). SEM and EDS analysis were performed on two of the specimens, showing an outer smooth surface and revealing presence of massive calcium phosphate, while the composition of the inner part of the propodus was calcium carbonate and isolated small pyrite crystals were observed. Thin sections of the two other concretions exposed different parts of two specimens in cross section. Lamination of the epicuticle and exocuticle could not be identified, while lamination of the endocuticle was clearly observed. Phosphate and calcium carbonate are established in irregular layers without a defined pattern. Phosphate layers can disappear laterally being replaced by calcium carbonate layers. Cuticle preservation probably included immediate post-mortem phosphatization of the cuticle, then shallow entombment of the specimens closing the phosphatization window, anaerobic decay and pyrite precipitation, and finally precipitation of abundant carbonate cement around the specimens. These processes occurred in the early diagenesis, in different microenvironments generated inside the specimens during decay and early burial. The lamination preserved in the endocuticle and the presence of pyrite crystals indicate that the studied specimens were probably carcasses remains and not moults, whose preservation were enhaced by early diagenetic processes and early burial. This is contribution R-249 of IDEAN.

Diversity of Decapod Crustaceans from Streams of Brazilian Cerrado, State of Maranhão

Andrade KSP, Araujo MSLC, Nunes JLS*
Universidade Federal do Maranhão, Universidade de Pernambuco, Universidade Federal do Maranhão

The fauna of freshwater crustaceans is widely distributed in Brazil, being dominated by crabs of the family Trichodactylidae H. Milne-Edwards, 1853 and the prawns of the genus Macrobrachium Bate, 1868 of the Palaemonidae family. The State of Maranhão does not have enough studies on freshwater crustaceans, thus, this is the first study to provide an update on the knowledge of the genus Macrobrachium and the family Trichodactylidae for the eastern region of Maranhão. Eight streams of the East of Maranhão were sampled with hand nets, sieves and trawl, passed in the bottom and submerged marginal vegetation for a period of 20 minutes in a stretch of 150m. A total of 526 specimens of shrimp were collected in five species: Macrobrachium amazonicum (Heller, 1862) (N = 119), M. acanthurus (Wiegmann, 1836) (N = 116), M. carcinus (Linnaeus, 1758) (N = 01), M. jelskii (Miers, 1877) (N = 235) and M. olfersii (Wiegmann, 1836) (N = 55). We also registered 22 specimens of Trichodactylidae crabs, distributed in four genera and four species: Goyazana castelnaui (H. Milne-Edwards, 1853) (N = 6), Dilocarcinus septemdententatus (Herbst, 1783) (N = 11), Sylviocarcinus pictus H. Milne-Edwards, 1853) (N = 3) and Valdivia serrata White, 1847 (N = 2). The species M. carcinus and M. olfersii were registered for the first time in the State, increasing the number of species of freshwater prawns in Maranhão, from four to six species. We have also developed an identification key of the genus Macrobrachium for the State.

Relative Growth of Swimming Crabs (Portunidae) from Potiguar Basin, Brazilian Northeast

Araujo MSLC, Silva ES
Universidade de Pernambuco

This work analyzed the relative growth of swimming crabs in the Potiguar basin, in the Northeast of Brazil. The material was collected in the months of May and November of 2003 and May and June of 2004. Measurements were taken for carapace width (CW), carapace length (CL), abdomen width (AW) in females and chelipod length (CLH) in males, considering CW as an independent variable. A total of 510 specimens were collected, being 176 Callinectes ornatus, 154 Achelous ordwayi, 64 Portunus anceps, 63 A. tumidulus, and 35 A. gibbesii. For C. ornatus, positive allometric growth was observed for CW x CL, in males and females, and for CW x AW and CW x CLH. For A. ordwayi, negative allometric growth was observed for CW x CL, in males and females, but with positive allometric growth for CW x AW and CW x CLH. For P. anceps, negative allometric growth was observed for CW x CL, in males and females, but with positive allometric growth for CW x AW and CW x CLH. For A. tumidulus, positive allometric growth was observed for CW x CL in males and allometric negative growth for CW x CL in females, but with positive allometric growth for CW x AW and CW x CLH. For A. gibbesii allometric positive growth was observed for CW x CL in males and females, and for CW x AW and CW x CLH. The present results provide additional information on the biometry and growth of Portunid crabs.

Climate Change Scenarios Effects on a Coral Reef Peracarid Community

Araújo-Silva CL, Santos PJP
Federal University of Pernambuco

This study aimed to test experimentally the effects of three different climate change scenarios on the structure of macrofaunal peracarid community. Samples were taken from artificial substrate units (ASUs), colonized by macrofauna from the coral reef subtidal zone of Serrambi beach (Brazil). In the laboratory, the ASUs were exposed to control (Ctrl) treatment and three climate change scenarios (Sc.) (increase of T° [0.6, 2, and 3° C], pH drop [0.1, 0.3, and 0.7 units]), and collected after 15 and 29 d of exposure. Peracarids showed significant sensitivity in the first 15 d of exposure in Sc. III. Scenario III together with Sc. II changed significantly the community after 29 d. Compared to control treatments, Amphipoda presented higher density in the less severe scenario (Sc. I) after 15 d but was negatively affected by scenarios II and III on both times. Tanaidacea also increases when exposed to Sc. I but contrarily to Amphipoda remained with higher density even after 29 d. Isopoda and Cumacea responded negatively to all scenarios. SIMPER analyses showed that dissimilarities were greatest between Ctrl and Sc. III, particularly after 29 d. Elasmopus longipropodus and Condrochelia dubia greatly contributed to these dissimilarities. These outcomes highlight the importance to study the climate change effects for benthic peracarids, especially to those that incubate their eggs. This characteristic decreases migration potential and hence could reduce ability to disperse as a response to a changing environment.

Cracking the Genetic Code of the Blue Crab, Callinectes sapidus

Bachvaroff TR, Plough LP, Decre BE, Chung JS
University of Maryland Center for Environmental Science, University of Maryland Baltimore County

Callinectes sapidus or the blue crab, is an economically and ecologically important species in the Atlantic Ocean and its estuaries. To better understand the biology, the mechanisms regulating growth and reproduction, and population diversity, we have begun to sequence the genome of C. sapidus, which is estimated at a haploid size of 2 billion bases. The sequencing approach was to generate high ~100 fold coverage using Illumina HiSeq, followed by ~10 fold coverage PacBio sequencing. This preliminary assembly will then be used for generating a linkage map and further scaffolding with HiC. In addition we have ~500 million Illumina RNAseq reads from various tissues using that were assembled into a transcriptome dataset using Trinity. The preliminary draft genome was assembled using the MASurCA software pipeline and contains 800 million bases in 12,000 scaffolds greater than 10kb. We will present results of transcript and repeat mapping to the preliminary assembly.

Diversification in the Caribbean Sea: Insights from Molecular Phylogenetics and Cryptic Species Delimitation Analyses in the Shrimp Genus Lysmata

Baeza JA, Sanjeevi P
Clemson University

The Caribbean Sea (CS) harbors a large proportion of species in the Neotropics. One outstanding yet poorly explored question is whether or not the CS is a 'cradle' or a 'museum.' If a cradle, speciation events should be observed in phylogenetic trees depicting the genealogy of related species ~3.1 mya after final closure of the Isthmus of Panama that resulted in the complete separation of the CS from the tropical eastern Pacific. If the CS is a museum, no such speciation events should be observed in phylogenetic trees. In this study, we developed molecular phylogenetic hypotheses for the genus Lysmata and studied the phylogeography of selected species. Diversification analyses revealed speciation events occurring earlier than 3.1 mya, supporting the notion that the CS acts as a cradle in the genus Lysmata. Additional phylogeographic studies in Lysmata wurdemanni revealed this shrimp to be a complex of cryptic species featuring no morphological disparity but considerable genetic distinctiveness. Species delimitations analyses demonstrated five cryptic species in L. wurdemanni: one of them restricted to the Virginian biogeographic province, two restricted to the western Atlantic Carolinian province and northern Caribbean province south of Cape Canaveral, and two restricted to the Gulf of Mexico (one species west and other east of the Mississippi river). These analyses also argue in favor of the notion that the CS is a cradle, with diversification taking place in peripheral areas. Landscape genetic studies are needed to continue improving our understanding of those processes driving diversity in the Caribbean province.

Sex (Phase) Ratio in Protandric Simultaneous Hermaphrodites (Caridea: Lysmatidae: Lysmata)

Baeza JA
Clemson University

Sex allocation theory (SAT) is one of the most successful subfields of evolutionary biology. SAT predicts the optimal sex ratio in gonochoric (separate sexes), protandric (male first), and protogynous hermaphrodites (female first). SAT also predicts the optimal sex allocation of strict simultaneous hermaphrodites. Importantly, no mathematical models predicting the optimal sex phase ratio (SPR) of protandric simultaneous hermaphrodites (PSHs) exist. In PSHs, individuals consistently mature and reproduce initially as males to become functional simultaneous hermaphrodites later in life. In this study, I first introduce a basic graphical+mathematical model predicting that SPR in PSHs should be skewed towards hermaphrodites. I used as a model system PSHs shrimps in the genus Lysmata to test this prediction. Empirical data does not support the theoretical expectation. First, the proportion of species with hermaphrodite-skewed SPRs (estimated during the main reproductive season) was not greater than expected by chance alone. Second, considerable temporal SPR variability was observed in some PSHs. For instance, in L. wurdemanni, the population was dominated by relatively small hermaphrodites during the peak reproductive season (Spring and Summer) but males dominated the population right before and after this main reproductive season. Our study suggest that SPR in PSHs is a highly labile population-level trait affected by environmental, including social, conditions.

The Private Sex Life of Symbiotic Decapod Crustaceans: Model Systems in Behavioral Ecology

Baeza JA
Clemson University

A symbiotic lifestyle is one of the most important environmental adaptations in decapod crustaceans. These symbiotic associations most often comprise small decapods and other much larger invertebrate partners that serve as hosts. Studies conducted during the last decades in symbiotic decapods have revealed most impressive morphologies, colorations, reproductive strategies, and social interactions. In this talk, I provide an overview of the mating system of selected representatives from major decapod crustacean clades that have adopted a symbiotic lifestyle. A literature review reveals five different mating system in decapod symbiotic decapod crustaceans: Social monogamy, Host-defense polygyny, Female-centered polygyny, Pure search polygynandry of mobile females, and Pure search polygynandry of sedentary females. I also compare the mating system of symbiotic species to that of their closest free-living relatives to reveal behavioral adaptations to the symbiotic mode of life. The comparative approach above suggests that the mating system of symbiotic crustaceans is mostly determined by a combination of host intrinsic characteristics, i.e., host relative size and abundance, and extrinsic environmental conditions, i.e., predation risk off hosts. Life history and experimental studies are needed to formally test the relative importance of intrinsic and extrinsic host characteristics in driving the mating system of symbiotic crustaceans.

Historical Demography in the Reef-Dwelling Caribbean Spiny Lobster Panulirus argus Revealed Using Ngs

Baeza JA
Clemson University

The Caribbean spiny lobster Panulirus argus is a keystone species in shallow water coral reefs and target of the most lucrative fishery in the Caribbean sea. We explored historical demography in P. argus using genotype-by-sequencing derived SNPs. We expected an increase in population size of P. argus from Florida, USA starting about 21,000 years ago, after the Last Glacial Maximum, when ice sheets started to retreat and subtropical shallow coastal waters warmed up. A total of 10 lobsters were collected from Alligator Reef, Florida Keys, Florida, USA. One microgram of gDNA extracted from each specimen was used for RAD library construction using established protocols. A panel of 1542 SNPs was obtained after interrogation of RAD-tags. This panel was then used to calculate a site frequency spectrum (SFS). The observed SFS for the Florida population of P. argus exhibited a non-normal distribution peaking at singleton SNPs. Three different demographic models (constant, exponential growth, and exponential growth after bottleneck) were tested within a model selection approach in the software dadi. Results indicated that lobsters most likely suffered a population bottleneck in the distant pass before experienced population expansion. In disagreement with expectations, population expansion started much later than 21,000 years ago. Studies exploring population connectivity and population-specific demographic history of the Caribbean spiny lobster P. argus are underway. Fisheries and conservation studies are expected to profit from the evaluation of genomic and population variability in this species using demographic models, as shown here.

Evidence of Contamination in Ucides cordatus at a Southern Brazil Mangrove

Baptista-Metri C, Costa-Junior FM, Roveda LF, Metri R
Colegiado de Ciências Biológicas, Universidade Estadual do Paraná, Rua Comendador Correia Junior, Curso de Ciências Biológicas

Landing crabs as Ucides cordatus are important socioeconomic in Brazil, and their populations are being affected by the environmental impact caused by the contamination of mangroves. The present study aims to evaluate the population and the presence of contaminants determined by metallic ions in a southern estuary of Brazil. Samples were taken in 3 mangroves at different antropogenic influence in Paranaguá Bay, southern Brazil: Palmito State Forest (formally conserved), Rio da Vila (polluted), and Rio Pequeno (recently formally conserved). For 40 individuals we measured: carapace width, length and height, abdomen width and length, height and thickness of the larger chaela, and wet weight. The concentration of Cd, Cr, Cu, Mn, Pb e Zn was obtained by ICP-AES. The mean size of the males presented differences between mangroves (FLC = 69.7 mm for Palmito State Forest individuals, 69.5 mm for Rio da Vila and 70.6 mm for Rio Pequeno; FP = 150,6 g for Palmito State Forest, 155,6 g for Rio da Vila and 155,3 g). The weight and width of carapace ratio obtained were also different for the mangroves indicating isometric growth for specimens from Palmito State Forest and from Rio Pequeno, and allometric negative for the Rio da Vila. Concentrations of chromium and zinc have exceeded the limits allowed by legislation, and must be affecting the crabs fitness. This work demonstrates the need to study the characteristics of the uçá crab population, to evaluate the quality and development of mangroves, since it has an important role for society.

Ecology of Sympagurus Pictus Smith 1883 in the Southern Gulf of Mexico

Barbosa-Nieto B, Gracia A, Vázquez-Bader AR*
Instituto de Ciencias del Mar y Limnología

The distribution and abundance of the pagurid S. pictus in the Mexican continental slope (300-1200 m depth) of the Gulf of Mexico (Tamaulipas-Yucatán) was analyzed through seven cruises carried in 2009-2017. Sampling was conducted on board the R/V JUSTO SIERRA of the Universidad Nacional Autónoma de México using a semi-commercial shrimp trawling net with a 18 m mouth and 4.5 cm mesh. S. pictus was found along the whole gulf in a bathymetric range of 313-813 am depth and temperature range of 7-10 °C with highest abundance during summer. Size range was 3.6-17.8 shell width and 3.1-15.7 shell length. Sex ratio during summer was 1:1 but varied in other seasons. Sex distribution presented a different pattern. Ovigerous females were mainly collected in a 400-600 m depth range in different seasons, suggesting a protacted spawning period with a peak in spring. Smallest ovigerous female found was 8.5 mm SW. Fecundity varied between 21-4630 eggs. Fecundity showed a high variation with body weight, although a significant relationship was presented ($P< 0.05$). Fecundity and female condition factor showed a linear relationship with less data dispersion.

The Reproductive Cycle of the Norway Lobster Nephrops norvegicus: Ovary Maturation and Staging Scales

Becker C, Cunningham EM
Queen's University Belfast

Sustainable management of crustaceans relies on knowledge of the reproductive cycle in exploited species. Maturity scales for female Norway Lobster, Nephrops norvegicus, have been subject to a series of changes and various scales are in use in different fisheries regions. To date, a unified, evidence-based scale has not been established. We have reviewed previous staging scales and propose a revised scale based on macroscopic and microscopic characteristics. In order to provide better-informed tools for future stock assessment, female stages were characterised through external observation on ovary colour, size and extension, and the progress of vitellogenesis in maturing oocytes. Our study clarifies several biological phases and reveals an alternative pathway in the reproductive cycle in females that resorb their ovaries instead of spawning. We demonstrate how to distinguish between immature ovaries in juvenile females versus the earliest ovary maturation stage in adults. The new scale also differentiates between "mottled" ovaries seen in two separate biological stages: the spent ovaries which undergo partial resorption in berried females, versus ovaries of females which fail to spawn, skip one reproductive cycle and undergo full resorption. To ensure consistent application, colours are assessed relative to international standards (RAL/Pantone). This new, practical staging scheme clarifies the correlation between microscopic characteristics and macroscopically observable details in gonad colour, size and texture. The proposed staging scale has the potential to improve the resolution of maturity analyses and identify a potentially reduced reproductive capacity of stocks in future demographic studies when females are observed to resorb their ovaries. This study was funded by Seafish (UK) and Kilkeel/Whitby Seafoods (UK) (grant number SR-7941610).

Age Determination of Decapod Crustaceans - Do Gastric Teeth Form Annual Growth Rings as a Record of Chronological Age?

Becker C, Dick JTA, Cunningham EM, Sigwart JD
Queen's University Belfast

The growth of crustaceans is fundamentally different from the continuous growth of most animals. Being cast in an exoskeleton, crustaceans grow episodically and only increase in size at the moult. In other animals, e.g. fish and bivalves, accretionary growth under fluctuating environmental conditions can become manifested as annual rings in hard structures, which are used to determine age. Crustaceans have been supposed to loose skeletal elements when they moult; however, an anatomical approach using the strongly calcified cuticle of gastric mill ossicles, was proposed in 2011. Cuticle bands are herein interpreted as annual growth rings since their number increases with body size and correlates with size-based age estimates. Since its first publication, this cuticle method has raised hope that the conundrum of aging crustaceans is finally resolved. We studied gastric mill ossicles with light microscopy, micro-computed-tomography and cryo-scanning electron microscopy, and followed their dynamics through the moult cycle. Our results confirm the presence of cuticle bands in ossicles; however, those were of low readability. The number of bands increased with body size, but varied in different structures of the same specimen. Moulting experiments and the comparison of intermoult versus recently moulted specimens and exuvia, revealed that ossicles are not retained. Histological sections of the gastric mill close to moulting further confirmed the complete loss and reformation of the banded cuticle at ecdysis. Our findings conflict with the idea that gastric mill ossicles accumulate annual growth rings and challenge their utility for crustacean age determination. This study was funded by Seafish (UK) and Kilkeel/Whitby Seafoods (UK) (grant number SR-7941610).

Performance of Amphipod Mesograzers - Direct and Indirect Effects

Beermann J, Boos K, Gutow L, Boersma M, Peralta AC
Helmholtz Centre for Polar Marine Research, University of Bremen, Simon Bolivar University

Predator presence can have non-consumptive effects on prey species, potentially influencing their interspecific interactions and thus the structure of entire assemblages. The performance of potential prey species may therefore depend on both the presence of predators and competitors. Small invertebrate herbivores ('mesograzers') often live in close association with seaweeds and many species select their habitat for the shelter it provides from predation. Here, we studied habitat use and food consumption of a marine mesograzing crustacean, the amphipod Echinogammarus marinus, in the presence/absence of a fish mesopredator, the sea scorpion Taurulus bubalis and an amphipod competitor (Gammarus locusta). The presence of the predator affected both habitat choice and food consumption of the amphipods, indicating a trade-off between the use of predator-free space and food acquisition. Without the predator, individuals were equally distributed over different microhabitats, but in the presence of the predator, most animals hid under a provided shelter and reduced their food consumption. Additionally, habitat choice of the amphipods changed in the presence of the competitor, also resulting in reduced feeding rates. The behaviour of E. marinus is apparently driven by trait-mediated direct and indirect effects caused by the interplay of predator avoidance and competition. This highlights the strong non-consumptive impacts of mesopredators on amphipod prey. The flexible responses of small crustacean consumers to the combined effects of predation and competition may substantially sculpt the structure of coastal ecosystems and the multiple species interactions therein.

Impact of Acanthocephalan Parasitism on the Fecundity of the Pacific Mole Crab, Emerita analoga

Bhaduri RN, Yamaguchi T, Munguia K, Sandhu R
California State University Stanislaus

Parasites may influence their hosts in multiple ways, ranging from physiological changes and behavioral modifications to altering certain life history traits, like fecundity, in their host populations. The acanthocephalan parasite, Profilicollis altmani, commonly infects the Pacific mole crab, Emerita analoga; yet, this parasite's effect on the crab's fecundity is unknown. Consequently, we examined the effects of parasitism on various aspects of fecundity of this mole crab species. Crabs were collected from the swash intertidal zone in Monterey Bay, California, in September 2017. We recorded crab's body size, egg-bearing status, egg developmental stage, parasite prevalence and infection intensity, parasite volume, and crab dry mass. To quantify fecundity, eggs from gravid crabs were carefully removed, counted and weighed. Of the 124 crabs examined, 94 (75.8%) were gravid and 30 (24.2%) were non-gravid. Parasite prevalence was 86.2% in gravid and 73.3% in non-gravid crabs. There was a significant positive relationship between parasite intensity and host body size, indicating that the acanthocephalan did not affect growth or survival of their crab host. Egg mass was unaffected by both infection intensity and mean cystacanth volume. No significant differences were noted when egg mass between uninfected and infected crabs were compared. Similarly, no significant difference was documented between different developmental stages in uninfected and infected gravid crabs. Our study suggests that the fecundity of E. analoga remains mostly unaffected by P. altmani.

Copepod Phylogeny and Systematics: the Current State and Future Directions

Bernot JP, Boxshall GA, Crandall KA
George Washington University, London Natural History Museum

The goals of this project are to summarize existing phylogenetic data on copepods, describe newly discovered parasitic copepod diversity, and develop new molecular markers for high-throughput approaches to copepod phylogenetics. To establish a preliminary phylogenetic framework for copepods, we completed a literature review of all interspecific molecular phylogenic studies of copepods. We added these studies to The Open Tree of Life and used the propinquity pipeline (Redelings & Holder 2017) to combine phylogenetic data on nearly 400 copepod species from 24 studies with taxonomic data on 11,000 copepod species from WoRMS. By combining the WoRMS taxonomy with previous phylogenetic studies through the OpenTree synthesis platform, we estimated a phylogeny of all copepods. Based on our resulting synthesis tree, only 3% of described copepods have been included in phylogenetic studies. To better understand the evolutionary relationships among copepods, a scalable approach is needed to efficiently generate sequence data across 11,000+ copepod species. To take advantage of the scalability of NGS, we are developing an ortholog set for a target capture approach to copepod phylogenetics using publicly available copepod genomes and transcriptomes to identify orthologous protein coding genes. Our initial comparison of two copepod genomes identified over 500 protein coding loci from 200–1,000bp each. We are using additional transcriptomes to validate our initial genomic orthologs and develop a more robust set of loci for efficient capture across copepods and related crustaceans. Once completed, we hope to accumulate data from a wide range of copepod taxa to generate a robust phylogenetic estimate for the Copepoda. With the resulting tree, we will take an in-depth look at the evolution of parasitism in this diverse group of crustaceans.

Multi-Locus Phylogenetic Analysis of Amphipoda Provides Insight Into the Evolution of the Pelagic Suborder Hyperiidea

Biancani LM, Osborn KJ, Cummings MP
Museum of Natural History, University of Maryland, College Park

Hyperiidea (Peracarida; Amphipoda) is an abundant and diverse suborder of amphipod crustaceans. No common morphological synapomorphy unites approximately 350 described species. Instead, hyperiid amphipods are defined only by an exclusively pelagic existence. Like many midwater animals, hyperiids possess a wide range of unique adaptations, including a vast array of visual strategies. Understanding these adaptations requires an accurate phylogenetic hypothesis onto which patterns of ecology and functional morphology can be mapped. Previous morphological and molecular analyses have led to uncertainty in the monophyly of hyperiids and their relationship to other amphipods, raising the possibility of convergent evolution of pelagic lifestyles in multiple amphipod lineages. Here we present results of a multi-gene phylogenetic analysis of a curated set of available amphipod sequences for 3 nuclear (18S, 28S, and H3) and 2 mitochondrial loci (COI and 16S). This is the largest analysis, to date, aimed at addressing the question of hyperiid monophyly and includes approximately 500 amphipod genera, 40 or which are hyperiids. Preliminary results support the monophyly of suborder Hyperiidea as well as monophyletic hyperiid infraorders Physosomata and Physocephalata (with enigmatic genera Cystisoma and Paraphronima included in Physosomata). We also find evidence of a potential sister relationship between hyperiids and several small, benthic, commensal amphipods including the genera Leucothoe, Anamixis, Paranamixis, Colomastix and Amphilochus. These taxa have not previously been considered close hyperiid relatives and this outcome may illuminate the phylogenetic placement of Hyperiidea within Amphipoda. These results are being used to inform taxon sampling for an ongoing transcriptome-based phylogenomic study.

A New Family of Tanaidacea (Tanaidomorpha) from the Deep-Sea

Błażewicz M, Jóźwiak P, Frutos I
University of Łódź, University of Hamburg

Although there have been years of intensive studies focused on better understanding the systematics of the Tanaidomorpha, it is still not fully resolved. This problem is compounded by a high number of species and genera which are described every year and high morphological inter- and infra-specific plasticity. As a consequence, twenty-seven genera and 54 species (6% of members of suborder Tanaidomorpha) remain unclassified to any currently defined family (family incertae sedis). During examination of Tanaidacea from various deep-sea collections from slope and/or abyssal regions of the Atlantic, SE Australia, and NW and Central Pacific, a series of distinct, but similar specimens were discovered and classified to seven new species: six of them to the genus Paranarthrurella Lang 1971 and one to the genus Armatognathia Kudinova-Pasternak 1987. Both genera are currently without family classification, but are considered to be closely related. Morphological analysis compared against molecular results based on the two markers (COI and 18S) revealed that Paranarthrurella and Armatognathia should be considered a new tanaidomorphan family.

An Organ of Equilibrium in Deep-Sea Isopods Revealed: the Statocyst of Macrostylidae (Crustacea, Peracarida, Janiroidea)

Bober S, Riehl T, Brandt A
University of Hamburg, Senckenberg Research Institute and Natural History Museum

Isopoda (Crustacea, Peracarida) from the deep sea are relatively well studied but little is known about their lifestyles or the functional morphology and anatomy. The isopod family Macrostylidae, for example, is rather small in size, usually less than 1 cm in body length, and occurs mainly in the deep sea between 3000–6000 m. This family features a paired subepidermal structure on the posterior end of the pleotelson. It has been reported only in this family and was first mentioned by Hansen in 1916, who hypothesized that it represents a pair of statocysts. Nevertheless, neither the structure nor the function has been investigated until now. The shape of some related features, however, has already been used for species differentiation thus indicating that phylogenetically as well as systematically valuable information may be inherent in this feature. Here, the anatomy of this structure was studied based on four species of Macrostylidae from the North Pacific and Atlantic Oceans. It was digitally reconstructed from his- tological sections. The paired structure comprised two tergal invaginations, each with distinct muscular attachments and a modified seta that distally held a statocyst on the shaft. This resembles equilibrium organs reported from other organisms and thus the statocysts hypothesis seems reliable. Using energy-dispersive X-ray spectroscopy, the substance of the statolith could be determined as silicon dioxide. Based on these findings, the function of this organ and its potential phylogenetic and ecological implications are discussed.

Does the Mid-Atlantic Ridge Affect the Distribution of Abyssal Benthic Crustaceans across the Atlantic Ocean?

Bober S, Brix-Elsig S, Riehl T, Schwentner M, Brandt A
University of Hamburg, German Centre of Marine Biodiversity Research (DZMB), Senckenberg Research Institute and Natural History Museum

A trans-Atlantic transect along the Vema Fracture Zone was sampled during the Vema-TRANSIT expedition in 2014/15. The aim of the cruise was to investigate whether the Mid-Atlantic Ridge (MAR) isolates the abyssal fauna of the western and eastern abyssal basins. Based on two separately treated genetic datasets of Macrostylidae and Desmosomatidae/Nannoniscidae we learned that most of the species were found at only one side of the MAR. We analysed those species of Macrostylidae and Desmosomatidae that were sampled across the MAR and complemented these with a species of a third family, Munnopsidae. With these datasets we were further able to consider the effect of different niche adaptations: Macrostylidae are infaunal (burrowing), Munnopsidae are considered epifaunal with pronounced swimming capabilities and Desmosomatidae and Nannoniscidae are partly able to swim, but are not as well adapted to swimming as Munnopsidae. We concluded that the MAR seems to be a dispersal barrier for the non-swimming Macrostylidae and weakly-swimming Desmosomatidae and Nannoniscidae. However, four species of Macrostylidae and Desmosomatidae did cross the MAR, but evidence for regular unrestricted gene flow is still lacking. For the swimming Munnopsidae we were able to detect persistent gene flow across the MAR.

New Macrostylidae (Isopoda) from the Northwest Pacific Basin Described By Means of Integrative Taxonomy with Reference to Geographical Barriers in the Abyss

Bober S, Riehl T, Henne S, Brandt A
University of Hamburg, Senckenberg Research Institute and Natural History Museum

During the KuramBio expedition in 2012, previously unknown Macrostylidae (Crustacea, Isopoda) were collected from the Northwest Pacific Basin near the Kuril–Kamchatka Trench. One morphospecies dominated the samples, but with a combination of morphological and molecular–genetic approaches two (semi)cryptic species were revealed. The females are morphologically indistinguishable and have thus been delineated by means of DNA data. The adult males, however, are distinguishable by their antennula and the type of aesthetascs. This is the first time that a new type of aesthetasc has been assigned to this family. Both species were described herein Macrostylis sabinae sp. nov. and M. amaliae sp. nov. For these two species evidence for sexual size dimorphism, in which the females are significantly larger than the males, was found. Macrostylis sabinae sp. nov. was widely distributed, so a biogeographical approach was followed and the dispersibility of benthic infaunal isopods across deep-sea trenches in the abyssal deep sea was tested.

Systematic Reassessment of a Caridean Shrimp from the Aptian Crato Formation, Araripe Basin, NE Brazil

Bondioli JG, Matos SA, Castilho AL, Varejão FG, Fürsich FT, Assine ML, Simões MG*
Universidade de São Paulo, Universidade Estadual Paulista, Friedrich-August-Universität Erlangen-Nürnberg

The fossil record of palaemonid shrimps comprises 21 species embraced within nine genera, ranging from the Late Jurassic (Tithonian) to the Oligocene. Beurlenia araripensis has been recognized as the only known South American, Cretaceous palaemonid. This is a key genus within caridean shrimps, since it represents the second oldest known Mesozoic freshwater palaemonid. However, some authors have noticed uncertainty on the palaemonid affinity of Beurlenia, based upon some morphological characters (e.g., presence of triflagellate antennules, two or more pairs of spines at distal extremity of telson) shared by extant palaemonid. New exceptionally well-preserved specimens of Beurlenia (coded as, GP/1E: 9490, 9863, 9864, 10630, 10631, 10862, 10863) from the basal laminated carbonate interval of the Early Cretaceous Crato Formation, Araripe Basin, northeastern Brazil, shed new lights on the morphology and affinities of this genus. The preservation of fragile morphological structures (e.g., antennules) and soft tissues (e.g., eyes and gills) indicates that all studied specimens are corpses, ranging from 41-49 mm in length. Despite the morphological variations in fossil palaemonids (e.g., presence of triflagellate or biflagellate antennules; serrate or smooth rostrum; spineless or spiny telson), the studied specimens show that Beurlenia is characterized by biflagellate antennules, a dorsally serrate rostrum, and telson with two apical spines. Finally, when preserved in the studied specimens the chelae of the second pereiopods are larger than those of the first, and the exopods are absent in all pereiopods. These characters allow B. araripensis to be referred to Palaemonidae.

Crustaceans Liberate Substantiel Amounts of Extracellular Enzymes

*Böök I, Saborowski R**
Alfred Wegener Institute

Extracellular enzymes are key drivers in the remineralization of organic matter in marine sys¬tems. According to the widespread view such enzymes derive mainly from bacteria. However, a large number of extracellular enzymes are released into the water by invertebrates through “sloppy feeding”, molting, and excretion. These enzymes have the potential to degrade orga¬nic matter and boost subsequent microbial growth. We investigated the extracellular enzyme activities in molts and egesta of different marine invertebrate species with sensitive fluorometric assays. Visualization of enzymes leaking from molts and fecal pellets was achieved by using agarose plates incubated with fluorogenic substrates. 4-methylumbilliferone (MUF) derivatives were used to detect enzymatic activity of selected enzyme classes: MUF-Phosphate for phos¬phatase, MUF-N-acetyl-beta-D-glucosaminide for exochitinase. Molts and feces were placed directly on agar plates and enzymatic activity was shown by clear fluorescence signals. Phosphatase activity was present in fecal pellets of isopods (Idotea baltica) in feces of the decapod shrimp (Palaemon varians) and the lobster Homarus gammarus. High chitinolytic activity was found in molts of all three species. The enzymes remained active for up to several days. Subsequent decrease of activity indicates degradation of the enzymes. Our results support the hypothesized important role of extracellular enzymes from marine invertebrates in remineralization processes. Further investigation will focus on the quantifica¬tion and detailed characterization of these proteins to distinguish them from microbial enzymes.

The First Complete Mitochondrial Genome of a Parasitic Isopod Supports Epicaridea as a Suborder and Reveals the Less Conservative Genome of Isopods

Boyko CB, Yu J, An J, Li Y
Hofstra University, Shanxi Normal University, China

The complete mitochondrial genome sequence of the holoparasitic isopod Gyge ovalis (Shiino, 1939) has been determined. The mitogenome is 14268 bp in length and contains 34 genes: 13 protein-coding genes, two ribosomal RNA, 19 tRNA and a control region. Three tRNA genes (trnE , trnI, and trnS1) are missing. Most of the tRNA show secondary structures which derive from the usual cloverleaf pattern except trnC which is characterized by the loss of the DHU-arm. Compared to the isopod ground pattern and Eurydice pulchra Leach, 1815, in the suborder Cymothoida, the genome of G. ovalis shows few differences, with changes only around the control region. However, the genome of G. ovalis is very different from that of non-cymothoidan isopods, and reveals that the gene order evolution in isopods is less conservative compared to other crustaceans. Phylogenic trees were constructed using Maxiumum Likelihood and Bayesian Inference analyses based on 13 protein-coding genes. The results do not support the placement of G. ovalis with E. pulchra and Bathynomus sp. in the same suborder; rather, G. ovalis appears to have a closer relationship to Ligia oceanica (Linnaeus, 1767), but this result suggests a need for more data and further analysis. Nevertheless, these results cast doubt that Epicaridea can be placed as an infraorder within the suborder Cymothoida, and Epicaridea appears to also deserve subordinal rank. Further development of robust phylogenetic relationships across Isopoda will require more genetic data from a greater diversity of taxa belonging to all isopod suborders.

Decapod Phylogeny: a Conflicted Past and the Way Forward

Bracken-Grissom HD, Wolfe J, Breinholt J, Crandall KA
Florida International University

Decapoda is a biologically diverse and economically important assemblage of crustaceans with a rich fossil record dating back approximately 360 million years into the Late Devonian. The morphological and ecological diversity is among the most impressive of all invertebrates, with representatives including shrimp, hermit crabs, spiny lobsters, slipper lobsters, true crabs, crayfish and king crabs. For decades, morphological and molecular studies have attempted to reconstruct the evolutionary relationships between the major lineages, but a consensus on decapod phylogeny is still under debate. Much of the uncertainty surrounding the evolutionary history of this ancient group stems from uneven and unrepresentative sampling across taxa and loci, conflicting data, and different analytical approaches. Here, we will review the pioneering molecular studies that have contributed to current understanding of higher-level relationships within Decapoda. We will start with a series of early studies and describe how the development of methods and technology allowed for the advancement of molecular phylogenetics. This will be followed by a discussion on new emergent methods in the field that can be applied to future phylogenetic and phylogenomic studies. We will conclude with presenting an updated decapod tree using an anchored hybrid enrichment phylogenomic approach that includes ~100 species across all major lineages.

NW Pacific Deep-Sea Crustacea At the Edge of the Changing Arctic Ocean in Times of Rapid Climate Change

Brandt A, Saeedi H
Senckenberg Research Institute Museum

The biology of the bathyal, abyssal and hadal benthic faunas of the north-western (NW) Pacific have been intensively investigated during four expeditions with both RV Akademik M.A. Lavrentyev as well as RV Sonne since 2010. These have provided data on the systematic, evolution and biogeography of the deep-sea fauna of the Sea of Japan, Sea of Okhotsk, the Kuril-Kamchatka Trench (KKT) and the NW Pacific open abyssal plain in order to study the biodiversity, biogeography of the benthic organisms in these areas, to compare more isolated deep-sea basins with more easily accessible ones and to test whether the hadal of the KKT isolates the fauna of the Sea of Okhotsk to the fauna of the open NW Pacific area. These data build the basis of the Beneficial (Biogeography of the northwest Pacific fauna. A benchmark study for estimations of alien invasions into the Arctic Ocean in times of rapid climate chance) project which aims to deliver a sound biogeographic baseline study of the NW Pacific area. These data will serve as a solid basis and benchmark for predicting potential species invasions supported by the retreat of Arctic Ocean sea ice. Thus our data will be beneficial for the assessment of state and quality of the Arctic marine ecosystem in a changing environment. Within some taxa, e.g. Crustacea we already identified close links to the Arctic Ocean which they can easily access via the deep Kuril Strait in 4400 m depth. Some examples of our work will be presented.

First Insights Into the Gene Network Governing Embryonic and Adult Neurogenesis in Procambarid Crayfish

Brenneis G, Schwentner M, Benton JL
Wellesley College, University of Hamburg

Two decades after its discovery, the system producing neurons in the midbrain of adult decapod crustaceans is one of the best understood invertebrate models of life-long neurogenesis. The neurogenic system in crayfish has proved particularly suitable for in vivo and in vitro approaches. As a result, studies on Procambarus clarkii have recently indicated a lack of neural stem cells (NSCs) in the adult neurogenic niche, suggesting instead replenishment of its neural precursor pool by hemocytes of the innate immune system. In contrast, embryonic neurogenesis is driven by “canonical” NSCs. To better characterize the cell types involved in “canonical” embryonic and “non-canonical” adult neurogenesis of crayfish, we identified members of gene families involved in arthropod neurogenesis/neural differentiation (SoxB, Achaete-Scute-Complex and Snail transcription factors, Prospero, Elav). We then performed in situ hybridization on embryos and adult brains, the latter coupled to in vivo cell proliferation experiments. Our embryonic data confirm gene expression in the expected neurogenic regions and cell types, as predicted by other arthropod studies. Further, we demonstrate expression of several genes in the adult system, including SoxB in the niche, Snail in some niche cells and migrating neural precursors, and Elav in advanced neural precursors and neurons. This is one of the first crustacean studies to address neurogenic gene expression at the cellular level. We show the suitability of this approach to characterize cell types along the embryonic and adult pathways, making it a crucial step towards unraveling the gene network governing neural differentiation of hemocytes in the adult brain.

New Data On the Development of Antarctic and Tropical Sea Spiders - Implications for the Evolution of Developmental Pathways in Pycnogonida

Brenneis G, Arango CP
Wellesley College, Queensland Museum

The life cycle of many sea spiders (Chelicerata, Pycnogonida) encompasses a small protonymphon larva as hatching stage, which subsequently undergoes parasitic, anamorphic development on an invertebrate host. Generally, this type of post-embryonic development is considered as plesiomorphic for Pycnogonida, despite gaps of knowledge for some elusive extant taxa. However, well-nested within the pycnogonid tree, several lineages show extended embryonic development – in some cases even complete epimorphosis. As of now, it remains unclear to what extent ecological factors have driven independent evolution of this developmental type, and conversely, to what extent it may be phylogenetically informative. Here, we used scanning electron microscopy and fluorescent histochemistry coupled to epifluorescence imaging or confocal laser scan microscopy to investigate developmental stages of three Antarctic Pallenopsidae and two tropical Nymhonidae. For the first time, we report extended embryonic development in some pallenopsid species. This indicates independent evolution of lecithotrophic development in cold water representatives of at least three extant pycnogonid lineages, being accompanied by a shortened anamorphic phase in two of them. Interestingly, we also discovered first examples of extended embryonic development in tropical shallow-water nymphonids, which in turn challenges the notion of a purely temperature-driven emergence of this developmental trait. Given putative close relationships of Nymphonidae with Callipallenidae – a group featuring extended embryonic development in all its representatives – this is suggestive of phylogenetic signal content of developmental features in certain parts of the pycnogonid tree. Systematic sampling across all major taxa coupled to proper phylogenetic analyses will help to illuminate this issue further.

Exceptionally Preserved Fossils Reveal the Origins of Crustacean Clades

Briggs DEG, Siveter DJ, Siveter DJ, Sutton MD
Yale University, Oxford University, University of Leicester, Imperial College London

The early fossil record of crustaceans is limited to sites of exceptional preservation due to the paucity of taxa with a biomineralized cuticle. Burgess Shale-type fossil deposits of Cambrian and early Ordovician age, which preserve flattened fossils primarily as carbonaceous films, continue to yield a remarkable diversity of arthropods. The great majority, however, fall low on the stem of living groups in phylogenetic analyses. Later Paleozoic fossils, preserved in three dimensions through mineralization in pyrite or calcite, postdate the initial diversification of marine arthropods and offer important insights into the earliest representatives of clades of living crustaceans. The late Ordovician Beecher's Trilobite Bed (~450 Myr BP) in upper New York State has yielded a pyritized myodocope ostracod showing brood care. Most notable, however, is the Silurian Herefordshire deposit (~430 Myr BP) in the Welsh Borderland, UK, which is a critical source of unique three-dimensional fossil arthropods, most preserving extraordinary details. Specimens from the deposit, which are reconstructed as virtual fossils based on physical-optical tomography, include a range of phyla. Among the diversity of arthropods are a marrellomorph, trilobite, pycnogonid, and horseshoe crabs, and crustaceans including several myodocopid ostracods, a pentastomid, a barnacle, a phyllocarid, and a novel form, Cascolus, which resolves as a stem-group leptostracan (Malacostraca). These early crustaceans preserve critical data on their appendages which illuminate the evolutionary history and phylogeny of the groups to which they belong. Exceptionally preserved deposits provide robust stratigraphic records that assist in calibrating the chronology of crustacean phylogeny.

Insect Wings and Body Wall Evolved from Crustacean Leg Segments

Bruce HS, Patel NH
UC Berkeley

Researchers have long debated the origin of insect wings, and central to this debate is whether wings evolved from an ancestral structure or represent a novelty. The former proposes that the proximal portion of the ancestral crustacean leg became incorporated into the body, which moved the leg's epipod (multi-functional lobe, e.g. gill) dorsally, up onto the back to form insect wings. The latter proposes that the dorsal insect body wall co-opted crustacean epipod genes to form a novelty, wings. To determine whether wings can be traced to ancestral, pre-insect structures, or are a novelty that arose by co-option, comparisons are necessary between insects and other arthropods more representative of the ancestral state, where the hypothesized proximal leg region is not fused to the body wall. To do so, we examined the function of five leg gap genes in the crustacean Parhyale hawaiensis and compared this to previous functional data from insects. Here we show, using CRISPR-Cas9 mutagenesis, that leg segment deletion phenotypes of all five leg gap genes in Parhyale align to those of insects only by including the hypothesized fused ancestral proximal leg region. We also show that Parhyale retains an additional proximal leg segment, the precoxa, with an epipod. Together, our data shows that the crustacean ancestor of insects had two additional proximal leg segments, which now form much of the body wall of insects, and that the insect wing evolved from the epipod of the ancestral precoxa. Thus, insect wings are not novelties that arose by co-option.

The Impact of Invasive Pigs (Sus scrofa) on Coconut Crabs (Birgus latro) on Guam

Brunson CE
University of Guam

The coconut crab (Birgus latro) is commonly hunted by locals on Guam to impress friends and family at fiestas. However, the invasive feral pig (Sus scrofa) appears to be a much more efficient hunter than man. This study sought to measure the impact of pig predation on coconut crab populations in the forests of Guam, Mariana Islands. Surveys were done by baited transect after sunset during the rainy season. Each transect was set with 20 bait stations from 15 to 20 meters apart in karst terrain within limestone forests in both preserve areas and public areas. All coconut crabs were caught and measured. Pig presence was noted by direct sighting or by evidence of their presence such as rooting and tree rubbing. Surveys of coconut crabs in areas with high pig presence found few or no crabs, even while human hunters were restricted from the area. Surveys with low or no pig presence showed higher numbers of crabs, even with human hunters active in the area. Surveys on the National Wildlife Refuge found very low numbers of crabs, which may be attributed to an extremely high feral pig presence due to peripheral fences which trap the pigs within the Refuge.

An Integrative Taxonomy Study of Cave-Dwelling Aeglids (Decapoda: Aeglidae) from Southeastern Brazil, with Description of Three New Species

Bueno SLS, Tavares MDS, Mantelatto FL, Vera-Silva AL, Moraes JCB
University of São Paulo

Most freshwater aeglid species inhabit epigean habitats. Cave-dwelling species of freshwater aeglids, however, have been reported from cave systems in the Alto Ribeira karst region, Ribeira de Iguape Hydrographic Basin, southeastern Brazil. We describe three new species from subterranean habitats from the same karst region. Descriptions were based on characters traditionally used in aeglid taxonomy. Molecular analysis and comparisons among subterranean and epigean species were based on the partial fragments of the 16S rDNA sequences obtained from the new species and retrieved from Genbank. Morphological and molecular data support the establishment of the new taxonomic entities of cave-dwelling aeglids. The molecular topology obtained reveals that stygobitic species form two distinct clades. This result suggests that dispersal of ancestral epigean aeglids towards the Alto Ribeira karst area, which successfully led to full adaptation and complete isolation of present-day assemblage of obligate cave-dwelling aeglid species in subterranean habitats, occurred twice in the evolutionary history of this freshwater decapod.

A Homage to H.H. Hobbs III: the Inspiration for Four Decades of Research On Decapods

Butler MJ
Old Dominion University

Professor Hobbs and I met in 1976 when we were "freshman" together at Wittenberg University; I was a undergraduate freshman and he a newly minted Assistant Professor. For four years he mentored me as a scientifically naive, but energetic student and in 1981 we coauthored what was my first peer-reviewed paper - ironically, in the inaugural issue of The Journal of Crustacean Biology. Horton "Beep" Hobbs remained a friend for the next four decades. He inspired my own close, richly collaborative, and informal approach to the education of students and he jump-started what was to become the focus of my laboratory's research on decapod crustaceans. This presentation will highlight Professor Hobbs' influence on my own career and research on crustaceans spanning the fields of early life history and connectivity, disease dynamics, mating systems, and fisheries biology - many of those studies conducted against the backdrop and influences of anthropogenic disturbance largely unfathomed when Professor Hobbs and I were "freshmen".

Blue Crab Population Genomics in the US Using Rad-Seq

Caballero IC, Mateos M, Hurtado LA
Texas A&M University

Restriction-site-Associated DNA Sequencing (RAD-Seq) is a very powerful genomic technique that allows at a relatively low cost the discovery and genotyping of thousands of Single Nucleotide Polymorphisms (SNP) for a species. The vast amount of SNPs generated can help to unveil even subtle levels of genetic differentiation. The objective of this study was to use double digest Restriction-site Associated DNA sequencing (ddRAD-seq) to examine genetic connectivity of the blue crab in the US Atlantic coast and Gulf of Mexico. Several population genetics studies have attempted to study population connectivity for this species, but conflicting results and potential problems with the markers used, as well as other issues, have obscured our understanding on this aspect. We conducted three separated sequencing runs, each with their own RAD-seq procedure, which represented different years. Each run included individuals from localities representing most of the US Gulf of Mexico portion, and for two runs individuals from Atlantic populations were also included. Two runs did not reveal any population structure, but some geographic differentiation is observed in the remaining run. We exhaustively examined the sequencing data to explain these differences. Our results provide an opportunity to discuss potential issues when analyzing RAD-seq data, especially shortcomings when pooling data from different runs, and considerations for experimental design using this methodology in population genetics studies.

Assessment of the Extinction Risk of the Colombian Freshwater Crabs

*Campos MR, Lasso CA, Acevedo Alonso A**
Universidad Nacional de Colombia, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Northern Michigan University

Freshwater ecosystems around the world are highly threatened by human activities, and recent conservation assessments suggest that a third to a half of aquatic species, including freshwater crabs, may be threatened with extinction. Freshwater crabs play an important role in the food chain and nutrient cycling in freshwater ecosystems because these crustaceans represent a high percentage of the biomass in these systems. Freshwater crabs are found in tropical and subtropical regions throughout the world and are assigned to five families, two of which (Pseudothlephusidae and Trichodactylidae) are the subject of the present study. Colombia is ranked sixth in the world for the size of its freshwater ecosystems, and its freshwater crabs are ranked second in the world for their diversity and endemism (81%). The 2008 IUCN global conservation assessment listed 101 species of freshwater crabs in Colombia of which 13.9% were classified as threatened, and 40.6% were Data Deficient. Here we report on the results of a country-wide reassessment of the freshwater crabs of Colombia carried out in 2015 that used the IUCN Red List protocols to assess the extinction risk of species based on new data on ecology, distribution, and threats. The study found 25% of species of Colombia's freshwater crabs to be in one of the three threatened categories, and that 7.7% were Data Deficient. The major threats to freshwater crabs in Colombia are deforestation and water pollution from agriculture, mining and urban development. Species of the Pseudothelphusidae are more affected by these threats, perhaps due to their distribution at higher altitudes where the impacts of urbanization are most felt. This study illustrates the need for the development of new conservation strategies and for more field studies of the freshwater crabs of Colombia.

A New Morphotype of the Phreatic Crayfish Cambarus hubrichti (Decapoda: Cambaridae) from an Ozark Spring Cave System, with Comments On Its Ecology

Carroll TM, Rogers C, Stern DB, Crandall KA
University of South Carolina Beaufort, University of Kansas, George Washington University, National Museum of Natural History, Smithsonian Institution

The subterranean waters of the Missouri Ozarks in the USA, harbor two reported blind crayfish species: Cambarus setosus and C. hubrichti. During surveys of phreatic (underwater) karst conduits and caves in the Salem Plateau region of Missouri by the Ozarks Cave Diving Alliance, blind Cambarus specimens were found that were not morphologically consistent with either reported species. Morphologically our material was referable to C. hamulatus (Cope, 1881) from Alabama and Tennessee. Qualitative and quantitative characteristics, both morphological and genetic, established them as new morphotypes of the Salem Cave Crayfish (Cambarus hubrichti Hobbs, 1952). Our molecular phylogenetic analyses indicated that our specimens cluster with C. hubrichti with 100% bootstrap support. This morphological variation demonstrates the need for molecular verification of morphological diagnoses in crayfish species, particularly those taxa in need of conservation. Incorrect determinations may artificially inflate or reduce distribution and threat assessment data sets, and affect conservation management decisions. In addition, we present habitat, feeding pathways, and distributional observations data, which suggest that this morphotype is highly dependent on heterotrophic or chemoautotrophic microbial communities.

Synchronism in the Naupliar Development of Sacculina carcini Is Explained By Synchronized Cell Division

Carton B, Audebert F, Tredez F, Galindo LA, Maury B, Rabet N*
Sorbonne Universités, Université de Versailles Saint-Quentin-en-Yvelines, UFR Sciences de la Santé Simone Veil

Cirripeds have a great morphological diversity adapted for various adult lifestyles. Our study focuses on Sacculina (Rhizocephala) which parasitizes other crustaceans, such as crabs. Due to the morphology of their nauplius larva, that sacculines were classified in the clade of the cirripeds. Recent observations of larval stages in Sacculina carcini led to the discovery of a morphological and anatomic synchronism in their development. The naupliar development of S. carcini is redescribed from a precise monitoring. Nauplii of the same brood were sampled every 4 hours, from the release of the larvae until the cypris stage. Our results indicate that the larval development of Sacculina is clearly different from an anamorphic model because the segmentation and morphogenesis of the appendages are synchronous. This allowed us to establish an evolutive hypothesis linked to the adaptation to a parasitic lifestyle within cirripeds. We used confocal microscopy and image processing to study the cellular mechanisms in the larval development of the thorax of the larva of S. carcini. A kinetic study during first 24h of S. carcini development allowed us to observe a synchronization of cell divisions. This would enable the establishment of a long-term mode for a synchronized segmentation. We also conducted a comparative study of two cirriped species: S. carcini and Semibalanus balanoides (Thoracica). Our results suggest the possibility of a cellular taxonomy and new arguments in favour of lecitotrophy, a larval adaptation linked to adult parasitism.

Genomic Consequences of Eusociality in Snapping Shrimps

Chak STC, Hultgren KM, Duffy JE, Rubenstein DR
Columbia University, Seattle University, Tennenbaum Marine Observatories Network, Smithsonian Institution

Eusociality is considered the apex of animal sociality. While the genomic underpinning of eusociality is being increasingly studied in advanced eusocial insects, little is known about the genomic changes associated with the early stage of eusociality. Here, we studied snapping shrimps in the genus Synalpheus, the only known group of eusocial animals in the sea that have evolved eusociality relatively recently. We found that eusocial Synalpheus species have 1) smaller effective population sizes, 2) high abundance of transposable elements and 3) larger genome sizes compared to their non-eusocial congeners. Our results suggest that although eusocial species may have ecological advantages, it may also carry genomic costs.

Are Barnacles Sessile Organisms? Drastic Movement of the Turtle Barnacle Chelonibia testudinaria

Chan BKK, Lin CC
Academia Sinica, National Taiwan Ocean University

Barnacles are sessile organisms and it is believed that they are sessile and cannot move. However, a previous study examined regular temporal photos of green turtles in the field revealed the turtle barnacle living on turtle carapaces appearing to have directional locomotion. However, no experiments have been conducted to examine this observation. In this study, we successfully re-attached the turtle barnacle Chelonibia testudinaria on acrylic surfaces. The reattached Chelonibia in an aquarium displaced at a distance > 20 cm after keeping in aquarium with aeration for 12 months. We hypothesize that the movement of barnacles can be related to different direction of water current. 18 individuals of turtle barnacles were equally assigned in three different experimental groups. Rostrum shell plate facing the current, Rostrum shell plate away from currents and control group (no currents). There were significantly differences in the distanced moved among these three groups (One-way ANOVA), with barnacles have rostrum plate facing current moved the greatest distance. In the rostrum facing current group, four turtle barnacles moved against the direction of flow (at 90 degree) and the average movement angle was 57.50 ± 38.38°. In the rostrum away from current group, four turtle barnacles followed the direction of current and the average movement angle was 268.50 ± 46.22°. Our results showed that the water current can stimulate growth, moving and movement angle of turtle barnacles However, the reason for the move is unclear and needs further studies to address this issue.

Is the Blue Swimmer Crab a Winner Or Loser of Climate Change?

Chandrapavan A, Johnston D, Caputi N, Kangas M
Western Australian Department of Primary Industries Regional Development

Resilience of species worldwide is currently being tested by the shifting climatic conditions, and their survival may depend on their status as a “winner” or “loser” of climate sensitivity and biophysical vulnerability. The blue swimmer crab Portunus armatus is a short-lived, fast growing and highly fecund species that is a popular recreational catch and supports several commercial fisheries along the coastline of Australia. It mainly inhabits inshore inlets and estuaries across a large latitudinal range thus exhibiting its inherent plasticity and adaptability. However, the south west coast of Western Australia (WA) is now considered a climate change hotspot with water temperatures rising above global trends. During the summer of 2010/11, an extreme marine heatwave event (1 in 100-year event) impacted the WA coastline which lasted 4 months and significantly altered the status of key fisheries. In one region of the State, Australia’s largest single highest producing blue swimmer crab fishery in Shark Bay collapsed from a recruitment failure while in another region of the State, improved recruitment success gave rise to stock expansion. Extreme events such as heatwaves are expected to become more common as the climate changes and so resource management of recreational and commercial fisheries in WA are focused on early identification of environmental changes and the need to be aware that recruitment and other biological parameters cannot be assumed to be stable. So responding to climate change is now about managing risks though flexible harvest strategies to achieve a balance between sustainability and economic viability.

Thylacocephalans from the Cretaceous Lagerstätten of Lebanon

Charbonnier S
Muséum National D’Histoire Naturelle

Thylacocephalans (Euarthropoda, Thylacocephala) were arthropods characterized by their “bivalved” carapace and three anterior prehensile appendages. It is still not clear how they used to live, or what their evolutionary history is. This presentation focuses on new thylacocephalans from the Late Cretaceous Konservat-Lagerstätten of Lebanon, which yielded the youngest representatives of the group. Three new genera and species are described in the Cenomanian sublithographic limestones of Hakel and Hadjoula, and two new genera and one new species are described in the Santonian chalky limestones of Sahel Alma. Among the specimens from Hakel and Hadjoula, Paradollocaris vannieri, Thylacocaris schrami and Globulacaris garassinoi are the first reports of thylacocephalans in the Cenomanian of Lebanon. Paradollocaris and Thylacocaris are assigned to Dollocarididae based upon their large optic notches limited by rostral and antero-ventral processes, their hypertrophied eyes, and their posterior notches with dorsal and ventral spines. Moreover, Thylacocaris presents a very peculiar character: an optic notch with two strong optic spines protecting the eye. Globulocaris is assigned to Protozoeidae based upon its small carapace with a distinct dorsal notch anterior to a strong postero-dorsal spine. Keelicaris deborae (Microcarididae) is also a new form in the Santonian of Lebanon. It presents a very unusual keel-shaped carapace with terraces and punctuations. The occurrence of such diverse fauna of thylacocephalans markedly increases the diversity of the group during the Late Cretaceous. The diversity and abundance of the Sahel Alma thylacocephalans pose also the problem of causes of their disappearance from the fossil record after the Santonian.

Rising Seawater Temperature on the Benthic Shrimp Assemblages Structure in Subtropical Coastal Waters–An Eight-Year Investigation

Chen HS, Wen TC, Chen K, Chen CY, Chen MH

National Sun Yat-Sen University, National Taiwan University, National Kaohsiung Marine University

This study aimed to understand the influence of rising seawater temperature on the species composition of benthic shrimp assemblages in subtropical coastal waters. Shrimp specimens were collected by a beam trawl onboard R/V Ocean Researcher III in coastal waters off Erren River (ER) and Kaoping River (KP) at depths from 15 to 25 m during two survey periods (2002-2004 vs. 2007-2010) in southwestern Taiwan. Abundance-weighted community temperature index (CTI) was used to elucidate the temperature performance of the assemblage. The results show that the shrimp assemblages were changed in (1) reducing the species number, (2) disappearance of cold-water dwelling species, and (3) shifting the dominant species ranks. The number of species decreased from 22 to 18 and from 22 to 13 in ER (higher latitude) and KP (lower latitude) sites, respectively. The relative abundance and frequency of occurrence of the warm-water dwelling species, such as Metapenaeopsis palmensis, Metapenaeus affinis, Metapenaeus ensis, increased, whereas the cold water species, such as Metapenaeopsis dalei and Trachysalambria curvirostris, decreased in 2007-2010. The rising CTI also revealed that the dominance of warm-water dwelling species increased and became a warm-water species dominant assemblage for both ER and KP. The above results suggest that rising seawater temperature, which could be attributed to global warming, might induce tropicalization and simplification of benthic shrimp assemblages in subtropical waters.

Crab Assemblages Changes in Relative to Environmental Factors in the Coastal Waters off Southwestern Taiwan

Chen TC, Chen MH, Meng PJ, Chen CY, Chen KS, Chen HS

National Sun Yat-Sen University, National Museum of Marine Biology and Aquarium, National Kaohsiung Marine University

Benthic crabs were collected at depths ranging from 12 to 31 m using a beam trawl onboard R/V Ocean Researcher III off two coastal areas, namely Cigu and Jiading, southwestern Taiwan in the periods of 2006–2010 and 2016–2017. Crabs of 4,358 individuals belonging to 11 families, 45 identified species, were collected. More specifically, 37 crab species belonging to 10 families were recorded from 2006 to 2010 in the two study areas, and 5 and 3 species of new records were collected off Cigu and Jiading, respectively, during the period of 2016–2017. The total numbers of identified crab species were 22 off Cigu and 36 off Jiading. The most dominant species by abundance off Cigu from 2006 to 2010 was Portunus argentatus (43%), and changed to P. sanguinolentus (26%) in the period of 2016–2017. Nevertheless, P. hastatoides was consistently the most dominant species off Jiading during the two study periods (72% vs. 74%). Cluster analysis revealed two geographic crab assemblages, namely the Cigu group and Jiading group. Portunus argentatus tended to increase in abundance with depth, whereas P. sanguinolentus was abundant with decreasing depth, salinity, and dissolved oxygen, as well as increasing of suspended particles. Portunus hastatoides preferred living in the habitat substrate of finer sand grain size. Five abiotic factors, including depth, salinity, suspended particles, dissolved oxygen, and grain size of substrate shaped the crab assemblages in the subtropical coastal waters.

Deep-Sea Tanaids of the Clarion-Clipperton Fracture Zone

Chim CK

National University of Singapore

A total of 1,174 tanaids from about 4,000 m depth at the polymetallic nodule fields of the Clarion-Clipperton Fracture Zone (CCFZ) were examined. These specimens were collected from the Singapore and United Kingdom exploratory areas during the ABYSSLINE I and II research cruises in the years 2013 and 2015. Quantitative data were obtained using the box corer and multiple corer. Tanaids accounted for 8% of the box core macrofaunal assemblage, superceded only by nematodes (28%), copepods (27%) and polychaetes (15%). While the majority of the tanaids were found at the topmost layer of the sediment (0–2 cm; 65%), these peracarids also occurred frequently (27%) at the 2–5 cm layer and occasionally (8%) at the 5–10 cm layer. Tanaids were rare in multiple core samples, and comprised only 0.08% of the meiofaunal assemblage. Specimens collected by the Brenke epibenthic sledge were highly diverse, including apseudoid and neotanaoid tanaids, which were rarely present in the box and multiple cores. These two superfamilies made up only 10% of the entire tanaidacean collection, while the other 90% consisted of paratanaoid tanaids. Preliminary results showed that the material was represented by two suborders, three superfamilies, nine families, 14 genera and about 40 species. Based on these findings, the total number of tanaid species in the CCFZ increases more than three-fold over from current literature records. Furthermore, gravid females and large numbers of mancas were present in our samples, suggesting that there are healthy populations of tanaids in the CCFZ.

Brachyuran Tree of Life Illuminates the Origin and Biogeography of Hydrothermal Vent Crabs

Chu KH, Tsang LM, Chan TY, Ng PKL

The Chinese University of Hong Kong, National Taiwan Ocean University, National University of Singapore

Organisms associated with hydrothermal vents are of great interest as their adaptation to this extreme environment is considered to be evolutionary novelty. The origin and biogeography of hydrothermal vent fauna are, however, poorly known except for several well studied taxa. We construct the most comprehensive tree of life for the brachyuran crabs using a dataset of eight molecular markers (two mitochondrial rRNA genes and six nuclear protein-coding genes) from more than 320 species in 93 families (representing ~90% of the 104 brachyuran families), including 13 of the 14 species from the hydrothermal vent crab family Bythograeidae, to determine the evolutionary origin and biogeography of Bythograeidae. The divergence times for different clades were estimated and superimposed with biogeographic reconstruction in order to reveal the evolutionary history of vent crabs. The inferred phylogeny reveals the polyphyletic nature of Bythograeidae, with one lineage closely related to Hypothalassidae, and members from Mathildellidae and Oziidae, and the other to Progeryonidae. Divergence time estimation suggests Paleogene origins for both lineages. Biogeographic analyses reveal independent invasions to the East Pacific deep water hydrothermal vent habitat, with one lineage subsequently colonized the other oceans whilst the remaining one diversified but restricted to East Pacific. The high morphological similarities of the two vent crab lineages are likely the result of convergence. Future analysis will focus on functional genes expressed in the two lineages to elucidate convergent evolution with respect to genetic and physiological adaptation. [This work is supported by a grant (14176317) from the Research Grants Council, HKSAR Government.]

Expression Profile of Crustacean Female Sex Hormone (Cfsh) and Its Functional Role During the Development of the Blue Crab, Callinectes sapidus

Chung JS, Ahn IS
University of Maryland Center for Environmental Science

Crustacean female sex hormone (CFSH) is required for the development of adult-specific female characteristics, specifically the parental care system of female blue crab, Callinectes sapidus. The presence of CasCFSH during the embryogenesis of this species is seen in the sinus gland of embryos at the hatching-imminent stage. Because crustacean sex dimorphism develops gradually throughout the life cycle, we aim to establish a relationship between CasCFSH expression and the development of phenotypes specific to female C. sapidus during its life cycle. In females, the levels of CasCFSH transcripts steadily increase, starting early from crab stages 3-4 to pre-puberty, while showing a decrease only at crab stages 15-16. The highest levels of CasCFSH transcripts occur at the pre-pubertal stage, which are ~5.6 fold greater than those of adults. Interestingly, the first visible secondary female characteristics: a pair of gonopores or triangular abdomen and 4 pairs of pleopods are seen as early as crab stages at ~3 (CW 5-7 mm) - 5 (CW 8-10 mm), respectively. The adult-specific female morphological features manifest only at the completion of pubertal-terminal molt, after developing gradually throughout the pubertal molt cycle. Specifically, spermathecae develop at early premolt stage (D0); ovigerous and plumose setae on pleopods at premolt stage (D0-4); gonopores and abdomen at the completion of ecdysis. Knockdown study of CasCFSH by injection of CasCFSH-dsRNA to the prepuberty females at specific molt stages provides further evidence that the gradual development of adult-specific morphological features depends on the constant presence of CasCFSH.

Photic Ecology in the Epipelagic High Arctic Polar Night: a Deep Sea Analogue?

Cohen JH, Last KS, Charpentier CL, Johnsen G, Berge J
University of Delaware, Scottish Association for Marine Science, Rutgers University, Norwegian University of Technology and Science, UiT The Arctic University of Norway

Light and vision play a large role in interactions among crustaceans in both the epipelagic and mesopelagic realms. While atmospheric light is typically considered to be the dominant source of photons to the underwater light field, bioluminescence provides an additional source of light in the mesopelagic to supplement atmospheric light. During Polar Night in the high Arctic, the sun remains 6° or more below the horizon throughout the diel cycle. During this time the epipelagic is a dim photic environment over an extended period, which would seem to favor bioluminescence and organisms adapted to detect dim light, much like the mesopelagic. In four years of sampling on the west coast of Svalbard during Polar Night (January 2014-2017), we have studied eyes and vision in crustacean zooplankton and micronekton (copepods, amphipods, and krill), and both the atmospheric and bioluminescent components of the light field in which they function. We find that the light environment is similar to the mesopelagic. Using structural and electrophysiological techniques, quantitative visual models, and empirical observations with autonomous platforms, we show focal crustaceans to possess similar optical designs, visual function, and light-mediated behaviors as comparable mesopelagic species, including diel vertical migration and entrainment of endogenous rhythms in visual sensitivity. We therefore suggest that the cocktail of light experienced by crustaceans during Polar Night has ecological relevance at high latitudes during this darkest part of the year, and this habitat can represent a deep sea analogue.

Taxonomic Revision of the Eastern Pacific Species of Stenocionops Desmarest, 1823 (Decapoda: Brachyura)

Colavite J, Windsor A, Santana W
University of São Paulo State, Universidade do Sagrado Coração, Department of Health & Human Services, Food and Drug Administration

The Amphiamerican genus Stenocionops is composed by seven extant and three fossil species. The Atlantic species of Stenocionops, until recently, presented several taxonomic problems, which is not the case for the Pacific species. However, the Pacific species are poorly studied. As is the case for several other majoid taxa, the absence of good illustrations and the poorly detailed original descriptions have resulted in dubious synonymic lists. Here, we aimed to review the Pacific species of Stenocionops and clarify the taxonomic problems involving this genus, such as the synonymy between S. angustus and S. contigua. As a result, all three species were redescribed and illustrated in detail, and a complete identification key for genus Stenocionops was developed.

Morphological and Molecular Investigations of the Macrocoeloma trispinosum and M. nodipes (Decapoda: Brachyura) and its Potential Cryptic Species

Colavite J, Windsor AM, Santana W
University of São Paulo State, Universidade do Sagrado Coração, Department of Health & Human Services, Food and Drug Administration

Rathbun, in 1925, recognized a complex of species in Macrocoeloma that she called "trispinosum-dicanthum group" and reported the existence of at least three groups of species in the USNM collections. This complex includes both species mentioned, M. nodipes and one third group she named “variety.” Several issues such as the superficial diagnoses and poor or contradictory illustrations of the original descriptions, the erroneous type-locality, and the absence of original type-materials biased the identification of species included in this group. This fact resulted in an extensive synonymic list and a confusing taxonomic history for all three species. An extensive literature review and the morphological analyses of specimens was compared to the distribution pattern of M. nodipes and M. trispinosum. The first step in resolving the above-mentioned taxonomic issues is to designate neotypes and sequence both species already accepted as valid, also the morphological differences and the DNA sequences are being compared in order to confirm or refute the existence of a cryptic species group.

Phylogenetic Evidence from Freshwater Crayfishes That Cave Adaptation Is Not an Evolutionary Dead-End

Crandall KA, Stern DB
George Washington University

Caves are perceived as isolated, extreme habitats with a set of uniquely specialized biota, which long ago led to the idea that caves are 'evolutionary dead-ends.' This suggests that cave-adapted taxa may be doomed for extinction before they can diversify or transition to a more stable state. However, this hypothesis has not been explicitly tested in a phylogenetic framework with multiple independent cave-dwelling groups. Here we use the freshwater crayfish, a group with dozens of cave-dwelling species in multiple independent groupslineages, as a system to test this hypothesis. Starting with an updated classification for the freshwater crayfish and coupling this taxonomy with multiple studies of phylogenetic history using the OpenTreeofLife phylogenetic synthesis approach, we consider historical patterns of lineage diversification and habitat transition as well as current patterns of geographic range- size and extinction risk. We find that while cave-dwelling lineages have small relative range- sizes and rarely transition back to the surface, they exhibit remarkably similar diversification patterns to those of other habitat types. Furthermore, phylogeny-based conservation prioritization does not distinguish cave species from species in other habitats. Finally, we analyze eye transcriptome-wide gene expression patterns across repeated instances of vision loss in cave crayfish and show that blind animals exhibit weak convergence in gene expression patterns. However, we find that this convergence is due to commonly increased rates of gene expression evolution relative to sighted species, signifying a loss of functional constraint in expression levels in response to reduction of selective pressure maintaining eye function. This suggests that cave-adaptation is not a 'dead-end' for freshwater crayfish, which has positive implications for our understanding of biodiversity and conservation in cave habitats and that the evolution of vision loss is driven by genetic drift in gene expression patterns.

Conservation of Freshwater Decapods and Responses to the Global Biodiversity Crisis

Cumberlidge N
Northern Michigan University

Freshwater ecosystems host a diverse endemic fauna including freshwater crabs, crayfish, and shrimps but freshwater habitats, and the animals that depend on them are now under imminent threat. Recent global IUCN Red List assessments of the freshwater crabs, crayfish, and freshwater shrimp revealed unexpectedly high numbers of species threatened with extinction. The majority of threatened decapods are restricted-range endemics living in habitats impacted by deforestation, alteration of drainage patterns, pollution, and over-harvesting for human consumption. The current strategies aimed at monitoring and quantifying the decline of the World's threatened freshwater decapod species are reviewed, along with the efforts to develop conservation measures to prevent further losses. The sustainable management of inland aquatic resources depends heavily on the availability of data on the diversity, distribution patterns, population trends, and threats. These data are all necessary in order to assess the extinction risk of freshwater decapod faunas and to develop conservation actions plans in response to imminent threats.

Sex, Allometry and Herbivory: Are Mesograzers Weird Or Is There Need for Reassessing Size-Consumption Relationships?

Cruz-Rivera E
University of the Virgin Islands

Experimental works on the relationships between crustacean size and feeding date back to the 1950s. Some of these classical studies are prominently cited in physiology textbooks and are the theoretical basis of calculations regarding the scaling up of metabolism-driven community and ecosystem processes. In general, it is expected that a linear inverse relation between feeding rate and animal size will occur, where larger adults will consume less food per mass or volume than juvenile ones. Yet, few direct tests of this exist for marine animals and even less is known about how gender or sexual behavior may affect these allometry-feeding relations. Studies on two mesograzers, the amphipod Gammarus aequicauda from Egypt and the crab Omalacantha bicornuta from the Caribbean demonstrated that these relations between consumption rates and consumer size are 1) strongly influenced by consumer sex and diet, and 2) sensitive to the allometric parameters used, with mass being a better predictor of consumption than the more widely-used body lengths. Furthermore, consumer sex influenced parameters that are independent of allometric scaling, such as food choice. Together, these results invite discussion and reassessment of consumer size-resource consumption relations for crustaceans, and possibly other invertebrate groups.

Sight Beyond Eyes? Evidence for Photosensitivity in the Bioluminescent Light Organs of Deep-Sea Shrimp Using Phylotranscriptomics

De Leo DM, Bracken-Grissom HD
Florida International University

Photoreceptor cells inside the complex eyes of animals are responsible for light detection and subsequent signaling cascades linked to vision. Though light detection in animals is typically associated with ocular photoreceptors, the ability to detect and respond to light can also occur in extraocular tissues and structures. Extraocular photoreception has been documented across a range of structures and taxa, including the dermal chromatophores of cephalopods, tube feet of echinoderms and the central nervous systems of arthropods. Despite the occurrence across diverse metazoans, knowledge regarding the functionality of extraocular photoreceptors remains limited. Deep-sea shrimp provide a unique system for examining extraocular photoreception as some genera possess autogenic bioluminescent light organs called photophores. These light emitting organs are thought to function in counterillumination and congener attraction. Preliminary evidence for the family Oplophoridae also suggests these photophores contain photopigment proteins (opsins) and other phototransduction genes that would allow for light detection. In this study, RNA was extracted from the oplophorid shrimp species Janicella spinicauda and Systellaspis debilis and sequenced on an Illumina HiSeq4000. Transcriptomes were assembled discretely from eye (n=16) and photophore (n=15) tissues and analyzed to characterize opsin diversity and visual pathway genes within a phylogenetic context. Gene expression analyses were also conducted to quantify differential opsin expression across tissue types. Our findings suggest photophores are light sensitive and may be used to fine-tune bioluminescent emissions during counterillumination. Furthermore, we illustrate the strength of employing next-generation sequencing and phylogenetic approaches towards the study of deep-sea sensory systems.

Are Some Cuticular Parts Conserved For Studying the Life History of Amphidromous Caridina Shrimps (Decapoda: Caridea: Atyidae)?

De Mazancourt V, Djediat C
Muséum National D'Histoire Naturelle

Amphidromous lifestyle, allowing some species of fish, gastropods and decapods to colonize freshwaters ecosystems from the sea still keeps some secrets. To study this lifestyle, sclerochronology has been used in the two former groups, focusing respectively on the otoliths and the operculum, both calcified parts preserved throughout the life of the animal and recording all the physico-chemical changes of their environment. However, such a feature was supposed to be lacking in crustaceans due to the molting process they undergo all during their life. In 2012, Kilada et al. proposed a novel technique to determine the age of some decapods using growth bands in the endocuticle of the eyestalk and gastric ossicles, suggesting that some parts of the cuticle were preserved through the molts. We tested the feasibility of using these anatomical parts to study the life traits of an amphidromous shrimp, Caridina multidentata. The small size of the specimens (>5 cm) and the difficulties to obtain the gastric ossicles led us to focus on the cuticle of the eyestalk. Vital markings were performed on specimens during one or several molt cycles and we could not reproduce the results obtained by Kilada et al. on other species since coloration did not seem to be retained in a specific area of the cuticle of C. multidentata. Finally, we studied the ultrastructure of the cuticle at different stages of the molt cycle and the exuvia with TEM microscopy to investigate the conservation of a part of it throughout the cycle.

The Complex Study of Complexes: the First Well-Supported Phylogeny of Two Species Complexes Within Genus Caridina (Decapoda: Caridea: Atyidae) Sheds Light On Evolution, Biogeography, and Ecology

De Mazancourt V, Klotz W, Marquet G, Mos B, Rogers DC, Keith P
Muséum National D'Histoire Naturelle, Southern Cross University, Kansas University

A key component of tropical freshwater ecosystems, atyid shrimps face multiple anthropogenic threats and thus need special attention. With more than 300 described species, Caridina genus is the most speciose of all the Caridea infra-order. Caridina spp. occupy diverse habitats in tropical freshwaters ranging from Africa to Polynesia. Some of these species are amphidromous, which allows them to have a wide distribution, while others are landlocked and are often endemic. Several species complexes have been recognized by different authors, based on common morphological features. For this study, we focused on two complexes: 'Caridina nilotica' and 'Caridina weberi'. After collecting specimens belonging to these two groups from most of their known geographical range, we sequenced seven mitochondrial genes and two nuclear markers, and performed a phylogenetic analysis which yielded the first well-supported tree for the genus Caridina. This tree allowed us to develop hypotheses regarding the potential dispersion barriers or avenues used by the different species, the habitats used by the different species, the adaptations that led to their colonization, and finally evolutionary hypotheses for the two species complexes. Our work provides new insights into the biogeography of the Indo-Pacific region and highlights new opportunities for further studies of the taxonomy of this group in order to fill knowledge gaps that currently impede the management and conservation of these species and their environment.

Crustacean Fouling Communities Along Southern Brazilian Coasts – Functionality, Connectivity and Possible Implications for Marine Bioinvasions

Desiderato A, Beermann J, Haddad MA
Universidade Federal Do Paranà, Curitiba, Alfred Wegener Institute Helmhotz Centre for Polar and Marine Research (AWI), Universidade Federal do Paranà, Curitiba, Brazil

Fouling communities can rapidly colonize any kind of hard substrates that are immerged in water. Although fouling on artificial substrates is known to harbour less diverse faunal communities than natural reefs, they provide refuge and work as stepping stones for non-indigenous species. Crustaceans are dominants component of marine fouling. Due to their diversity, abundance and adaptability, crustaceans represent excellent model organisms for the study of marine fouling and the biology of associated cosmopolitan alien and/or invasive species. Here we present the first preliminary results of a project that was designed to assess the ecological significance of marine fouling with respect to community composition, functionality and connectivity between sites. We studied the succession of crustacean fouling on artificial hard substrates that were positioned in different estuaries within the Lagamar Biosphere Reserve. Three estuaries were regarded in this region: the Iguape/Cananeia complex, the Paranaguá Estuarine Complex and Guaratuba Bay. A fourth, highly impacted bay (Babitonga Bay) was used for comparison, including two international ports such as Paranaguá. Amphipoda was the most abundant and diverse component in the fouling communities at all sites with a dominance of the filter-feeding Caprellidae as well as the tube-building Ischyroceridae and Corophiidae. The amphipod communities were subject to spatio-temporal shifts in their assemblage structures. Furthermore, some species such as Paracaprella pusilla, Stenothoe valida and the cosmopolitan Monocorophium acherusicum were found in all locations. Subsequent molecular analyses such as the Single Nucleotide Polymorphism with these select species are expected to elucidate the connectivity among remote fouling communities.

Parametopella cypris (Amphipoda: Stenothoidae), A New Sneaky Alien in a North Adriatic Lagoon

Desiderato A, Mucciolo S, Turicchia E, Ponti M, , Krapp-Schickel T
Universidade Federal Do Paranà, Curitiba, University of Bol, University of Bologna, Italy, Forschungsmuseum A. Koenig

Pialassa Baiona is a northern Adriatic coastal lagoon located about 60 km south of the famous Venice lagoon. It is affected by many types of anthropogenic disturbances: influx of nutrients and pollutants from civil and industrial wastewater treatment plants, warming from power plant effluents, fishing, shipping and hunting activities, dredging operations, and invasion of non-native species due to the connection with the sea through the Ravenna port channel. During the biennial monitoring of the status of the environmental quality of the lagoon through the analysis of the recruitment of the fouling communities, the amphipod Parametopella cypris Holmes, 1905, was found. So far this species had only been recorded from the US east coast, from Cape Cod to Florida, where it is found in association with hydrozoans. In Pialassa Baiona this amphipod was found in August 2014, together with the hydrozoan Ectoplauera crocea (Agassiz, 1862) and the bryozoan Amathia verticillata (Delle Chiaje, 1822). To our knowledge, this is the first report of the presence of P. cypris in Europe and the Mediterranean Sea. Given the small number of specimens found, the establishment success of this species in Mediterranean lagoons is to be assessed. Also, its presence may have been overlooked, because of its similarity to the co-occurring "cosmopolitan" species Stenothoe valida. In order to facilitate the identification of P. cypris, we provide a detailed illustration of the male, and of distinctive traits from congeneric species, as well as of S. valida.

Tracking Human Impact and Remediation of Temperate Lakes That Have Experienced Eutrophication Using Living and Subfossil Records

Diana ON, Garelick S, Leonard-Pingel J, Michelson AV
Virginia Wesleyan University, Brown University, the Ohio State University at Newark

Few studies describe the long terms effects of remediation to combat the effects of eutrophication in lakes. Here, we employ preserved lacustrine archives to both quantify human effects and track the progress of eutrophication and subsequent remediation. We sampled three currently-impacted lakes and three previously-impacted, but remediated lakes for living communities and time-averaged death assemblages of ostracodes in Wisconsin. Low live/dead agreement in impacted lakes results from a mismatch between the living community altered by human impact and the time-averaged death assemblage, reflecting pre-impact conditions, but live/dead agreement in remediated lakes is unknown. Furthermore, if low live/dead agreement is truly caused by human activity and remediation is recorded by preserved ostracode assemblages, then both human impact and remediation should be reflected in sedimentary archives. To test this, we extracted sediment cores from one currently-impacted and one remediated lake in Wisconsin. We find that live/dead agreement in remediated lakes is high, like unimpacted lakes. Sedimentary archives reveal high concentrations of preserved ostracod valves corresponding coincident with European settlement and eutrophication. This continues to the present the still-impacted lake, but lessens at the time of remediation in the remediated lake. Our remediated lake core also shows a decrease in the percent abundance of the low-oxygen tolerant species Candona eliptica at the time of remediation. Our results thus demonstrate that preserved ostracode assemblages can record human impact and remediation and that successful remediation can be tracked by the return of high live/dead agreement.

Species of Porcellanid Crabs from the Northern South China Sea

Dong D, Li X
Chinese Academy of Sciences,

The diversity of porcelain crabs (Decapoda: Anomura: Porcellanidae) is high in the subtropical regions of the West Pacific. We examined hundreds of porcellanid specimens deposited in the Marine Biological Museum, Chinese Academy of Sciences and materials recently collected from waters of northern coast of the South China Sea (China mainland). The collections contain 40 species belonging to 10 genera. Among them, 3 species of the genus Polyonyx Stimpson, 1858 were found new to science, and 3 species of the same genus were firstly discovered in the South China Sea. The three new species were observed living within sponges, polychaete tubes and coral reefs, respectively, demonstrating the wide adaptability of this genus to the commensal habitats in this area.

A Journey Into the Unknown: Past, Present and Future Studies of the Elusive Crustacean Y-Larvae

Dreyer N, Grygier MJ, Chan BKK, Høeg JT, Olesen J
Natural History Museum of Denmark, National Taiwan Ocean University, Academia Sinicia, Marine Biological Section

Discovered 130 years ago, The Facetotecta remain one of the most elusive crustacean groups. Knowledge of all aspects of their biology is based exclusively on larval instars, typically comprising only a single instar or even only a single larva. Historically, early studies reported the morphology of single larval types of "nauplius y". Later studies comparatively studied the larval stages, including the "cypris y" and the slug-like, very likely endoparasitic "ypsigon" into which it has recently been shown to metamorphose, and related these to larvae of other thecostracans. To date, only one genus, Hansenocaris, with 11 formally described species has been proposed in the Facetotecta, but many undescribed forms exist, particularly in East Asian waters. Many aspects of the biology of the Facetotecta are yet to be unraveled, and our work is proceeding along four tracks. First, we are describing a hitherto unreported and overwhelming diversity of nauplii and cyprids both within and between locations in Taiwan and Okinawa using SEM, high-speed video, light microscopy and digital stacking software. Second, we will attempt to fully characterize the metamorphosis from the cypris to the ypsigon stage by histology and TEM. Third, we will construct a molecular phylogeny used to base a new classification and to trace larval character evolution. Fourth, to identify the adults, which constitute one of the biggest enigmas in marine biology, we will use an array of molecular techniques to locate them in the field or in their host(s).

Almatium Sp. from the Middle to Late Triassic Madygen Formation, SW Kyrgyzstan and the Structure of the Calmanostraca

*Elsea PK, Hegna TA**
Western Illinois University

The Madygen Formation is a noted terrestrial and aquatic lagerstätten found in SW Kyrgyzstan. Among the notable animals that it contains is a provisional new species of branchiopod crustacean belonging to the genus Almatium. The main differences between the Madygen Almatium specimens and specimens of Almatium from elsewhere lie in discontinuous proportional differences in the shape of the carapace. Larger samples may eventually demonstrate that these proportional differences are allometric and that the Madygen Almatium specimens are part of a single, highly variable species of Almatium across the Triassic of Asia. Traditionally, Almatium has been placed in the Kazacharthra—a clade of unique notostracan-like branchiopod crustaceans. Together with the notostracans, they form the clade called the Calmanostraca. However, owing to the morphological heterogeneity of the purported kazacharthrans, there is very little morphological support for the monophyly of Kazacharthra. A phylogenetic analysis (parsimony and Bayesian) of the Calmanostracans demonstrates this by finding essentially no structure to the kazacharthrans, and failing to recover their monophyly in the Bayesian analysis. Even so, many kazacharthrans remain very poorly known—it is possible that as they become better known, their phylogenetic resolution will increase.

Nested Distribution of the Peracarida of Bernardo O'Higgins National Park (S Chile) Channels and Fjords

Esquete P, Aldea C
Universidade de Aveiro, Facultad de Ciencias & Instituto de la Patagonia

The Crustacea Peracarida is of the most diverse and abundant taxa in benthic ecosystems, and a potential tool for marine biogeography hypothesis testing due to the absence of dispersive phase together with a variety of displacement capacities. Nevertheless, the knowledge of the biodiversity and distribution patterns of the Peracarida is still scarce in many areas of the ocean world. On the other hand, Bernardo O'Higgins National Park (BONP), located in the Chilean Channels and Fjords ecoregion is an area of very unique, fragmented ecosystems that offers an excellent opportunity for the study of the distribution patterns of the faunas in habitats with environmental gradients. With the aim of studying the biodiversity and distribution patterns of the benthic communities in BONP, 20 sites were sampled by scuba divers at 5 and 15 m depth by scrapping quadrats of 25x25cm. A total of 561 individuals belonging to 60 peracarid nominal taxa were identified, with a high proportion (30%) of singletons. The most ubiquitous species was the isopod Exosphaeroma gigas, whereas the most abundant were two undescribed species of amphipods, Paramoera sp1 and Polycheira sp1. These results revealed a nested distribution pattern within the channels (T=20.762º; p<0.01), on which the faunas of the sites located at the innermost part or the channels appear as a subset of those at the outer sites.

Discovering the Tanaidacea of Caribbean Mesophotic Reefs

Esquete P, Schizas N, Chatterjee T
Universidade de Aveiro, University of Puerto Rico, Indian School of Learning

Mesophotic reefs are characterized by low light adapted reef communities occurring in tropical seas. Unlike their shallower counterparts, they are largely understudied and even baseline diversity studies are almost inexistent. This work deals with the Tanaidacean specimens collected in the framework of the 2016 Nekton/XL Catlin Deep Ocean Survey in Bermuda, Deep-CRES program of the University of Puerto Rico, and three mesophotic cruises (2010-2012) in US Caribbean. Samples consisted on corals, algae and rhodolits were taken by technical divers and Triton submersibles at depths ranging 45-330m. A total of 291 individuals belonging to 15 morphospecies of four families were found, all of them but two (Synapseudes erici and Hoplolemius propinquus) are new to science. Just like the typical situation for shallow water samplings, the number of species per sample was relatively low, ranging from 1 to 9. The most abundant and widespread species belonged to the genus Paraleptochelia, followed by one belonging to Sinelobus. This work will be the first study focusing on Tanaidacea of mesophotic reefs, and represent a contribution to the knowledge of the diversity of the Caribbean Sea.

The Tanaidacea of the Iberian Margin and Adjacent Abyssal Plains: Diversity and Connections

Esquete P, Garcia-Herrero A
Departamento de Biologia & Cesam, Universidade de Aveiro

Amongst the Peracarida, the Tanaidacea is perhaps most sedentary order; Tanaidacean species are known to live in tubes and/or buried in the sediment, with no or little swimming capacity. This condition, together with the absence of a larval dispersive phase, lead to a tendency to local speciation and endemicity. On the other hand, the continental margins of the Iberian Peninsula host a variety of geomorphological oceanographic settings: bottom currents run from the Mediterranean Sea and the north Atlantic, passing by cold seeps, submarine canyons, coral mounds and other structures resulting in a remarkable habitat diversity. In this work, we compiled all the georeferenced records of Tanaidaceans corresponding to the Iberian continental margin and adjacent abyssal plains (48.57^{o}–32.22^{o}N, 14.436^{o}W¬–5.77^{o}E; 210-4800m depth) available from the literature, OBIS datasets (total: 122 records) and identifications of the biological collection of the Biology Department of the University of Aveiro, coming from 13 oceanographic cruises carried out between 2000 and 2014 in the framework of different international projects (855 records). Biogeographical analyses were performed with QGIS and VNDM/NDM software. There are significant differences regarding the amount of data at different areas: there is no data at the Galician Bank, or Mediterranean margin north to Alboran sea; The eastern area of the gulf of Cadiz called "El Arraiche" showed the highest endemicity values, but also the majority of the records; A significant percentage of species are shared between El Arraiche and Alboran, and also between the Portuguese and Cantabric margins.

Diversity, Disparity and the Evolutionary Radiation of Symbiotic and Non-Symbiotic Portunid Crabs

Evans N
National Museum of Natural History, Smithsonian Institution

Recent phylogenetic analyses of Portunidae have revealed that all symbiotic taxa of the subfamily Caphyrinae are derived within the nonsymbiotic genus Thalamita (subfamily Thalamitinae). Totaling 12 genera and approximately 190 species, Thalamitinae now constitutes the most diverse portunid clade and exhibits some of the family's greatest morphological diversity (i.e., disparity). However, while much of the morphological disparity within this clade appears to be associated with the emergence of symbiotic taxa (now subtribe Caphyrina; 4 genera, 40 spp.), Thalamitinae's greatest species diversity accumulated in multiple lineages of the non-symbiotic genus Thalamita s.l. (76 spp., including the newly described genus Thranita Evans, 2018). This pattern appears to contradict current hypotheses that the evolution of symbiosis in crustaceans may promote large adaptive radiations, generating greater diversity than that of closely related nonsymbiotic clades. Here I use fossil calibrated molecular dating, geometric morphometrics, and model-based phylogenetic comparative methods to investigate patterns of diversity and disparity (carapace shape and body size) associated with the evolutionary radiation of symbiotic Caphyrina taxa and nonsymbitoic Thalamita s.l. clades. To a lesser extent, patterns of allometric disparity are also discussed, providing a better characterization of novel morphology in these crabs. This work provides a small but important counterpoint to our current understanding about the emergence of symbiosis and patterns of diversification in crustaceans.

A Synthesis Phylogeny of the Thecostraca: Integrating Diverse Phylogenetic Efforts Into a Comprehensive Phylogeny for Barnacles

Ewers-Saucedo C, Owen CL, Perez-Losada M, Hoeg J, Glenner H, Chan BKK, Crandall KA
Zoological Museum of the Christian-Albrechts University, Henry Jackson Foundation, George Washington University, National Museum of Natural History, Smithsonian Institution, University of Copenhagen, University of Bergen, Academia Sinica

The Thecostraca, which include the Facetotecta, Ascothoracida and Cirripedia, is a highly variable crustacean group in terms of both morphology and biology. While work on phylogenetic relationships among the Thecostraca at both high and low taxonomic levels has been prolific, there has been little integration across those levels and across groups working on barnacle evolution. To fill this gap in barnacle systematics, we present here a new 'synthesis' tree approach that maps phylogenetic hypotheses onto underlying hierarchical taxonomic information. This results in an integration of both phylogenetic and taxonomic information into a single phylogenetic hypothesis for the entire Thecostraca. To construct our synthesis tree, we included 27 phylogenetic studies, and merged them with the comprehensive Open Tree of Life Taxonomy. We show that much of the Thecostracan taxonomy needs to be re-evaluated: only 18 of 38 families with phylogenetic information were monophyletic. Comparing the distribution of taxa with and without geographic information available at the GBIF and OBIS online databases revealed that the coasts of the USA, Europe and Australia have the highest density of records, both of species with and without phylogenetic information. Unsurprisingly, the deep sea and Antarctica have very few records. However, all regions have species with geographic information, which have not been included into phylogenetic studies. This study highlights both solved and resolved areas for future phylogenetic studies, and the resulting phylogenetic reconstruction can be used to answer large-scale comparative questions about adaptations, radiations and trait evolution.

A Review of Crustacean Sex Ratios in the Light of Sexual System Evolution

Ewers-Saucedo C
Zoological Museum of the Christian-Albrechts University

In animals, males either coexist with hermaphrodites or females, or are completely absent. Therefore, the sexual system can be described by the male frequency – the sex ratio. When males are absent in a population, the sexual system must either be hermaphroditism or parthenogenesis. When males occur at low frequencies, the other sex is hermaphroditic, making the system androdioecious. Lastly, at high male frequencies, the other sex is likely female, and the system is dioecious (gonochoristic). Crustaceans have evolved all of these sexual systems, with a surprisingly high frequency of androdioecy, which is extremely rare elsewhere in the tree of life. In the present study, I review sexual systems in crustaceans, focusing on androdioecy as the connecting stage between hermaphroditism and dioecy. In theory, life history and mating system are two important factors to shift sex ratios, and therefore sexual systems. I will assess these factors in crustaceans with different sexual systems, as far as data exist, and add new data from the androdioecious barnacle Chelonibia testudinaria. I show that the mating system differs between androdioecious species that are ancestrally hermaphroditic or dioecious, and that life history strategies play an important role when androdioecy evolved from hermaphroditic ancestors, but less so when the ancestors were dioecious.

Cloning Crayfish Cell Culture

Faulkes Z, Deleon H, Thomas J
the University of Texas Rio Grande Valley

The parthenogenetic marbled crayfish, Marmorkrebs, is an emerging model organism. For example, it is the only decapod crustacean with a sequenced genome, and several labs have used Marmorkrebs as a model for embryonic development. One difficulty in studying embryonic cells is that eggs contain a large amount of yolk, which can make imaging embryonic cells difficult. We successfully isolated and cultured cells from early stage Marmorkrebs embryos, and confirmed their identity using DNA sequencing. Cellular and molecular tools for use in crayfish are underdeveloped compared to other model organisms, and cultured embryonic cells could provide a new testbed for those techniques.

Preliminary Phylogenetic Analysis of the Enigmatic Cycloidea

Feldmann RM, Schinker M, Schweitzer CE, Maguire E
Kent State University

The crustacean Cycloidea comprise a heterogeneous assemblage of small, ovoid creatures ranging in age from Carboniferous to Late Cretaceous. Although some exhibit well-defined head regions, antennal structures, and short, jointed appendages, variations in other morphological features suggests that they do not comprise a coherent group. Preliminary phylogenetic analyses, based upon examination of as many type and figured specimens as possible, coupled with photographs of other non-type specimens, suggests that the current systematic arrangement requires re-evaluation. Selection and coding of characters for analysis is limited and subjective, in part, because of preservational bias. Appendages were not scored because of paucity of specimens. Cuticle is absent in nearly all specimens; preservation is generally moldic. Specimens may expose dorsal surfaces, ventral surfaces or, rarely, internal features including gill bundles. Although representatives of Carboniferous species from Great Britain and the United States may be numerous, most taxa are based upon one, or just a few specimens. Previously named taxa were proposed based upon different preservational aspects necessitating reconsideration. Of the 45 named species arrayed into 16 genera, specimens documenting 6 species have been lost, 2 species are probable synonyms, and at least 2 may be referable to taxa other than Cycloidea. The current cladistic analysis suggests six well-defined clades and a few unresolved taxa. Shape of the carapace, small size, and presence of short legs with hooked dactyli on some species suggest either benthic or parasitic lifestyles.

Did Sexual Selection Hinder Survival of Ostracode Species Through the K/Pg Mass Extinction?

Fernandes Martins MJ, Hunt G, Thompson C, Lockwood R
Smithsonian Institution, National Museum of Natural History, The College of William and Mary

Sexual selection is a special case of natural selection that relates to investment in traits that help organisms compete for mates. Sexual selection is suggested to affect the probability of species extinction: Investment in expensive traits that do not directly increase survival may elevate extinction risk when conditions change, in particular under extreme ecological shifts. However, empirical testing has been restricted to the living biota, where indirect proxies are used to calculate extinction. Thus the role of sexual selection in dictating extinction selectivity will remain largely untested without the inclusion of fossil data. We developed a study system using ostracodes that allows us to examine the role of sexual selection in fossil lineages. In cytheroid ostracodes the male shell is systematically more elongate than that of females, and the sexes can be assigned even in fossils. Moreover, as verified in the living fauna, the strength of dimorphism can be taken as an indicator of the intensity of sexual selection. By leveraging the rich fossil record of these organisms, we can test sexual selection as a driver of extinction selectivity across the Cretaceous/Paleocene mass extinction. Here we report the preliminary results of an investigation using the fossil record of early Paleocene (Danian) cytheroid ostracodes from the US Gulf Coastal Plain. We digitized the valve outlines of adult specimens, and used mixture modeling to identify sex clusters in samples. We successfully estimated sexual dimorphism in body size (difference in log area between the sexes) and shape (difference in log length/height ratio) for 35 populations assigned to 24 species and 14 genera. Comparing dimorphism data between the Late Cretaceous and Paleocene, we observe a systematic reduction in size and shape dimorphism in the Paleocene. This is most recognizable by the absence in the Paleocene of species with males that are much bigger and much more elongate then females, a style of dimorphism that reflects higher investment in mating traits. Our results suggest that aspects of resource allocation (survival vs reproductive investment) may be an important factor for species survival at the end Cretaceous mass extinction.

Genetic Structure of Calanus helgolandicus (Calanoida:Copepoda) from the Deep Balearic Sea

Figueroa NJ, Cartes JE, Figueroa DF, Scott N
University of Texas Rio Grande Valley, Instituto de Ciencias del Mar

Calanus helgolandicus (Copepoda: Calanoida) is widely distributed in epipelagic waters of the Atlantic, Mediterranean and the Black Sea. The species is also very abundant at bathypelagic/abyssopelagic depths. In the Balearic Sea (western Mediterranean), C. helgolandicus was the dominant zooplantkon (> 95% of specimens collected) near the bottom at 2170 m depth. The objective of our project was to compare the genetic structure of C. heloglandicus from the deep Balearic Sea to that of previous studies that defined, unique and distinct populations in the English Channel-North Sea, the Adriatic Sea, and the Black Sea (this population is deemed C. euxinus). We targeted two mitochondrial regions, cytochrome oxidase I (COI) and the small ribosomal unit (16s). Haplotype network analyses show that the Balearic Sea had a high proportion of individuals with the same, dominant haplotype found in the UK-North Sea population. This is consistent with the Atlantic origin of Mediterranean fauna. Our gene flow and AMOVA analyses show that all populations are significantly different from each other, except for the near-bottom deep population in the Balearic Sea and the neritic population from the Black Sea. This surprising connection could be explained by the hydrography of the region. The Black Sea receives an inner flux of saltier water from the Mediterranean, while the outer flux from the Black Sea occurs at surface. Past colonization of the Black Sea by deep (not by surface) populations could explain the high affinity between C. helgolandicus from the deep Balearic Sea and those from the Black Sea.

First Data of Tanaidacea from the Tidal Channels of the Gulf of Gabès (Central Mediterranean Sea,Tunisia) with the Discovery of Three New Species

Fersi A, Esquete P, Neifar L, Dauvin JC*
Université de Sfax, Universidade de Aveiro, Laboratoire Morphodynamique Continentale et Côtière

The distribution and abundance of Tanaidacea were studied for the first time in the tidal channels of the Gulf of Gabès (Tunisia). Samples we taken at 26 sites during four seasons (spring, summer, winter and autumn) from March 2016 to January 2017. Each sample consisted in four replicates of a 0.1 m^2 Van Veen grab (total 0.4 m^2). A total of 2,896 individuals of eight species of Tanaidacea were identified. Apseudopsis was the most diversified genus with four species: two new species were discovered and a new record of Apseudopsis ostroumovi; until new only in the Black Sea was recorded for the first time in the Mediterranean Sea. Apseudes was the second most diversified genus with three species. The species richness and abundances were higher in winter than during the other seasons. The Tanaidacea structure was linked to the location of the channels in the Gulf of Gabès. High abundances were recorded in the most polluted channel near an emissary of phosphogypsum. This highlights that these species were very resistant and tolerated pollution. Moreover, some malformation anomalies were recorded in Apseudopsis individuals in this high polluted channel.

Virus Prevalence in Proximity to Flow-Through Blue Crab Aquaculture in a North American Atlantic Estuary

*Flowers EM, Johnson AF, Aguilar R, Schott EJ**
University of Maryland School of Medicine, University of California San Diego, Smithsonian Environmental Research Center, University of Maryland Center for Environmental Science

From New England to Argentina, the blue crab Callinectes sapidus is a crucial benthic-pelagic link in Atlantic estuarine ecosystems and supports fisheries worth hundreds of millions of dollars. Across this range, blue crabs are infected by a pathogenic reovirus, termed CsRV1, at prevalences up to 78%. Soft crabs are a value-added product created by holding pre-molt crabs in short term aquaculture until ecdysis. Soft crab culture is often conducted in flow-through systems that draw water from the estuary and return effluent to the same waters. Studies in the US show that crab mortality during soft crab production is often over 25%, and recent work indicates that the majority of dead crabs carry CsRV1 at high levels. To assess whether flow-through shedding increases CsRV1 infection among wild crabs near soft crab aquaculture effluents, we used a quantitative PCR assay to measure the prevalence of the CsRV1 genome in crabs captured in scientific trawls both near to and far from active flow-through shedding aquaculture. A total of 898 crabs, caught at 5 sites on multiple dates in 2012 and 2013, were analyzed. Virus genome prevalence was highly variable across time and space. Generalized Linear Models were used to investigate the relationship between CsRV1 prevalence and crab sex, size, season and location. In 2012, crabs close to shedding systems had a higher probability of CsRV1 infection. Larger crabs had a higher probability of CsRV1 infection, leading to the hypothesis that as crabs age (grow), they are more likely to acquire CsRV1.

Loss of Wound Melanization Response in the Cave Shrimp Troglocaris

Fong DW, Bilandžija H, Laslo M, Porter ML
American University, Ruđer Bošković Institute, Harvard University, University of Hawai'i at Mānoa

Many species adapted to aphotic subterranean habitats have lost all body pigmentation. Yet, melanization is an important component of wound healing in arthropods. We amputated appendages in a variety of cave-adapted and surface-dwelling arthropods. A dark clot formed at the site of injury in most species tested, including even albino cave-adapted species. The dark coloration of the clots was due to melanin deposition. The speed of wound melanization was uncorrelated with a difference in metabolic rate between surface and cave populations of an amphipod. The chelicerate Limulus polyphemus, all isopod crustaceans tested, and the cave shrimp Troglocaris anophthalmus did not melanize wounds. The loss of wound melanization in T. anophthalmus was an apomorphy associated with adaptation to subterranean habitats, but in isopods it appeared to be a symplesiomorphy unrelated to colonization of subterranean habitats. We conclude that wound melanization i) is an important part of innate immunity because it was present in all major arthropod lineages, ii) is retained in most albino cave species, and iii) has been lost several times during arthropod evolution, indicating melanization is not an indispensable component of wound healing in arthropods.

Long-Term Population Dynamics of a Stygobiont from a Hypotelminorheic Habitat

Fong DW, Farmer W
American University

Weekly interval multiple-mark multiple-recapture estimates of the population sizes of the troglomorphic amphipod crustacean, Stygobromus tenuis potomacus, at two adjacent seepage springs (sites B and C) associated with hypotelminorheic habitats were conducted during the winter through early summer months in 2014, 2015 and 2017 using both Schnabel (S) and Schumacher-Eschmeyer (S-E) methods. Estimates based on S and S-E methods were similar, but the estimates fluctuated over the years and differed between the two seepage springs although they were only < 3 m apart. Estimated values and 95% CI in parentheses were: 2014: ~ 440 (320 – 660) in B and ~ 640 (450 – 790) in C; 2015: ~ 1,270 (990 – 1940) in B and ~ 5,400 (1,300 – 15,000) in C; 2017: ~ 3,450 (2,270 – 9,570) for C with B having ceased flowing. The number of ovigerous females also differed between sites B and C each year and fluctuated over time at each site. Our results indicate that long-term monitoring is necessary to reveal the population dynamics over time and the extensive variation in population dynamics between sites in proximity as well as the ephemeral nature of such habitats.

Early Post Hatching Stages of Nymphon Australe Hodgson 1902, an Example of Direct Development in the Pycnogonida

Fornshell JA
Smithsonian Institution

Using scanning electron microscopy, we describe the first and second post hatching stages of Nymphon australe Hodgson 1902. Upon hatching, the animals have a pair of three segmented cheliphores, a pair of three segmented larval appendages II or III? Three underived buds of walking legs, 1, 2 and 3 are also present. The second post hatching stage has seven-segmented walking legs 1 and 2 and a three-segmented walking leg 3. The fourth walking leg is present as an underived bud in this stage. The paired primordia of ventral ganglia of the ventral chord are present on the epidermis. The digestive system is still incomplete; the proctodeum has not appeared by the second post hatching stage. The tubercle with the four eye has not appeared by the second post hatching stage. The first two post hatching stages of Nymphon australe display several characteristics of embryonic development including the mechanism of ventral nerve chord ganglia formation, limb bud development, the incomplete development of the digestive tract as indicated by the absence of the proctodeum and the presence of underived limb buds. Further the absence of a distinct metamorphosis into the adult form accompanied by apoptosis resulting in the loss of structures found in a larval stage, but not the adult. It is proposed that these facts may be interpreted to indicate that in the Pycnogonida, embryonic development is incomplete at the time of hatching. Also that these animals exhibit a form of direct development.

Sight Beyond Eyes? Are Photophores of Deep-Sea Crustaceans Able to Both Emit Bioluminescence and Sense the Background Light Intensity?

Frank TM
Nova Southeastern University

Counterillumination is used extensively by deep-sea crustaceans to hide their silhouettes from visual predators swimming below them. Utilizing ventral photophores, they are able to emit bioluminescence that precisely matches the intensity of downwelling light being blocked by their bodies, so that their silhouettes disappear. How they are able to achieve such a close match is not well understood, but a recent discovery (Bracken-Grissom lab) that photophores possess opsins suggest that the photophores themselves might be light sensitive. To examine this possibility, electrophysiological recordings were conducted on the cuticular photophores of Oplophorus gracilirostris, Systellaspis debilis and Janicella spinacauda (Family Oplophoridae) and hepatic photophores (Organs of Pesta) from Sergestes sp. (Family Sergestidae). The crustaceans were collected alive and without exposure to light on several NSF funded research cruises, with experiments conducted both on shipboard and on land. No responses were obtained from any of the cuticular photophores in response to varying intensities of light. The larger hepatic photophores gave repeatable responses to light when the eyes were also exposed to the light stimulus. When the electrode was placed in the water bath next to the eyes, or in muscle tissue next to the photophores, no responses were observed; the response returned when the electrode was again placed in the photophore. When a filter blocked the light stimulus to the eyes, however, the response from the hepatic photophores also disappeared. These results will be discussed with respect to the role of hepatic photophores in mediating the counterillumination response.

Shrimps of the ‘Cuapetes–Palaemonella Complex’ (Caridea: Palaemonidae) on Their Way to Primary Symbioses

Frolová P, Horká I, Ďuriš Z
University of Ostrava

The majority of the coral reef shrimps Palaemonidae are associated with various invertebrates. However, the target group of our study is basally separated from the main group of symbiotic palaemonids and contains 10 genera. The most species-rich of these are Cuapetes and Palaemonella. The members of the complex exhibit wide variety of lifestyles (from predominate free-living to both facultative and obligatory symbiosis) and, therefore, the complex may represent an appropriate model for the study of the evolution of symbiosis in palaemonid shrimps. To this end, however, the reliable phylogeny of the complex must be inferred. According to both ML and BI phylogenies based on four molecular markers (16S rRNA, CO1, H3, and 18S rRNA), the polyphyletic genus Cuapetes is represented by four independent lineages, whereas Palaemonella seems to be paraphyletic as it includes the genus Vir and Atlantic Cuapetes americanus. Furthermore, a representative of a new genus was found in a material from Papua New Guinea raising the number of known genera within the complex to 11. The results of the Ancestral State Reconstruction suggests that the ectosymbiotic shrimps evolved from free-living ancestors independently several times. While some of these diverged into the entire clades of ectosymbionts (Vir, Philarius, Harpilius, Ischnopontonia and Anapontonia), others represent an isolated ectosymbiotic species (C. amymone, C. kororensis, C. nilandensis, and P. pottsi) within the clades dominated by free-living relatives. The study is supported by project SGS/PřF/18, and program of Support for science and research (RRC/10/2017). P. Frolová is scholarship holder of Ostrava city.

Discovering Biodiversity with Genetics and Morphology: a New Deep-Sea Amphipod Family

Frutos I, Jazdzewska A, Hendrycks E
University of Hamburg, University of Lodz, Canadian Museum of Nature

Within the marine crustaceans, Amphipoda are one of the most diverse groups among the Peracarida. However, knowledge of amphipod diversity in the deep-sea is still very poor, due to the vastness of the deep-sea and the difficulty in collecting at great depths (especially below 2000 m depth). This study of amphipods collected during six different deep-sea expeditions carried out in both the North and South Atlantic (IceAGE, Vema-TRANSIT, DIVA2 and DIVA3 expeditions) and the north-west Pacific Oceans (SokhoBio and KuramBio expeditions), revealed the discovery of a new amphipod family. Based on two mitochondrial genes (COI and 16S) and morphological features, a total of 205 individuals have been identified belonging to eight new species. These species are allocated to a new genus and a new family. One species was found south of Iceland, two in the central Atlantic, two in the South Atlantic and three at the Kurile- Kamchatka area in the north-west Pacific. The relative close proximity of some of them and their occurrence at both sides of a ridge (Mid Atlantic Ridge) or trench (Kurile- Kamchatka Trench) provides additional information about the connectivity between abyssal plains and the biogeographic distribution of amphipod fauna in the deep-sea.

A New Mesosignum Species (Crustacea: Isopoda: Mesosignidae) from Abyssal Bottoms of the Puerto Rico Trench

Frutos I, Sorbe JC
University of Hamburg, Station Marine

The family Mesosignidae was erected by Schultz (1969) to accommodate the genus Mesosignum Menzies, 1962. Later on, George (2003) assigned the fourteen known species into five genera: Bermudasignum, Costasignum, Japanosignum, Kurilosignum and Mesosignum. Currently, the genus Mesosignum comprises ten species (three of them undescribed). With an exclusive deep-sea distribution, Mesosignum species are mainly reported from the tropical latitudes of the eastern Pacific and Caribbean Atlantic, but also from Antarctic waters. Within the framework of the German multidisciplinary Vema-TRANSIT project on board of the new RV Sonne, the benthic macrofauna of the Puerto Rico Trench area (northwestern Atlantic) was sampled using a multinet camera-epibenthic sledge. Samplings were carried out in January 2015 at 6 stations located between 4552 and 8340 m depth. Within the isopod material collected, nine specimens (male, female and manca stages) were ascribed to a new species of the genus Mesosignum according to the following discriminating features: whole body with dorsal denticulations, anterolateral projections of pereonite 2 broadest at proximal end, lateral margins of pereonites and pleotelson with teeth, pleotelson with a pair of distolateral projections and rounded distal margin with 4–6 apical teeth, bearing a submarginal row of teeth on ventral side. The new species was recorded in one station at 4552 m depth. The world distribution of the currently 11 known species of Mesosignum is provided as well.

Molecular Regulation Mechanism of Sex-Determination and Sex Differentiation in Penaeid Shrimp

Fuhua L, Shihao L, Qing G, Jianhai X
Chinese Academy of Sciences

Understanding the mechanism of sex determination and differentiation in shrimp will facilitate the development of biotechnologies for the culture of monosex populations. In recent years, we have focused our study on the sex differentiation and development of shrimp. Genes related to sex-determination and sex differentiation, including sex lethal (Sxl), transformer 2 (Tra-2), doublesex (Dsx), crustacean hyperglycemic hormone (CHH), and insulin-like androgenic gland hormone gene (IAG) and insulin-like androgenic gland hormone receptor (IAGR) were isolated and characterized. Sxl, Tra-2 and Dsx are homologs of genes in sex determination cascade of Drosophila. The expression patterns of sexual dimorphism of these genes show that they are important during sex determination or sexual differentiation. IAG, which controls sexual differentiation of crustacean, has two spliced isoforms and is mainly expressed in AG. The expression of IAG was regulated by Dsx and CHH in shrimp. An IAGR, which was mainly detected in AG and testis, could interact with two types of IAGs. The expression of IAGR was regulated by CHH. The data provides not only new clues to understand the molecular mechanism of sex determination and sexual differentiation of crustacean, but also possible target for developing sex control agents.

Looking For Sacculina (Rhizocephala, Cirripedia)

*Galindo LA, Pellen F, Rabet N, Audebert F**
Université de Versailles Saint-Quentin-en-Yvelines, Sorbonne Universités

Sacculina is the most common cirriped parasite in marine and brackish waters. It includes 85% of all rhizocephalan diversity although there is not a clear synapomorphy that gathers all these species together. We revised the phylogenetic relationships within Sacculinidae and stablished limits and contains of genus Sacculina. Cytochrome oxidase I (COI) sequences were obtained from the Sacculinidae collection deposited at the Museum National d'Histoire Naturelle, Paris. The 200 COI sequences were used to estimate a gene tree using Bayesian inferences. Subsequently, one individual per lineage was sequenced for the 18S and 28S rRNA genes. Rhizocephala emerged as monophyletic and a sister group of Thoracica. Within the "Kentrogonids", Peltogastridae was found to be paraphyletic. One clade included all species previously considered as Sacculina merged with other genera (ex. Loxothylacus or Heterosaccus), rendering the current concept of "Sacculina" as polyphyletic. Clearly, the tree showed two mayor diversification events within the Sacculina-clade, and only one contained Sacculina carcini, the type species of the genus. Not a clear biogeographic pattern was revealed from the phylogeny. Atlantic and Indo-pacific species can be siblings, and sympatric species may not be closely related, suggesting the occurrence of repetitive colonization events. Given that different lineages were found to parasitize the same decapod species, this suggests a strong convergence of the Sacculina phenotype traits adapted to parasitism. Clearly, the history of life traits of Sacculina are much more complex than expected and classification of this group does not reflect its evolutionary path.

Operational Sex Ratio and the Degree of Assortative Mating Among Crustacean Sympatric Species

Galipaud M
University of Zurich

When living in sympatry, closely related species sometimes interact sexually. If such interbreeding produces unfit hybrids, selection is expected to lead to assortative preferences, where members of each species prefer to mate with their own kind. This simple model yet overlooks the effect of demographic parameters such as adult and operational sex ratio on competition for mate access and on resulting mating patterns. I here present a simulation model of mating interactions between 2 species in sympatry, taking explicitly the competition emerging from pairing dynamics into account. I can show that initially similar mating preferences can lead to strikingly different interbreeding patterns under different values of adult and operational sex ratio, ranging from assortative mating to competitive exclusion of one species by the other. This model helps predicting the fate of crustacean species sexually interacting in sympatry. Females of many crustacean species have very restricted periods of sexual receptiveness, right after moulting. This dependence of copulation on female moulting cycle leads to heavily male biased operational sex ratio, male-male competition and the evolution of precopulatory mate guarding. Such extended periods of pairing in turn limit the availability of preferred mating partners and increases competition for their access. In natural populations, mate guarding duration can vary widely according to temperature (because it affects female moulting cycle length) or adult sex ratio for instance. These variations in mate guarding duration should therefore strongly affect the degree of assortative mating among sympatric crustacean species, eventually determining their ability to coexist.

Next Generation Sequencing and an in Silico Approach Identifies an Endo-Beta-1,4-Mannase, a Novel Highly Expressed Hemicellulase Within the Herbivorous Christmas Island Red Crab, Gecarcoidea natalis

Gan HM, Austin C
Deakin University

The Christmas Island red crab, Gecarcoidea natalis, is mainly herbivorous, consuming mostly brown leaf litter. It utilises specialised cellulase and hemicellulase enzymes to digest substantial amounts of cellulose and hemicellulose. To comprehensively examine the type and level of expression of these enzymes, the transcriptome of the midgut gland (main digestive tissue) was sequenced using next generation sequencing and the carbohydrase enzymes characterised using an in silico approach. Transcripts of seventy carbohydrase enzymes were identified. This included highly expressed cellulase and hemicellulase enzymes. Four transcripts of an endo-β-1,4-glucanase ("classic cellulase") had the highest combined total expression. Out of these four transcripts, one was previously sequenced and the others may represent novel endo-β-1,4-glucanase subfamilies. The next three transcripts, in descending order of expression were a novel endo-β-1,4-mannase (hemicellulase), a previously sequenced β-1,3-glucanase (laminarinase)(hemicellulase) and an amylase. The endo-β-1,4-mannase, which hydrolyses the hemicellulose mannan, had the highest expression out of all of the carbohydrase transcripts. It was expressed in the midgut gland but not in the muscle or gill. The endo-β-1,4-mannase is a novel and previously missed hemicellulase whose high expression suggests that it may have an important digestive function. Indeed the endo-β-1,4-mannase may be more important, in terms of the amount of metabolisable sugars produced, than the endo-β-1,4-glucanase ("classic cellulase"), as its activity within the digestive fluid, was higher than that of the endo-β-1,4-glucanase. The enzyme activity also confirms homology modelling that suggests that the endo-β-1,4-mannase transcript would be translated into a functional enzyme.

New Records of Caridean Shrimps (Crustacea Decapoda Caridea) from China Seas

Gan Z, Li X
Chinese Academy of Sciences

Four species of caridean shrimps collected from the East China Sea and South China Sea represent new records for the Chinese waters: Lysmata kempi Chace, 1997; Lysmata lipkei Okuno & Fiedler, 2010; Chlorocurtis jactans (Nobili, 1904) and Rhynchocinetes conspiciocellus Okuno & Takeda, 1992. The diagnostic characters and illustrations of these four species are presented, with remarks on their taxonomy. The identification keys of these species from Chinese waters are provided.

Modelling Larval Dispersal and Connectivity of the Blue Crab (Callinectes sapidus) for Florida Coastal Waters

Garavelli L, Criales MM, Ghannami M, Crowley C, Gandy R, Chérubin L*
Pacific Northwestern National Laboratory, University of Miami, Ecole Nationale Supérieure de Techniques Avancées Bretagne, Fish and Wildlife Research Institute (FWRI), Florida Atlantic University

Although the blue crab Callinectes sapidus covers a large geographic range, from Texas to Florida and from Florida to New Jersey, there is no clear understanding of the connection among blue crab subpopulations. Based on genetic studies and natural population breaks, the fishery of the blue crab in the Gulf of Mexico has been managed as an east and a west stock, each one modeled with no exogenous sources of recruits to the population. To understand the potential connectivity among subpopulations of blue crab in the eastern Gulf and Florida's Atlantic coast we developed a high-resolution biophysical model parameterized with species-specific early life-history information, sub-grid turbulence motion and settlement habitats. Simulations were run monthly during 2015 releasing particles from three onshore and three offshore stations at each of eleven spawning sites located in western and eastern Florida coastal waters. Connectivity matrices estimated the likelihood that each spawning event contributes to the neighboring populations. Results indicate a high percentage of local retention at the western Florida stations. However, a connection is evident between the offshore Panama City station and both Mississippi, Alabama and Louisiana waters and the south Florida coast. At the eastern Florida stations there is also a clear connection with the Georgia coastal region. These results are of particular interest given the potential of long distance connectivity as it relates to homogenizing the genetic structure and the use of more accurate models for blue crab assessment.

Rediscovery of the Presumed Extinct Horseshoe Shrimp (Lightiella serendipita) in San Francisco Bay, California, USA

Garcia C, Flanagan AM, Rogers DC, De La Cruz S
U.S. Geological Survey, Kansas University

Cepahlocarida are considered among the most primitive crustaceans alive today. The species Lightiella serendipita was first discovered in San Francisco Bay in 1953. Since then, despite several attempts to find it, the species was not observed for three decades and was presumed extinct. In 2017, a total of 13 adult L. serendipita specimens were serendipitously found as part of an on-going USGS study in central San Francisco Bay. Previously only 8 specimens had been collected – two juveniles, four adults, and two of unknown life stage. Benthic cores (10 cm dia. x 10 cm deep) were partitioned into "shallow" (0-4 cm) and "deep" (4-10 cm) sections to assess vertical distribution of macroinvertebrates within the sediment. Environmental factors sampled included water temperature, salinity, dissolved oxygen, pH, sediment grain size (percent sand, silt, and clay) and chemical composition (e.g., sediment organic matter). Lightiella serendipita were generally found in sediments with low organic matter (1.7-3%), high sulfate concentrations (594.6-1647 ppm SO4), fine loam textures (12.8-36.2% sand; 35.6-58% silt; 22.8-37.6% clay), and within the deep core sections. Interestingly, specimens were consistently observed in cores containing tube-forming Polychaeta (i.e., Sabacco elongatus and Capitellidae), suggesting L. serendipita may have a commensal relationship with sedentary polychaetes as do other Cephalocarids such as Lightiella incisa. The perceived absence of L. serendipita may be attributable to the sampling methods used in previous detection efforts and underscores the importance of sampling design. Additional studies are planned to understand basic ecology, benthic community, and habitat associations of this newly rediscovered species.

Litopenaeus vannamei Digestive Metallo Peptidases Compensate For Anti-Nutritional Sbti in Feed

García-Carreño F, Maytorena Verdugo C
CIBNOR

The aim of this work was to study mechanisms of homeostasis of the digestive system of the whiteleg shrimp Litopenaeus vannamei when fed anti-nutritional soybean trypsin inhibitor (SBTI). In a previous work, we tested if the shrimp could respond against SBTI in feed with the increase in the digestive proteolytic activity. This time we tested the time of response against the inhibitor and also how the two major digestive trypsin phenotypes change the proteolytic activity. In groups fed SBTI, the total proteolytic activity, trypsin and chymotrypsin decreased during food transit time (2–4 h), but increased at 23 h postprandial. Three metallo peptidases absent in the control group were identified in groups fed SBTI; individuals with trypsin phenotype CBA increased the activity of two metallo peptidases at 4 h of SBTI ingestion, while, individuals with trypsin phenotype CB increased the activity of three metallo peptidases at 23 h postprandial. The first evidence of feedback by the digestive system in the whiteleg shrimp fed SBTI was 1 h postprandial, with a concomitant increased in metallo peptidases activity at 4 h or 23 h depending on the trypsin phenotype in each specimen

A Synergistic Peptidase Network Mediates Food Protein Digestion in the American Lobster Homarus americanus (Edwards, 1837)

García-Carreño F, Rodríguez Siordia I
CIBNOR

The American lobster [Homarus americanus (Edwards, 1837)] is an omnivore decapod with generalist and opportunistic feeding habits, in which gastric fluid cysteine and aspartic peptidases are the main proteolytic enzymes. Using in vitro assays, the network of concerted acting peptidases belonging to aspartic and cysteine catalytic mechanisms that hydrolyze bovine serum albumin (BSA), hemoglobin, and actin was elucidated. The role of each class of peptidases in protein digestion was evaluated by monitoring the hydrolysis of each substrate in the presence of single or mixed specific peptidase inhibitors. Peptidases of the gastric fluid can hydrolyze BSA, actin, and hemoglobin. Hemoglobin was hydrolyzed by cysteine and aspartic peptidases but not by serine ones. Results suggest that hydrolases act synergistically. Hydrolysis of BSA and actin is carried out by a multienzyme network mechanism. Although cysteine peptidases hydrolyze about 50% of BSA and actin, aspartic peptidases are required to fulfill the task; when aspartic and cysteine peptidase activity is absent, no hydrolysis of the substrates happens at all. Serine peptidases seem not to contribute to the analyzed substrates hydrolysis at the conditions of the assay.

Rapid Colonization and Historical Introductions? - First Insights Into the Biogeography of Palaemon varians in the Baltic Sea

Geburzi JC, Meenke H
Kiel University

he ditch shrimp Palaemon varians (Leach, 1814) inhabits brackish coastal waters and estuaries along European coasts. In the Baltic Sea, it occurs only in fjords, separated bights and lagoons, but is absent from the open sea, resulting in a rather disjunct distribution. Little is known about the biogeography of P. varians in the Baltic Sea, and it has been debated whether its colonization is the result of a recent natural range expansion or an introduction. To investigate the population structure and colonization history of P. varians in the Baltic Sea, we sampled six populations along the southwestern Baltic Sea coast and compared them to specimen from the neighbouring southeastern North Sea on the basis of a 538bp fragment of the COI gene. The results revealed a clear separation between the North and Baltic Sea populations with haplotypes unique for each basin, and a lower genetic diversity in the Baltic Sea (2 haplotypes) compared to the North Sea (7 haplotypes). This result points in fact to a rather rapid colonization of the Baltic Sea. Curiously, we detected a single haplotype that was shared between the island of Sylt (North Sea) and the Schlei Fjord (Baltic Sea). These two sites are not directly connected by water, but were both trading places in medieval times, connected by a short overland route. We therefore hypothesize an additional historical introduction of P. varians into the Baltic Sea.

Seeking for Salinity: Larvae of an Invasive Crab Perform Horizontal Migrations to Optimize Development Conditions

Geburzi JC, Weiler N
Kiel University

The ability to successfully reproduce is a crucial step for alien species to become established in new environments. For alien decapods in particular, this step is however not a trivial one, as their planktonic larvae often have narrower tolerances towards abiotic conditions than the adult individuals. The Asian crab Hemigrapsus takanoi (Asakura & Watanabe, 2005) is the most recent alien brachyuran in the Baltic Sea, northern Europe. Our study aimed to clarify whether H. takanoi is able to perform its full larval development under the brackish conditions of the Baltic Sea, and thus to maintain a self-sustaining population in this newly invaded ecosystem. Plankton samples were taken regularly in two consecutive summers in Kiel Fjord (Germany, southwestern Baltic Sea) around the initial site of introduction of H. takanoi, both near- and off-shore. From the samples, we were able to reconstruct the full larval cycle of H. takanoi, consisting of five zoea and one megalopa stage, ultimately confirming the successful establishment of the crab in the Baltic Sea. The samplings further revealed that only zoea I larvae occur at the low-salinity near-shore hatching sites, while all further zoeal stages only occur in off-shore waters with higher salinity. Considering the lack of tidal or any other regular current patterns in Kiel Fjord, we hypothesise an active, purposive horizontal migration of the early zoeal stages of H. takanoi along the salinity gradient. This adaptation allows H. takanoi larvae to optimize development under variable salinity conditions and likely promotes the species' invasion success.

First Multigene Phylogeny of the Cumacea (Peracarida)

Gerken S, Meland K, Glenner H
University of Alaska, University of Bergen, Norway

Species of the peracarid order Cumacea are globally distributed members of marine soft-bottom communities. Locally, species of Cumacea can occur in high densities, often with high species diversity within only a few square meters of sediment. As prominent inhabitants of benthic habitats, both in terms of quantity and biodiversity, surprisingly little is known about the phylogeny of the order. Here we present the first multigene analysis (nuclear 18S, 28S; mitochondrial CO1, 16S, 12S, CytB) of the phylogenetic relationships within the Cumacea. The analysis includes 76 species, representing 26 genera from seven of the eight cumacean families. The only family lacking representation is the Ceratocumatidae, in which the species are very rare and largely restricted to depths below 500 meters. Monophyly of the order is strongly supported, as is the telson/pleotelson division. Most families are recovered as monophyletic, with the exception of some Antarctic Leucon that do not fall within the rest of the Leuconidae, and the Gynodiastylidae which arise from within the Diastylidae.

The Phylogenetic Position of Freshwater Barnacles

Glenner H, Høeg JT, Rees DJ, Rybakov A, Schubart C
University of Bergen, University of Copenhagen, Russian Academy of Sciences, Universität Regensburg Institut für Zoologie

Barnacles (Cirripedia) are predominantly a marine taxon. Within two of the three suborders that constitute Cirripedia, Thoracica (the sessile and pedunculated barnacles) and Acrothoracica (the burrowing barnacles), no truly freshwater dwelling species have ever been reported. In the remaining suborder, Rhizocephala (parasitic barnacles), four species are known to have been able to establish themselves in full freshwater habitats, as parasites of freshwater crabs. In the present paper we present molecular data that indicates a single marine-to-freshwater transition in a lineage, which is either closely related to, or positioned within the sacculinid genus Heterosaccus. Morphological characters in the settling larva, the cypris, further support this evolutionary event.

A Fishery in Flux: Claw Removal and its Impacts on Survival, Behavior, and Physiological Stress in the Jonah Crab (Cancer borealis)

Goldstein JS, Carloni J, Kibler RD
Wells National Estuarine Research Reserve, New Hampshire Fish and Game Department, University of New Hampshire

Found in coastal and shelf waters along the Atlantic coast of North America, from Newfoundland to Florida, Jonah crab (Cancer borealis) have been captured as incidental bycatch in the New England lobster industry for over 80 years. In the last 20 years however, Jonah crabs have become an alternative fishery target and landings have more than quadrupled. This has necessitated evaluation of the current status and prospective long-term health of the fishery. The biological implications of harvesting Jonah crab through the live removal of claws remain mostly unknown. The goal of this ongoing research is to evaluate current harvest practices (claw removal) and the implications on the health and behavior of Jonah crabs. Preliminary results from laboratory trials (n = 232 total crabs) suggest that double-claw removal incurs markedly more mortality (~74 %) compared with single-claw removal (~56 %) and control animals (~19 %). Physiological stress, assessed through concurrent haemolymph analyses suggest elevated levels of glucose and lactate in de-clawed crabs. Continued studies on behavior (feeding) and growth are ongoing in an effort to better understand Jonah crabs and manage this rapidly developing fishery in New England waters.

Impacts of Repeat Spawning on Lipid Content and Fecundity-Associated Regulatory Pathways in Giant Tiger Shrimp, Penaeus monodon

*Goodall JD, Botwright N, Coman GJ, Wade NM**
The University of Queensland, CSIRO Aquaculture, Queensland Bioscience Precinct, Bribie Island Research Centre

Low fecundity of domesticated Giant Tiger Shrimp (Penaeus monodon) is a major constraint to the development of selective breeding programs and supply of genetically improved broodstock. Greater understanding of the molecular pathways controlling reproduction could assist in increasing fecundity though improved nutrition or genetic selection targeted on key reproductive pathways. The present study sought to characterize the early tissue composition and gene regulatory changes that contribute to decreased fecundity in a homogeneous population of domesticated P. monodon fed identical high-performance maturation diets. Results suggested that lipid composition had a greater influence on reproductive performance than total lipid content, and that the specific fatty acids were critical to maintaining reproductive performance in P. monodon. In particular, the variability in ovarian arachidonic acid (ARA) resulted in a significant positive correlation with the expression of prostaglandin synthesis genes, PmcPLA2 and PmCOX, with significant variation in the expression of PmCOX, PmPGFS, PmPGE1 and PmPGE3 in groups with high or low ARA content. Further RNAseq analysis identified a total of 757 genes with greater than 2-fold expression increase or decrease in groups with high or low ARA content, but genes extremely poor assignment to functional gene ontology groups. Differential gene expression analysis demonstrated that variation in ARA has direct impact on the synthesis of key downstream prostaglandin synthesis genes, which have potent roles in broodstock egg production and maturation, and elucidates a suite of currently uncharacterized genes for P. monodon that may influence reproductive performance.

Mission Shrimpossible – the Circulatory System of Penaeus vannamei with Special Focus On Lacunar Structures

Göpel T, Wirkner CS
Universität Rostock, Allgemeine & Spezielle Zoologie

Ever since early anatomists started investigating arthropod morphology, the circulatory system has drawn major attention. In recent years, modern 3D imaging techniques and features have again increased morphological descriptions of this in some groups remarkably complex organ system and its features have served as source of phylogenetic relevant characters e.g. in Malacostraca. This led to a major shift in our understanding of the vascular part, i.e. the heart and associated arteries. However, when leaving the arteries, the hemolymph is channeled through a highly complex system of lacunae and sinuses which are still not readily understood. Therefore, detailed three-dimensional investigations are necessary to not only understand the structural but also the ontological nature of this elusive system. To this end, we investigated the circulatory system of the white leg shrimp Penaeus vannamei using micro computed tomography complemented with histological sections and confocal laser scanning microscopy followed by virtual 3D reconstruction. Our results comprise detailed visualization of the vascular system and – for the first time – also the three-dimensional structure of the lacunae and sinuses. Based on the lacunar morphology, we are now able to understand the functions of major lacunar subsystems in the broad context of hemolymph circulation in decapod crustaceans.

Shrimp Population Resiliency to Mega Oil Blowouts in the Gulf of México

Gracia A, Murawski SA, Vázquez-Bader AR
Instituto de Ciencias Del Mary Limnología, University of South Florida

Accidental oil spill impact on fishery resources is of great concern due to its economic and social importance. Shrimp fishery is a valuable activity in the whole Gulf of Mexico. The effects of two mega oil spills (IXTOC 1979 and Deepwater Horizon 2010) on shimp fisheries in the northern and Southwestern GoM are analyzed. Shrimp fisheries did not show a population collapse during and after oil spill. Pink and White Shrimp Recruitment and spawning stock variations following 1979 oil spill were found inside natural annual variations. Shrimp stocks in the NGoM neither registered an apparent impact related to Deepwater Horizon blowout, even though, studies showed a general increasing trend in spawning biomass and recruitment. Pink and White Shrimp Stock-Recruitment Relationships models show a high capacity to stand/recover either from natural or man made impacts by taking advantage of good environmental conditions. In the SWGoM combined artisanal and industrial fishing effort rather than IXTOC oil spill is more likely the main factor causing Pink and White Shrimp fisheries collapse. Constranting the reduced fishing effort in the NGoM allowed shrimp stocks rebuilding. Shrimp population reproductive strategy with a high reproductive potential result in high resiliency to oil spill impacts.

Deepwater Shrimp of the Southern Gulf of Mexico

Gracia A, Vázquez-Bader AR
Instituto de Ciencias del Mar y Limnología

A systematic study along the Mexican continental slope (300-1200 m depth) of the Gulf of Mexico (Tamaulipas-Yucatán) was conducted on board the R/V JUSTO SIERRA of the Universidad Nacional Autónoma de México, to study crustacean biodiversity and potential fishery resources. The benthic fauna was sampled day and night using a semi-commercial shrimp trawling net with a 18 m mouth and 4.5 cm mesh. Thirteen species of deepwater shrimp of the families Aristeidae, Benthecisymidae, Solenoceridae and Penaeidae were found. Most abundant large size deepwater shrimp species in almost 200 hauls were Giant red shrimp Aristaemorpha foliacea, Scarlet shrimp Aristeopsis edwardsiana and Royal red shrimp Pleoticus robustus that together represented 90 % of the total catch. Other like Aristeus antillensis, Penaeopsis serrata and Parapenaeus politus were less abundant with minor size. Higher catches were consistently found in the 300-700 m depth range. Mean biomass and catch per unit effort registered values were 609 + 832 g/ha and 2.5 + 3.3. kg/h. CPUE reached values as high as 16 kg/h, which are in the range registered in several deepwater shrimp fisheries in the world. An area of 60,000 km2 was estimated where potential fishing grounds can be located. Shrimp abundance and value could be attractive enough for developing a deepwater shrimp fishery which can cause an impact on the fragile deepwater benthic ecosystem. The eventual utilization of deepwater shrimp must consider a sound fishery plan to assure sustainable exploitation while minimizing impacts on the fragile deep-sea ecosystem.

Elucidating the Presence and Expression of the Crustacean Hyperglycemic Hormone of the Red Deep-Sea Crab, Chaceon Quinquedens

Green SR, Chung JS
University of Maryland Center for Environmental Sciences

Crustacean hyperglycemic hormone (CHH), a member of CHH superfamily in decapod crustaceans, is known as multiple functioning hormone. To date, over >100 CHH sequences are known, while little has been known about the CHH from deep-sea cold-water crustacean species. The fishery of the red deep-sea, Chaceon quinquedens, a data-poor species is currently federally managed in the US. We aimed to understand if crustacean hyperglycemic hormone (CHH) in the red deep-sea crab, Chaceon quinquedens play a role in female reproduction. We first isolated the full-length cDNA of CHH sequence using PCR with degenerate primers and 5'/3' RACE and then measured the levels of CHH in the sinus gland and its expression in the eyestalk ganglia of females. As expected two forms of CHH are found in the sinus gland by RP-HPLC combined with a dot blot assay (CHH1 and CHH2): with a ratio of CHH1:2 at 1:4. The full-length cDNA sequence for CHH (ChqCHH; 957 bp) obtained using a degenerate PCR combined with 5'and 3' RACE includes 5' UTR 360 bp, ORF 420 bp, and 3' UTR 177 bp. The ORF translates to a signal peptide, CHH precursor relate-peptide, dibasic cleavage site and 73 aa mature hormone, an amidation site and tribasic cleavage site. The putative amino acid sequence of ChqCHH is most closely related to Cancer productus CHH IIb isoform. The levels of ChqCHH in the sinus gland and its expression in the eyestalk ganglia are elevated in the females at early vitellogenic stages, implying its function in early vitellogenesis.

The Joint in Between - Intrabasal Joints and Their Relevance for Malacostracan Phylogeny

Grams M, Richter S
Universität Rostock

A dicondylar thorax-coxa joint permitting promotion/remotion followed by a dicondylar coxa-basis joint performing abduction/adduction is presumably the plesiomorphic pattern in the thoracopods of Eumalacostraca. Peracarids differ from this pattern and Mysidacea (Mysida and Lophogastrida) stand out in particular as both their thorax-coxa and coxa-basis articulations permit abduction/adduction, while an additional intrabasal joint permits promotion/remotion. This intrabasal joint is formed by a membranous gap between an anteriorly located proximal triangle and the rest of the basis. Interestingly, an intrabasal joint of this nature is also present in Euphausiacea, and, with structural differences, in Anaspidacea, which in contrast exhibit the plesiomorphic articulation pattern between thorax-coxa and coxa-basis. A µCT and cLSM-based comparison of the complex limb musculature (around 20 functionally differentiated muscles) is conducted, enhancing our 3-dimensional and functional understanding of these intrabasal joint constructions in the different groups. The possible homology of the intrabasal joint is discussed and used to evaluate various phylogenetic hypotheses, e.g. Eucarida vs. Xenommacarida and the monophyly vs. polyphyly of Peracarida. While the shift in mobility is believed to have evolved in favor of the peracaridian marsupium, Euphausiacea and Anaspidacea do not have a marsupium, so other biological roles need to be assumed in these two taxa.

A Tour of the Fantastic Diversity of Body Forms of “Nauplius Y” (Crustacea: Thecostraca: Facetotecta), as Exemplified By Populations in Okinawa and Taiwan

Grygier MJ, Dreyer N, Olesen J, Høeg JT
National Taiwan Ocean University, University of Copenhagen

Twelve named species of Hansenocaris and a roughly equal number of other variously designated “types” of facetotectan larvae, some based exclusively on specimens of “nauplius y”, have been characterized in the literature. Especially in East Asian waters, many remain unpublished. Aside from a handful of enthusiasts, zoologists have had no chance to see their true diversity of form. This is unfortunate, inasmuch as the Facetotecta are known only from the nauplius and cypris larvae and a subsequent slug-like juvenile stage, the ypsigon. Extensive plankton sampling and laboratory rearing of facetotectans conducted at Sesoko Island, Okinawa, in 1996-97 and 2003-2005 and at Keelung and Green Island, Taiwan, in 2017 has allowed us to recognize dozens of undescribed species, particularly of lecithotrophic forms. Here we try to show the scale of this diversity, using SEM photographs of whole nauplii and stacked digital DIC photographs of late (usually last) naupliar molts. Besides the already familiar forms that resemble miniature horseshoe crabs, others are long and attenuate, or long and cylindrical, or variously capsule-shaped, pot-bellied, discoidal, downturned-triangular, downturned-stubby, or even bent at a nearly 90 degrees. Some have the labral swelling semicircular, trapezoidal, or hoe-shaped, or drawn out into a short or long spine, or have lateral “trunk” spines, or extremely reduced or enlarged furcal spines. Despite this diversity it is easy to recognize specimens of nauplius y: no frontolateral horns, no furcal setae but (usually) a pair of furcal spines, and a long dorsal “trunk” surface distinct from the cephalic shield.

A New and Mysterious Internal Structure of Nauplius Larvae: a "Ghostly" Support Sling For the Y-Cypris Present Within Last-Instar Exuviae of Nauplius Y (Crustacea: Thecostraca: Facetotecta)

Grygier MJ, Olesen J, Dreyer N, Høeg JT
National Taiwan Ocean University, University of Copenhagen

The Facetotecta, or "y-larvae", undergo a metamorphic molt from the last nauplius to the cypris in which a free carapace, six pairs of natatory thoracopods, and a segmented thorax and abdomen develop. Unlike in earlier naupliar molts, the cephalic shield and the so-called "facio-trunk" usually remain together at the last molt, and the posterior "trunk" portion, while hollow, is not empty. In mounted preparations examined by phase or differential interference contrast (DIC) microscopy, a ghost-like image of part of the cypris thorax, particularly the thoracopods and even their setae, is commonly visible inside the naupliar exuviae, and may be universally present. To investigate this "ghost", we used DIC and digital photographic stacking, plus SEM, on slide- or stub-mounted last naupliar molts of an assortment of undescribed species of Facetotecta that had been reared from planktonic lecithotropic nauplii to the cypris stage at Sesoko Island, Okinawa, Japan, and Keelung, Taiwan. These techniques showed that the "ghost" is a delicate, three-dimensional, fibrous structure, essentially a sling-like mold or matrix with struts attached to the outer cuticle and pairs of deep pockets that previously held the thoracopods of the developing cypris y. Whether it is endoskeletal in nature, the (partial) exuviae of an additional instar, or something else is currently unknown. Nothing similar has been reported in other thecostracans, or in other crustaceans that undergo a similarly abrupt metamorphosis at the last naupliar molt, but we expect that some of their exuviae will also prove to hold "ghosts".

Temperature Dependent Energetic Demands and Food Acquisition in the Marine Isopod Idotea emarginata

Gutow L, Kellermann R, Wang HY, Lannig G
Alfred Wegener Institute Helmholtz Centre For Polar Marine Research

Temperature is a major driver of physiological processes on all levels of biological organization. Accordingly, in the light of global climate change, studying the performance of marine species at different temperatures is becoming increasingly important to understand upcoming changes in ocean ecosystems. Small herbivorous crustaceans are important trophic links in coastal marine food webs. They consume considerable amounts of marine primary production. Simultaneously, they provide an important food resource for predators from higher trophic levels, including commercially important fish species. We studied energetic requirements and food acquisition in the marine isopod Idotea emarginata from the North Sea. In laboratory experiments, the isopods were maintained for three days at different temperatures (5 to 25°C). The respiration of I. emarginata increased continuously with temperature, indicating high energetic demands at elevated temperatures. Food consumption also increased from low to moderate temperatures but dropped at high temperatures, indicating that the rates of secondary somatic processes are decreased to safeguard oxygen supply to fundamental metabolic processes. However, a lower food uptake may result in a progressive shortage of carbohydrates to sustain elevated levels of cellular metabolism at high temperatures. Our results indicate an increasing mismatch between energetic demand and supply in small marine invertebrates due to rising seawater temperatures.

The Burrowing Amphipod Sunamphitoe Lessoniophila Induces Major Damage in the Large Kelp Lessonia Berteroana in Northern Chile

Gutow L, Poore AGB, Díaz MA, Villalobos VA, Jerosch K, Thiel M
Alfred Wegener Institute Helmholtz Centre for Polar Marine Research, University of New South Wales, Universidad Católica del Norte

There is growing evidence that small marine herbivores can substantially affect the performance and biomass of large kelp species when their grazing activity is concentrated on particularly vulnerable or structurally important algal tissues. In the SE Pacific, the small herbivorous amphipod Sunamphitoe lessoniophila burrows into the stipes of the large kelp Lessonia berteroana, causing a characteristic wound healing response in the kelp. Excavation of the stipes leads to conspicuous local damage and, finally, to the loss of stipes above the burrow. In a kelp forest in northern Chile, we quantified the occurrence and distribution of amphipod burrows and the consequences of the infestation for individual algae. About one third of the stipes surveyed was infested by S. lessoniophila. The number of burrows per stipe increased with stipe length. Burrows were concentrated in the middle of the stipe with few burrows in the most basal and apical sections of the stipes. About 50% of all burrows were occupied by amphipods, including adult males and females and juveniles. Assemblages of amphipods inside the burrows often comprised females with juveniles from multiple cohorts indicating repeated local reproduction and parental care. The resultant extended residence times of multiple individuals inside burrows enhances the probability of stipe breakage. By compromising the physical structure of the kelp, small amphipod grazers can induce substantial biomass loss in coastal kelp beds thereby channeling considerable amounts of seaweed primary production into the detrital pathway of coastal marine food webs.

Distribution of Pelagic Shrimps in the Southeast Pacific (Decapoda, Dendrobranchiata and Caridea)

Guzman GL, Rivera J, Escribano R
Universidad Arturo Prat, Universidad de Concepción

The knowledge of the mesopelagic fauna in Chile has increased in the last twenty years. At present, 81 species of shrimps have been cited in waters off this country, including the waters surrounding the seamounts of the Salas y Gomez Ridge and the Juan Fernandez submarine dorsal. Most of the available information is based in taxonomic reports and no information about the distribution of this group has been provided. Here, we analyzed the distribution of the pelagic fauna of Shrimps (Caridea and Dendrobranchiata) collected during two surveys offshore of Chile, from about 70ºW to 110ºW and from 27ºS to 33ºS. A total of fourteen species were collected using a Tucker net from zero to 1000 m depth. Seven species of Dendrobranchiata belonging to Sergestidae and Benthesicymidae were found in same proportions, and an additional species of Solenoceridae. Seven species of Caridea, of which five belong to Oplophoridae and two to Pandalidae. Funchalia woodwardii and Gennadas kempi were identified and registered for the first time in this area. We observed a differential distribution in relation to water masses identified in the study area. Some species were distributed close to the South American coast and seamounts, while others were more oceanic. In the samples, far away from the land masses, only Dendrobranchiates shrimps were observed, whereas in the samples close to land masses both Caridean and Dendrobranchiata shrimps were found. We discuss the distributions of these species in according to those reported in the literature about global biogeographic patterns of epipelagic and mesopelagic fauna.

An Unusual Type of Mantis Shrimp Larva

Haug C, Haug GT, Haug JT
LMU Munich

Mantis shrimps are impressive benthic predators when they are adults. When they are larvae, they are part of the plankton, but likewise predatory. Mantis shrimp larvae can grow to astonishing sizes of about 50 mm, especially the so-called alima larvae of squillid mantis shrimps. Yet, also another type of mantis shrimp larva, the erichthus, can grow to astonishing sizes, for example those of lysiosquilloid mantis shrimps. Only recently we reported a number of different new types of erichthus larvae with very large and prominent shields. Among them was a specimen with a shield roughly resembling a flying saucer. Here we report a new specimen strongly resembling the 'flying saucer' specimen in overall shape but with differences concerning the raptorial appendages. As the specimen was partly damaged, we decided to remove the appendages and document them in detail. All structures were photographed on a fluorescence microscope exploiting the autofluorescence capacities of the cuticle. Especially fine setae were additionally documented using phase-contrast transmitted-light microscopy. All images were enhanced by recording each image detail as a stack that was later on fused into a single sharp image, and by stitching several such optimised image details into large panorama images.

Ontogeny of Fossil and Extant Xiphosuran Chelicerates and Its Contribution to Species Delineation and Evolution of the Group

Haug C
LMU Munich

Today we have only four species of xiphosuran chelicerates (horseshoe “crabs” or “sword tails”). In contrast, the fossil record provides a remarkable number of xiphosuran species. However, the validity of many of the fossil species has been doubted subsequently. Some species could, for example, be identified as groups of deformed specimens. In general, the species delineation among fossil xiphosurans remains difficult. One group of fossil xiphosurans is Euproops, with specimens occurring in different 300 million years old deposits. Two well established species are Euproops danae from North America and Euproops rotundatus from Great Britain. However, new individual-rich finds of Euproops sp. from North-Western Germany questioned species delineation within Euproops. The German form is known from 10 instars of which the early stages resemble the American species (E. danae), while the later stages are virtually indistinguishable from the British species (E. rotundatus). I will present ontogenetic data for all three forms, providing important characters for discriminating the different species of Euproops. In a larger comparison, the early post-embryonic development of species of Euproops differs from that of extant xiphosurans, especially in the developmental timing. Representatives of extant Limulus polyphemus hatch with a less far developed morphology than their fossil relatives, relying on yolk nutrition at first. Interestingly, the different body parts develop at varying speed in different embryos of L. polyphemus, but achieve a very similar hatching morphology. The comparison between ontogeny in extant and fossil xiphosurans indicates that heterochronic events played an important role in the evolution of xiphosurans.

I Am Not a Larva, But I Look Like One – Erroneous Identifications Among Larval Material and What We Can Learn from Them

Haug JT, Haug C
LMU Munich

Sorting plankton samples is a hard task; there are so many forms and so much material. Naturally, we all make mistakes. Yet, making mistakes is not the main problem, but the way we deal with them. Often, when identified, such mistakes are simply corrected. In this way, we do not gain very much besides the correction. Instead we should ask what the specimen has in common with the specimen it had been mistaken for. Why has a certain specimen been mistaken for a certain type of larva, but is something different? Especially in regularly occurring cases of misidentification, these mistakes must be based on specific traits. After checking different historical museum collections we can sum up some common misidentifications and also draw possible conclusions from them. Examples include pelagic mysid shrimps that were mistaken for crab megalopa larvae, or deep sea amphipods that have been sorted among decapod larval material. A very common triplet of intermixing are larval forms of the alien-like decapod Amphionides reynaudii, phyllosoma-type larvae of achelatan lobsters, and the alima and erichthus larvae of mantis shrimps. Certain morphological features must be the basis for these mistakes, always leading to the same results in very different collections. A similar morphology that leads to such misidentifications could point to similar functions in only distantly related groups. With this, these mistakes may already provide a rough indication for cases of convergence and allow us to further explore this still not well formulated concept.

I Know What a Larva Is – a Look At Specimens That Mess with Our Concepts

Haug JT
LMU Munich

We all seem to know what a larva is, right? But do we agree? Apparently not! The literature is full of approaches of defining what a larva is and what is not, and even more so what a certain type of larva is. Different authors consider very different types of criteria and come to rather different conclusions. I will discuss cases in which specimens – modern-day as well as fossil ones – ignore common definitions, for example by exhibiting morphologies that can best be termed 'intermediate'. These may either occur between two larval phases, which are apparently not as strictly separated as generally thought, or even between larva and juvenile. Other larval forms represent cases of unexpected sizes. These examples demonstrate that larval morphology is still more variable than what we have so far recognised. The true diversity of crustaceans is most likely far beyond that indicated by taxonomic measures: the extreme richness of larval forms concerning their morphologies is an indicator that also in ecological aspects larval forms are highly diverse, possibly even more so than adult crustaceans. Super-sized larvae in various groups furthermore point to long periods of life in the plankton and that crustacean larvae have major impact on this important part of the oceanic ecosystem. It seems astonishing that in the age of bio-conservation and protection of biodiversity our knowledge of the true diversity of crustacean larvae is still rather limited.

Reproduction At Depth - the Reproductive Morphology of Hydrothermal Vent Crabs

Hayer S, KöHnk S, Kabus J, Boretius S, Gorb SN, Kihara T, Brandis D
Christian-Albrechts-University Kiel, Deutsches Primatenzentrum (DPZ), Deutsches Zentrum für Marine Biodiversitätsforschung (DZMB)

Little is known about the Bythograeidae – a brachyuran family that is endemic to hydrothermal vents. Up to date, six genera have been described with 14 species. Almost everything we know about this family is based on a single species of the genus Bythograea. Hydrothermal vent crabs are very similar to shallow-water brachyurans in their basic biology, but have also evolved characteristics specific for life at hydrothermal vents (Dittel et al., 2008). To expand our knowledge about reproductive anatomy of these crabs, we investigated the female seminal receptacle and the male gonopods of the genus Austinograea. To do so we used a combination of different methods: histology, magnetic resonance imaging (MRI), micro computed tomography (µCT) and scanning electron microscopy (SEM). The results show a seminal receptacle, which fundamental characteristics are homologous to shallow-water brachyurans. Especially conspicuous is the proportion of glandular epithelium within the seminal receptacle, which differs from other brachyuran species. The morphology of the gonopods is described in great detail. In conclusion, the reproductive system of Austinograea combines classic characteristics of other known Brachyura, yet distinct specific traits can be found in these organs too.

The Genome Survey of Chthamalus challengeri (Cirripedia:Chthamalidae)

*Hee-Soo K, Hyunkyong KD, Won K**
Seoul National University

Chthamalus challengeri Hoek, is a predominant species in the rocky intertidal zone of tropical and sub-tropical shores. It prefers the upper part of exposed rocky shores and endures strong surf and strong sunlight. We conducted genome survey of Chthamalus challengeri as a preceding step to obtain genetic information through whole genome sequencing. The genomic DNA for sequencing was extracted from adult specimen. A total of 135.4 GB of raw data were generated using the Illumina Hiseq X platform. We confirmed the quality of raw data using FastQC program. The total 110.8Gb of filtered data were used for K-mer analysis to estimate genome size of Chthamalus challengeri using JELLYFISH. The total sum of each K-mer individual for K-mer size of 17, 21, 25 bases pairs was 99.1 Gbp, 96.1 Gbp and 93.2 Gbp, respectively. The genome size of Chthamalus challenger was estimated to be approximately 0.91Gb based on K-mer measurement. In addition, we expect that Chthamalus challenger has high heterozygosity genome through clear two picks shown in K-mer analysis graph.

Buttresses and Muscles: First 3D Reconstructions of Brachyuran Axial Skeletons and Intrinsic Musculature - Why Swimming Crabs (Portunidae) Are Able to Swim

Hazerli D, Richter S
Universität Rostock

Swimming crabs (Portunidae) are decapod crustaceans which possess the extraordinary ability to swim using their 5th pereiopods, something which other brachyuran crabs are unable to do. Not all the morphological differences between swimming and non-swimming crabs are as apparent as those concerning the shape of the 5th pereiopods, however. Less obvious but important differences are found in the endophragmal system, better referred to as the “axial skeleton”, where the extrinsic musculature of the 5th pereiopods has its origin. Information on the axial skeleton is still sparse in the literature because of the difficulties associated with preparing, illustrating and naming elements of this complex structure. We use micro computed tomography and virtual 3D reconstruction to examine and visualize for the first time the axial skeleton and the extrinsic and intrinsic musculature of the 5th pereiopods of three European crab species: the swimming crab Liocarcinus depurator, the non-swimming Cancer pagurus, and the in some respects intermediate Carcinus maenas. We also compare the capacity for deflection of individual articulations of the pereiopods. Our results enable us to provide an updated list of morphological features that explain why only a swimming crab such as Liocarcinus has the ability to swim.

Raman Spectroscopic Analysis of the Composition of Clam Shrimp (Laevicaudata, Spinicaudata, Cyclestherida) Carapaces: a Novel Dual Mineralization System

Hegna TA, Czaja AD, Rogers DC
Western Illinois University, University of Cincinnati, Kansas University

Clam shrimp are a paraphyletic group of bivalved branchiopod crustaceans including the Laevicaudata, Spinicaudata, and the Cyclestherida. In the published literature, the mineral content of the unique carapace (formed by molt retention in Spinicaudata and Cyclestherida) is variously ascribed to calcite or calcium phosphate. To better understand the mineral composition of clam shrimp carapaces, we analyzed the composition of the modern carpaces of one species of laevicaudatan, thirteen species of spinicaudatan (including both cyzicids, leptestheriids, and limnadiids), one species of cyclestherid, and two species of the notostracan Triops (as an outgroup comparison within Branchiopoda) via Raman spectroscopy. The results were surprisingly variable. The outgroups species of Triops varied in either having no mineral content to having a slight amount of calcium phosphate in their carpaces. The laevicaudatan, Lynceus planifascia, likewise had a minor calcium phosphate peak. The leptestheriid, Leptestheria compleximanus, had a strong calcium phosphate peak and a strong calcium carbonate peak. The seven limnadiids were variable; varying from no mineral content to strong dual calcium carbonate and calcium phosphate peaks. The five cyzicids tended to have strong calcium phosphate peaks and some amount of calcium carbonate as well. The cyclestherid, Cylcestheria sp., had no mineral content. The results support the conclusion that spinicaudatans primitively have a unique dual mineralization system in their carapace that utilizes both calcium phosphate and calcium carbonate, with the calcium phosphate ability being primitive. This dual mineralization system is novel in branchiopods and warrants study from material scientists.

The Fossil Record of Branchiopod Crustaceans

Hegna TA
Western Illinois University

The higher-level phylogeny of modern branchiopod crustaceans is relatively well understood. However, we do not have a firm grasp on divergence dates or character state transitions between the major clades. Rehbachiella from the upper Cambrian of Sweden is pretty firmly established as a stem group branchiopod. The anostracans and notostracans are two of the earliest branching lineage of branchiopods; they have stem group representatives in the Devonian known from the Rhynie Chert and the Strud Lagerstätte. Possible crown group representatives for both are known from the Mesozoic. The understudied Triassic Grès à Voltzia Lagerstätte contains possible stem group phyllopods and diplostracans. Laevicaudatans have a published record in the Permian and possible soft-part preservation known from the Jurassic. However, owing the character-poor nature of these fossils, it is impossible to tell if they represent crown-group laevicaudatans. Spinicaudatans have a rich record of carapaces. The earliest known total group spinicaudatans come from the Devonian (though there is reference to some possible late Silurian fossils). The leaiids are an enigmatic extinct diplostracan lineage thought to be closely related to the spinicaudatans. They have a record that extends from the Devonian to the Triassic. Cyclestherids have an enigmatic fossil record. There are no examples of cyclestherids preserved with soft-parts, so the only character used to assign fossils to this lineage is the shape of the carapace. According to that metric, cyclestherids have a record that begins in the Devonian. Cladocerans are late-comers, with a record that begins in the late Jurassic.

The Protein Phosphorylation Regulation in Pathogenesis of Tremor Disease of Eriocheir sinensis Caused by Spiroplasma Eriocheiris

Hou L, Gu W
Nanjing Normal University

Spiroplasma eriocheiris, has been identified as a novel lethal pathogen of E. sinensis tremor disease (TD). The direct cause of TD is infection of the thoracic ganglion of E. sinensis by S. eriocheiris. Previous reports confirmed that abnormal protein phosphorylation modification plays a crucial role in the etiology of neurological disease in the other animals. Our study was designed to examine the role of protein phosphorylation modification in the occurrence of TD. In the current study, the phosphoproteomic changes of E. sinensis thoracic ganglion after S. eriocheiris infection were obtained. A total of 6,040 phosphorylation sites in 2,451 protein groups were identified. The proteins with quantitative ratios above 1.5 or below 1/1.5 are deemed significant. Among the quantified proteins, 349 phosphorylation proteins are up-regulated and 331 phosphorylation proteins are down-regulated when compared to the control sample. To further understand the function and feature of the identified and quantified proteins, we annotated function or feature of proteins from several different categories, including gene ontology (GO), and KEGG pathway and so on. Many phosphoproteins, as well as potential signal pathways associated with the development of the nervous system and signal transmission were found, including Glycogen synthase kinase 3β, synaptotagmins, calcium/calmodulin-dependent protein kinase type II, vesicle-associated membrane protein, Wnt signaling pathways, Calcium signaling pathway, and Synaptic vesicle cycle, and so on. The present work could serve as a basis for future studies to understanding the role of protein phosphorylation regulation in pathogenesis of TD of E. sinensis caused by S. eriocheiris.

Brachyury and Engrailed Genes Identified from Penaeid Shrimp Genomes and Transcriptomes

Hertzler PL, Baugh WM, Wei J, Droste AP, Yuan J, Ziang J
Central Michigan University, Ocean University of China

The recent publication of genomes and developmental transcriptomes for several penaeid shrimp species (Decapoda: Dendrobranchiata: Penaeidae) has allowed the identification of shrimp orthologs of genes involved in embryonic development. Our objectives were to identify the coding sequence (CDS) and gene structure of the transcription factors brachyury (bra), known in other animals to be involved in mesoderm and/or endoderm specification and regulation of gastrulation movements, and engrailed (en), involved in segmentation and neural specification. We mined the sequence databases for bra and en from the shrimp species Marsupenaeus japonicus, Litopenaeus vannamei, and Penaeus monodon. Additional sequence was obtained by PCR from an outgroup dendrobranchiate Sicyonia ingentis (Sicyoniidae). The CDS encoded shrimp Brachyury (Bra) proteins of 551-552 amino acids containing the highly conserved T-box DNA binding region. The N-terminal Smad1-binding domain was absent in shrimp Bra, as in dipteran insects. The R1 repressor domain was the best conserved of the C-terminal regulatory domains, which were widely divergent compared to other species. The penaeid shrimp bra gene consisted of six exons, with splice sites conserved with other phyla across the animal kingdom. Real-time PCR showed that shrimp bra mRNA was strongly expressed during gastrulation. We also obtained the complete CDS for en from several penaeid shrimp species, which encoded a protein of 252 amino acids. Phylogenetic analysis identified this as en1, known to be expressed in neuronal tissues in higher crustaceans. The penaeid en gene consisted of three exons containing the CDS, with splice sites conserved with the caridean shrimp Caridina multidentata.

Host Driven Phenotypic Plasticity of Coral-Inhabiting Barnacle

Hsu WC, Chan BKK, Fraser CML
National Taiwan University, Biodiversity Research Center

Coral-inhabiting barnacles are obligatory symbionts of scleractinian corals and fire corals. They are belong members of the superorder Thoracica, order Sessilia, family Pyrgomatidae in taxonomy. Coral-inhabiting barnacles have a cup-shaped or tubular base, different from another families of barnacles. The base structure is imbedded by coral skeleton. The base elongates with the upward growth, and they grow at the same rate as the host coral. If the barnacle base grows too slowly, it would be easily covered and entombed by the host coral. Conversely, if the barnacle grows more rapidly than then host coral it would protrude, and become more exposed to predation. Therefore, the same species of barnacle may have different growth rates and morphology when found in different host corals. The purpose of this study was to examine phenotypic plasticity in coral-inhabiting barnacles. Coral-inhabiting barnacles were collected from host corals by SCUBA diving and identified using molecular biology. To examine the growth pattern of barnacles, shell length and base depth were measured by electronic vernier scale. The results show that coral-inhabiting barnacle have phenotypic plasticity in patterns of growth. Barnacle plasticity occurs between different places in the same coral, different coral growth forms, and different coral species. Nobia grandis also has different shell shape and cirrus color in different host coral species. The growth rate of host corals often changeable. Phenotypic plasticity plays an important role in adapting varied host coral for coral-inhabiting barnacles.

Taxonomy of Coastal Talitrids of Australia (Amphipoda: Peracarida)

Hughes LE
Life Science, Natural Histroy Museum

Talitrid amphipod are the only terrestrial amphipod family and are noted for being more diverse in the Southern Hemisphere. Preliminary assessment of coastal Australian talitrids recognised a high level of endemic undescribed genera and species based on morphological studies. A two-year assessment of museum specimens included a morphometric growth stage analysis of male sexual dimorphic characters for populations and species from around mainland Australia and Tasmania. The recognised continuum of some species level characters alters what is known of described species and generic boundaries within the Talitridae. Research is continuing on the description of new species/genera along with the redescription of historic types. Nearing completion, the research will deliver comprehensive distributions, user friendly identification guides and contribute to further understanding evolution within the Talitridae.

A Worldwide Phylogeny of the Snapping Shrimp Genus Alpheus Using Anchored Hybrid Enrichment

Hultgren KM, Hurt C, Bracken-Grissom H
Seattle University, Tennessee Tech University, Florida International University

Snapping shrimps in the genus Alpheus have been model organisms for studies of host specialization, population genetics, and molecular evolution, yet few multi-locus phylogenies exist of this large and diverse group. Part of the difficulty is due to the presence of pseudogenes and other gene duplication events, and the extremely large genomes (4-20 pg) of alpheid shrimps. Here we present a phylogeny of 29 species of snapping shrimp from the genus Alpheus, with the goal of resolving deeper species group relationships and examining the monophyly of species groups proposed by Coutière. Utilizing specimens collected worldwide and spanning eight species groups, we present a phylogeny using markers generated with Anchored Hybrid Enrichment. Preliminary results suggest that at least three of the established species groups in the genus Alpheus are paraphyletic, and that specialized host behavior (symbioses with echiurans, gobies, and corals) has evolved multiple times within this genus.

Which Way to the Island? Diversity and Origin of Freshwater Gammarids from Mediterranean Islands

Hupalo K, Mamos T, Rewicz T, Wrzesinska W, Karaouzas I, Plaiti W, Boulaaba S, Grabowski M
University of Lodz, Hellenic Centre for Marine Research, Université de Carthage, Tunisia

The Mediterranean Region is known as one of the most prominent biodiversity hotspots worldwide. However, majority of studies upon Gammaridae of the Mediterranean focused mainly on marine species, leaving aside the freshwater counterparts. So far, around 120 freshwater species of two genera, Gammarus and Echinogammarus, have been reported from the area, with only 15 known from the islands. Considering the recent discoveries of high cryptic diversity in European gammarids, we conclude that number of species already reported may be underestimated. A set of 443 individuals from 98 locations on Sicily and Crete, along with the reference areas, were amplified for several mitochondrial and nuclear markers. The reconstruction of time-calibrated phylogeny, done using BEAST software, have shown that on Sicily, E. sicilianus forms a sister group to all the Apennine Echinogammarus and diverged from them at the time when the island formed. Another Sicilian species, E. adipatus, has a different origin and probably migrated through the land connection between Calabria and Sicily. On Crete, a new species of Gammarus has been discovered, which diverged from its closest relative from Peloponnese around the time of the isolation of Crete, supporting the species' continental origin. Besides, we confirmed presence of three species of Echinogammarus on Crete, including two potentially new for science. Moreover, a substantial level of cryptic diversity was found both on the islands and in the reference areas. The multi-marker phylogeny revealed a high complexity of the evolution of the freshwater gammarids from the islands.

Population Genetics Inferences of the Blue Crab in the US Based on Microsatellites

Hurtado LA, Macedo D, Caballero IC, Mateos M, McCay S
Texas A&M University

The blue crab is a keystone species found in estuarine habitats of the US Atlantic coast and Gulf of Mexico, and historically represents a multibillion-dollar fishery in the US. Although several population genetics studies have attempted to study population connectivity and genetic diversity in this species, conflicting results and potential problems with the markers used, as well as other issues, have obscured our understanding on these aspects. The objective of this study was to examine, for the first time, large-scale genetic connectivity of the blue crab in the US using microsatellites. We genotyped samples from the Chesapeake Bay, in the US Atlantic, and from nine localities along the US Gulf of Mexico coast, using 16 microsatellites that have 100% power to detect significant genetic differences for values as low as FST = 0.005. High levels of genetic diversity were estimated (average alleles per locus = 18.12; expected heterozygosity = 0.74), and effective population size appears to be very large. Consistent with the high long-distance dispersal potential of this species, which has a combined pelagic larval duration and postlarval megalopal stage of 5–10 weeks, very low levels of genetic differentiation were detected for the blue crab among the 10 localities examined. The high connectivity in this crab has a limit in its native range, however, as US populations appear to be highly differentiated from those in southern Brazil. Estimations of genetic diversity and effective population size can serve as baseline to monitor temporal changes for this species in the US.

First Record of Six Species of Mantis Shrimp from Korea (Crustacea: Stomatopoda)

Hwang HS, Ahyong S, Kim W
Seoul National University, Australian Museum, University of New South Wales

Stomatopods or mantis shrimps are predatory crustaceans found mostly in tropical and subtropical regions. More than 480 stomatopod species have been described worldwide (Ahyong 2001, 2004), of which only seven species have been recorded in Korean waters. We performed taxonomic research on a series of stomatopods collected by SCUBA diving and commercial fishing trawlers from the coastal waters of Korea. As a result of this study, thirteen species of stomatopods are now recorded in the Korean fauna. Six are first reported from Korean waters. Among them, four belong to the superfamily Squilloidea Latreille, 1802 (Levisquilla inermis (Manning, 1966), Anchisquilla fasciata (De Haan, 1844), Cloridopsis scorpio (Latreille, 1828), Miyakella nepa (Latreille in Latreille, Le Peletier, Serville & Guérin, 1828)) and two belong to the Lysiosquilloidea Giesbrecht, 1910, one each in Tetrasquillidae Manning & Camp, 1993 (Acaenosquilla latifrons (de Haan, 1844)) and Nannosquillidae Manning, 1980 (Acanthosquilla multifasciata (Wood-Mason, 1895)). Through the present study, the superfamily Lysiosquilloidea is reported for the first time from Korean waters. A checklist of the thirteen species of Korean stomatopods is provided with photographs.

Distributional Patterns of Small Brooding Crustaceans (Tanaidacea) from Abyssal Regions Around the World

*Jakiel A, Jóźwiak P, Błażewicz M**
University of Łódź

Deep-sea dwelling tanaidacean crustaceans are an important component of deep-sea ecosystems. As they actively dwell in the sediments and lack a dispersal larval stage (juveniles develop in a brood pouch), tanaids are assumed to have limited dispersal and thus a narrow distributional range. The members of Apseudidae (Apseudomorpha) that walk/swim over the sediments or burrow in most upper layers are considered to have a potentially wider distribution than tube-building members of the Pseudotanaidae (Tanaidomorpha). During four deep-sea expeditions DIVA3 (SW Atlantic), KuramBio (NW Pacific) and JPIO (Central Pacific), collections of Apseudidae and Pseudotanaidae were analysed and examined. Morphological identification was compared against molecular results (68 COI sequences of Apseudidae and 68 COI sequences of Pseudotanaidae). Species delimitation was achieved by applying ABGD, GMYC and PTP. From the results, 18 species of Pseudotanaidae were identified and confirmed by morphological results and all of them are new to science. From the twelve identified taxa of Apseudidae, six of them are already known. For most numerous species haplotype network was investigated. In the Central Pacific, analysed distributions were restricted to the most closely located sampling stations. Tanaidacean species from DIVA3, KuramBIO and JPIO collections were much more widely distributed, with maximum distances of 1856 km, 850 km and 372 km respectively, were detected.

Pseudotanaidae of the Iceage – a Tip of the Iceberg in the Tanaidacean Diversity in the North Atlantic

*Jakiel A, Stępień A**
University of Lodz

Iceland is located at the junction of the Mid-Atlantic Ridge and the Greenland-Scotland Ridge. In result of this topography, ocean area is divided on four different basins, that are under influence of various water masses. Generally the southern basins are bathed by the warm water originating in the southern part of North Atlantic, while the northern basins by the polar water from the Arctic Ocean. The submarine ridges hampers the interaction between water masses, thus it is suggested that fauna composition and biological process between ridges are different. The Icelandic Animals Genetic and Ecology (IceAGE) project aimed to understand how underwater physical structures (e.g. submerged ridges) and non-physical barriers (e.g. temperature, salinity) affect the distribution of benthic organisms. Samples have been collected from wide depth range (117~2750 m), at different localities around Iceland.During IceAGE cruises large collection of tanaidaceans (Crustacea: Peracarida) was obtained. Members of the family Pseudotanaidea were a dominant part of that collection. In the material five species of pseudotanaids were identified, four of them were new for science. One of the species was widely distributed, however morphometric analysis highlighted significant differences between specimens collected in Northern and Southern Icelandic basins. It is supposed, thus, it is complex of species. Furthermore the diversity and distribution of the Pseudotanaidae in the North Atlantic was assessed based on literature data and new records from the IceAge. Most of those taxa have a limited zoogeographical range. The Bray-Curtis similarity separated the pseudotanaid fauna into five zoogeographical groups.

An Alternative Draft Genome of Portunus (Portunus) trituberculatus and Comparative Genomic Analysis Across Decapod Species (Decapoda: Brachyura: Portunidae)

Jeong JH, Koo HY, Kim W
Seoul National University, Sangi University

The great popularity as marine food species of decapod crustaceans such as Portunus (Portunus) trituberculatus, brings importance in terms of both economic value and ecological conservation. Understanding the genomic structures of decapod species thus provide useful information applicable to their fisheries and conservation. However, genomes of the decapod crustaceans known currently comprised of only 7 species, and comparative study of their genomes is not published yet. In the present study, we conducted de novo whole genome assembly and gene annotation of P. (P.) trituberculatus and compared its genomic information with selected species of genomes of crustacean genomes currently available. The scaffold N50 of our draft genome was 617 bp while the assembled genomic size was 1.18 Gb, which covered 84.3 % of the estimated genome size. Then, according to our annotation result, we collected non redundant arthropodan core orthologous genes from P. (P.) trituberculatus, other decapod species and selected arthropod taxa for phylogenomic analysis. Also, we further analysed the Hox gene family structures among currently known crustacean genomes and our draft genome.

Genetic Selective Breeding and Genome Sequencing of Penaeid Shrimp

Jianhai X
Chinese Academy of Sciences

Since 2008, the local cultured commercial line imported from Chia Tai, Kona Bay and OI (Ocean Institute) were collected, together with our own cultivated "Kehai 1 were selected as the breeding base group. Using the line breeding method combined with the cross-test breeding method, the individuals with the high performance in different families were selected. After seven consecutive generations of selection, four lines including fast growth group (A series), high survival / high fecundity line (B series), high survival / fast line (C series), high fecundity line (D series) were established, and the two-hybrid breeding system were established: the A series were mated with B series to produce the female parent (AB), which shown advantage in growth and survival. The C series and D series were mated to produce male parents (CD), which shown advantage in both fecundity and high survival. AB and CD were mated to produce commercial line (ABCD), which was named as “Guangtai NO.1”. The growth rate of Guangtai NO.1 increased by 37% and the survival rate increased by 20% compared with the local breed. In the high-level pool culture mode, the growth rate increased by 16%, breeding survival rate increased by 30% compared with the SIS. Based on the second and third generation high-throughput sequencing technology, we obtained 828 Gb high quality Illumina data and 133 Gb PacBio sequencing data for Litopeneaus vannamei, covering 319 and 50 times of its genome respectively. The hybrid assembly method which was suitable for the characteristics of high repetition genome were successfully constructed, as as result we assembled the whole genome work frame. The Contig N50 is 57 KB and the Scaffold N50 is 600 KB, with the genome coverage 77%, gene region coverage reached 92%. The genome structure, the characteristics of the shrimp genome and the evolution characteristics of prawn were analyzed with comparative genomics method. Using the methods of integrating genomic method, including transcriptomic and proteomic data, the function genes related to the growth of shrimp, molting and resistance were selected and discovered, including prawn disease resistance related gene: VEGF3, SOCS, thrombospondin, Descam, genes related to the growth of the prawn molting: EH, crustacyanin, IGFB. Use similar method, we have assembled the Penaeus chinesis genome and obtained a better results (the Contig N50 was 53kb, the Scaffolg N50 was 127kb). Further investigation and improvements of the two prawn genomes are still ongoing.

The Rise and Fall of a Coastal Marine Embayment Blue Swimmer Crab Fishery

Johnston DJ, Marks R, Denham A, Hesp A, de Lestang S, Caputi N
Western Australian Department of Primary Industries and Regional Development

Cockburn Sound, a temperate coastal marine embayment in Western Australia, once supported a productive blue swimmer crab (Portunus armatus) fishery. Initially a commercial gillnet fishery around 100 t in the 1970’s/80’s, catches increased in the late 1990’s to around 350 t, following conversion from gillnets to traps. Catches then declined dramatically and the fishery closed in 2006 co-incident with low recruitment and egg production. This decline was attributed to heavy fishing pressure (reducing abundance of mated pre-spawning females) and environmental conditions (cooler temperatures affecting spawning success, noting Cockburn Sound lies near the southern end of the distribution for P. armatus). After re-opening, total catches never rose above ~ 80 t, recruitment and stock spawning biomass levels declined again, and the fishery was subsequently closed. This was unexpected given low catches relative to historic levels, suggesting that factors other than fishing pressure may be important. A stock-recruit-environment relationship indicated that, in addition to biomass, good recruitment is associated with high water temperatures during spawning. Other possible factors contributing to low current stock levels include i) reduced environmental productivity (indicated by low summer chlorophyll-a and declines in populations of other species, including in aquaculture), ii) increased predation (associated with rebuilding of fish stocks), iii) annual changes in proportion of berried females, and iv) critical depensation (associated with extremely low crab population size). The factors contributing to current low stock levels are likely to be complex and inter-related, begging the question; can a productive fishery again be expected if current environmental conditions persist?

Evolution of Freshwater Crabs in Lake Malawi in the African Rift Valley

Johnson EC, Cumberlidge N
Northern Michigan University

Lake Malawi is the southernmost great lake in the African Rift Valley and is home to a single freshwater crab species, the Malawi blue crab (Potamonautes lirrangensis) (Rathbun, 1904). While previous studies have focused generally on phylogeny (Daniels et al., 2015), biogeography, and conservation of Afrotropical freshwater crabs (Cumberlidge et al., 2009), little is known about the species diversity and the phylogenetic relationships of the freshwater crabs of Malawi, including Lake Malawi. This large Rift Valley lake is well known for its rapidly evolving species of cichlid fish; however, little information is present regarding the evolution of the notably species-poor freshwater crabs present in the same lake. The Malawi blue crab is currently assigned to P. lirrangensis, and while its distribution includes other Rift Valley lakes besides Lake Malawi and the Congo River basin, its current taxonomic assignment remains controversial. A detailed molecular analysis of this widespread morphologically similar-looking species may reveal distinct genetic lineages within the taxon from elsewhere in its range that could prove to be different, but cryptic, species. Through detailed examination and identification of distinct morphological characters, coupled with next generation RAD sequencing, this study aims to accomplish the following: (i) Assess the true diversity of Malawi’s freshwater crab fauna; (ii) Determine the species status of the Malawi blue crab as either widespread or unique to Lake Malawi; and (iii) Study evolutionary adaptation in Lake Malawi freshwater crab fauna.

Temporal and Spatial Trends in the Reproductive Biology of Blue Swimmer Crabs in Temperate and Subtropical Environments in Western Australia

Johnston DJ, Marks R, Hesp A, de Lestang S, Caputi N, Chandrapavan A
Western Australian Department of Primary Industries and Regional Development

Over the past two decades, several blue swimmer crab stocks in Western Australia have experienced marked declines, resulting in extended periods of closure for the two largest crab fisheries. Whilst one of these fisheries (Shark Bay) has essentially recovered, the other (Cockburn Sound) has not, despite now being closed for four years. Though not fully understood, the marked declines in both these stocks were attributed to high fishing pressure and environmental factors, including the effects of an extreme marine heat wave event in 2010/11. The need to understand why not all crab stocks have recovered, despite receiving full protection, and help facilitate robust management into the future based on reliable scientific advice, has prompted a detailed re-investigation of the biology of crab stocks in the State. This talk details results from recent reproductive studies, comparing key reproductive variables (size at maturity, batch fecundity, timing and duration of spawning, and amount of spawning activity (i.e. proportions of berried females) over time of stocks in different environments, including in temperate and subtropical waters. The marked changes in abundance of crab stocks in Western Australia over recent years, and accompanying data sets, provide an ideal basis for exploring the extent to which changes in abundance are accompanied with changes in reproductive biology. Attention is also given towards improvements we have made in the analysis of reproductive data for blue swimmer crabs in Western Australia.

Presence of Three Groups Among Populations of Common Intertidal Hermit Crab Pagurus minutus (Decapoda; Paguridae) in East Asia

Jung J, Kim W
Seoul National University, Ewha Womans University

A systematic study was conducted to examine the color variation and genetic differences among the individuals of Pagurus minutus. In this study, P. minutus were collected along the entire coast of South Korea, east coast of Honshu, west coast of Kyushu, Okinawa Islands of Japan, and Taiwan. Based on the difference of color and cytochrome c oxidase subunit I (COI) sequence, the individuals of P. minutus were divided into three groups: Major Group (MAG), Minor Group (MIG), and Taiwan-Okinawa Group (TOG). MAG commonly inhabits the entire coast of South Korea (except its northeast coast), east coast of Honshu and west coast of Kyushu of Japan. MIG predominantly inhabits northeast coast of South Korea, while a small proportion of the group inhabits west coast of South Korea and west coast of Kyushu in Japan. TOG restrictively inhabits Taiwan and Okinawa Islands of Japan. The background color and stripe pattern on the lateral surface of the ambulatory leg differ among these three groups. The COI divergence between MAG and MIG (9.82-11.46%), MAG and TOG (8.00-11.03%), and MIG and TOG (7.76-10.74%) was larger than the minimum interspecific divergence for other Pagurus species (5.59%). The average COI divergence between two TOG subgroups inhabiting Taiwan and the Okinawa Islands (3.06%) was larger than the average intraspecific divergence among hermit crabs (0.63%) but smaller than minimum interspecific divergence for other congeneric species (5.59%). Based on the results of the color pattern and COI analysis, MAG, MIG, and TOG are considered as three cryptic species.

Why a Functional Approach to Comparative Morphology Matters: Examples from Snapping Claws of Shrimps and Amphipods

Kaji T
University of Alberta, Edmonton

Form and function cannot be separated from one to another, but a functional perspective has not received much attention in morphological studies. We present two model cases where enhanced understanding of joint function helps explain the evolutionary origins of dramatic snapping claws in caridean shrimps and mearidaen amphipods. Both studies examine joint morphology specialized for “latching”, a mechanism that facilitates high-speed claw closing. These claws achieve ultrafast closing (which creates cavitation bubbles and subsequent shock waves and sounds) via novel latching mechanisms in the joints that allow muscle-contraction energy to be stored and released suddenly. Based on comparative functional morphology of many species in both taxa — including lineages that retain ancestral joint features — we describe how impressive novel functions derived evolutionary from mundane joints that had no latch mechanism. In both cases, the evolutionary change of form itself was subtle, but the functional consequences were large enough to cross a threshold to a wholly novel function. Such functional innovation may contribute more widely to evolutionary adaptation and diversification in other organisms, but the importance of subtle morphological differences in these examples were only recognized by careful examination of function. Such a functional approach brings a new explanatory power to better understand morphological diversity from an evolutionary perspective.

Seeing Things from a Different Angle - The Reproductive Morphology of Xantho poressa

Kabus J, Hayer S, Boretius S, Brandis D
Christian-Albrechts-University Kiel, Deutsches Primatenzentrum (DPZ)

The genus Xantho Leach, 1814 has an exclusive Mediterranean–Atlantic distribution and shows a great interspecific as well as intraspecific morphological variability (d‘Udekem d’Acoz, 1999). All four species of the genus as currently defined are restricted to the northeastern Atlantic Ocean and the Mediterranean Sea. Xantho poressa Olivi, 1792 is a widely distributed species of crab from the Black Sea, Mediterranean Sea and parts of the eastern Atlantic Ocean which normally lives in the shallow subtidal zone (0–2 m) in a wide range of habitats. To gain a new tool in studying intra- and interspecific variation of the genus Xantho on a morphological level, we developed a reference model of the copulatory system of Xantho poressa. Since the reproductive system of this species is entirely unknown, we used histological methods, magnetic resonance imaging (MRI) and micro computed tomography (µCT) to analyze the female reproductive organs. The results show a vagina and seminal receptacle which leans highly to the lateral side. In this case a rarely described epithelium around the seminal receptacle seems to play an important role in the fertilization process. Photographs of the male gonopods were used to understand the copulatory process. In summary the reproductive system of Xantho poressa can give some insight in the otherwise well-known genus Xantho.

Phylogeny and Divergence Times of Lake Baikal and Subterranean Candonidae Ostracod Lineages

Karanovic I, Sitnikova TY
Hanyang Univeristy, Limnological Institute, Siberian Branch, Russian Academy of Sciences

The family Candonidae is one of the most diverse freshwater ostracod groups in terms of number of taxa and ecological adaptations. They are a significant component of the Lake Baikal ostracod fauna and a predominant one in subterranean waters around the world, with many short-range endemics. All candonid lineages have representatives in subterranean waters, and five out of eight tribes exclusively inhabit these ecosystems. In Lake Baikal, 104 described species show an unprecedented morphological diversity, but they are classified into only three genera, one of them endemic to the lake. Competing hypotheses about the origin of highly disjunct subterranean lineages received some attention in morphology-based cladistic studies. However, phylogenetic relationships of candonid tribes and genera have not yet been tested using molecular markers. We reconstruct their phylogeny based on 16S, 18S, and 28S rRNAs, using Bayesian inference methods. Exploiting a rich ostracod fossil record for molecular divergence time estimates, we use four taxa to calibrate the root and three internal nodes. The resulting trees show an incongruence between molecular and fossil divergence time estimates, with the former suggesting older ages. Baikal candonids have a close phylogenetic relationship with Palearctic clades, but their deep divergence is indicative of separate genera. Our results also suggest a monophyly of tribes that today live exclusively in subterranean waters, and we offer several hypotheses of their evolutionary history. Broader implications of this study are some or all of the following: missing fossil record, inadequate systematics, problematic molecular dating, and marine origin of subterranean lineages.

Instant Taxonomy: Choosing Adequate Characters for Species Delimitation and Description through Congruence between Molecular Data and Quantitative Shape Analysis.

Karanovic T, Lee S, Lee W
Hanyang University

The lack of university funding is one of major impediments to taxonomy, partly because traditional taxonomic training takes longer than a PhD course. Understanding ranges of phenotypic variability for different morphological structures, and their use as characters for delimitation and description of taxa, is a tedious task. We argue that the advent of molecular barcoding and quantitative shape analysis make it unnecessary. As an example, we tackle a problematic species-complex of marine copepods from Korea and Japan, approaching it in a way that a starting taxonomist might do. Samples were collected from 14 locations and the mitochondrial COI gene was sequenced from 42 specimens. Our phylogenetic analyses reveal four distinct clades in Korea and Japan, and additional nine belonging to a closely related complex from other parts of the Northern Pacific. Twenty different morphological structures were analysed for one Japanese and two Korean clades using landmark-based two-dimensional geometric morphometrics. Although there is no single morphological character that can distinguish with absolute certainty all three cryptic species, most show statistically significant interspecific differences in shape and size. We use five of them to describe two new species from Korea, and to redescribe Tigriopus japonicus Mori, 1938 from near its type locality.

Photoreception and the Role of Serotonin On Photobehavior of Gammarus minus

Kennedy MD
American University

Intricate adaptations to their visual systems have allowed amphipods to thrive in extreme habitats like caves. Photoreception is required not only for vision, but also for hormone stimulation and photobehavior. Serotonin, a neurotransmitter modulated by light exposure, plays a vital role in many physiological processes like escape, reproduction, and feeding. Serotonin function can be altered by anthropogenic contaminants in the environment like antidepressants. The purpose of this study is to research photoreception in Amphipoda and assess the impact of altered serotonin pathways on photobehavior. Using a preference assay, subterranean and surface populations of Gammarus minus are characterized as photonegative, photopositive, or photoneutral before and after exposure to the antidepressant hydrochloride fluoxetine (Prozac®), a common selective serotonin reuptake inhibitor. Results will provide a basic understanding of amphipod photoreception and the role of serotonin on photobehavior, and lend insight into the evolution of invertebrate visual systems.

Global Conservation of Freshwater Crayfish

Kawai T
Wakkanai Fisheries Research Institution

Freshwater crayfishes (Astacoidea and Parastacoidea) have over 650 species and are globally distributed in temperate regions of Africa (Madagascar), Australia (including New Zealand and Papua New Guinea), eastern Asia, Europe, and the Americas. Freshwater crayfish have a unique evolutionary history. They live only in freshwater, they do not have a planktonic stage, and they frequently occur in smaller habitats, such as; swamps, springs, and bayous. This has led to high levels of endemism and local populations have are easily effected by anthropomorphic activities. Indeed, many species have been designated as endangered at the global level. Effective conservation strategies could be developed from an understanding of their evolution. Advanced conservation strategies are presented with several excellent examples through international collaboration.

The Reproductive System of Limnopilos naiyanetri (Hymenosomatidae) Indicates a Thoracotreme Affiliation

Kienbaum K, Vehof J, Becker C
Humboldt-Universität zu Berlin, Queen's University Marine Laboratory

The eubrachyuran Hymenosomatoidea MacLeay, 1838 is a group of crabs, widely distributed in tropical and subtropical regions ranging from marine to freshwater habitats. Even though, the biology of this taxon has been studied to some extent, its phylogenetic relationships are far from clear. Based on spermatozoal characters, larval development, and morphology, some authors suggested a close affinity of hymenosomatid crabs to heterotreme dorippoids or majoids. However, many of these characters are ambiguous, and the few molecular studies did not provide convincing solutions either. To address this issue, we studied the reproductive system of the hymenosomatid freshwater species Limnopilus naiyanetri using histology and scanning electron microscopy. The females show the characteristic organization of the paired eubrachyuran reproductive system. Additionally, a bursa (an accessory sperm containing cuticle cavity) is present that lies in close proximity to the oviduct orifice and the crescent-shaped vagina. The male copulatory system is characterized by paired long first and relatively short second gonopods, and a pair of sternal gonopores equipped with a penis. Both, the female and male reproductive organs reveal a number of correspondences to thoracotreme crabs. The seminal receptacle is largely lined by a very thin and highly expandable cuticle and dorso-laterally by a monolayered glandular epithelium. The male gonopods, the sternal genital opening, and the penis also resemble the thoracotreme situation. Thus, our results indicate that Hymenosomatidae are most likely part of the Thoracotremata. In contrast to this, a close majoid-dorippoid-hymenosomatid affiliation is not supported.

Comparative Transcriptome Analysis of Two Tetraclitella Species, T.chinensis and T.multicostata

*Kim HK, Kim HS, Kim W**
Seoul National University

The morphology of shell and number of plates are taxonomic characters in Barnacle. Within Tetraclitella Hiro, 1939, T. chinensis and T. multicostata are easily distinguished by the growth forms and number of holes in the shells. However, there are little significant genetic divergence between two species in two mitochondrial genes (12S rDNA and COI) and no distinct differences were observed in cirri, mouth parts and their setation. In this study, we conducted the first comparative analysis of de novo trascriptome assembly of RNA sequencing for two species, T. chinensis and T. multicostata. Using the Illumina sequencing technology, we sequenced 32,926,730 trimmed data of T. chinensis and 33,944,188 of T. multicostata. Comparison of two species transcripts against the Uniprot database produced 22,475 and 21,421 positive matches for T. chinensis and T. multicostata transcriptomes, respectively. Based on the DAVID gene functional annotation system, we analyzed gene ontology enrichment of two species to classify the functions of unigenes. Genes concerning binding for T. chinensis and cellular process for T. multicostata were most abundant genes in the biological process. The results suggested that transcriptome profiling is useful tool to understand evolutionary changes according to ecological adaptation of T. chinensis and T. multicostata.

The Genome Survey of Chthamalus challengeri (Cirripedia:Chthamalidae)

*Kim HS, Kim HK, Kim W**
Seoul National University

Chthamalus challengeri Hoek, is a predominant species in the rocky intertidal zone of tropical and sub-tropical shores. It prefers the upper part of exposed rocky shores and endures strong surf and strong sunlight. We conducted genome survey of Chthamalus challengeri as a preceding step to obtain genetic information through whole genome sequencing. The genomic DNA for sequencing was extracted from adult specimen. A total of 135.4 GB of raw data were generated using the Illumina Hiseq X platform. We confirmed the quality of raw data using FastQC program. The total 110.8Gb of filtered data were used for K-mer analysis to estimate genome size of Chthamalus challengeri using JELLYFISH. The total sum of each K-mer individual for K-mer size of 17, 21, 25 bases pairs was 99.1 Gbp, 96.1 Gbp and 93.2 Gbp, respectively. The genome size of Chthamalus challenger was estimated to be approximately 0.91Gb based on K-mer measurement. In addition, we expect that Chthamalus challenger has high heterozygosity genome through clear two picks shown in K-mer analysis graph.

An Integrated Approach to the Phylogenetic Position of Microcerberidea Lang, 1961 (Peracarida, Isopoda)

*Kim JH, Lee WC, Karanovic I**
Hanyang University, University of Tasmania

The suborder Microcerberidea comprising over 40 species, 8 genera and 2 families is one of the typical minute isopod highly specialized to the narrow space including marine interstitial and subterranean environment. The phylogenetic placement of the Microcerberidea is classically defined as a sister group of Asellota. However, previous studies to discuss on the origin of microcerberid and the detail relationship with other asellotan group are still controversial and requires additional works. Here we present the first molecular phylogenetic assessment of relationship between Microcerberidea and other related taxa. Furthermore, the cladistic analysis using morphological characters that appear synapomorphies for the studied groups are presented. To address this, we chose two species of Coxicerberus, representing Microcerberidea, collected from Korea and Australia for three ribosomal DNA (16S, 18S and 28S) and analyzed individual and concatenate datasets with other NCBI data using Bayesian Inference and Maximum Likelihood. For the cladistics study, 50 characters of 8 genera of Microcerberidea and 10 genera of Asellota were coded and analyzed with Maximum Parsimony method. Our analysis of both morphological and molecular data yielded consistent result representing the fresh water asellotans such as Stenasellidae and Asellidae are the most closely related to Microcerberidea while, other marine group, Janiroidea is to be distantly related. Our result possibly proposes that the current subordinal rank of Microcerberidea should be reconsidered and reassigned to the family level rank included in Asellota.

New Genus or Just New Species?

Kim SH, Lee YG, Kim YH
Dankook University

The purpose of this study is to raise the biodiversity of Korea by reporting new species though the collection of Cumacea. Specimens were collected mainly with a light-trap from the shallow coastal waters of Korea during 1994–2012. As a result, three new species belonging to the family Bodotriidae were collected from Korean waters. These three new species probably belong in the genus Bodotria (subfamily Bodotriinae) and the characteristics are as follows: carapace often with lateral carina; pereonite 1 fused to carapace and invisible in lateral view; exopods only on the first pair of pereopods; pereopod 2 without distinct ischium; uropod, endopod uniarticulate or biarticulate. However, major differences were also found between our three new species and the genus Bodotria: pereopod 5 absent; uropodal peduncle shorter than species of the genus Bodotria. Especially, Bodotria n. sp. 1, pereopod 1 very long and with 9 long setae in propodus. In hence, the three new species possibly belong to a new genus in subfamily Bodotriinae.

Crustaceans from Fossil Cold Seep Environments

Klompmaker AA, Nyborg T, Brezina J
University of California, Berkeley, Loma Linda University, South Dakota School of Mines and Technology, Mizunami Fossil Museum

Crustaceans including decapods, copepods, amphipods, cumaceans, tanaidaceans, ostracods, and isopods are major components of modern marine methane seeps, where they play a key role in structuring these hotspots of diversity in relatively deep waters. There is every reason to suspect they were common too in ancient seeps, but relatively few studies have focused on crustaceans from fossil seep deposits thus far. We hypothesize that crustaceans can be commonly found in Meso-Cenozoic seeps when many of the aforementioned groups were present and/or radiated. To this end, we review the global fossil record of crustaceans in seeps for the first time using the primary literature and newly collected specimens from the Late Cretaceous of South Dakota, USA. We find that seep crustaceans are much more common than previously known, are found on each continent, and occur more frequently starting in the Jurassic. Decapod crustaceans are represented by body fossils and traces (coprolites, repair scars in mollusks, and burrows), whereas only body fossils of ostracods and barnacles are known. Other groups are lacking. While modern seep decapods are dominated by galatheoid squat lobsters, alvinocaridid shrimps, king crabs, and true crabs, the fossil record is consisting primarily of callianassid ghost shrimps and true crabs thus far. Preservation and recognition are likely to have influenced this discrepancy. Finally, the relatively unexplored fossil record of seep crustaceans provides many opportunities for systematic and paleoecological research.

How Common Are Isopod Parasites in Decapod Crustaceans Throughout the Meso-Cenozoic?

Klompmaker AA, Robins CM, Fraaije RHB, Portell RW, De Angeli A
University of California, Berkeley, Oertijdmuseum, University of Florida, Museo Civico "G. Zannato"

Parasites substantially influence the structure of modern marine ecosystems, but the prevalence, diversity, and importance of parasitism throughout the Phanerozoic is poorly known. The best-known record of parasites in fossil crustaceans is evidence attributed to epicaridean isopods found in decapods. Such parasites can have dramatic effects on the host, including castration. Although these soft-bodied isopods do not fossilize, their swellings (ichnotaxon Kanthyloma crusta) are readily visible in the gill chamber region on dorsal carapaces of fossil decapods. Here we test the hypothesis that the prevalence of isopod infestations decreased through time by studying >5000 specimens from 13 Late Jurassic – Miocene assemblages from Europe and North America. Infestation percentages are significantly higher for Late Jurassic – Early Cretaceous species occurrences relative to those from the Late Cretaceous – Miocene interval. Decreases are also evident using genus-level occurrences and whole assemblages, supporting earlier notions based on less refined methods. This decline cannot be explained by collecting and preservational factors. Instead, this trend may, in part, be explained by a drop in the abundance of commonly infested primitive lineages such as homolodromioid brachyurans and galatheoid squat lobsters, among other factors. Possibly, parasitism contributed to the decline of these clades. This macroevolutionary trend adds to the rapidly increasing knowledge about the importance of parasitism in deep time and opens the door for new studies.

Crustaceans in the Tropics: Still Much to Discover

Knowlton N
Smithsonian National Museum of Natural History

The tropics are the epicenter of marine biodiversity, and crustaceans are no exception in this regard. Crustaceans are among the most diverse and ecologically important members of coral reef communities, where they form important symbioses with other invertebrates, support the base of coral reef food chains, and even shape the ecology of other reef dwellers through their sounds. This diversity has also provided model systems for understanding the processes of speciation in the sea and the evolution of true social behavior. Nevertheless, crustacean diversity is still poorly known, although DNA-based tools are contributing to rapid improvements in our understanding. In the past, DNA sequencing of individual organisms has revealed considerable cryptic diversity, and this process continues to this day. More recently, the high-throughput sequencing revolution has documented the extraordinary diversity of small crustaceans that typically go uncounted in traditional ecological surveys, and these approaches can also provide tools for examining the contribution of crustaceans to coral reef trophic relationships. In this talk I will review some highlights of these research trends, with a particular focus on snapping shrimp, one of the most diverse of all crustacean lineages, and on the discoveries emerging from studies of environmental DNA.

Dynamics of Amphipod Assemblages Associated with Sargassum Yezoense Beds On the Coast of Otsuchi Bay

Kodama M, Kawamura T, Nakamoto K, Ohtsuchi N, Hayakawa J, Kitagawa T, Watanabe Y
The University of Tokyo

Amphipod assemblages in algal beds include various functional groups each adapting different environments. Canopy part and understory part of algal communities are distinct microhabitats showing different seasonal fluctuation, and therefore, amphipod assemblages in the two parts are expected to fluctuate differently in response to different patterns of environmental change. In this study, we compared species compositions and its seasonal changing patterns of amphipods including various functional groups between canopy and understory parts of Sargassum yezoense beds. Paired-samplings on the canopy and the understory parts using 25×25 cm2 quadrats were conducted monthly from July 2015 to June 2016 on the coast of Otsuchi Bay, Japan. Amphipod abundance (inds/m2), species-richness and Shannon's diversity index were generally greater in the understory part than in the canopy part. In the canopy part, the abundance increased in early summer and decreased in late summer, followed by the abundance fluctuation of dominant species Jassa morinoi (tube-dwelling filter-feeder). In the understory part, the abundance increased in late summer and decreased in autumn, explained by the abundance fluctuations of various species, especially free-living deposit-feeders such as Quadrimaera pacifica. These differences in seasonal fluctuation of assemblage structures were probably caused by the different response of functional groups to the defoliation process of S. yezoense. In early summer, S. yezoense began defoliation, and withering algal bodies in the canopy part provided preferable habitat to tube-dwelling filter-feeders. By late summer, S. yezoense thalli were dropped off, and deposited in the understory part as detritus i.e. food source for deposit-feeders.

Regional Variation in Life-History Strategies of Penaeids and Their Resilience to Changing Temperatures

Koefoed IK, Loneragan NL, Kangas K, Hordyk A
Murdoch University, Department of Primary Industries and Regional Development, University of British Columbia

Penaeid prawns (or shrimp) are a high-value seafood commodity supporting large industrial-scale and artisanal fisheries around the world. Many of these prawn fisheries are tropical and sub-tropical and are thus potentially affected by rising sea temperatures. Temperature is known to influence the life history of organisms, with the metabolic theory of ecology (MTE) and the temperature-size rule (TSR) both predicting that ectotherms grow faster, mature earlier, but reach a smaller size in warmer waters than in cooler waters. However, these predictions have seldom been investigated for penaeids, despite having implications for stock assessment and management, particularly in tropical regions which are often relatively data-poor. A meta-analysis of published life history data for 22 penaeid species (four genera) from around the world was carried out to evaluate how the life history parameters of penaeids vary with temperature (using latitude as a proxy), both between species and within species. This meta-analysis was then used to examine the predictions of the MTE and TSR for the von-Bertalanffy growth parameters Linf and k and two of the Beverton-Holt life history ratios; M/k and Lmat/Linf. Understanding how life history parameters estimated from these ratios compare to the results of empirical studies from different regions and temperatures can facilitate discussion on the use of the Beverton-Holt ratios for informing stock assessments in data-poor penaeid fisheries.

Bring Out Your Dead: Reconstructing a Decapod Biocoenosis Through Quantitative Taphonomy and Functional Morphology

Kornecki KM
Rensselaer Polytechnic Institute

The Blue Springs locality (BSL) of the Maastrichtian Coon Creek Formation (CCF) crops out in Mississippi in what was a large bay of the Western Interior Seaway. The BSL is fossiliferous, with excellent preservation of a diverse assemblage of decapod taxa (Kornecki et al., 2017). A recent paleo reconstruction of CCF “Dakoticancer australis Assemblage” community (Bishop, 2016), proposed trophic relationships of major fossil groups and included some discussion of individual species’ predator-prey relationships. Whereas Bishop (2016) cited modern intertidal zones and “warm sea bottoms” as modern analogs, isotopic and biomarker analyses (Vrazo et al., 2018). suggested that the depositional environment was a shallow, nearshore marine environment further north in Tennessee and postulated that environments within the bay to the south would be offshore. These hypotheses were tested using quantitative taphonomy (corpse vs. molt preservation, articulated vs. disarticulated) and functional morphology of associated decapods to provide further insight on the CCF paleo community, particularly regarding depositional environment vs. the “living” assemblage. The ratio of molts to corpses of Dakoticancer australis Rathbun, 1935 and Tetracarcinus subquadratus Weller, 1905 suggests that molts may have been deposited in what was an intertidal zone and do not represent the dominant living taxon, though they may migrate up-slope for mating or molting events. The presence and accumulation of flat, phosphatic concretions (proposed to be large “rip-up clasts”), glauconite, and other factors support an interpretation for a reducing environment and potential for anoxic episodes or pockets, increasing preservation potential of molts and less calcified decapods, such as mud shrimps.

A New Species of the Deep-Sea Spongicolid Genus Spongicoloides (Crustacea, Decapoda, Stenopodidea) and a New Species of the Glass Sponge Genus Corbitella (Hexactinellida, Lyssacinosida, Euplectellidae) from Seamount Near the Mariana Trench, with a Novel C

Kou Q, Gong L, Li X
Chinese Academy of Sciences

A new species of the deep-sea spongicolid genus Spongicoloides Hansen, 1908 and a new species of the euplectellid genus Corbitella Gray, 1867 are described and illustrated based on the material recently collected by the ROV 'Faxian' near the Mariana Trench. The new deep-sea spongicolid species can be distinguished from the congeneric species by a series of morphological features and the validity was supported by the molecular phylogenetic analysis. Based on the microscleres of regular hexaster and oxynohexaster, the new sponge species can be distinguished from other Corbitella species easily. The new euplectellid sponge species is the host of the new spongicolid shrimp species and it is the first discovery of the association between the genera Spongicoloides and Corbitella. The present study increased the species diversity of both genera as well as brought insight into the commensal relationships between spongicolid shrimps and their sponge hosts.

Chemoreceptor Proteins in the Decapods: Variant Ionotropic Receptors Galore, Some Shared, Some Unique

*Kozma M, Schmidt M, Derby CD**
Georgia State University

A major class of chemoreceptor proteins in all protostomes, including crustaceans, is a variant subfamily of ionotropic glutamate receptors called Ionotropic Receptors (IRs). IRs exist as heterotetrameric ion channels, with the particular combination of subunits determining sensory function. IRs are best studied in insects, which have “conserved” IRs that are orthologs expressed across protostomes, and “divergent” IRs that are unique to each species. Our study examined IRs in transcriptomes from two chemosensory organs – antennules and legs – of four decapod crustaceans – Panulirus argus, Homarus americanus, Callinectes sapidus, and Procambarus clarkii. We identified protostome-conserved IRs, arthropod/tetraconate-conserved IRs, decapod-conserved IRs, and species-specific IRs. Each decapod species has over 50 IRs in its antennules and legs. Many more IRs are expressed in the antennules than legs, with little overlap between the two. This suggests that the antennule, which is the olfactory organ, has additional olfactory IRs to detect a broader range of chemical stimuli including pheromones. Immunocytochemistry shows that the co-receptor IR25a is expressed in most chemoreceptor cells in P. argus but in a smaller subset of cells in H. americanus, suggesting a functional diversity to the co-receptors. Decapod transcriptomes also have homologs of conserved IRs that in insects mediate hygro- and thermoreception, and homologs of other known insect chemoreceptors, TRP channels and Gustatory Receptors. Our results show that decapod crustaceans have an abundance of chemoreceptor proteins. An understanding of the functional roles of these receptors requires determining their expression patterns in individual chemosensory neurons and the central projections of those neurons.

A Review on the Life History of the Stone Crab Menippe mercenaria: Implications For Fishery Management

Kroenke C, Baeza JA
Clemson University

The stone crab Menippe mercenaria is heavily fished in the USA. This study reviews the life history of M. mercenaria to identify knowledge gaps relevant to the sustainable management of this fishery. Menippe mercenaria is abundant from Virginia to Texas. Adults are omnivorous but primarily feed on mollusks. Female spawning seasons vary by geographical location. In one reproductive season, females lay an average of six clutches, brooding approximately one million eggs. Larval release is correlated with circadian rhythms and tidal cycles. Temperature and salinity are key factors in the rate of larval development and mortality. Megalopae settle on a variety of substrates: mud, sand, rock, oysters, and seagrass beds. Chemical and physical cues play a role in inducing metamorphosis and megalopae ignore exudate cues from adults. Predation on M. mercenaria appears limited. Juveniles growth more quickly than adults, which molt once each year, with a final molting near age seven. M. Mercenaria show highly ritualized confrontational behaviors that are unique compared to other crustaceans. Males mate with recently molted 'soft' females, but may engage in pre-copulatory pairings before females have molted. Fishery regulations are inconsistent across the region, and likely outdated due to climate change. Claw-removal fisheries appear to cause moderate mortality and diminished reproductive performance. Our review suggests that additional studies on the population genetics, effect of claw removal, and reproductive performance of M. mercenaria are needed if this fishery is to be managed towards the goal of sustainability.

Effects of Habitat Type on a Marine Mesopredator's Foraging Efficiency

Kulp RE, Floros N, Peterson BJ
Stony Brook University, University of North Carolina Wilmington

Benthic predators forage in multiple habitats, each of which can differ in its structure density. This variation could alter the predators' foraging efficiency, thus altering their top-down control on the community. However, few studies have examined structure density effects in multiple habitat types. In a series of functional response mesocosm experiments, the foraging efficiency of the decapod mesopredator, Dyspanopeus sayi, was tested in a soft-bottom structured habitat, Zostera marina, and hard-bottom structured habitat, Crepidula fornicata shell hash. Increasing densities of the bivalve prey, Mytilus edulis, were placed in one of four mimicked structure habitat density mesocosm treatments (no structure, low [- 1SD of field mean], middle [field mean] and high [+ 1 SD of field mean]). Unlike typical submerged aquatic vegetative habitat density studies, Z. marina structure did not have a negative effect on D. sayi foraging efficiency regardless of shoot density. In contrast to their predation in the Z. marina habitat, D. sayi was less likely to consume M. edulis in C. fornicata habitat beyond the low habitat density. The differential foraging behavior in each habitat type was likely a result of differential prey accessibility in the habitat structure. In addition, the prey used, M. edulis, had limited mobility, which may have influenced the relationship between structure type and density and D. sayi's ability to find prey. Our results indicate that habitat type and prey mobility need to be considered to understand how habitat complexity alters predator foraging efficiency.

Freshwater Diaptomid Copepods on the Rocky Outcrops of the Western Ghats: Distribution, Ecology and Biogeography.

Kulkarni MR, Pai K
Savitribai Phule Pune University

Rocky outcrops are exposed rock surfaces, often devoid of woody vegetation. Temporary aquatic habitats often form on these outcrops, and despite being globally known to harbour unique biota, they remain largely understudied and neglected. Rocky outcrops also occur in the Western Ghats of Maharashtra, India (Northern Western Ghats, NWG), a region largely understudied for its invertebrate diversity, especially freshwater micro-crustaceans. The NWG have a geological history influenced by Deccan volcanism ca. 65mya, and comprise of distinct geo-morphological regions. Diaptomid copepods in such habitats were studied to a) document their diversity b) analyse their distribution and ecology and c) highlight their biogeography. Outcrops were classified as High-Level Ferricretes (HLF, >700m), Low-Level Ferricretes (LLF, 0-700m) or Basaltic Mesa (BM, 400-1300m) based on geo-morphological data. Samples (n = 185; 82 sites) collected from temporary habitats on these outcrop types were examined. Exploratory statistical and GIS-based methods were used for data analysis. Twelve species of diaptomid copepods (including three new species), representing eight genera and two subfamilies were observed. Highest species richness was observed on HLF outcrops, often occurring as multi-species (2-4 species) assemblages. Diaptomid fauna varied between outcrop types, and species distributions were influenced by altitude, latitude, electrical conductivity, hydrology and geology. Taxa with Gondwanan, Oriental, Palaearctic and endemic Indian affinities were observed. The studied outcrops face considerable anthropogenic pressures and such studies on their diversity and ecology can prove valuable for habitat conservation programs. We illustrate this using data on distribution, ecology, biogeography and genetics for a recently described diaptomid species.

Private Parts for Private Property: Evolution of Penis Size in Hermit Crabs

Laidre ME
Dartmouth College

Evolution has generated enormous diversity in animal genitalia. However, the importance of private property in driving penis size evolution has rarely been explored. Here I introduce a novel hypothesis, the 'private parts for private property' hypothesis, which posits that enlarged penises evolved to prevent the theft of property during sex. I tested this hypothesis in hermit crabs, crustaceans which carry valuable portable property in the form of a shell and which must emerge from this shell during sex, risking social theft of their property by eavesdroppers. I compared relative penis size (penis-to-body ratio) across nine closely-related species. Species carrying more valuable, more easily stolen property had significantly larger penis size than species carrying less valuable, less easily stolen property, which in turn had larger penis size than species carrying no property at all. These patterns in penis size were not explained by alternative hypotheses. Instead, the results suggest larger penises evolved as morphological adaptions to facilitate safe sex, in which individuals retain their valuable property by extending a long penis outside the shell to copulate. This hypothesis may likewise apply to other taxa, including those with valuable but non-portable property.

Description of the Setae on the Pereiopods of Scyllarid Lobsters, Scyllarides aequinoctialis, S. latus, and S. nodifer, with Observations on the Feeding Sequence During Consumption of Bivalves and Gastropods

Lavalli KL, Malcom CN, Goldstein JS
Boston University, Educational Testing Service, Wells National Estuarine Research Reserve

This paper examined the morphological and behavioral aspects of slipper lobster feeding. Using Scanning Electron Microscopy (SEM), the gross morphological structure of all pereiopods were described for three species of scyllarid lobsters: Scyllarides aequinoctialis, S. latus, and S. nodifer. Five types of setae within three broad categories were found: simple (long and miniature), cuspidate (robust and conate), and teasel (a type of serrulate setae). Setae were arranged in a highly organized, row-like pattern on the ventral and dorsal surfaces. Comparisons among species demonstrate that S. nodifer bears the same setae and setal pattern as S. latus, but S. aequinoctialis differs. The setal patterns of slipper lobsters contrast with those of nephropid and palinurid lobsters, likely due to the more rigorous use of the pereiopods in accessing their food. Feeding sequences of S. aequinoctialis on bivalves were videotaped, analyzed as Markovian chains, and showed a complex suite of behaviors involving contact chemoreception by the antennules as part of an initial assessment of food items, followed by mouthpart and leg probing, and eventual wedging behavior as previously described. Feeding sequences of S. latus on gastropods and bivalves also demonstrate extensive use of the pereiopods (instead of the mouthparts) to pry these prey items from the substrate and then to remove the foot. Use of antennules for food assessment and recruitment of many of the perieopods for food handling with minimal use of mouthparts also contrasts with the feeding sequences typical of nephropid and palinurid lobsters and may be an important adaptation.

Isolating Insulin-Like Androgenic Gland (Iag) Hormone Cdna Sequence of the Red Deep-Sea Male Crab, Chaceon quinquedens

Lawrence AL, Green SR, Chung JS
Institute of Marine Environmental Technology

Insulin-like androgenic gland factor (IAG) found in decapod crustaceans is known to regulate male sexual development. IAG is produced in the male-specific endocrine tissue, androgenic gland (AG); however, its expression has also been observed in other tissues of decapod crustacean species including, Callinectes sapidus and Scylla paramamosain. We isolated the cDNA sequence of IAG from the AG of male red deep-sea crab, Chaceon quinquedens using 5' and 3' rapid amplification of cDNA ends (RACE). The full-length ChqIAG cDNA sequence (1555 nt) translates to an ORF of 151 aa including: 19 aa signal peptide, 32 aa B chain, 56 aa C chain, and 44 aa A chain. The putative ChqIAG amino acid sequence is similar to those found in other crab species, including C. sapidus and S. paramamosain, which are clustered together phylogenetically. We are currently investigating the role of IAG in the onset of sexual maturity of male decapod crustaceans.

First Male Specimen of Sea Spider Pycnogonum spatium (Pycnogonida: Pycnogonidae) from the Green Island, Taiwan

Lee D, Chan BKK, Kim W
Seoul National University, Academia Sinica

The sea spider genus Pycnogonum Brünnich, 1764 consists of 73 species which are characterized by thick and robust body, well developed proboscis, and absence of chelifore and palp. Pycnogonum is divided into the three subgenera based on the character states of the male oviger. In subgenus Pycnogonum, oviger has 8-9 segments with terminal claw; in subgenus Retroviger, oviger has 4-7 segments with or without terminal claw; in subgenus Nulloviger, oviger is absent. Pycnogonum spatium Takahashi, Dick & Mawatari, 2007 was described as a new species based on a female specimen collected by beam trawl at Amami Island, Kagoshima. One sea spider specimen was collected by SCUBA diving at Green Island, Taiwan. This specimen generally agrees with the description of P. spatium in terms of having a cylindrical proboscis with a flat lip, strong middorsal tubercles on the trunk, and wide intervals between the lateral processes. However in this specimen, oviger is absent and there is one small gonopore on ventrolateral coxa 2 of each 4th leg. In comparison with the female, the length of trunk body is shorter, and intervals between lateral processes are narrower. With these characteristics, we conclude that this specimen is the male Pycnogonum spatium and this species comes into the subgenus Nulloviger.

Color Variation in Female Green Crabs, Carcinus maenas

Lee KT
George Mason University

Carcinus maenas, the green crab or shore crab, is a wide-spread invasive species, important in shaping shallow marine communities. Individual crabs come in a range of colors from yellow or light green through orange to dark red. In male crabs, this coloration, which develops during intermolt periods, affects physiological tolerance in individual crabs, their distribution on the shore, their aggressiveness, and their ability to attract mates. Evidence suggests that crabs which are molting frequently, putting their resources into growth, stay light colored, while crabs which are molting infrequently turn red, sacrificing their environmental tolerance for increased mating success. Most of the data on color variation in C. maenas has been collected in male crabs. For many years I have been collecting physiological, ecological and color data on female crabs. Salinity tolerance, distribution on the shore, aggression, and color change over the course of the summer have all been collected via a variety of methods including laboratory studies, behavioral trials, mark-recapture studies, and population sampling. In laboratory studies, red females have decreased physiological tolerance, but do not show increased aggressiveness when compared to green females. In the field, red females are much more common than red males, often outnumbering even green females. Over the course of a summer, the pattern of color change in female crabs differs from the pattern in male crabs. These data show that female crabs show color variation similar to that exhibited by male crabs but with important differences.

Studying Molt-Stage Dependent Changes in the Blue Crab Callinectes sapidus By Transcriptomic and Metabolomic Approaches

Legrand E, Schock TB, Chung JS
University of Maryland Center for Environmental Science, National Institute of Standards Technology, Hollings Marine Laboratory

Crustacean growth requires numerous molting events to complete their life cycle from hatching to adulthood, the process of which is orchestrated by hormones. In decapod crustaceans, two different types of hormones are intimately involved in this process: the inhibitory neuropeptides produced in eyestalk ganglia and ecdysteroids secreted by Y-organ. Importantly, the ecdysteroids in hemolymph are closely related to molt stage: low at intermolt and high at premolt. The exact mechanism that triggers the initial increase of ecdysteroids at early premolt is still unknown. This project aims to gain a better understanding of the molting process in the blue crab, Callinectes sapidus, using transcriptomic and metabolomic analyses. Specifically, we aimed to identify the initial changes occurring between the intermolt animals and those entering the early premolt stage. To this end, the following experiments were set out to determine if there are differences between 1) intermolt and premolt stages of the prepubertal females and 2) intermolt of intact adult females and early premolt induced by a bilateral eyestalk ablated. Based on the transcriptomic analysis, expression levels of candidate genes that are known to be involved in ecdysteroidogenesis, have been measured in the Y-organ by qPCR assays. Expression levels of Spook, Cyp49, HR4, are positively related to the hemolymph ecdysteroid concentrations. The metabolomic study using NMR shows significant differences in the hemolymph between intermolt and premolt stages. To conclude, both transcriptomic and metabolomic approaches have identified molt-stage dependent changes, in correlation with the increase of ecdysteroids.

Recognizing the Caribbean Sea Lesser Antilles as a “Hot Spot” of Decapod Crustacean Biodiversity

Lemaitre R, Poupin J
Smithsonian Institution, Institut de Recherche de L’ecole Naval

The decapod crustacean fauna from the Caribbean Lesser Antilles (LA) is evaluated based on recent intensive biodiversity surveys in French islands (St. Martin, Guadeloupe, Martinique), Dominica, and Curaçao, museum collections, and taxonomic literature. The LA is found to be a “hot spot” of decapod diversity, even though the historical rate of species discovery shows that the decapod fauna is still imperfectly known. Numerous species complexes have been recognized and are yet to be understood. The region has thousands of islands at the core of the Caribbean zoogeographic province, covering three main archipelagos, each with its own zoogeographic characteristics: United States and British Virgin Islands (VGI); islands of the Caribbean arc from Anguilla to Trinidad (ICA); and islands off Venezuela (IOV) from Los Testigos and Margarita to Aruba. A total of 910 species are found in ICA, 548 in IOV, 374 in VGI, and 1044 in the entire LA of which 992 (95%) are marine, 25 (2.4%) terrestrial, and 27 (2.6%) freshwater. Differences in diversity can be attributed to unequal sampling efforts, but are also correlated with number of islands and richness of habitats. Comparisons show ICA more diverse (910), followed by IOV (548) and VGI (374); of the LA total, 886 (84.8%) are distributed exclusively in the western Atlantic, 77 amphi-Atlantic (and/or Mediterranean), 60 cosmopolitan, 16 trans-Panamanian, 5 non-native or invasive, and 80 exclusively in LA. The zoogeography of LA decapods is compared with other oceanic areas in the Atlantic and Pacific. The list of species is available online: http://crustiesfroverseas.free.fr/iles.php?ile=Antilles

Multiple Spectral Channels in Branchiopods: Vision in Dim Light and Neural Correlates

Lessios N, Cohen JH, Rutowski RL, Sayre ME, Strausfeld NJ
University of Arizona, University of Delaware, Arizona State University

Animals that have color vision possess multiple spectral classes of photoreceptors. For true color vision, species of Pancrustacea (Hexapoda + Crustacea), integrate spectral information in the second and third optic neuropils, and centrally in optic glomeruli. Branchiopod crustaceans possess only two optic neuropils, the lamina and optic tectum but nevertheless express four or more rhabdomeric opsins in their compound eyes. Here we describe experiments and correlative neuroanatomy that explains the retention of chromatic pathways in a simple crustacean visual system. To identify the most likely number of spectral photoreceptor classes in their compound eyes, we used electroretinographic recordings and multi-model inference based on modeled spectral absorptance. Recordings from the retina provide support for four spectral channels. Histological methods were used to characterize parameters that could explain signal summation at low light intensities, incorporating spectral sensitivities. Candidates for spatial summation in the lamina have been resolved using immunocytology as well as selective silver and dye staining to demonstrate systems of terminal collaterals from photoreceptors extending tangentially to provide substrates for photoreceptor signal pooling. We propose that spatial summation from compound eye ommatidia provides sufficient signal for vision at intensities equivalent to those of terrestrial habitats under dim starlight. Our findings suggest four spectral photoreceptor classes have been maintained in these species of Branchiopoda primarily for luminance detection in the absence of optic lobe neuropils used by other pancrustaceans for fine-scale spectral discrimination.

The Brains and Sensory Specializations in the Midwater Hyperiid Amphipods

Lin C, Cronin TW, Osborn KJ
Smithsonian Institution, University of Maryland Baltimore County

Studying the nervous systems of animals with highly specialized sensory systems often provides insight into how a brain has evolved in response to the animal’s natural surroundings. However, correlations between the modifications of certain brain regions and an animal’s ecology are mostly suggestive, due to a lack of intermediate forms among closely related species. Here we present a group of crustaceans that provides an excellent opportunity to study how brains adapt when light limitations have driven the evolution of a diverse morphology of eyes. Hyperiidea is a suborder of amphipod crustaceans that are abundant members of zooplankton at mesopelagic depths (200-1000 m), where sunlight is reduced to increasingly dim and downwelling blue light. At least 10 different eye types are found, ranging from no eyes, tiny simple eyes, to several forms of compound eyes. Using techniques in neuroanatomy, we show that neural arrangements in the visual brain area generally follow the malacostracan-insect ground pattern, but with various modifications. Photoreceptor axons project to the first optic neuropil (lamina), whose axons, in turn, project to the second optic neuropil (medulla). One exceptional taxon, Paraphronima spp., possesses a true third optic neuropil (lobula) and three additional ones after the lobula, an arrangement that has never been described. While the neural organization of each hyperiid reflects the result of sensory adaptation in its own surroundings, mapping all the neural and habitat characteristics onto the hyperiid phylogeny enables us to reconstruct the evolutionary history of sensory adaptations in this closely related but highly diverse group.

Carcinofauna Composition from South Pernambuco Continental Shelf, Southwestern Atlantic

Lucatelli D, Souza-Filho JF, Andrade RM
Universidade Federal De Pernambuco

The aim of this work was to designate the composition and distribution of the carcinofauna along the Tamandare Bay (South Pernambuco), which comprise a Marine Protected Area (MPA) "Costa dos Corais". The samples were collected by R/V Velella using dredge and Van-Veen grabs. The continental shelf was divided in three portions: Inner (0-20 m), Mid (20-40 m) and Outer (>40 m) shelf. The samples were transformed to log (x+1) and analyzed on redundancy analysis and CAP. A total of 3.516 specimens were collected. Seven groups of Crustacea were identified: Amphipoda, Cumacea, Decapoda, Leptostraca, Ostracoda, Stomatopoda e Tanaidacea. Among these, only Leptostraca showed a restricted bathymetric distribution, being collected around 40 m (mainly on Mid shelf). Tanaidacea (n= 1.228), Amphipoda (n= 1.179) and Isopoda (n= 522) were the most representative orders. The first one was the most abundant among all crustacean. Crustaceans showed a higher abundance on Mid shelf and lower on Inner shelf. Cumacea and Ostracoda were more representative on Inner and Outer shelf, respectively. Leptostraca had no representatives on Inner shelf. Regarding the type of substrate, the Inner shelf was composed by a variety of substrate (from mud to gravel). Mid and outer shelves was defined by coarse-sand and gravel. The CAP analysis presented tanaidaceans and amphipods preferring coarse substrate on Mid and Outer shelf. This work is the first to study the carcinofauna of Tamandare, contributing with the knowledge of this group for the MPA "Costa dos Corais".

Extreme and Contrasting Population Structures of Freshwater Atyid Shrimps in Hong Kong

Ma KY, Chow LH, De Grave S, Chu KH
The Chinese University of Hong Kong, University of Oxford

The Caridina and Neocaridina shrimps of family Atyidae constitute a major component of stream ecosystems in Hong Kong. Nonetheless, while two of the nine local species are considered threatened in the IUCN Red List, the lack of understanding on their genetic diversity and population genetics structure significantly hampers conservation management. By a combination of extensive sampling and genetic assessment using mitochondrial COI and microsatellite markers, we scrutinized the fine-scale population structure of all the atyid species in Hong Kong. Our results reveal contrasting phylogeographic patterns, ranging from wide range genetic panmixia observed in two amphidromous species, to strong population structure in most of the freshwater obligates, among which, population differentiation of the two threatened atyids is evident at an extremely small scale of even less than a kilometre. Such pronounced population structuring of the freshwater obligates may be attributed to the species' limited dispersal ability, high level of inbreeding and marked demographic fluctuations associated with climate changes since the Pleistocene. The results not only lay the foundation for future scientific research on the local freshwater fauna, but also bridge the critical knowledge gap in formulating effective conservation plans. [The present work was supported by a research grant (project no. 74/2015) from the Environment and Conservation Fund, HKSAR Government, China.]

The Evolution of True Crabs Through Time: Insights from the Tropical Americas

Luque J
University of Alberta, Edmonton

A full understanding of the evolution of novel forms requires evidence of their origins. This must be inferred via study of genotypic and phenotypic variation in living forms and clues from the fossil record. However, the early evolutionary history of some morphologically diverse groups is obscure because few early-splitting branches have living descendants, molecular data are currently unavailable for many key extant species, and useful fossils are rare or incomplete. This is the case for true crabs, or Brachyura, a diverse and economically important group whose evolutionary history and phylogenetic relationships remain unresolved. Moreover, while crab fossils from higher latitudes are relatively well known, records from tropical settings are scarce and fragmentary. I present new crustacean-rich assemblages from the Mesozoic and Cenozoic of tropical America, and explore the phylogenetic relationships across the main fossil and extant Brachyura lineages in light of these new discoveries. Analyses of morphological data from fossil and extant taxa under different tree search methods support the view that podotreme brachyurans (crabs with sexual openings at the base of the legs) form a paraphyletic grade, and that some derived podotreme groups might be closer to Eubrachyura than to less inclusive podotremes. Furthermore, our findings also reveal that the evolution of shovel-like and paddle-like legs, and the loss of a typical 'crab-like' form, or 'decarcinization', have occurred independently at least five times since the Cretaceous. The versatility of the crab body form, and the interplay between development and ecological invasion, may act as drivers of morphological innovation.

Volcanic Mass-Death Events and Exceptional Fossil Preservation: Lessons from the Ancient Romans

Maguire EP, Feldmann RM, Schweitzer CE, Casadio S, Thiel BA
Kent State University, Universidad Nacional de Rio Negro

When volcanic ash enters marine systems following explosive eruptions, it can have devastating effects on the biota, causing respiratory distress by blocking inhalant passages and lacerating soft tissue. Evidence of respiratory distress is observed in some fossil decapods, which have been preserved with their third maxillipeds in an unusual gaping position. Rivers can deliver massive quantities of ash to marginal marine settings, forming extensive hyperpycnal flows capable of travelling 10's of kilometers along the sea floor. Sedimentation rates during these high-density flows can be greatly enhanced, making escape nearly impossible. Fossil evidence suggests that mortality of the inhabitants of affected areas is nearly total, and distinctive "pioneer taxa" are found following such deposits. Computed tomography scanning of specimens from Argentina reveals the preservation of delicate gill structures rarely seen in the fossil record, and examples of exceptional preservation in association with volcanic ash are known from several localities around the world. The ancient Romans utilized the unique qualities of volcanic ash in cement making, and found that ash mixed with lime, and poured under seawater made a most resilient concrete. Ancient Roman sea walls constructed in this manner still stand today. We hypothesize that the same qualities the Romans exploited for cement-making may contribute to the exceptional fossil preservation observed in some specimens. Modern research on Roman concrete has found that the fine-grained, cryptocrystalline silica component of ash facilitates pozzolanic reactions, producing early resilient diagenetic cements. Further testing will be needed to determine how these properties contribute to fossil preservation.

The Effect of Temperature on Larval Development of Ucides cordatus (Linnaeus, 1763) in a Climate Change Scenario

Marochi MZ, Costa TM
São Paulo State University,

Climate change already affects the marine environment. One of the main effects is the increase of coastal waters temperatures. Consequently, it can affect the stability of populations. In this sense, our aim was assess how the increase of ocean water temperature (based on IPCC predictions) may affect the coastal environment and population dynamics, using as model organism the semiterrestrial crab *Ucides cordatus*. Thus, we evaluated 1) the survival and duration of larval development until zoea III stage and 2) the morphological variation. We hypothesized that the survival rate will decrease in warmer temperatures and affect the development duration and morphology. Zoea I larvae (396) from six females were individualized in 5 ml acrylic plates with artificial sea water (salinity 30) and submitted to three water temperatures: 25°C (control), 27°C and 29°C until they reach zoea III stage. Daily the zoea larvae were fed and the water was changed. Results revealed influence of water temperature during larval development from zoea I to zoea III in survival rate, duration of larvae development and morphology. The survival rate was lower in warmer temperatures (27°C and 29°C) accompanied by reduced development time and morphological variation. These results confirm our initial hypothesis, and, in summary, if the IPCC predictions for ocean superficial waters temperature increase occurs, a reduction in colonization rate (by new offspring) and consequently in population size is expected. Therefore, our results reveal a negative effect during larval development of Ucides cordatus caused by water temperature increase.

Seasonal Expression of Digestive Enzyme Genes in the Brown Shrimp Crangon crangon (Decapoda, Caridea)

Martinez-Alarcon D, Teschke M, Hagen W, Saborowski R
University of Bremen, Alfred Wegener Institute

The brown shrimp Crangon crangon is valuable specie for the North Sea ecosystem, where it is highly abundant and has an important role as a predator and as a prey. It represents an important target in coastal fisheries. Previous studies revealed distinct seasonal pattern in metabolic processes. Activities and numbers of enzyme-isoforms increased during the early summer but were reduced during autumn and winter. The brown shrimp is apparently well prepared to thrive in a highly variable environment. However, it is still unknown, how this species manages to cope with the seasonal environmental changes of the North Sea at the metabolic level. Here we analysed the seasonal gene expression of digestive enzymes in C. crangon. The objective of this research was to learn about the modulation of digestive enzymes in the brown shrimp during the seasons of the year. We found that Trypsin, Cathepsin L and triacylglycerol lipase show differential expression between seasons. None of the enzyme genes involved in carbohydrate metabolism showed seasonal differences. The results here obtained help to better understand about the biochemical strategies that allow C. crangon to inhabit a variable environment.

Hepatopancreas Transcriptome Analysis of the Brown Shrimp, Crangon crangon (Decapoda, Caridea), Reveals Expression of Polymorphic Digestive Enzymes

Martinez-Alarcon D, Harms L, Hagen W, Saborowski R
University of Bremen, Alfred Wegener Institute

The brown shrimp Crangon crangon shows high reproduction rates, feeds opportunistically on endo- and epibenthic organisms and is apparently well adapted to variable environmental conditions. Previous electrophoretic studies revealed a high level of polymorphism and no consistent phenotype of digestive enzymes between individuals. In order to understand the biological reason of digestive enzymes polymorphism and underlying biochemical processes, we performed a transcriptome-based study of digestive enzymes of C. crangon. Detailed sequence analyses of triacylglycerol lipase, phospholipase A2, alpha-amylase, chitinase, trypsin and cathepsin L were performed to identify putative isoforms. The number of isoforms varied among enzymes: for lipases, phospholipase A2 showed a higher number of isoforms than triacylglycerol lipase, while carbohydrase chitinase showed a higher number of isoforms in comparison with alpha amylase. Furthermore, cysteine proteinases showed a lower polymorphism than serine proteinases. We propose that the expression of polymorphic digestive enzymes indicates high plasticity in food utilization by the brown shrimp. Alternative splicing may be the driving force of the heterogeneous patterns of digestive enzymes in C. crangon.

New Aptian Necrocarcinoidea from the Early Cretaceous Romualdo Formation, Araripe Basin, Brazil

Matos SA, Castilho AL, Bondioli JG, Custódio MA, Fürsich FT, Assine ML, Simões MG*
Universidade Estadual Paulista, Universidade de São Paulo, Universidade Federal do Amazonas, Friedrich-August-Universität Erlangen-Nürnberg

Necrocarcinoidea is an Early Cretaceous to Oligocene group of marine, basal raninoids (frog crabs), represented by Araripecarcinus ferreirai in the Brazilian Cretaceous. Initially, this was interpreted as a freshwater portunoid crab, but subsequent studies demonstrated that they belong to Necrocarcinidae. Here, we record two new fossil specimens of necrocarcinoid crabs from the Romualdo Formation, Araripe Basin, northeastern Brazil, which were found in the Sobradinho section, Jardim County, Ceará State. At the study area, this formation is a ~98 m-thick siliciclastic-dominated sedimentary succession, mainly composed by concretion-bearing black shales and fossil-rich siltstones, also recording a metric-thick carbonate interval about halfway-up. The unit records the main marine transgression during the late Aptian in the NE interior of Brazil. Fossil crabs were recorded in siltstones, locally placed ~ 48 m above the base of the unit. The specimens are tiny (~5 mm width) and represented only by carapace remains. They may correspond to exuviae or disarticulated carcasses. Morphologically, the carapaces close resemble those of Orithopsidae crabs, and may be referred to Planocarcinus and Aetocarcinus (?), respectively. These genera were also recorded in Aptian-Albian deposits of Colombia and United States, respectively. Therefore, the paleobiogeographic distribution of this group of crabs is extended into the NE Brazilian interior. Yet, they represent another unquestionable fossil evidence of marine invertebrates in the Romualdo Formation. Finally, our data suggest that the necrocarcinoid fauna that thrived in the Araripe Basin during the Romualdo Formation transgression was more diverse than previously realized.

Effects of Prey Densities and Dietary Supplementation on the Larval Development of the Blue Crab Callinectes sapidus Rathbun, 1896 (Brachyura: Portunidae)

Maurer L, Chung JS
University of Maryland Center For Environmental Science

Variation in larval development related to duration and number of stages is common among arthropods. This variation appears to be influenced largely by environmental factors such as prey availability and temperature, but the primary causes are poorly understood. We examined the effects of prey density and the use of polyhydroxybutyrate (PHB), an energy-storage compound, on larval duration and survival during the early development of the blue crab, Callinectes sapidus (Rathbun, 1896), using hatchery-raised animals at constant temperature (21–23 °C). We also determined the daily food consumption by zoeae and the number of zoeal stages that are required to reach the final megalopa stage. Newly-hatched zoeae of C. sapidus were reared until megalopae in 24 well plates under high and low prey density with and without PHB supplementation (50 and 100 mg/l). Food consumption only was significantly different when a high density of Artemia, used as food, during later development. The zoeae raised under a high prey density had a shorter duration by having fewer zoeal stages and greater survival rate than those with a low prey density. PHB supplementation, with a combination of a high prey density, increased the incidences of stage skipping without changing the duration of zoeal development. Prey density, possibly affecting the nutritional status of larvae, is a critical factor that influences the zoeal development of C. sapidus.

Interaction Between Host Lgbp and Pathogenic Enolase Promote Spiroplasma eriocheiris Invasion Into Macrobrachium Rosenbergii Hemocytes

Meng Q, Ning M, Xiu Y, Wang W
Nanjing Normal University

Spiroplasma eriocheiris, as an aquaculture pathogen without cell wall, has led into enormous economic losses in aquaculture. The Macrobrachium rosenbergii hemocytes have been shown to be major target cells in S. eriocheiris infection. It is established that host-pathogen interactions could be a prerequisite for invasion and colonization, particularly for cell wall-less S. eriocheiris. The study focused on the identification of interactions proteins between S. eriocheiris and its freshwater crustacean host, M. rosenbergii. Six potential receptor proteins of the prawn hemocytes were identified including Ras-related nuclear protein, lipopolysaccharide and beta-1, 3-glucan binding protein (MrLGBP), beta-Actin, prophenoloxidase, beta tubulin and alpha-tubulin. Bacteria binding assays and confocal microscope observed that S. eriocheiris colocated with MrLGBP. Four ligand proteins of MrLGBP were isolated and identified as enolase, transketolase, acetaldehyde dehydrogenase, and DNA directed RNA polymerase subunit beta. The interactions between the MrLGBP and its ligand protein enolase was confirmed by co-immunoprecipitation and colocalization. The competitive assays suggest that hemocytes viability was increased resulting from competitive binding of enolase to MrLGBP. And, the overexpression of MrLGBP could decrease copies of S. eriocheiris in Drosophila S2 cells, which result in increasing of cells viability. In addition, RNAi knockdown of MrLGBP made M. rosenbergii more sensitive to S. eriocheiris infection, leading to less survival rate of prawns. In conclusion, as the identified of interactions proteins, MrLGBP and enolase played important roles in the process of S. eriocheiris infecting M. rosenbergii hemocytes.

Investigation of Ultrastructures in the Eyes of Larval Stomatopod Crustaceans

McDonald MS, Porter ML, Feller KD
University of Hawaii at Manoa, University of Cambridge

Light detecting systems leading to vision are widespread in the animal kingdom, but not all eyes are built the same. There is a wide diversity of eye types and capabilities, and one of the most intriguing is the stomatopod crustacean eye. As adults, stomatopods have arguably the most complex eyes in the animal kingdom. However, during the larval phases the eyes are physiologically and morphologically distinct from the adult. Upon metamorphosis, the adult retina grows in adjacent to and replaces the larval retina. While the adult visual system has been well studied, there is a gap in understanding of the larval visual system. The stomatopod eyes are remarkably adapted to the pelagic environment, with transparent apposition optics that utilize screening pigments and eye shine to remain camouflaged in the open environment. However, it is generally assumed that all crustacean larvae have similar compound eyes regardless of adult complexity. We hypothesize that the larval stomatopod eyes are more complex than previously assumed, and that there are differences in the larval eye specializations among species that relate to the corresponding adult eye complexity. In order to test this hypothesis, the ultrastructure of the larval eyes from multiple stomatopod species were imaged using transmission electron microscopy (TEM). Various structures were examined throughout the eye in order to identify novel structures and differences among species. Follow up studies will use physiological and behavioral methods to understand how the anatomy is related to the function and use of the larval eye.

Searching Through the Abyss – Comparing Isopod Family Composition from Two Different Depths from Northern and Southern Deep-Sea Areas off the East Coast of Australia

Merrin KL, Hughes L
Museums Victoria, Natural History Museum

The Isopoda are an important component of deep-sea ecosystems. One group, the Asellota, is the dominant sub-order found within the deep-sea (Brandt et al. 2004, 2007). Within Australian waters, our knowledge of deep-sea Asellota is just beginning (Poore 2002). During May to June 2017, scientists on the R.V. Investigator conducted the first deep-sea latitudinal sampling program along the abyssal regions of the east Australian coastline. Collections were made with a Brenke epibenthic sled at two depths, 2500 and 4000 metres, from 41.6°S in the Tasman Sea, Tasmania to 23.7°S, the northern terminus of the abyssal basin in the Coral Sea, Queensland. Here we compare the composition of isopod families collected from the southern abyssal region to that of the north. Preliminary sorting documents a rich fauna, with a high percentage new to science. We found that the Munnopsidae was one of the more prominent families in both regions, while other families such as the Nannoniscidae, Haplomunnidae and Thambematidae were represented only by a few individuals. The use of a Brenke sled along with dedicated on-board and post trip processing has provided a legacy of high quality research material.

Comparative Analysis and Phylogenetic Context of the Spermatozoa Ultrastructure in Grapsoidea Macleay, 1838

*Miranda I, Zara FJ, Mantelatto FL**
Paulista State University, University of Sao Paulo

The superfamily Grapsoidea are presented in Brazil by the families Gecarcinidae, Grapsidae, Sesarmidae and Varunidae. Comparative studies on the spermatozoa ultrastructure have demonstrated to be informative and valuable to elucidate the phylogenetic relations among different groups, especially in Brachyura. The knowledge on the spermatozoa of grapsoid crabs distributed along the Brazilian coast is, however, insipid. Thus, our goal is to describe and compare the spermatozoa ultrastructure of the grapsoid crabs collected on the coast of São Paulo state and analyze patterns of distribution of the morphological characters from the spermatozoal analyses in a phylogenetic tree generated using mitochondrial and nuclear markers. For that purpose, adult males of 10 genera and 13 species were included (Geograpsus lividus, Goniopsis cruentata, Pachygrapsus gracilis, Pachygrapsus transversus, Aratus pisonii, Armases angustipes, Armases ricordi, Armases rubripes, Sesarma rectum, Cyclograpsus integer, Cyrtograpsus angulatus, Neohelice granulata and Plagusia depressa). Preliminary results indicate that the presence of perforatorial chamber, apical buttom, periopercular rim, accessory opercular ring and thickened ring are informative characters but each family has its peculiarities. By the end of this project, we expect to contribute to understand the evolutionary history of male reproductive system in Grapsoidea and in comparison with the remaining groups in Brachyura. Financial Support: Ciências do Mar II - Procs. 2005/2014 - 23038.004308/201414; #1989/2014 – 23038.004309/201451 ; BIOTA-FAPESP – Proc. 2010/50188-8; CNPq – Proc. 304968/2014-5

Phylogenetic Approach of the Mexican Freshwater Crabs Genus Tehuana (Decapoda: Pesudothelphusidae), Using Morphologic and Genetic Evidence

Moreno-Juarez EG, Villalobos-Hiriart JL
Universidad Nacional Autónoma De México

The freshwater crabs of the genus Tehuana include a group of eight species, which are distributed along the southeastern of Mexico through the states of Veracruz, Oaxaca, Tabasco and Chiapas. Morphologically are characterized by the presence of a first par male gonopods slender and cylindrical proximally and distally depressed; the main axis shows an evident conical meso-distal prominence as well as a medial constriction on the lateral surface; in addition, on the inner surface of the proximal lobe of the caudo-marginal projection, a strong and sharp carina protrudes. The morphology and distribution of each species of this genus has been well studied, but in areas with complexes geological histories and orographic conformations, the crabs populations present evident morphological variations among them and with the nominal species, which makes difficult its taxonomic determination. In this work two phylogenetic reconstructions, morphological and molecular, were carried out. The morphological analysis of parsimony in TNT, included somatic and reproductive (first male gonopod) characters. The molecular consisted of an analysis of Bayesian Inference in Mr. Bayes, analyzing three markers, two mitochondrial (COI and 16S) and one nuclear (H3). In our results the genus Tehuana was retrieved as monophyletic group and sister of the genus Pseudothelphusa, with a strong statistical support, also there were found species that comprise complexes of forms, in the particular case of T. poglayenorum, the specimens of several localities were recovered as lineages independent of the nominal species.

Metabolic Effects of a Viral Infection (CSRV1) on the Blue Crab Callinectes sapidus in Southern Brazil: Preliminary Results

*Model JFA, Vogt EL, Lima MV, Trapp M, Schott EJ, Vinagre AS**
Federal University of Rio Grande Do Sul, Institute of Marine and Environmental Technology (IMET), University of Maryland Center for Environmental Sciences (UMCES)

Basic metabolic parameters are useful indicators of health status, including viral infection. In a previous study (Flowers et al. 2016), Callinectes sapidus Reo-Like Virus (CsRV1) was identified in C. sapidus collected in Southern Brazil. This study was developed in order to identify which metabolites could be affected by CsRV1 infection. Male (n = 26) and female crabs (n = 8) were caught from 2013 to 2015 in Lagoa de Tramandaí estuary (-29.97, -50.15), Brazil. The crabs were kept in tanks (natural photoperiod, 20‰, 25±2°C) and fed with squid. After 14 days, hemolymph and tissue samples were collected. Legs were preserved in 95% ethanol at 4°C and shipped on dry ice to IMET for RNA extraction and analysis of CsRV1 genetic material using RT-qPCR. Samples with greater than 100,000 virus genome copies per mg muscle were considered infected. The levels of glucose, triglycerides, cholesterol and total proteins in the hemolymph were determined using commercial enzymatic assays. The levels of glycogen and lipids in the tissues were determined according to Inohara et al. (2015). Data homogeneity was analyzed with Levene test, and afterwards, the data were submitted to Student´s t, 2 way ANOVA or Kruskal-Wallis tests. In males, CsRV1 decreased glycogen and triglycerides levels in the anterior gills and hepatopancreas, respectively. In females, CsRV1 did not cause any significant difference in the metabolites analyzed. Further studies are necessary and will contribute to understanding the interaction of stress and infection, and the development of sustainable exploitation of this species.

Establishment of Long-Term Crustacean Epithelial Cell Culture

Morgan SR, Rumney BM, Malik FT, White N, Parker AR, Meek KM, Albon J
Cardiff University, Lifescaped, Somerset House

Myodocopid ostracod bodies are enclosed within a thin, bivalved carapace. In Skogsbergia lerneri, the carapace is transparent, yet maintains the durable physical attributes necessary for survival. A single cell layer on the internal carapace surface is responsible for its formation. As a step towards a better understanding of carapace biosynthesis, the aim of this study was to develop a long-term culture of the Skogsbergia lerneri epidermis. First a method to dissect the ostracod epidermal layer from the carapace was optimised based on sterility, cell viability (live/dead labelling) and proliferation (EdU incorporation assay). In brief, relaxants (MgCl2), disinfectants (betadine) and antimycotics (amphotericin B) were tested. Optimal media for maintaining cell viability and proliferation during culture at 37°C and 25°C was determined within various media (DMEM, M199, L-15, Schneider's insect media) and supplements (including FBS, GlutaMAX™, non-essential amino acids). Cell viability was deemed optimal during culture within M199 media supplemented with 10% FBS, 0.25μg/ml amphotericin B, 200μg/ml penicillin-streptomycin, 10% non-essential amino acids and 2mM GlutaMax at 25°C. Decontamination of dissected ostracod carapaces prior to epithelial removal was not included in the optimised protocol due to toxic effects. 60% cells remained viable after 4 weeks in culture. Additionally, 13% epidermal cell proliferation was observed in vitro. This novel method for the long-term culture of viable crustacean (ostracod) epidermal cells has great potential to i) augment our understanding of the complex ostracod carapace biosynthesis and ii) to advance the field of crustacean cell biology, particularly for in vitro toxicity testing.

Exploring the Effect of Phyletic Dwarfism on the Static Allometry of Reproductive Traits: Fecundity, Egg Size, and Reproductive Output in the Pygmy Crab Petamithrax pygmaeus

Mullen H, Baeza JA
Clemson University

The marine crab Petamithrax pygmaeus is one of the smallest crabs in the superfamily (Majoidea) reaching body sizes no larger than 7.0 mm carapace width (CW). Little is known about the reproductive biology of marine invertebrates exhibiting phyletic dwarfism. This study reports on egg production (fecundity, egg size, and reproductive output) of this dwarf species. Fecundity varied between 75 and 310 eggs crab-1 with a mean ± SD of 150 ± 53 eggs crab-1 and increased significantly with female CW. Embryo volume varied between 0.13 and 0.19 mm3 with a mean ± SD of 0.15 ± 0.01 mm3 and did not increase with female CW. Reproductive output (RO) represented a mean ± SD of 5.92% ± 2.05% of female dry body weight (DBW), and a significant correlation was observed between female DBW and dry weight of the egg mass. The brood mass (RO) of P. pygmaeus increased proportionally (isometrically) with increases in female body size. Fecundity and egg size are within expected ranges for minute species of crabs in the superfamily Majoidea and thus, phyletic dwarfism does not appear to affect reproductive performance in this species.

Effects of Extended Day Length on Vitellogenesis of Intertidal Crab P. cinctipes

Neufeld M, Gunderson AR, Stillman JH, Tsukimura B
California State University

Intertidal organisms, such as the porcelain crab, Petrolisthes cinctipes, live in a dynamic environment. They are exposed to varied tides, temperatures, and day lengths. These abiotic factors may act as stressors, having physiological effects on P. cinctipes. They may rely on temperature and/or day length cues to become reproductive. Previous studies in our laboratory have shown that P. cinctipes are reproductive in the winter months during a new moon. Reproductive output can be measured through the yolk protein, vitellogenin (Vg). We can determine the Vg concentration in P. cinctipes hemolymph using an enzyme-linked immunosorbent assay (ELISA) (Delmanowski et al. 2017). To determine whether reproduction is dependent on day length, crabs were collected on both full and new moons. They were exposed to extended day lengths for seven days using overhead light sources. Pre- and post-treatment hemolymph samples were taken before and after treatment. Vg concentrations were measured using the ELISA. Extended day length increased the levels of Vg in crabs collected during full moons. Crabs in the control group showed decreased levels of Vg. This effect was most pronounced in gravid crabs. Vg levels did not change in crabs collected under new moons. The ELISA cannot discern between Vg and vitellin (Vn), which might be released by oocytes during degradation. The increased levels of Vg could be showing an increase in Vn, which means that oocytes have been resorbed in response to stress conditions. To determine whether the ELISA detected Vg, in-depth RNA analysis is required.

Insights Into What Is Inside: New Observations of the Relationship Between Parasitic Barnacles and Their Host Shrimps

Nagler C, Starck M, Glenner H
University of Bergen, Ludwig-Maximilians University of Munich

Parasites are ubiquitous abundant and play an important role in marine habitats. Among crustaceans, parasitism is frequent. Parasitic barnacles (Rhizocephala), mainly parasitic castrators of other crustaceans, show remarkable morphological adaptations to their lifestyle. The adult female parasite consists of a body that can be differentiated into two distinct regions: a sac-like structure containing the reproductive organs (externa), and a nutrient-absorbing, root like system situated inside the host`s body (interna). The ramifying simplicity of the interna has made it difficult to describe the morphology of the parasite. Using histological cross- and longitudinal sections of Sylon hippolytes infesting Pandalina brevirostris, we describe new details of the topographic organization of the interna of S. hippolytes inside its host. Due to the close distance between the parasite's interna and the neurosystem of the host, it seems that the parasite is using the neurosystem as a guiding structure to the gut. Most of parasites interna is entangled around the host`s gut suggesting a straightforward functional interpretation. By comparing infested with a non-infested shrimp, we reveal new specifics concerning the common rhizocephalan interpretation as parasitic castrators. Although it has been proposed that rhizocephalan parasitism results in the castration of their hosts, achieved by absorbing the entire reproductive energy of the host, we observed fertilized eggs and embryos in the host shrimp. Taken together, we add new and significant information to our global understanding of parasitic barnacles, of the interactions between them and their hosts and morphological adaptations of these parasites for such a lifestyle.

Proteomic and Metabolomic Responses in Hepatopancreas of Whiteleg Shrimp Litopenaeus vannamei Infected By Microsporidian Enterocytozoon Hepatopenaei

Ning M, Wei P, Wang W, Meng Q
Nanjing Normal University

Enterocytozoon hepatopenaei (EHP) causes hepatopancreatic microsporidiosis (HPM) in shrimp. HPM is not normally associated with shrimp mortality, but is associated with significant growth retardation that is not clearly noticeable until 2-3 months of cultivation. In this study, the responses induced by EHP were investigated in hepatopancreas of shrimp L. vannamei using proteomics and metabolomics. Among 154 up-regulated proteins, several proteins (e.g., peritrophin-44-like (P44L) protein, alpha2 macroglobulin isoform 2 (α2M) and prophenoloxidase-activating enzymes (PPAE),) were related to pathogens infection and host immunity. Several down-regulated proteins (e.g., Ferritin, Rab and cathepsins D) also meant that EHP injections could induce L. vannamei immune response. Other proteomic biomarkers, farnesoic acid o-methyltransferase (FAMeT) and juvenile hormone esterase-like carboxylesterase 1 (CXE1), resulting in increased shrimp sesquiterpenoid hormone levels. And, the ecdysteroid-regulated protein (ERP) was up-regulated after EHP infection further demonstrated that the ecdysteroids were down-regulated to prevent the shrimp from molting. Both proteomic KEGG pathway (e.g., “glycolysis / gluconeogenesis” and “glyoxylate and dicarboxylate metabolism”) and metabolomics KEGG pathway (e.g., “galactose metabolism” and “biosynthesis of unsaturated fatty acids”) data indicated that energy metabolism pathway may be significantly down-regulated in the hepatopancreas when infected by EHP. More importantly, the changes of hormones regulation and energy metabolism could provide much-needed insight into the underlying mechanisms of stunted growth in shrimp after EHP infection. Altogether, this study demonstrated that proteomics and metabolomics could provide an insightful view into the effects of microsporidia to the shrimp L. vannamei.

Crossing Experiment and Genomic Analysis of Genus Neocaridina in Japan

Niwa N, Shigeto K, Hashimoto K, Sakaguchi T, Hoshino E, Mihara M
Kyoto University , Kobe Senior High School

Crossing Experiment and Genomic Analysis of Genus Neocaridina in Japan

Niwa N, Shigeto K, Hashimoto K, Sakaguchi T, Hoshino E, Mihara M
Kyoto University, Kobe Senior High School

Neocaridina denticulata denticulata [Iralic] (De Haan, 1849) (Caridea: Atyidae) is a freshwater shrimp distributed in western Japan used as live bait for fishing. Due to recent decrease in population density, some unknown species of Neocaridina [Iralic] spp. have been imported from China and Korea, and they can be bought at pet shops and Internet websites. Recently, a closely morphological form of an alien Neocaridina [Iralic] species was reported intermingling in various parts of Japan. To observe the ability of hybridization between the native and alien species, lab work was conducted. Due to absence of morphological character difference, genomic analysis was made, and a family tree was obtained. The observed shrimp were collected from Sugo River of Hyogo Prefecture and Hayafuro River of Okayama Prefecture. Molecular work was performed on a male-parent from Sugo River (K-11 M), which is considered an alien or a hybrid of an alien species and a Japanese pure-line, and a female-parent from Hayafuro River (K-11 F), which is considered a Japanese pure-line, using 16S rRNA and CO-I genes. Offspring (F1) examination using molecular work confirmed hybridization within the native species and between the alien and the pure-line species, parent (K-11 M) belongs to Clade2, while F1 and parent (K-11 F) belong to Clade3. The molecular work results showed evidence of at least two Japanese subspecies populations, which belong to the genus Neocaridina [Iralic]. These species existed in Japan before introduction of the alien Neocaridina [Iralic]species.

Carcinonemertidae (Nemertea): Ribbon Worms in Search of a Family History Among Crabby Hosts

Norenburg JL, Santos CD, Schwartz LC, Goetz FE, Maslakova SA, Wirshing HH, Gonzalez VL
Smithsonian National Museum of Natural History, University of South Carolina, University of Oregon

We used Sanger sequencing data from 5 genes to test monophyly and species-level diversification of Carcinonemertidae (Coe 1902), and to assess the degree of co-evolution of these egg-predators living as obligate symbionts on decapod crustacean hosts. We used transcriptome data and morphology to test phylogenetic rooting of the family. Carcinonemertids, comprising 21 current valid species, are associated primarily with crabs, including almost all sufficiently studied harvested species. To assess genetic diversity and co-evolution with host lineages, we surveyed 68 potential host species, of which 44 are newly recognized as hosts, a 70% increase to the previous number of known hosts. We demonstrate that carcinonemertids are monophyletic and that their genetic diversity is much greater than expected, almost equal to their putative parent suborder. Assessment of co-evolution, however, yields mixed signals and points to the need for much wider taxon sampling of potential hosts. Two multigene studies (Thollesson & Norenburg 2003, Andrade et al. 2014a) confidently place Carcinonemertidae as a sister-clade to the suborder Distromatonemertea. This contrasts sharply with the universally accepted traditional classification placing them within that suborder, which a third multigene study does support (Kvist et al. 2015). Our new phylogenomic data supports the first two studies but, owing to inadequate taxon sampling for transcriptomes, cannot refute the third. Our new confocal microscopical observation of rhynchocoel musculature weakly supports the first two studies. The deep genetic divergence and host distribution of carcinonemertids probably reflects an ancient association with decapod crustaceans but may also reflect an accelerated molecular clock.

Tracking the Blue Crab Spawning Migration Using Carapace Biogeochemistry

Ogburn MB, Gilmour CC, Johnson EG, Hines AH
Smithsonian Environmental Research Center, University of North Florida

The blue crab, Callinectes sapidus, supports the largest fishery in the Chesapeake Bay and is a key component of the estuarine food web. Multi-jurisdictional (MD, VA, Potomac River) blue crab management is focused on protecting female spawning stock, but the relative contribution of different nursery habitats to the spawning stock is unknown. In female blue crabs, which have a functional terminal molt at maturity, biogeochemical (stable isotope and trace metal) signatures may provide a path forward for evaluating relative contributions of nursery habitats to the spawning stock. We conducted a large-scale field experiment to determine: 1) spatial and temporal variation in nursery habitat biogeochemical signatures, 2) whether signatures remain stable during the spawning migration, and 3) the relative contribution of nursery habitats to the spawning stock. Spatial and temporal variation were determined using recently-mated female blue crabs collected from 21 sites in the Chesapeake Bay during fall 2014 and spring 2015, representing individuals likely to make up the majority of the summer 2015 spawning stock. A mark-recapture experiment was conducted at the same time to obtain migrating crabs of known age and tributary of origin. Actively-spawning crabs were collected in July 2015 from the spawning area of the lower Chesapeake Bay. Crab carapace material was analyzed for stable isotopes (C, N) and 17 trace metals. Preliminary results of discriminant function analyses suggest that >60% of the spawning stock derives from high salinity tributaries of lower Chesapeake Bay, indicating the importance of these nursery habitats in sustaining the population and fishery.

Linking Operational Sex Ratio and Reproductive Output of Chesapeake Bay Blue Crabs

Ogburn MB, Richie KD, Aguilar R, Hines AH
Smithsonian Environmental Research Center

Mature female blue crabs, Callinectes sapidus, receive their lifetime supply of sperm during mating at the time of their molt to maturity, and use this stored sperm to produce multiple broods of offspring during one or more spawning seasons. Male-biased blue crab harvest has the potential to alter the operational sex ratio and reduce reproductive output due to sperm limitation, but a lack of information on changes in sperm quantity during long-term storage inhibits our ability to evaluate whether sperm limitation occurs in Chesapeake Bay. We used a large scale mark-recapture study to study sperm storage in the field. In fall 2014, 5190 recently-mated mature female blue crabs were tagged and released in 12 locations throughout Chesapeake Bay. Initial sperm stores were quantified for additional crabs obtained at the time of tagging. The sperm stores of recaptured crabs were compared to expected initial sperm stores. Results indicated that sperm quantity declined more than 90% from the time of mating to fertilization of the first brood, with subsequent declines likely related to fertilization. Simulations of brood production suggest that the sperm limitation likely due to intensive male-biased harvest could be leading to a 5-10% reduction in reproductive output of the Chesapeake Bay blue crab spawning stock.

Relationship Between Ontogenetic Habitat Shift and Decorating Material Preference in Japanese Kelp Crab Pugettia quadridens

Ohtsuchi N, Kawamura T, , Kurogi H, Watanabe Y
The University of Tokyo, National Research Institute of Fisheries Science, Japan of Fisheries Science

Various spider crabs change their habitat ontogenetically, whereas it is also known that some decorator crabs change their decorating materials (DM) in both field and captive condition. This study examined the ontogenetic changing patterns of DM preference in Japanese common kelp crab Pugettia quadridens with concerns to their ontogenetic habitat shift (OHS) from small red algal turfs in subtidal zone to Sargassum fusiforme beds near low tidal mark. Two experiments were performed in captive condition to examine the following two hypotheses: 1) P. quadridens decorate themselves selectively and change DM preferences ontogenetically, and therefore OHS is facilitated; 2) they decorate themselves opportunistically to be matched in their habitat environment, and therefore emigrant individuals are kept staying in new habitat. First, the ontogenetic changes in DM preference among four dominant macroalgae species (S. fusiforme and three branched red algae species) were examined by using single adolescent and full-grown crabs. Second, the ontogenetic changes in DM preference between S. fusiforme and red algae Gelidium elegans in different condition (1:10, 1:1, 10:1 in wet weight ratio) were examined by using single immature and adolescent crabs. The results in the first experiment indicated that P. quadridens constantly prefer S. fusiforme to red algae. The second experiment revealed that P. quadridens decorates opportunistically when they are immature, but they decorate selectively by S. fusiforme as they grow. In conclusion, DM preference do not facilitate OHS in P. quadridens, but ontogenetic changes of decorating tactics contributed to completion of OHS.

Video Recordings of the Swimming Behavior of Nauplii and “Tessmann’s Larvae” of Several Kinds of Ascothoracida from Taiwan (Crustacea: Thecostraca: Synagogidae, Petrarcidae, Lauridae)

*Olesen J, Kolbasov GA, Petrunina AS, Chan BKK, Dreyer N, Grygier MJ**
University of Copenhagen, Moscow State University, Academia Sinica, National Taiwan Ocean University

Ascothoracida are parasites of anthozoans and echinoderms. Many brood their nauplius larvae, release lecithotrophic nauplii, or undergo embryogenesis directly to the subsequent a-cyprid stage. Some, however, release apparently planktotrophic nauplii with long, heavily armed appendages. Their bobbing motion while swimming and the grand, sweeping movements of their antennae are distinctive, but photographs of living ascothoracidan larvae are rare, and no videos appear to be available to zoologists. In September, 2017, at Green Island, Taiwan, we employed semi-high-speed (162 fps) video photography using an Olympus IX70 inverted microscope, a Basler ace USB 3.0 digital camera with a SONY sensor (1936 x 1216 pixels), and various software (e.g., TroublePix ver. 2.35.0.6095, Filmora ver. 8.4.0) to document the limb movements and body motions during swimming of first- and/or second-instar nauplii of Sessilogoga sp. (Synagogidae) and Petrarca sp. (Petrarcidae) released in the laboratory by adults infecting antipatharian and scleractinian corals, and nauplii of probable Baccalaureus sp. (Lauridae) from the plankton. Behavior of laurid a-cyprids (so-called “Tessmann’s larvae”) from the plankton was recorded the same way. SEM micrographs were also taken. It is noteworthy that the naupliar antennules do not simply point forward, but bend downward to participate in the power stroke, and that the mandibles’ movements are restricted compared to those of the antennae. The laurid and petrarcid larvae are morphologically similar to others of these families described earlier using light microscopy, but the nauplii of Sessilogoga differ from known forms in the cephalic shield outline and distribution of marginal pores.

Hyperiid Amphipods as a Model of Midwater Adaptation

Osborn KJ
Smithsoanian NMNH

Hyperiid amphipods are ubiquitous in the midwater - all oceanic water below the surface and above the sea floor - and are found exclusively in this largest of earth's habitats. The variation found in hyperiid eyes is likely the result of adaptation to and diversification within the midwater. The extreme variation in their visual systems, along with them being a relatively small group (only about 350 species described so far) and quite hardy compared to most midwater animals, make them an ideal group to explore midwater adaptations. My objective is to explore the evolution of hyperiid visual systems and behavior by integrating traditional functional morphology, physiology, behavior, ecology, brain anatomy, and phylogenetics through multiple collaborations. I will provide an overview of the project, discuss how each piece informs the others, and summarize what we have learned about hyperiid associations with gelatinous zooplankton.

Regional and Local Species Distribution of Cladocera (Crustacea: Branchiopoda) in the Indian Sub-Continent

Padhye SM
Katholieke Universiteit Leuven

Cladocera are an important freshwater zooplankton group commonly found in most freshwater habitats around the world. The Indian subcontinent though remains the least studied in terms of their diversity & distribution. My objective thus was to study the cladoceran zoogeography & patterns across a regional and local scale with emphasis on distribution across different habitat types locally. Information from published literature was used for faunal comparisons within different regions of the subcontinent while sampling data from Pune region, India was used for assessing local distribution patterns. Regionally, cladoceran faunal complementarity increased with distance with a turnover of tropical to temperate species across the latitudinal gradient. Chydoridae comprised of nearly 90% of the total fauna. Daphnia species were broadly distributed into 3 zoogeographical groups within the subcontinent based on the mean Temperature due to altitudinal and latitudinal gradients. A Gondwanan relict and an Amphi-Pacific distributed species were discovered in the Western Ghats along with 9 oriental endemics. Local faunal composition mirrored the regional pattern of richness. Rarefaction showed water reservoirs had the maximum species (34) while pools had the least (19). Family level species composition between the habitat types varied significantly. Beta diversity indices showed a higher faunal similarity between water reservoirs and rivers. Few species associated with specific habitats while many were generalists occurring in all types. Species like Kurzia longirostris & Chydorus parvus distributed along a salinity gradient. Moina micrura was abundantly observed in eutrophicated habitats while Daphnia carinata was restricted to rock pools above 1000 m a.s.l.

Evolution and Development Of Novel Forms: Insights from Crustacean Limbs

Palmer R
University of Alberta, Canada

Fundamental questions in development and evolution can be addressed using comparative and experimental studies of crustacean limb morphology. Examples from our own research include: How reversible is development (developmentally plastic gain versus loss of limb segments)? Is direction of asymmetry in an individual determined developmentally at the local level (independently in different body segments) or at the global level (consistently across all body segments)? Are genes leaders or followers in evolution (phylogenetic patterns of asymmetry variation)? How do stunning novel morphologies - like the spectacular claws of snapping shrimp - evolve from unspecialized precursors (reconstructing the evolutionary history of snapping claws in alpheid and palaemonid shrimp)?

Planktonic Estimates of Stomatopod Diversity

Palecanda SP, Feller KD, Porter ML
University of Hawai'i at Mānoa, University of Cambridge

Stomatopods (Crustacea, Stomatopoda), are well studied for their aggressive behavior and unique visual system. Like many crustaceans, stomatopods undergo indirect development, passing though several larval stages before reaching maturity. Though we know little about the ecology of larval stomatopods, when looking at the overall diversity of stomatopods they are a valuable resource for information. Adult stomatopods can be difficult to catch, a problem shared amongst many marine invertebrates due to inaccessible habitats and sometimes cryptic nature. By sampling from the planktonic community, less collection time and effort is required to obtain accurate measures of diversity within a particular region. Using consistent, annual collection methods from 2006 to 2016, stomatopod larvae were taken from the waters around the Lizard Island reef platform in Eastern Australia. Cytochrome oxidase I (COI) mitochondrial DNA sequences were generated from each larval sample and compared to a database of known adult CO1 sequences tied to morphological species identifiers. The previous literature identified 30 adult species of stomatopods within the Lizard Island reef platform, of which 28 species have CO1 data available. Using phylogenetic analysis, we identified 21 of these species from larvae. An additional 11 potential species were found only from larvae. By sampling consistently before and after ocean stressors, such as cyclones in 2013 and 2014 and up until the major coral bleaching event at Lizard Island in 2016, we provide an accurate snapshot of shifts in diversity over time. Such temporal estimates will become increasingly important in times of rapid environmental change.

Where Do Coastal Anthropogenic Stressors Present More Threats to Crustacean Diversity?

Pappalardo P, Wares J
University of Georgia

Recent efforts to map human impacts on marine ecosystems show that human impacts associated with climate change are rapidly increasing and allow us to identify areas of higher threats to species diversity. Our goal is to identify areas where crustacean diversity is threatened by climate change or other stressors (such as fishing, pollution, etc.). Because different groups of crustaceans may be differently affected by each stressor, we generated global maps of crustacean diversity for different taxonomic groups. We focused on coastal and shelf areas and calculated species richness of barnacles, shrimps, crabs, lobsters and amphipods by ecoregion using the Marine Ecoregions of the World (Spalding et al. 2007) and occurrence data from GBIF (www.gbif.org). We then correlated species richness with different types of global stressors reported for each ecoregion (Halpern et al. 2014). Areas with low accumulated human impact, such as the poles, are also areas with lower diversity for most groups. Despite the differences in the location of the hotspots of diversity between taxonomic groups, the ecoregions with higher species richness correlate with intermediate or high levels of climate change stressors. Within temperature and tropical latitudinal zones, larger ecoregions harbor more species. The areas of the globe with higher human impact also coincide with areas of most recent discovery of species. We show regions with high diversity for each group and high impact scores for climate change and other stressors that should be targeted for conservation efforts.

Towards a Revision of the Cristimenes Commensalis Complex (Crustacea, Decapoda, Palaemonidae)

Park JH, De Grave S, Kim W
Seoul National University, Oxford University Museum of Natural History

The genus Cristimenes Ďuriš and Horká, 2017 is an echinoderm associated group of Palaemonidae, consisting of three species. C. cristimanus and C. zanzibaricus are associated with echinoids and C. commensalis is associated with crinoids. The genus is widespread in tropical and temperate regions of the Indo-West Pacific area, and is easily distinguishable from related genera by the unique carpo-propodal articulation of the second pereopod. C. commensalis differs from other the two species of the genus by their host affiliation and the morphology of the ambulatory dactylus. Bruce (1982) already reported that some specimens of C. commensalis have a small supraorbital teeth and a reduction of lateral carinae, which is here further explored. Specimens of C. commensalis were examined from across the Indo-West Pacific area, including the Korean Peninsula. Based on morphological evidence and molecular analyses, C. commensalis is divided into 5 clades. In the COI barcode sequence, the minimal interspecific divergence amongst clade is 13%. The C. commensalis complex is thus demonstrated to comprise five pseudo-cryptic species. Here, we present the morphological characters across the five clades and related palaemonid genera, as well as its phylogenetic position within the family.

Local Navigation in a Mantis Shrimp

Patel RN, Cronin TW
University of Maryland Baltimore County

Stomatopods, better known as mantis shrimp, are crustaceans which commonly inhabit holes in benthic marine environments for use as burrows. Many stomatopod species forage at extended distances from these burrows before returning back to their homes, risking predation. Since many mantis shrimp are central place foragers living in structurally complex environments, we hypothesized that these animals use landmark navigation and/or path integration to navigate their benthic environments. To determine which mechanisms are employed, Neogonodactylus oerstedii were placed in circular arenas in a glass roofed greenhouse, with their burrows submerged from view. Foraging paths in the presence and absence of a landmark adjacent to the burrow were recorded. We found that return trips in the presence of the landmark were more direct than trips in the landmark's absence. However, the initial direction of the return trips were generally oriented towards the burrow regardless of the presence of the landmark. Further, in the absence of a landmark, path lengths home were statistically indistinguishable to the beeline distance to the burrow before a search behavior was initiated. To determine if N. oerstedii employ path integration when returning to their burrows, animals were translocated along a platform to a new location before homeward paths were initiated. These translocated animals exhibited homeward paths oriented towards the direction of the burrow had they not been moved, rather than towards the actual direction of their burrow. These results indicate that N. oerstedii use landmark navigation in parallel with a path integration system to return to their burrows.

The Evolutionary Dynamics of Extreme Movement in Mantis Shrimp (Stomatopoda)

Patek SN, Muñoz MM
Duke University, Virginia Tech

In addition to their renowned biomechanical capabilities, the diversity of forms across mantis shrimp (Stomatopoda) have enabled new insights into the interface of physics and evolution. Here I present an overview of our research that has examined the costs and consequences of diversification of the extraordinarily fast strikes of mantis shrimp. Techniques including geometric morphometrics, linkage mechanics, and evolutionary rate analyses have revealed a rich space of morphological diversity that is fundamentally limited by the size and biomechanical construction of the fast-moving raptorial appendages.

You Are What You Eat, You Are Where You Live - Caime Part 2 - Trace Metals in Crustacea: Biomonitoring of the Marine Environment

Peart R, Schnabel K, Handler MR, Wysoczanski RJ, Frontin-Rollet GE, Graham AEM, Seabrook C
National Institute of Water & Atmospheric Research, Victoria University of Wellington

The state and health of our marine environment is paramount to our societal and economic wellbeing. One approach towards assessing and preserving the uniqueness of our marine estate is understanding the chemistry of the organisms occupying it. The uptake of elements from the environment into their bodies makes them recorders of their chemical environment. This, in turn, allows for the monitoring of events that might occur over time, such as changes in levels of trace metals resulting from offshore mining activities, urban development, or ocean acidification. Here, we present the second part of the CAIME (Crustacea As Indicators for the Marine Environment) study which includes preliminary trace element baseline data for shallow marine Amphipoda from around New Zealand. Thirty trace elements from four amphipod species (Ampelisca chiltoni, Podocerus sp., Ischyrocerus sp., Apohyale sp.) have been analysed using acid digestion techniques combined with inductively coupled plasma mass spectrometry, and preliminary results are compared with those for Decapoda (CAIME II). The results show distinct patterns between species and locality and indicate a potential for evaluating natural variations and consequently unusual changes across a range of geographic localities. Further, the results provide the potential to compare across two orders of crustaceans that occupy very different habitats and trophic niches. These two presentations will cover the hypotheses and implications of the first results of this 3-year programme and how any changes in the marine environment can be assessed in the future.

Amphipods - Turning the Wheel of Carbon in the Deep Sea

Peart RA, Nodder SD, Lörz AN
National Institute of Water & Atmospheric Research, CeNak, Zoologisches Institut und Museum

To understand the intricacies of the movement of carbon between surface waters and the ocean seafloor, a time-series project was established in 2000 (-2012), capturing environmental data in subtropical and subantarctic waters off eastern New Zealand. These data are used to understand carbon sequestration via the biological pump, especially the role of pelagic amphipods in modulating the flux of carbon to the deep-sea. These animals were collected as “swimmers” that actively swam (not sunk) into 1500 m-deep, moored mid-water sediment traps and are regarded to be representatives of the resident deep-ocean zooplankton community that utilise the sinking organic material (also collected). Abundance and diversity of the amphipod species/groups, or their ecological responses (i.e., reproductive cycles, feeding niches), is related to variations in surface production and carbon flux. Since many of these pelagic amphipods are preyed on by various fish species, these data will improve food web models of ecosystem structure and functioning. These samples have also provided a wealth of information on amphipod diversity from the “twilight - midnight” zones over depths of the Southwest Pacific that are rarely sampled. The first five years of amphipod samples from the time-series have been investigated, yielding information on amphipod abundance, weight and diversity in proportion to the contents of the traps. Preliminary results are presented along with a correlation analysis between the amphipods collected, organic carbon flux and other environmental variables, related to biophysical (mixed-layer depth, sea-surface temperature, primary production) and climatic processes (El Niño-Southern Oscillation, Southern Annular Mode).

Is There Host-Associated Differentiation in Marine Herbivore Amphipods?

Peres PA, Azevedo-Silva M, Andrade SCS, Leite FPP
University of São Paulo, University of Campinas

Plant-herbivore interactions may play an important role on the evolution of small terrestrial and marine herbivore. Some authors consider amphipods as insect equivalents in the marine realm because of their strict relation to the host macroalgae, which was already explored regarding macroalgae chemical defenses. Different host species provide distinct selective pressures for their associated animal populations, which may act as divergent selection pressure towards adaptive traits related to each host. This phenomenon has been called host-associated differentiation (HAD), and can lead to ecological specialization, or even ecological speciation. However, it is still unexplored if amphipods may be insect equivalents in terms of HAD. Here, the species Cymadusa filosa (Amphipoda, Ampithoidae) and its host macroalgae were used as models to test the hypothesis that amphipods present HAD, being genetically and morphologically structured because of differences in host traits. Furthermore, it was tested if there are differences among populations from distinct localities because of limited dispersion in amphipods. Microsatellites were used to access the genetic diversity, along with geometric morphometric analyses for morphology. Our results indicate that there was no HAD regarding genetic and morphological features. Individuals seem to be highly mobile in local scales or to have a juvenile based dispersal, and they seem capable to disperse among localities by rafting. Two distinct morphological groups were formed probably because of environmental conditions of localities. HAD in marine environments is probably context-dependent, and should be explored in different species and scales, so we can have a better appraisal of marine plant-herbivore interaction.

How the Genetic Diversity Is Organized Along the Distribution of Neotropical Mangrove Crabs?

Peres PA, Mantelatto FL
University of São Paulo

Patterns and processes that explain the genetic diversity of species are current evolutionary biology topics. Assessing genetic variation across species ranges can elucidate trends in how genetic diversity is spatially organized. There are four hypotheses regarding the spatial distribution of intraspecific genetic diversity: 1) latitudinal trends; 2) core-marginal trends; 3) latitudinal-core-marginal trends; 4) highly-dispersal species trend. The most explanatory hypothesis depends on the taxon, but there are cases in which general patterns emerge when comparing a great number of species. As far as we know, there are no records of studies using Brachyura to test for general patterns regarding spatial organization of genetic diversity along western Atlantic distribution. Crabs are a potential group to test such hypotheses because of their diverse biological features, many species’ range encompasses great geographical areas, and this is a well-succeeded group in terms of adaptive evolution. Here, we explore which of the hypotheses best explain the distribution of genetic variation in seven mangrove crabs from the Neotropical Atlantic. Citochrome oxidase I (COI) sequences were generated for Aratus pisonii, Sesarma rectum, Armases angustipes, Leptuca thayeri, Ucides cordatus, Goniopsis cruentata using populations from Santa Catarina – Brazil, to Florida – USA. Nucleotide diversity and haplotypic were used as estimators of genetic diversity. We found that Aratus pisonii best explanator was the latitudinal trend model, while for all other species the highly-dispersal species model was the most fitted. Our dataset indicates that species-specific mechanisms may be acting on genetic diversity distribution, and, for now, general patterns were not found.

Diversity Patterns and Multiscale Analysis of Callyspongia vaginalis Dwelling-Crustacea in Campeche Bank Coral Reefs

Perez-Botello AM, Guerra E, Simões N
Posgrado Ciencias Biológicas, UMDI-Sisal

The tubular sponge Callyspongia vaginalis is a solitary and dominant organism in the Gulf of Mexico and the Caribbean Sea coral reefs. Previous studies suggest the sponge’s aggregations will form animal forests, shaping habitats and providing three-dimensionality to the reefs. This work has two main objectives: (1) Describe the relationship between the guest symbiont diversity with the sponge complexity. (2) Analyze the explained variation percentage of C. vaginalis associated fauna by (i) reef processes, (ii) local factors and (iii) sponge morphology. The complexity was measured with an index that summarizes the sponge morphological characteristics. The host species changes were analyzed in three scales: reef, local and individual. To calculate the significance and variation percentage of each level a PERMANOVA test was performed. This test indicates that the species richness changes are significant at each scale. The highest percentage of variation is explained by Reef processes, followed by local factors, and sponge complexity. The correlation between complexity and species richness is positive, an increase in complexity means an increasing in species number. In conclusion, the three scales of analysis provide significant explanation of the sponge dwelling-community changes. The potential to host species are directly related to the sponge heterogeneity. This process could be mediated by colonization-dispersion cycles and refuge competition. At the same time, the reef processes will be determining which dwelling-species will be found in each reef. Recognizing the contribution of each scale to the accumulated observed patterns is essential to understand the link between biological processes and geographic patterns.

Transcriptomic Analyses Illuminate the Molecular Basis of Troglomorphy in the Molnár János Cave System

Pérez-Moreno JL, Balázs G, Bracken-Grissom HD
Florida International University

Animals that inhabit subterranean environments often undergo various distinct physiological, morphological, and behavioral modifications, referred to as "troglomorphy", as they transition to life in perpetual darkness. However, the molecular basis behind these troglomorphic changes remains poorly understood. Important questions remain to be answered concerning the mechanisms involved in the loss or enhancement of traits at the transcriptomic level, and their role in the evolution of cave organisms. In this study we investigate the transcriptional basis behind two sensory traits involved in troglomorphy (vision loss and chemoreception) in natural populations of cave crustaceans from the Molnár János Cave System in Budapest, Hungary. To achieve this, we employed comparative transcriptomic and phylogenetic methods on both surface and cave-dwelling natural populations of an emerging model cave species, the isopod Asellus aquaticus, and of the amphipod Niphargus hrabei. By sequencing and assembling robust de novo transcriptomes, we identified and characterized differentially expressed genes and pathways between surface and cave populations of the aforementioned species. With such, we aim to improve our understanding of patterns of molecular evolution in the depths of caves and other extreme environments.

Rise of Shrimp Diversity from the Araripe Basin (Cretaceous: Aptian/Albian): the First Solenoceridae (Decapoda:Dendrobranchiata)

Pinheiro AP, Santana W, Oliveira GR, Alencar DR, Saraiva AAF
Universidade Regional do Cariri/URCA, Universidade Sagrado Coração/USC, Universidade Federal Rural de Pernambuco-UFRPE

The Araripe Basin is known worldwide about the preservation quality and quantity of its fossils. In the last years, the number of crustacean fossils from that basin is increasing rapidly, most of them shrimps from several families. Until now, two carideans, two sergestideans and one Luciferidae are known from the area. Here we present a new finding to increase the number of species and a different family to this group. The specimens collected is considered to be a Solenoceridae shrimp by the presence of a rostrum shorter than the antennular peduncle, a post-orbital spine and a well-marked cervical sulcus. The new shrimp differs significantly from the other known Dendrobranchiata species of the Araripe Basin. It is easily distinguished from Araripenaeus timidus, which has a marked sinuous cicatrix in the sixth abdominal somite and Paleomattea deliciosa that has its sixth abdominal somite two times longer than the anterior somites. Both characteristics are not observed at this new shrimp material.

First Lessepsian Decapod Crustacean in the Tyrrhenian Sea

Pipitone C, Vega Fernández T
CNR-IAMC, Stazione Zoologica Anton Dohrn

The vast majority of lessepsian species i.e., those that enter the Mediterranean through the Suez Canal, remain confined to the eastern Mediterranean. Very few lessepsian immigrants have reached the western basin. Among decapods, the westernmost records come from northern Tunisia, which is exactly at the boundary between the western and eastern basins. Pilumnus minutus De Haan, 1835 is considered a lessepsian species. After its first Mediterranean record in 1933 (Egypt) it was reported only recently from the Aegean and Black Sea coasts of Turkey. The objective of this poster is to report recent findings of P. minutus from the western basin. Twelve individuals of P. minutus were found in samples of macrobenthic fauna collected with a suction sampler in 2005 on submerged artificial reefs made of concrete boulders in the Gulf of Castellammare (Sicily, southern Tyrrhenian Sea, western Mediterranean) at about 15 m depth. The distribution of P. minutus in the eastern Mediterranean follows the same diffusion pattern observed in many other lessepsian immigrants that is, from the Sinai area to the Aegean Sea. Our record is the first lessepsian decapod from the Tyrrhenian Sea and one among very few lessepsian species found in the western basin overall. The temporal gap between the first (1933) and the successive (2000) record of this crab in the eastern Mediterranean, as well as the spatial gap between those records and our Tyrrhenian record, are likely due to the fact that P. minutus may have been misidentified with autochthonous Pilumnus species.

Population Genomic Analyses of the Blue Crab Callinectes sapidus: Novel Tools and Resources

Plough LV, Chung JS
University of Maryland Center for Environmental Science

Recent advances in high-throughput sequencing are transforming our understanding of the ecology and evolution of non-model marine species, such as the blue crab, Callinectes sapidus. Here we report recent work developing a genotyping-by-sequencing (RADseq) approach for genome-wide genotyping of blue crabs to study connectivity and gene flow across its range. For our pilot analysis, we generated data for more than 9,600 single nucleotide polymorphisms (SNPs) in 35 crabs from Panama City Beach, FL, Agawam River, MA, and Porto Alegre, Brazil. Principle components analyses revealed very distinct clustering of the Brazilian samples from the U.S. populations, and analysis of population structure between the two U.S. populations revealed low but significant genetic differentiation (FST = 0.0103), with FST values ranging from -0.05 to 0.48. Finally, results of population assignment tests for the two U.S. populations demonstrated that the full marker dataset provided good power to assign individuals back to their population of origin (~83% and 92% success for Panama City Beach and Agawam River, respectively), while a data set with only 500 SNPs was less successful (~60-70%). Overall, this work demonstrates the great utility of high-throughput sequencing technologies for characterizing fine-scale patterns of gene flow and genetic structure in blue crabs, and for assignment of individual crabs to population of origin. Sequencing of additional populations in the Gulf of Mexico, the Caribbean, and in South America is ongoing, and we will report the latest results of our parallel efforts to develop additional genomic resources such as a high-density linkage map.

Molecular Phylogeny Reveals Diversification Rate Shifts in Crangonidae (Decapoda, Caridea)

Poon KKY, Ma KY, De Grave S, Chan TY, Chu KH
The Chinese University of Hong Kong, University of Oxford, National Taiwan Ocean University

Crangonidae is the fourth most speciose caridean family, comprising over 220 extant species from 23 genera. Characterized by its extraordinary thermal-tolerant capability and broad distribution range, crangonid shrimp offers attractive opportunities to investigate the correlation between historical events (i.e. sea level/temperature fluctuations) and the contemporary species distribution and diversity. Nevertheless, such investigations have been hampered by the lack of a robust generic phylogeny. In the present study, we reconstruct the first comprehensive fossil-calibrated phylogeny of Crangonidae, based on two mitochondrial and five nuclear protein-coding gene markers. Our findings suggest this family, along with most genera, is monophyletic with strong statistical support, while Philocheras, the largest genus in this family, is polyphyletic, comprising at least three distantly related lineages. Crangonidae originated in the Upper Triassic (~ 250 - 204 mya) according to the divergence time estimation. Since Upper Cretaceous (~ 100 - 66 mya), a clade, comprising Crangon and seven other closely related genera, exhibited significant increase in diversification rate following a dispersal to North Pacific Ocean. This result implies that paleogeographic and paleoceanographic changes, such as continental drift and sea level fluctuation, might have influenced the spatial distribution and diversification rate shifts in this group. [The present work was supported by a research grant (project no. 41476146) from the National Natural Science Foundation of China.]

Impacts of Small Crustaceans On the World's Largest Seaweeds

Poore AGB, Gutow L, Thiel M
University of New South Wales, Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Universidad Católica del Norte

Herbivorous amphipods and isopods are abundant in vegetated marine substrates worldwide, but their impact on the plants they inhabit is poorly known. They may benefit their hosts if consuming epiphytes or have negative effects if consuming host tissue. We review the evidence for ecological impacts of crustacean mesograzers on the largest marine macroalgae – kelps from the order Laminariales – and present recent research from the kelp forests of New Zealand and Chile. We quantified the distribution of mesograzers and algal damage and used grazing experiments to test the impact of the amphipod Pseudopleonexes lessoniae on Macrocystis pyrifera, the amphipod Sunamphitoe lessoniophila on Lessonia berteroana and the isopod Amphoroidea typa on Lessonia spicata and Macrocystis pyrifera. Combined, these studies show that low levels of tissue loss due to grazing can have large, disproportionate effects on kelp growth and biomass due to preferential consumption of valuable tissue, modification of blade morphology and physical damage that leads to stipe loss. Understanding these interactions is important given the critical role of herbivory in regulating the biomass of marine primary producers and the likelihood that grazer populations will be altered in regions of reduced fish abundance.

Evolution of Light Production and Detection in Pleuromamma Copepods

Porter ML, Chen JWT, Blanco-Bercial L, Maas AE, Goetze E, Iwanicki T
University of Hawaii at Manoa, Bermuda Institute of Ocean Sciences

The copepod genus Pleuromamma (Calanoida: Metridinidae) consists of 16 bioluminescent species that exhibit diel vertical migration. Previous studies of several Pleuromamma species identified multiple luciferase genes from single individuals and reported bimodal bioluminescence emission spectra, but the ecological significance of this system is unknown. In order to investigate the evolution of bioluminescence in this group, the potential for multiple biochemical pathways controlling bioluminescence in single species, and the evolution of the associated visual systems, we will identify expressed opsin and luciferase transcripts from transcriptomes of two species - P. robusta and P. xiphias. These results will be compared to patterns of opsin expression identified from shallower-living, non-bioluminescent calanoid copepods. Continuing studies are generating comparable transcriptomes for an additional five Pleuromamma species for an in-depth examination of the evolution of vision and light production across the genus.

Horton H. Hobbs' III Contributions and Legacy in Crustacean Biology

Porter ML
University of Hawaii at Manoa

Dr. Horton H. Hobbs III (1944-2016) had a prolific career, publishing almost 250 peer-reviewed papers, chapters, and books, including the description of five new genera and 33 new species of crustaceans as well as numerous studies of cave crustacean biology and ecology. In addition to his outstanding scholarship, his incredible collegiality, and his numerous contributions to crustacean biology, he was also an inspirational mentor whose enthusiasm for research inspired many young scientists to pursue careers involving crustaceans. To honor all of these aspects of Dr. Hobbs' career in science, I will highlight his contributions to crustacean taxonomy, biodiversity, and ecology, as well as his influence on my research career and his impact on crustacean biology.

A Transcriptomic Approach for Large-Scale Functional and Evolutionary Analyses On Crustacean Gene Regulation

Qin J, Chu KH
The Chinese University of Hong Kong

Crustaceans include many species of major ecological and economic importance. While transcription factors (TFs), neuropeptides and their interactions play important roles in regulatory mechanisms of growth, reproduction and development in crustaceans, which are vital to fisheries, aquaculture, and biodiversity conservation, the lack of genome sequences for most crustacean species makes it very difficult to study these two groups of genes in a system-wide scale. Therefore, we have developed a comprehensive bioinformatics pipeline for identifying TFs and neuropeptides, and investigating their functions and evolution based on transcriptome data, Hidden Markov model and domain tree construction. Curated and newly sequenced transcriptomes from 250 crustacean species were used to dissect the neuropeptide-TF regulatory systems of crustaceans. Gene families of neuropeptides and TFs were identified from de novo assembled transcripts in these species. Known crustacean neuropeptides and TFs could be identified in most species, indicating the reliability of our approach. Moreover, several gene families that have not been characterized in current databases and publications were found to be potential novel neuropeptides and TFs. Functional and evolutionary analyses on each gene family were also performed computationally and results were deposited in our databases. Our results reveal evolutionary novelties for the crustacean neuropeptide-TF regulatory system, provide useful information in understanding gene regulatory mechanisms, and fill the knowledge gap of gene regulation in crustacean biology. [This study was supported by a National Natural Science Foundation of China (project no. 41606143) and a Direct Grant for Research from The Chinese University of Hong Kong (project no. 4053187).]

Evolution of Mitogenome Reorganization in Crustaceans: from the Extreme Case of Sacculine to a More Classical Situation in Branchiopods

Rabet N, Audebert F, Galindo LA, Bonillo C
Sorbonne Universités, UFR de Sciences, Université de Versailles Saint-Quentin-en-Yvelines

We used next-generation sequencing (NGS) to investigate the organization of the mitochondrial genes and phylogenetic relationships of a number of crustacean species. NGS provides information on the genome of several species simultaneously and allowed the organization of the mitogenome and a portion of the nuclear genome around the 18S to be reconstituted. Most species maintain an identical mitogenomic organization, but in some cases reorganization is observed. Thus among the Branchiopoda, we confirmed a very limited reorganization among the Anostraca, which does not include the family of Tanymastigidae in whom greater reorganization has been observed. In Spinicaudates, we also identified reorganizations, such as in Eulimnadia. These mitochondrial reorganizations provide punctual phylogenetic information relevant to Branchiopoda systematics. In the sacculines (Cirripedia, Rhizocephala), the situation is different because the mitogenomic organization of each species appears to be specific. In the extreme context of the sacculines, a group lacking morphological character, the mitochondrial genome can serve us as a fundamental taxonomic marker.

NGS Sequencing On Brazilian Spinicaudatan Diversity

Rabet N, Rogers DC, Ferreira AO, Lacau S, Bonillo C
Sorbonne Universités, Kansas University, MUNDI Biologia Integrada Ltda, Universidade Estadual do Sudoeste da Bahia, UMS 2700 OMSI, MNHN

Spinicaudata (Branchipoda) are relatively common temporary pool organisms. The systematics and taxonomy of this group are relatively confusing due to strong intraspecific variation which obscures interspecific informative traits. We are exploring Spinicaudata diversity through integrated NGS sequencing and morphological analyses. We review the research history of this group in Brazil and present data on selected specimens from Brazil. We identified four genera from two families. We present the first Brazilian records of Leptestheridae plus evidence for three Limnadiid genera: Eulimnadia, Metalimnadia and a new genus also known from Bolivia. The results suggest that Metalimnadia demonstrates strong endemism since four individuals analysed represent four species with a particular rate of evolution. The new genus is cryptic with respect to Eulimnadia, which further demonstrates the morphological difficulties in this group and the need for genetic analyses to advance clam shrimp systematics and taxonomy.

The Large Branchiopods of New Caledonia

Rabet N, Timms B, Charpin N, Bonillo C
Sorbonne Universités, Australian Museum, Vies d'Ô douce

New Caledonia is known for high faunistic and floristic endemism. Only two large branchiopods species were previously known from this island before the "La Planète Revisitée" expeditions: " Triops longicaudatus intermedius Longhurst 1955" and Lynceus insularis Olesen et al. 1996. We present the methods and results of our surveys, which used satellite technology and specific focused investigations based on local conditions. We conducted direct sampling of adult animals and sampled dry sediments for for resting eggs. Representative specimens were sequenced using NGS methods. This method allowed us to identify five species all with a strong Australian affinity. Two species are geographically limited, are probably endemic, and are affected by mining or agricultural activities. Two species are more widely distributed and do not seem threatened. The last species inhabits all areas including mining zones and presents a clear genetic structure suggesting the beginning of a radiation phase. The latter is threatened locally by urbanization and mining activity.

Exploring the Microbiome of Callinectes sapidus (Maryland Blue Crab)

Ramachandran P, Reed E, Windsor AM, Ottensen A
Office of Regulatory Science US Food and Drug Administration

The Atlantic Blue Crab (Callinectes sapidus) is a revered part of the diet of Marylanders and non-Marylanders alike. Describing the microbiome of this popular species provides valuable information to better understand health risks for crab aquaculture and also risks to consumers from handling or consuming inadequately cooked parts. The shotgun metagenomic data presented here provide culture-independent and PCR-bias free insight into the native microbiome and distinct groupings of microbial taxa associated with different body regions. Crab parts used for this study were categorized as legs, claws, meat, and viscera. Each part was homogenized and DNA was extracted using the Qiagen DNEasy Blood and Tissue kit prior to Nextera XT library preparation. For culture dependent description, crab parts were incubated at 37°C in mBPW broth for 24 hours prior to DNA extraction. Libraries were sequenced on an Illumina Nextseq 550 and data were analyzed using Cosmos ID bioinformatic pipelines. The data supported previous work describing a core Proteobacteria community; in this case comprised of Vibrio, Shewanella, Ralstonia and Pseudoalteromonas. Interestingly, Alivibrio was associated only with the viscera, Exiguobacterium was absent only from the viscera, and Citrobacter was unique to meat. Surprisingly, the claws and meat were more diverse than the viscera, hosting Psychrobacter spp, Propionibacterium, Shewanella, Exiguobacetrium, Providencia, Ralstonia, Proteus, Clostridium, Pseudoalteromonas, Lysinibacillus, Enterococcus, and Vibrio. Uncultured crabs were dominated by Psychrobacter and Propionibacterium, while cultured parts were dominated by Shewanella, Exiguobacetrium, and Vibrio. The cultured crab microbiota also supported the growth of Exiguobacterium, Lysinibacillus, Shewanella and Enterococcus. Incidence of Vibrio spp. was significant in all cultured parts except for claws. Phage elements also provided interesting contrasting signatures between cultured and uncultured crab parts. Uncultured crabs were dominated by Psychrobacter phages and Hop trefoil cryptic virus and cultured crabs were dominated by Lactococus, Vibrio and Enterobacteria phages.

Do We Have the Guts to Age Crustaceans? Evaluating Potential Age Structures for Three Alaska Species

Rebert AL, Kruse GH, Webb JB, Tamone SL, McNeel KW
Alaska Department of Fish & Game, University of Alaska Fairbanks, University of Alaska Southeast, Juneau

Banding patterns are observed in the endocuticle of gastric mill ossicles and eyestalks of red king crab (Paralithodes camtschaticus) and snow crab (Chionoecetes opilio), and eyestalks of spot shrimp (Pandalus platyceros). Recent research supports an age determination method based on these banding patterns; however, processing methodologies for these structures have not been established. Further, species-specific evidence is needed to determine whether these patterns indicate actual age or growth. The objectives of this project are to: (1) describe optimal species-specific methods for producing and evaluating band counts for red king crab, snow crab, and spot shrimp; and (2) use differences in shell condition to test whether band counts indicate growth for snow crab. For each species, we comprehensively thin-sectioned structures, evaluated each section for banding pattern presence (readability), and developed band count criteria. To address objective 1, we used generalized additive models to describe readability across structures to find the location that optimizes the production of readable sections. For objective 2, we used a one-way ANOVA to compare band count and endocuticle measurements among shell conditions. Results indicated preferred structures, locations, section orientation, and thickness. Results also indicated that there is no relationship between band count and shell condition for terminally molted snow crab. These results describe optimal methods for processing crustacean structures and suggest that the potential age structures may not continue to produce bands after terminal molt. Further evaluation is needed to validate potential age relationships and the use of this technique for age estimation.

Understanding Peaks of Diversity and Endemism of Crustacea in the Gulf of Mexico

Reaka ML, Lauer D
The University of Maryland, College Park

The objective of this research was to understand the relationship between diversity, endemism, depth, and geographic location of all the major taxa of crustaceans that occur in the Gulf of Mexico. We used the database that resulted from Gulf of Mexico: Origins, Waters and Biota (Felder and Camp 2009) to quantify the depth distributions and endemic status of all species in each crustacean Order. We found that, for all Crustacea combined, diversity is highest in shallow water and in the northern/eastern sectors of the Gulf of Mexico, although some individual taxa show other patterns. “Depth endemism” is highest in shallow water; 34% of species in 0-10m occur only there. Lower peaks (5-8% of species in each depth zone) of depth endemism are found on the upper continental shelf for some groups (myodocopan ostracods and tanaids at 500-1,000m; lophogastrids at 1,000-2,000m). “Horizontal endemism” (“Gulf endemics”) for all crustaceans = 13.3% (sufficiently high to designate the Gulf of Mexico as a separate biogeographic province for Crustacea). Some taxa show exceptionally high horizontal endemism (50-75% in cephalocarids, branchiurans, leptostracans, tanaids; 20-49% in myodocopan ostracods, stomatopods, mysids, amphipods, isopods, cumaceans; 10-19% in copepods, decapod lobsters). We hypothesize that these patterns are driven by speciation/extinction dynamics, where speciation > extinction in the northeastern sectors (endemics likely are young species), extinction > speciation in northwestern and southwestern sectors (leaving old “relicts” as endemics).

Best Practices for Depositing Voucher and Type Material in Museum Collections

Reed KJ, Ahlfeld K, Moser W*
Smithsonian Institution, National Museum of Natural History, Department of Invertebrate Zoology

The Smithsonian Institution, National Museum of Natural History, Department of Invertebrate Zoology routinely accepts, catalogs, and curates designated voucher and type specimens from all extant invertebrate taxa (except foraminifera, insects, myriapods and non-marine chelicerates). Due to modern shipping and permitting issues, we strongly encourage prospective donors to adhere to our best practices in the following areas: Notification, Specimen Curation and Documentation. Notification: Before you ship specimens, please contact the curator in charge of the collection (a list of collections and responsible curators is available at http://invertebrates.si.edu/) or the collection manager. If you wish to donate a large collection, be aware that the acquisition will need to be approved by the IZ Collection Committee and may require additional review time. Please do not send manuscript type specimens until your manuscript has been accepted for publication. Finally, do not ship any specimens for deposit until you have received departmental approval. Specimen Curation: Specimens sent for catalog numbers must be clearly separated, sorted, labeled with taxa and locality data, and housed in appropriate storage containers. In addition to the data on the label, please provide appropriate specimen and locality data in a spreadsheet. Documentation: To expedite processing time, please provide a signed Deed of Gift form or gift letter and copies of all relevant permits. We will not accept specimens collected in violation of international, local, state or Federal regulations or in violation of the Lacey Act or the Endangered Species Act.

Portray of a Global Species: the Parasitic Barnacle, Anelasma squalicola

*Rees DJ, Schnabel K, Finucci B, Drewery J, Leslie R, Noever C, Salvanes AG, Glenner H**

University of Bergen, NIWA, Marine Scotland, Department of Agriculture, Forestry and Fisheries

The presence of cosmopolitan species in the marine realm is highly debated and studies have repeatedly demonstrated that global or cosmopolitan species, with a seemingly morphological uniformity, turn out to be geographically distinct cryptic species when molecular methods are applied. In this study we present data that strongly indicates that the stalked barnacle, Anelasma squalicola, is a true global species. Widespread in deeper waters on a wide variety of shark species, the barnacle is recorded from off Greenland, the British Isles, Spain, the Mediterranean Sea the Azores, the Canary Islands, the Gulf of Mexico, South Africa, Australia, New Zealand, and Chile. DNA sequences for nuclear ribosomal genes (18S and 28S), from populations throughout most of the barnacle's distribution range, reveal no genetic differentiation. Variation in mitochondrial sequences (Control Region and COI) show no geographical pattern and is mainly due to local allocations of private alleles, and we conclude that A. squalicola represents a single globally distributed species. The evolutionary significance of this discovery will be discussed in the presentation

Hematodinium in Georgia: Where Are We Today?

*Richard K, Pham J, Frischer ME, Dunn PH**

Georgia Southern University, University of Georgia

Hematodinium perezi is a highly pathogenic parasitic dinoflagellate found in blue crabs (Calinectes sapidus) and other decapods along the Atlantic and Gulf coasts of the United States. Two decades ago (1998-2004) during a severe regional drought, high prevalence of Hematodinium infections were implicated in the major decline of the blue crab fishery in the state of Georgia. Commercial landings declined from an average of 4,200 metric tons in 1956-1995 to less than 1,000 metric tons in 2004. Following the end of the drought in 2004, crab landings partially recovered but remain well below pre-drought levels (an average of 1,600 metric tons from 2005-2017). The goal of this ongoing study is to determine whether Hematodinium may still be playing an important role in preventing a full recovery of the blue crab fishery in Georgia. Hemolymph samples from adult blue crabs were collected monthly since April 2016 and screened for the presence of Hematodinium using a previously developed 18S rRNA-targeted diagnostic PCR assay. Preliminary results indicate that the prevalence of Hematodinium in Georgia's blue crabs is typically between 20% and 40%, very similar to the prevalence observed during the fishery collapse of the late 1990s and early 2000s. These results suggest that Hematodinium may still be playing a large role in the population dynamics of C. sapidus in Georgia's waters.

Adaptive Potential of Calanus pacificus Copepods Along the Northern California and Oregon Coast

Rhodes ACE

University of Vermont

Objective: This project sought define the range of the two previously identified coastal subspecies Calanus pacificus californicus (sourthern range) and Calanus pacificus pacificus (northern range) as well as any significant subpopulations. Methods: In May 2017, copepods were collected using plankton tows at 61 stations off northern California and Oregon, from 3 km to 125 km offshore. Twenty-seven stations, mostly nearshore, contained Calanus pacificus. Ten of the stations were chosen for analysis using genome-wide single nucleotide polymorphism (SNP) genotyping with 2bRAD to detect haplotypes. This genetic data can provide historic rates of adaptation in the species and subspecies as well as information on the potential of Calanus pacificus to adapt to persistent warm water events. Summary: Calanus pacificus is a ubiquitous northern Pacific Ocean copepod species that is an important prey item for many marine fish and bird species. The Northern California and Oregon coasts have been undergoing an unusual warming event, colloquially referred to as the "warm blob", an influx of warm Pacific Ocean water that persisted throughout 2015 and into 2016 off the Oregon coast. While novel species can be detected by traditional taxonomic measures, it is difficult to determine whether subpopulations of morphologically identical individuals in the same species are moving into the area as well. The results of this study provides a baseline description of nearshore population structure in Calanus pacificus.

Multiple Immigrations Into the Subterranean Habitat in the Tasmanian Anaspides (Malacostraca) – Timing and Adaptation

Richter S, Hoepel CG, Reinhardt M, Ahyong ST

Universität Rostock, Australian Museum

Anaspidacea is an enigmatic taxon within Malacostraca with uncertain phylogenetic affinities. The best known genus Anaspides is endemic to Tasmania and shows a remarkable geographical and vertical distribution. Seven species are recognized to date, occurring in freshwater habitats such as lakes, streams, tarns and also in caves. We studied the genetic differentiation within the morphologically recognized species and a dating of speciation is given using a molecular clock approach. Significantly, however, the molecular data suggest several more species than so far described. Special focus is laid on the multiple instances of immigration of Anaspides into the subterranean habitat. Immigration is known to have happened at least three times independently across Tasmania (Mole Creek, Mt. Field, Ida Bay/Hastings), but our data suggest that this number could actually be higher. Remarkably, surface and cave forms sometimes share the same COI-haplotypes. Entry into subterranean habitats appears to have occurred in the Pleistocene rather than Tertiary and may represent opportunistic expansion into new habitats created by the action of glacial meltwaters on existing karst formations. Morphological differences between surface and cave forms affect pigmentation, the shape and spination of the telson and the shape and pigmentation of the eyes. We studied brain anatomy using MicroCT and found that differences in eye shape and pigmentation are reflected by variations in the number of ommatidia and the size of the optic lobe. The optic lobes are only significantly reduced in certain cave forms, however, which might reflect differences in the point in time of immigration into caves.

A Hyperdiverse Late Jurassic Squat Lobster Assemblage

Robins CM, Klompmaker AA
University of California, Berkeley

Decapod crustaceans are rarely fossilized in great enough numbers for large assemblage studies. One notable exception is the Friedrich Bachmayer collection of over 7000 individual decapods from the Late Jurassic Ernstbrunn Limestone of Austria, by far the largest known Mesozoic decapod collection in the world consisting of over 80 species. The fossil galatheoid anomurans (squat lobsters) within this collection have been the subject of two taxonomic monographs in the last decade, and comprise approximately 30% of the total decapod assemblage, presenting a unique opportunity for an assemblage-level study. All identifiable carapaces, discounting external molds, were tallied, totaling 2170 specimens. Of those, 1665 were identifiable to the species-level across 53 different species, representing the richest fossil galatheoid assemblage in the world. Two species are still undescribed. Rarefaction curves for both genera and species have leveled, implying that the majority of taxa have been collected. Several diversity metrics that take into account the number of specimens per species also indicate that the assemblage is very diverse. The Shannon Index for Ernstbrunn is 2.50; for comparison, this index is only 1.12 for a mid-Cretaceous (Albian) galatheoid fauna from Koskobilo, Spain (482 individuals across 10 species). The Simpson Index (1-D) gives a value of 0.83 for Ernstbrunn and 0.58 for Koskobilo (i.e. evenness is higher for Ernstbrunn). The large assemblage also allowed for additional study of parasitic infestation prevalence, preserved as large swellings on the branchial regions of infected individuals. Infestation percentages are statistically random across species.

Conservation Status of the Large Branchiopods (Branchiopoda: Anostraca, Notostraca, Laevicaudata, Spinicaudata, Cyclestherida)

Rogers DC
University of Kansas

The large branchiopods (fairy shrimp, tadpole shrimp and clam shrimp) are flagship animals for the conservation of seasonal wetlands. These animals live in seasonally astatic aquatic habitats on all continents and many islands. However, these habitats tend to occur on level open land, which tends to be desirable for development or other land conversion activities. Although fairy shrimp biodiversity is reasonably understood, the biodiversity of the other groups are limited due to morphological plasticity, numerous cryptic taxa, and confounding genetic systems. Furthermore, most taxa are known from only their type locality. Specific threats to large branchiopod conservation are discussed, including; habitat conversion, agriculture, recreation, and invasive species.

Population Structure of Creaseriella anops in the Yucatan Peninsula, Mexico

Ruiz Cancino G, Perez-Losada M, Crandall KA, Mejia Ortiz LM
Universidad De Quintana Roo, George Washington University

The isopod Creaseriella anops is an endemic monotypic species and is an abundant faunal component in the groundwater ecosystems in the Yucatan Peninsula. The aim of the present study was to determine population structure and basic knowledge about phylogeography of the species. A total of 2093 individuals were included in the analysis of the population structure for three localities. Isopods were identified based on their developmental stage. Total length and total width were measured, sex ratio was calculated with the proportion of females among the total males with validation using a chi-squared test. The equation Y=aXb was used to calculate the divergence from the isometry. The size at sexual maturity was determined by adjusting the logistic function of the proportion of mature specimens. Additionally, a DNA region coding for the Cytochrome Oxidase subunit I (COI) was sequenced from 35 individuals across five populations. The populations comprised all stages of the life cycle from all sample locations. There were no distinct peaks visible in the distribution of C. anops, suggesting continuous reproduction. Males consistently predominated over females with respect to abundance; whereas, female mean size was significantly larger than males (the average sizes at first sexual maturity was estimated to be 15.74 mm for females and 14.64 mm for males). The manca stage showed a negative allometry, suggesting an adaptation to the cave environment and successful reproduction. Sixteen unique haplotypes comprised three independent networks. Phylogenetic analysis showed three distinct clades which corresponded to three geographic groups. A pattern of isolation by distance was detected and may indicate an ancient founder event with possible limited gene flow. This suggests the possibility of incipient speciation, although the species is present in all Yucatan Peninsula.

Understanding the Structural Properties of the Skogsbergia Lerneri Carapace

Rumney BM, Morgan SR, Lewis P, Malik FT, White N, Paker AR, Albon J, Meek KM
Cardiff University, Lifescaped, Somerset House

The aim of this study was to investigate the structure and composition of the Skogsbergia lerneri ostracod carapace in order to determine what underlies its transparency and durable nature. The 2D and 3D architecture of the carapace at the nanoscale and microscale have been probed using transmission and scanning electron microscopy (TEM, SEM respectively), 3D serial block face SEM (SBFSEM) and nonlinear microscopy (two photon excited fluorescence [TPEF] and second harmonic generation [SHG]). Additionally, SEM energy dispersive X-ray spectroscopy (EDX) enabled carapace elemental composition analysis. Spectral imaging at a 920nm excitation wavelength produced chitin derived SHG signals at 460nm and broader TPEF signals at 540nm. Ultrastructural analysis of adult carapaces identified a thickness of ≈11µm; of which the exocuticle and endocuticle comprised 25% and 20% respectively. The endocuticle had an organised chitin matrix (lamination ≈100nm), which was absent in the exocuticle. The crystalline layer, lying between these two layers, was evident from instar 2 and comprised 54% of total thickness. During development, the endocuticle increased from 5 to 16 layers and exocuticle complexity increased. 3D modelling revealed twisted pore canals, characteristic of carapace honeycomb structures. High calcium (6.16%), magnesium (1.77%) and oxygen (20.34%) levels in the carapace, particularly the crystalline layer, were indicative of carbonate crystals, like calcite. With no novel layers identified in the carapace, the endocuticle chitin matrix can be inferred to allow transparency, however the thicker crystalline layer and disorganised exocuticle could influence the carapace's physical properties. Further investigation into crystal composition and exocuticle organisation is warranted.

Determining the Effects of Nitric Oxide on Procambarus fallax Forma Virginalis

Rymut JA
Fairleigh Dickinson University

Ethanol (EtOH) effects inducible nitric oxide synthase (iNOS) activity by inhibiting the production of iNOS in cells. Acute doses increase the production of nitric oxide (NO) and endothelial NOS (eNOS). At higher dosages, ethanol impairs endothelial functions. NO has been found to suppress the feeding response in pond snails, Lymnaea stagnalis, induce synaptic depression in crayfish, and inhibit the swimming rhythm of Xenopus laevis tadpoles. This in vivo study will be performed in order to determine if synaptic depression is caused by free radical NO and determine if overall movements are decreased in Procambarus forma fallax virginalis (P.f.f virginalis) in the presence of NO. It was hypothesized that there will be a depression in synaptic activity and less movement in crayfish exposed to free radical NO. A probe will be inserted near the cerebral ganglion to assess depression in synaptic inputs. Movement will be tested by placing crayfish into a partitioned tank and counting each movement across a partition as one movement. Movement will be tested on both an individual and group level to determine if group activity will be a variable factor. NO will be introduced through the usage of ethanol, an L-arginine supplement, and chlorhexidine in an approximate range of five to ten parts per million (5 mg/L and 10 mg/L).

Synthetic and Natural Microparticles - Coping with the Dirt

Saborowski R, Korez S, Weidung M, Riesbeck S, Gutow L
Alfred Wegener Institute

Continuously increasing production and careless use of plastic goods have caused massive litter problems in many parts of the world. Due to river runoff and gradual degradation of big plastic pieces into micro size ones, plastic enters the marine environment. Numbers of studies increased continuously during the last decade emphasising the hazard of plastic pollution to marine organisms. Many invertebrate species and, particularly, crustaceans may ingest microplastics but also huge numbers of natural microparticles such as small mineral grains like silt or fine sand, diatom frustules, chitin fragments, or cellulose fibres. Since crustaceans are able to cope with such natural microparticles they may serve as suitable models to distinguish the specific effects of microplastics from natural responses. In laboratory studies with isopods and shrimps we offered food which was blended with synthetic and natural microparticles. Feeding rates of isopods, Idotea emarginata, did not change when microplastics were added to the food but enzyme activities showed high scatter and inconsistent results. Shrimps, Palaemon varians, increased oxidative stress responses in the midgut gland when fed with microplastics but also when the food contained natural silica shells or titanium dioxide nanoparticles. Current research is in progress to identify the physiological background of the oxidative stress response. Our results indicate that comparative studies on the effects of natural and synthetic microparticles are essential to distinguish between natural reactions and adverse toxicological effects in crustaceans.

The Sea Spiders (Arthropoda: Pycnogonida) from the Late Jurassic of Solnhofen

Sabroux R, Audo D, Charbonnier S, Corbari L, Hassanin A
Muséum National D'Histoire Naturelle, Yunnan University

Sea spiders (Arthropoda: Pycnogonida) form a unique group of arthropods of which the oldest unambiguous fossil dates back to the Silurian (ca 425 million years). All extant species belong to the order Pantopoda characterized by cylindrical legs and an unsegmented, reduced abdomen, whereas the eight Paleozoic species exhibit a large panel of morphologies, including legs specialized for either paddling or walking, and various number of abdomen segments. Instead, the three Mesozoic fossils are assigned to Pantopoda. They all originate from the unique site of La Voulte-sur-Rhône, France (Callovian, ca 165 million years), remnant of a Middle Jurassic deep water environment. In the present study, we examined the morphology of nine undescribed fossil sea spiders from the Solnhofen-type outcrops of Germany, a remnant of the shallow lagoons of the European tropical archipelago of the Late Jurassic (ca 150 million years). We performed various macrophotographic techniques with image stacking, in order to reveal inconspicuous structures. All the fossils are pantopods, and two are even assigned to already described genera: the Middle Jurassic Colossopantopodus, and the extant Eurycyde. Other fossils are poorly preserved, however peculiar features indicate in some cases possible affinities to other extant genera. The existence of four extant families in Jurassic (Ammotheidae, Ascorhynchidae, Colossendeidae, Endeidae) suggests that the diversification of Pantopoda occurred prior to Middle Jurassic.

Unraveling the Phylogenetic Relationships Winthin Sea Spiders Using Mitochondrial Genomes

Sabroux R, Corbari L
Muséum National D'Histoire Naturelle

As an original trait among arthropods, sea spiders (Arthropoda: Pycnogonida) show a strong lability of the cephalic appendages (chelifores, palps, ovigers), that can be either present or absent in almost all possible combinations. Therefore, the cephalic appendages are key characters for the discrimination of the eleven families commonly accepted in recent classifications: for instance, Phoxichilidiidae have chelifores, no palp and ovigers only in males. Traditionally, it has been considered that those cephalic appendages have been lost progressively along sea spider evolution. However, previous morphological and molecular phylogenies were not able to address this issue because interfamilial relationships remained unresolved. In the present study, we sequenced the mitochondrial genome of about 60 species from nine families to better understand the evolution of cephalic appendages. Different methods of tree reconstruction were conducted to estimate the robustness and reliability of the nodes. Our dataset provides a strong signal for deep relationships and our phylogenetic results revealed that cephalic appendages have emerged and disappeared several times during the evolutionary history of sea spiders, whereas some other morphological features, not always considered as important, represent true synapomorphies.

Disentangling Cryptic Species Complexes and Understanding Diversification in ‘Marbled Shrimps’ Saron spp. (Caridea: Hippolytidae): an Integrative Taxonomy Approach

Sanjeevi P, Frolová P, Duris Z, Anker A, Baeza JA
Clemson University, University of Ostrava, Czech Republic, Universidade Federal de Goias

Shrimps belonging to the family Hippolytidae exhibit remarkable morphological and ecological disparity. Among hippolytids, the genus Saron is recognized for its astonishing coloration. Two species, S. rectirostris, and S. inermis, can be easily identified and distinguished from congeners based on morphological traits. By contrast, two other species, S. marmoratus and S. neglectus exhibit considerable morphological and color variability suggesting the existence of cryptic entities within each species. Herein, we used an integrative taxonomic approach to test whether or not S. marmoratus and S. neglectus represent cryptic species complexes. The results of multivariate analyses (PCA and DFA) based on 19 morphological traits did not reveal different entities in each of the two species. On the other hand, phylogenetic analyses based on mitochondrial (16S) and nuclear (H3) genetic markers, as well as single and multi-locus species delimitation approaches (ABGD, mPTP, GMYC, BPP) revealed the existence of 5-8 and 5-7 divergent lineages in S. marmoratus and S. neglectus, respectively. The above suggests that the genus Saron has likely undergone a series of allopatric/sympatric speciation events in the Indo-Pacific. The present study provides a valuable insight on cryptic species diversity in caridean shrimps, a clade with considerable ecological relevance.

Effects of Interspecific Interactions and Increased Population Density on Vitellogenesis in Intertidal Crabs P. cinctipes and P. manimaculus

Sayavong N, Gunderson AR, Stillman JH, Tsukimura B
California State University

Climate change via anthropogenic activities is causing ever rising temperature changes, affecting community dynamics in the rocky intertidal. Physiological stress from increased temperature may force heat-stressed species to move into cooler environments. As a result, interspecific interactions and increased population density may threaten the fitness of both species involved through increased behavioral conflicts. Reproductive output can be measured through the concentration of a yolk protein vitellogenin (Vg) and may be used as a measure of fitness in the crab species. The development of the Enzyme Linked Immunosorbent Assay (ELISA) in our lab has allowed to quantify Vg concentration in the hemolymph of the crabs (Delmanowski et al 2017). To investigate the effects of species interactions and increased population density, P. cinctipes and P. manimaculus were collected from November 2017 through February 2018 and were put into interaction treatments. Hemolymph samples were taken from each crab before and after a seven-day heat and density stress treatment. To quantify the effects of both treatments, the ELISA was used to quantify hemolymph levels of Vg before and after treatment/control. Increased interspecific species interactions (higher densities) decreased Vg levels and thermal stress decreased Vg levels in P. cinctipes. These data suggest that P. cinctipes relocation due to thermal stress places these crabs at higher densities with an interspecific grouping of crabs, appears to decrease Vg levels, suggesting a decline in reproductive output. Energy typically used towards reproduction, appears to be redirected to competition.

Taxonomic Revision of the Genus Pagurus Fabricius, 1775 “Provenzanoi” Group (Decapoda: Anomura: Paguridae) from the Western Atlantic

Santana W, Lima D
Universidade do Sagrado Coração, Universidade de São Paulom

The Pagurus “provenzanoi” group currently comprises 26 hermit crab species distributed along the Western Atlantic and Eastern Pacific. The Atlantic component is represented by 12 species, occurring from Massachusetts to Argentina. Due to several problems of identification and doubts concerning the distributional boundaries involving these species, the aim of this study is to provide a taxonomic revision of the “provenzanoi” group, including a diagnosis, illustrations of the main diagnostic characters, and remarks about taxonomic issues of all 12 species. Specimens from the entire range of distribution of the “provenzanoi” group were analyzed from several carcinological collections. After the analyses of the material we could observe that: i) Pagurus brevidactylus and P. provenzanoi can be quickly differentiated by the setation of the chelipeds; ii) P. brevidactylus and P. criniticornis may represent a complex of sibling species; iii) P. trichocerus is a valid species; iv) P. annulipes and P. carolinensis have a restrict distribution in the east coast of United States and Gulf of Mexico; v) P. protuberocarpus remains known only from the type locality. The number of spines in ocular acicles, length of the antennal flagellum, length of the setae on antennal articles, shape and armature of the left cheliped and posterior margin of the telson were most valuable for identification purposes.

Taking a Deeper Look – A Fossil Isopod Revisited By ‘Virtual Paleontology’

Schädel M, Nagler C, Haug JT
Ludwig-Maximilians-Universität, University of Bergen

Fossils often lack supposedly crucial characters. It is ironic that this is especially often the case for fossils from so called Konservat-Lagerstätten – fossil sites that are known for exceptional preservation. For example: with few exceptions, such as chert and amber, exceptionally preserved fossils are in most cases distinctly compressed. In addition to this common loss of the third dimension the crucial characters are often on the “wrong side”. Here, we present a fossil from a type of deposit that is not likely to bear exceptionally preserved fossils (high energy environment). Yet, the surrounding rock consists of small spheres of lime (oolite) which prohibited compression. The fossil is a three dimensionally preserved isopod crustacean. The dorsal morphology of the new specimen indicates that it is a representative of Eonatolana geisingensis, already known from this locality. By scanning the fossil in a micro-CT we gained insight into the so far poorly known appendage morphology of this species and reconstructed the morphology with the aid of labeling contrasted structures, rendering these as surface models. This virtual paleontology method not only revealed the structure of the locomotory appendages, but also allowed the interpretation of the mouthparts. The newly observed details support the systematic interpretation of E. geisingensis as an non-parasitic representative of Cymothoida. Often, the non-parasitic forms within Cymothoida have been united in the supposedly monophyletic group Cirolanidae. Due to lack of well formulated apomorphies the monophyly of this group is however doubtful. Thus, we consider Eonatatolana geisingensis as Cymothoida incertae sedis.

Exceptionally Preserved Fossils of Minute Infective Larvae – 90 Million Years Old Window Into the Evolution of the Parasitism of Epicaridean Isopods

Schädel M, Perrichot V, Haug JT
Ludwig-Maximilians-Universität, Université de Rennes

Isopoda is an ingroup of Peracarida and must be considered an overall evolutionary successful group. Isopods have conquered numerous habitats from the deep sea to dry desert and exhibit various feeding strategies. In most isopods the early post-embryonic stages strongly re semble the adults. The obligate parasitic epicarideans form an exception. Their life cycle is complex and includes a host switch and extreme sexual dimorphism. This requires two highly mobile stages. One of them is the cryptoniscus larva. After detaching from its copepod larval host, it becomes plan ktic and searches for its definitive host. Within Epi caridea there are different strategies to feed on the definitive hosts right up to endoparasitism. The most specialised form is the inhabitation of the gill chamber which can be indirectly traced back to the Jurassic period, i.e. 200-142 million years ago, based on specific deformations of the hosts. Here, we present the so far oldest record of epicaridean body fossils from a rare sample of French Cretaceous amber of about 90 million years in age. This represents a rare kind of preservation where marine organisms were trapped in resin in a coastal environment. With the help of high-resolution composite fluorescence microscopy, we shed light on their highly specialised morphology that was already present in the Cretaceous and discuss implications of this find on the evolution of the synecological relationship between parasites and their hosts

Unknown Unknowns: What Would We Not Know About Pancrustacea Without Fossils

Schram FR
University of Washington

Everyone recognizes that fossils do tell us a lot about evolution within Arthropoda. But if we had no fossil record, what would we have missed amongst the Pancrustacea? We would never know – so they could not be missed. Nevertheless, it is interesting to play the game of "unknown unknowns." First of all, our understanding of biodiversity would be depleted. Exact numbers remain vague, but as an example, in the Class Oligostraca the ostracods have around 14,500 living species and subspecies, and estimates indicate that another 56,000 ostracods are extinct species residing only in the fossil record. That is a great deal of missing diversity. Second, our understanding of body plan disparity would suffer. For instance, we would not know about several members of Class Multicrustacea such as: Cyclida (an infraclass of the Subclass Hexanauplia), Pygocephalomorpha (an extinct peracaridan order of Infraclass Eumalacostraca), and Thylacocephala (an enigmatic infraclass, probably of Multicrustacea). Gaps in understanding the evolution of living crustaceomorphs have also fallen prey to the effects of unknowns. Before World War II, branchiopods served as a kind of ancestral type. That is until 1943 when Mystacocarida were discovered. Before 1955, Cephalocarida were unknown. Not until 1981, were Remipedia unveiled. Each of these groups in turn served as a succession of avatars for ancestral types of crustaceans. Then between 2010-2013, DNA sequence data overturned all our old ideas: Hexapoda united with the paraphyletic crustaceomorphs to present us with a new reality, class Pancrustacea, which included the merger of three of the "old ancestors" of the crustaceans—branchiopods, cephalocarids, and remipedes—into a new subclass Xenocarida. How are we now to make sense of the evolution of hexapods from crustaceans? Can new "unknowns" provide insight? Such is indeed, and continues to be, the case. We not only have new insights about the radiations of crustaceans based on real fossils (Briggs et al., this meeting), but also from newly recognized crustaceomorphs we can now perceive what crustaceans evolved into (insects) and how they might have done it (via xenocaridans).

You Are What You Eat, You Are Where You Live - Caime Part 1 - Trace Metals in Crustacea, Biomonitoring of the Marine Environment

Schnabel K, Peart R, Handler MR, Wysoczanski RJ, Frontin-Rollet GE, Graham AEM, Seabrook C
National Institute of Water & Atmospheric Research, Victoria University of Wellington

The state and health of our marine environment is paramount to our societal and economic wellbeing. One approach towards assessing and preserving the uniqueness of our marine estate is understanding the chemistry of the organisms occupying it. The uptake of elements from the environment into their tissues and particularly into their exoskeleton makes them recorders of their chemical environment. This, in turn, allows for the monitoring of events that might occur over time, such as changes in levels of trace metals resulting from offshore mining activities, urban development, or ocean acidification. Here, we present the first part of the CAIME (Crustacea As Indicators for the Marine Environment) study which includes preliminary trace element baseline data for shallow marine Decapoda from around New Zealand. Thirty trace elements have been analysed from two decapod species, the coastal crayfish (Jasus edwardsii) and deep-sea squat lobster (Munida gracilis) using acid digestion techniques combined with inductively coupled plasma mass spectrometry, and preliminary results are compared with those for Amphipoda (CAIME I). The results show distinct patterns between species and locality and indicate a potential for evaluating natural variations and consequently unusual changes across a range of geographic localities. Further, the results provide the potential to compare across two orders of crustaceans that occupy very different habitats and trophic niches. These two presentations will cover the hypotheses and implications of the first results of this 3-year programme and how any changes in the marine environment can be assessed in the future.

Paleoecology of Podotrematous Crabs and Galatheoid Anomurans

Schweitzer CE, Feldmann RM
Kent State University

Paleoecology of fossil podotrematous crabs is only beginning to be studied. Preliminary analysis of members of podotrematous families indicates that families preferentially inhabited specific types of environments as defined by rock type. Many dromiacean families are predominantly recovered from carbonate environments, whereas homoloids and raninoids exhibit a broader environmental preference. Extant families, in general, exhibit broader environmental preferences than extinct groups. Within families, genera in Dromiacea and Homoloidea as well as the anomuran Galatheoidea demonstrated niche partitioning during the Late Jurassic. Correspondence analysis of 29 Late Jurassic decapod collecting localities in Europe demonstrated sponge-microbial versus coral bioherms exhibited distinct podotrematous and galatheoid decapod faunas. Of 50 genera examined, 30 never were recorded from sponge-microbial environments, whereas all taxa occurred at least once in coral dominated environments. Genera within six families were only collected from coral facies, and genera within only two families were predominantly collected from sponge-dominated facies. Among members of Raninoida, some families are predominantly associated with siliciclastic environments, whereas others are dominantly collected from carbonates. Niche partitioning among podotrematous brachyurans and galatheoids parallels that seen at the infraorder level in Decapoda, wherein specific groups of decapods generally inhabit specific types of environments, which remains consistent through time.

Crustacean Phylogenomics with Special Focus On Malacostraca and Branchiopoda - Designing Taxon-Specific Matrices Increases Accuracy in Phylogenomic Analyses

Schwentner M, Richter S, Rogers DC, Giribet G
Harvard University, University of Hamburg, Universitat Rostock, Kansas University

The phylogenetic relationships among and within main taxa of Tetraconata (or Pancrustacea) are still debated. Here we present the most taxon-rich phylogenomic data set focusing on crustacean lineages that is based solely on genomes and Illumina-generated transcriptomes, including 89 representatives of Tetraconata, with 26 species of Malacostraca and 36 species of Branchiopoda. To explore the sensitivity of results to particular analytical conditions, seven matrices with different gene occupancy and taxon representation criteria (comprising up 864 orthogroups and 242,530 amino acid positions) were analyzed under five different analytical approaches. Taxon-specific matrices for Malacostraca and Branchiopoda were designed to maximize gene occupancy and resolution of these clades. Oligostraca, Multicrustacea, Allotriocarida, Copepoda, Malacostraca, Thecostraca, Branchiopoda, Cephalocarida, Remipedia and Hexapoda were monophyletic and well supported across most analyses. The traditional taxon Maxillopoda which is in conflict with the concepts of Oligostraca and Multicrustacea was never recovered. Within Branchiopoda, Phyllopoda, Diplostraca, Cladoceromorpha and Cladocera were monophyletic. Within Malacostraca, the clades Eumalacostraca, Decapoda and Reptantia were well supported but recovery of clades like Caridoida or Peracarida was highly depending on the analysis. The malacostracan-specifc matrix consistently placed Stomatopoda as sister taxon to all other Eumalacostraca (i.e. Caridoida) and recovered Peracarida as monophyletic. From the latter and other examples, we can empirically show that taxon-specific matrices are highly effective for improving resolution within targeted taxa and that certain models and analytical methods, namely CAT-GTR and Dayhoff recoding, performed better than other methods in resolving recalcitrant nodes. However, no approach confidently resolved all nodes across the tree.

Climate Change Enhances Disease Outbreaks in Crabs and Lobsters

Shields J
Virginia Institute of Marine Science

Over the last two decades disease outbreaks have been increasingly reported from several commercially important crustacean fisheries. Environmental stressors, including increasing temperatures, extensive hypoxia due to eutrophication, and presumptive exposures to contaminants, have been implicated as contributory factors in these outbreaks. Environmental stressors can alter the homeostasis of crustacean hosts by weakening or compromising their defensive responses thereby increasing their susceptibility to pathogens. Environmental stressors also favor microbial pathogens by improving their reproductive capacity, particularly in response to temperature or nutrient loading, leading to faster rates of population growth that can overwhelm host defensive capabilities. The role of environmental stressors in the emergence of pathogens has been difficult to delineate because stressors have complex biotic and abiotic interactions. This presentation highlights the role of increasing temperature due to climate change in the emergence of several disease syndromes in important commercial species. Insights will be provided into how multiple factors contribute to the emergence of disease outbreaks. Examples include outbreaks of epizootic shell disease, Neoparamoeba pemaquidensis, calcinosis and blindness in clawed lobsters, Hematodinium in snow crabs and blue crabs, and viral infections in shrimp and lobsters. Collaborative laboratory, field and in silico studies offer a means to coordinate sampling and focus research questions to gain further understanding of these types of outbreaks.

Comparative Study of the Effects of Light On Photophore Ultrastructure from Two Families of Deep-Sea Decapod Crustaceans: Oplophoridae and Sergestidae

Sickles JE, Blackwelder PL, Frank TM
Nova Southeastern University

With little refuge and a three-dimensional hunting ground, mesopelagic animals have evolved a variety of adaptations to avoid being easy prey. Among these are counterillumination, i.e. a silhouette camouflaged from predators below via ventrally directed bioluminescent light produced in photophore organs. While counterillumination is used extensively throughout the marine environment, little is known about the mechanisms used to enable animals to precisely replicate the intensity and wavelength of downwelling light. In unpublished data by H. Bracken-Grissom, photophores from Oplophoridae shrimp were found to contain opsin proteins, a component of all known visual pigments, giving rise to the suggestion that photophores themselves might be light sensitive. In the study presented here, the cuticular photophores of Systellaspis debilis and Janicella spinicauda (Oplophoridae), and the hepatic photophores of Sergestes armatus and Sergestes sargassi (Sergestidae), were exposed to various light regimes and then fixed for transmission electron microscopy. Preliminary data indicate that light exposures alter photophore organelle structures, similar to what has been found in other studies on photoreceptors exposed to damaging levels of light.

Evaluation of Males Reproductive Quality of the White Shrimp Litopenaeus vannamei in Commercial Maturation System

Silva EF, Castelo-Branco T, Da Costa L, Da Silva Y, Nolé L, Lira AS, Batista A, Guerra M
Instituto Federal De Educação, Ciência e Tecnologia da Paraíba, Universidade Federal Rural de Pernambuco

The objective of the study was to evaluate the males reproductive quality of the white shrimp Litopenaeus vannamei in a commercial maturation system. The reproductive quality was determined by spermatophore weight, counting and sperm viability of seven animals with 0, 21, 44 and 84 days in the maturation system. Each male was weighed individually and one spermatophore was extruded manually and weighed. This spermatophore was homogenized in an eppendorf tube with 1 mL of calcium-free saline solution and quantified in a hemocytometer. The viability of sperm was assessed by staining with propidium iodide and 6-carboxyfluorescein diacetate (PI-CFDA). For animals entering in the maturation system (day zero), a significant lower weight (35.62±2.59 g) was observed in relation to the animals with 21 (40.50±2.55 g), 44 (41.65±4.53 g) and 84 days in the system (44.72±1.89 g). However, the spermatophore weight (day 0: 0.12±0.006g; day 21: 0.11±0.40g; day 44: 0.16±0.01g; day 84: 0.12±0.008g) and number of sperm cells (104 cells/mL) (day 0: 698.0±192.01; day 21: 920.0±300.0; day 44: 1047.5±545.4; day 84: 594.0±336.2) did not differ among the four groups analyzed. For the sperm viability, the animals with 84 days of maturation showed a higher viability (91.40±5.17%) in relation to the animals entering in the maturation system (79.40±18.28%). Animals with 21 (86.80±6.53%) and 44 days (91.20±4.65%) did not present significant differences among the other. L. vannamei males with approximately three months kept in commercial maturation systems, present higher sperm viability in relation to those shrimp entering in the system.

Population Structure and Size At First Maturity of the White Shrimp Litopenaeus schmitti On the North Coast of Paraíba State, Northeastern Brazil

Silva EF, Craveiro C, Nolé L, Lira AS, Castro Neto H, Gonzalez E, Lucena Flávia, Peixoto S, Soares R
Instituto Federal De Educação, Ciência e Tecnologia da Paraíba, Universidade Federal Rural de Pernambuco

The present study aimed to investigate the population structure and size at first maturity of Litopenaeus schmitti in Paraíba state, northeastern Brazil. Between December 2016 and November 2017, specimens were collected through artisanal fishing using a trawl. Specimens were weighed (TW) and the carapace length (CL) and total length (TL) were measured. To determine the size at first maturity of females, the CL was used, in which the percentage of the relative frequency of adults in each size class with a range of 0.1 cm was estimated. A total of 1,710 specimens were collected, corresponding to 966 females and 744 males, representing the proportion of 56.49% and 43.51%, respectively. Females presented significantly larger size and weight than males ($p<0.05$). Males had a mean TL of 11.73±0.97 cm, with a size range of 8.3 to 15.5 cm, whereas the females had a range of 5.6 to 18.5 cm and mean TL of 12.22±6.67 cm. For CL, mean values were 2.43±0.40 cm and 2.45±0.53 cm for males and females, respectively, with a range of 1.56 to 4.75 cm for males and 1.16 to 4.5 cm for females. Mean TW was 12.64±3.38 g for males and 14.22±8.40 g for females, with a range of 4.4-34.1 g and 2.2-59.8 g, respectively. The carapace length at first maturity (CL50) in females was estimated at 2.20 cm. This information may contribute to the elaboration of guidelines for the sustainability of L. schmitti fishery on the north coast of Paraíba, Brazil.

Eat Microplastics, Die Early? Do Microplastics Lead to Higher Mortality of Barnacle Larvae?

Sing-Pei Y, Chan BKK
National Taiwan University, Academia Sinica

Plastic litter negatively impact the marine life. Plastic debris smaller than 5 mm in diameter are classified as microplastics. Microplastics can be generated during plastic manufacturing or came from degradation of larger plastic fragments in the nature enviroment. Compared to macroplastics, the influence of microplastics on marine life are still largely unknown. Although most studies have evaluated the effect of microplastics on responses of adults but relatively less studies focus on larvae. Another constrain is the short experiment time. In the present study, we used barnacle naupliar larvae (Amphibalanus amphitrite), as a model organism for crustacean larvae, to investigate the ingestion of four sizes of polystyrene microbeads (diameter 1.0, 6.8, 10, 20 μm respectively) at four concentrations(1000, 100, 10, 1, 0 beads ml -1). After exposing to microplastics from nauplii to cyprids, nauplii mortality, development time, growth and metamorphosis rate were not significantly different from control which didn't receive any microplastics. Moreover, feeding ability of nauplii were barely effected at highest concentration (1000 beads ml -1). Nauplii appeared to prefer feed on microplastics, when microalgae and microplastics were presented at the same amount. After ingestion, microplastics was egested together with digested algal materials within two hours. Fecal pellets contained microplastics with digested algal materials sank to the bottom rather than float in water column. As a result, ingestion of microplastics by zooplanktons can transform microplastics to the benthic environment.

Carcinonemertes conanobrieni - A Newly Described Nemertean Parasite Infecting the Caribbean Spiny Lobster, Panulirus Argus, and its Effect on Host Reproductive Performance

Simpson LA, Baeza JA
Clemson University

Panulirus argus comprises one of the most commercially valuable fisheries in the Greater Caribbean. Here we describe a new species of Carcinonemertes parasite found to be infecting P. argus and the effects it has on the host. Panulirus argus males, non-gravid, and gravid females were captured along the Florida Keys reef tract, and searched for the presence of Carcinonemertes infection to determine host use, infection prevalence, and intensity. Furthermore, infected gravid females were also used in estimating the impact that infection had on three levels of reproductive performance (reproductive output, fecundity, and brood mortality). We found that all male lobsters (n=30) and all but two non-brooding female lobsters (n=30) showed no signs of infection by this nemertean worm, while all but 7 out of 114 sampled gravid female lobsters were infected by Carcinonemertes conanobrieni. When investigating the impact that infection had on the reproductive performance of gravid females, we found that the interaction between intensity of infection and embryo stage had a significant impact on fecundity (F=7.1792, d.f.= 1, 74, P= 0.0092). The interaction between egg stage and infection status was marginally significant on reproductive output (F=3.68, d.f.= 1, 74, P= 0.0591). We also found no effect of infection on brood mortality of female lobsters. We believe that C. conanobrieni has the potential to have a significant impact on the health of the lobster fishery in the Florida Keys, and the presence of this worm should be taken into account when considering new fishery management strategies.

Mating Dynamics of Eastern Bering Sea Snow Crab: Preview of Genetic Analysis

Slater LM, Jackson TM, Kruse GH, Grant WS, Habicht C, Grauvogel Z, Cheng W, Webb JB, Pengilly D, Daly B
University of Alaska Fairbanks, College of Fisheries & Ocean Sciences, Alaska Department of Fish and Game

Snow crab (Chionoecetes opilio) in the eastern Bering Sea (EBS) support the largest and most valuable crab fishery in Alaska and are managed with a large-male only harvest strategy. We collected measures of female sperm reserves and archived spermathecae samples annually over a 10-year period to improve understanding of mating dynamics. Evaluating spatiotemporal trends in female sperm reserves has provided critical insight into functional relationships among female reproductive potential, maternal characteristics including reproductive stage (primiparous and multiparous) and size, and mating success. However, inferences about mating dynamics is hampered by a lack of empirical information on contributing male mates, including the extent to which polyandry within a mating season and interspecies mating occurs, the latter as evidenced by the presence of viable snow-Tanner hybrid crab in the EBS. We will develop and validate genetic markers and determine the number and species of males that contributed to the sperm reserves of primiparous and multiparous snow crab in the EBS over our 10-year study. Additionally, we will look at the paternity of brooded embryos to evaluate whether the sperm reserves contains a complete record of male mates. These empirical data will improve our inferences about mating dynamics based on measures of female sperm reserves and sex ratios. This is the first year of our study, so we will present our research objectives and approach.

Mating Dynamics of Eastern Bering Sea Snow Crab: Inferences Based On Female Sperm Reserves and Sex Ratios

Slater LM, Jackson TM, Webb JB, Pengilly D, Kruse GH, Daly B
Alaska Department of Fish & Game, University of Alaska Fairbanks, College of Fisheries and Ocean Sciences

Snow crab (Chionoecetes opilio) in the eastern Bering Sea (EBS) support the largest and most valuable crab fishery in Alaska and are managed with a large-male only harvest strategy. Snow crab have a terminal molt, which is associated with maturity in females and the competitive advantage of a relatively larger chela size in males. However, males are functionally mature and capable of mating prior to their terminal molt. We collected measures of female sperm reserves, a direct indicator of mating success, annually over a 10-year period to improve understanding of mating dynamics. We found most primiparous females received sufficient sperm to fertilize their first clutch but had insufficient remaining stores for subsequent clutches. Multiparous crab had heavier sperm reserves than primiparous crab, indicating most females did re-mate. Along the ~400 nautical miles of surveyed EBS shelf, we found sperm reserves to be heaviest in the southeast and lightest in the northwest, opposite to the trend in mature female abundance. Stock assessment surveys provide estimates of crab abundance approximately five months after the mating season. Relating sperm reserves to sex ratios based on the number, size, and shell condition of available males will allow us to make inferences about mating dynamics, such as spatiotemporal variations in the male competitive hierarchy and the relationship between the harvested portion of the stock and female contributions to population renewal processes. Additional research is underway using genetic markers to provide empirical information about male mates, which will improve our inferences about mating dynamics.

Individual and Environmental Risk Factors for the Atlantic Blue Crab (Callinectes sapidus) Mortality in Soft-Shell Aquaculture Practice Associated with Reovirus Infection

Spitznagel MI, Small H, Shields J, Lively J, Schott EJ
University of Maryland Center for Environmental Science, College of William & Mary, Louisiana State University

Production of soft-shell crabs using Atlantic blue crab (Callinectes sapidus) frequently results in over 25% mortality, presumably from an array of aquaculture stresses. An endemic virus pathogenic to crabs, Callinectes sapidus reovirus 1 (CsRV1), is found at low viral loads in 20% of all wild crabs surveyed in the eastern US, but at high loads in most crabs dying in aquaculture. It is unknown how geography, aquaculture methods or crab characteristics affect crab mortality and CsRV1 infection rates. We measured crab mortality and CsRV1 infection intensity in Chesapeake Bay and Louisiana soft crab aquaculture in 2016 and 2017. Using an RT-qPCR assay, we compared viral loads in live and dead crabs with host and environmental factors. CsRV1 load was the primary correlate of crab death in aquaculture; over 106 virus genomes per mg crab muscle tissue were found in 48% of mortalities surveyed. Crab mortality and CsRV1 infection rates were higher in flow-through aquaculture systems than in recirculating systems. Higher salinity correlated with higher prevalence and intensity of CsRV1 infections in aquaculture crabs but not with crab mortality. CsRV1 infections were found in over 70% of dead aquaculture crabs from the Chesapeake Bay region but only 17% of aquaculture mortalities from Louisiana, where salinity was lower and culture practices more selective. The findings suggest that while CsRV1 is a ubiquitous pathogen of American blue crabs, its negative effect on soft shell production can be limited by the use of environmental and harvest controls in aquaculture.

Is the Mediterranean Slipper Lobster, Scyllarides latus, in the Levant Affected By Climate Changes?

Spanier E, Goldstein JS
University of Haifa, Israel, Wells National Estuarine Research Reserve, Maine Coastal Ecology Center

The Levant basin in the Eastern Mediterranean represents the warmest ‘edge’ in the wide distribution range of the Mediterranean slipper lobster, Scyllarides latus. This region has also been highly affected by recent SST increases, especially in the shallow shelf. We set out to examine how climate change may affect these lobsters. Lobsters are rare or absent in the nearshore in the fall when they are assumed to move to deeper waters to avoid the high, and possibly unfavorable, coastal water temperatures. A mark-recapture study of tagged lobsters was conducted in a coastal marine reserve in Israel. Concurrently a separate set of lobsters were exposed in the laboratory to the same thermal profiles as in the field and their locomotion was assayed using an activity wheel. Field results showed that indeed lobsters tagged in shallow waters moved (mean linear distance of 3.4 km) to deeper, cooler waters over the course of 2-2.5 warner months. Laboratory results confirmed this pattern (under similar thermal profiles), and also revealed that warming water temperatures elicited an increased response in all lobsters, resulting in markedly longer movements (mean 5.4 km, over a similar timeframe). Since lobsters molt in late fall, increased water temperatures cause molting challenges and sometimes death in S. latus. Only further studies may clarify if lobsters adapt their behavioral-ecology to these changing conditions or if their Levantine populations are susceptible to collapse as observed in some other inshore indigenous invertebrates in the Levant

First Insight Into the Cumacea Fauna from the Gulf of Guinea

Stępień A, Mühlenhardt-Siegel U, Błażewicz M
University of Lodz, Universitat Hamburg

In November 2012 monitoring investigation off the cost of Ghana in the Gulf of Guinea, in the frame of the Ghanaian marine environmental monitoring programme was organized. Survey was made in cooperation with Institute of Marine Research in Bergen (Norway) on the RV Dr Fridtjof Nansen and resulted in obtain large collection of Cumacea. Cumacea are small, benthic crustacean, classified to Peracarida. Member of that group occur in almost all habitats, in wide depth range. Small sizes of Cumacea and sexual dimorphism makes difficulties in recognition and describing species. Currently, there are more than 1500 species known, however it is supposed that this number is highly underestimated. From the west-north part of Africa, 61 species has been described so far, but 1/3 of them was found deeper than 1000m. Material for the present investigation was collected from 146 station in depth range 50-1000m, from sandy and muddy bottom. Cumacea was represented by 211 specimens, that were classified to 71 morphospecies, 7 families and 12 genera. Family Bodotriinae was the most rich in genera (5 genera recognized); the most speciose genera was Diastylis (Diastylidae) with 8 morphospecies recognized. Most of the morphospecies were rare, their frequency of occurrence in samples being lower than 10%.

Direct Aging of Decapod Crustaceans with Application to Red Deep-Sea and Jonah Crabs

Stevens BG, Wilson J
University of Maryland Eastern Shore

The difficulty of estimating age for crustaceans has long been an impediment to modern scientific management of their populations, due to the perceived lack of hard body structures, such as scales, otoliths, or bones. A recent advancement within the field of crustacean aging is the discovery of growth rings or bands in the eyestalk or gastric mill. We have used this technique to estimate age of the red deep-sea crab Chaceon quinquedens, and Jonah crab, Cancer borealis. Gastric mills were removed and embedded in epoxy, sectioned with a diamond-bladed saw, and photographed at 80X magnification. Bands were observed and counted by three independent viewers. Results for both species were mixed. Estimated ages ranged from 2 to 14 for red deep-sea crab, and from 2 to 5 for Jonah crab. Only the data for Chaceon could be fit to a von-Bertalanffy growth model, but the fit was poor due to high variability and low sample size. Agreement between multiple viewers was poor for Chaceon but it is unclear whether this is due to inherent variability, or the relatively constant environment in which they live. Other challenges include lack of known-age crabs for validation. Major questions about this technique still remain, however, and recent publications raise some doubts about whether age bands in gastric ossicles are true annuli. Nonetheless, the method shows great promise and may lead to improvements in management of crustacean populations.

Phylogenetic Relationships and Compartive Morphology Among the Spider Crabs Libinia Leach, 1815 (Majoidea: Epialtidae)

*Tamburus AF, Mantelatto FL**
University of Sao Paulo

The spider crab genus Libinia contains 10 valid species that occur only in the American continent in mud bottoms on variable depths. There are distinct phylogenetic hypothesis that include Libinia with different sister groups (Herbstia, Leucippa, Notolopas, Pisa, Rochinia, Taliepus), which belong to the superfamily Majoidea, but relationships of the genus are not solved. Two groups of species (Libinia ferreirae and L. spinosa in Brazilian coast / Libinia dubia, L. emarginata and L. erinacea in Gulf of Mexico) share similar habitat, depths and morphological similarities that made the identification difficult, especially of smaller specimens, justifying a comparative study of them. Thus, this study aims to investigate the relationship among the species of the genus and clarify the taxonomic position of those two groups. We analyzed the morphology through the comparison of adult and young specimens using new characters and others already used before. A phylogenetic tree was built from fragment of mitochondrial DNA sequences (16S and COI) by the maximum likelihood method. The taxonomic position of Brazilian and Gulf of Mexico species was solved with consistent characteristic that define them. The phylogenetic tree supported Libinia as a monophyletic clade positioned as a sister group of a clade composed by (Stratiolibinia + (Notolopas + Herbstia)), and the relationship with Notolopas and Herbstia support previous phylogenetic proposals made for the superfamily, while the addition of Stratiolibinia is a contribution of the present study Financial support: BIOTA-FAPESP – Proc. 2010/50188-8; Ciências do Mar II - Proc. 2005/2014 - 23038.004308/201414; CNPq – Proc. 142082/2015-5; 304968/2014-5

Exploring Crustacean Hox Gene Evolution Using Functional Genomics

Sun DA, Patel NH
UC Berkeley

The Hox/Homeotic family of genes helps determine the identity of segments and associated appendages along the anterior-posterior (AP) axis in diverse animal species. Changes to the timing and location of Hox gene expression can create remarkable changes in an animal's body plan. This project explores how the Hox genes have evolved across the diverse body plans of crustaceans. Our lab has previously investigated the function of Hox genes in the amphipod crustacean Parhyale hawaiensis. Using CRISPR-Cas9 mutagenesis targeting the Parhyale Hox genes, we identified homeotic transformations that reveal the role of each Hox gene in patterning the Parhyale body plan. Other previous work has suggested that changes in body plans between different groups of crustaceans are mediated by changes to Hox gene expression. For example, in decapod and isopod crustaceans, the Hox gene abd-A is expressed in a different set of segments than in Parhyale; this change in expression correlates with a change in the body plan. We used the Assay for Transposase Accessibility of Chromatin with next-generation sequencing (ATAC-Seq) to identify candidate cis-regulatory elements that may control Hox gene expression in the amphipod Parhyale hawaiensis. By examining the function of these elements in a particularly well-studied crustacean model system, we hope to develop a picture of how Hox genes are regulated in crustaceans, and to develop hypotheses about how this regulation can evolve to produce new crustacean body plans.

A New Species of Whale Louse (Crustacea: Amphipoda: Cyamidae) Found on Cuvier’s Beaked Whale Ziphius cavirostris

Tandberg AHS, Stokkan M
University of Bergen

Five specimens of Cyamidae were picked from the body of a recently deceased individual of Cuvier's beaked whale, Ziphius cavirostris Cuvier, 1823, which stranded in western Norway in early 2017. Autopsy of the whale revealed large quantities of waste plastic blocking its intestines and the observation triggered international media attention. We identified the cyamids to the genus Platycyamus Lütken, 1870 based on the gill-shape, the relatively similar sized gnathopods and separated peraeon segments. The new species differs particularly in characteristics of the legs from the North Atlantic Platycyamus thomsoni (Gosse, 1855), known to inhabit the bottlenose whale Hyperoodon ampullatus Forster, 1770, and from P. flaviscutatus Waller, 1989, known from Beardius bairdii Stejneger, 1883, in the Pacific. An about 1500 bp long sequence mitochondrial Cox 1, retrieved from three specimens showed no intraspecific variability. By comparing with other available data in GenBank we computed mean p-distances of 0.245 - 0.253 to sequences from Cyamus Latreille, 1796 and from Isocyamus Gervais & van Beneden, 1859, respectively. A Cox 1 gene tree using Caprellidae sequences as outgroup placed Platycyamus at the base of the Cyamidae, somewhat contrary to ideas about Cyamus being the most primitive of the group. A global haplotype network of Z. cavirostris based on CytB and 16S sequences placed the whale specimen as most closely related to individuals recorded around the Bahamas.

Morphological Variation of the Pennsylvanian Horseshoe Crab Euproops danae (Meek and Worthen, 1865) from the Lower Mercer Shale of Windber, Pennsylvania, USA

Tashman JN, Feldmann RM, Wells NA, Schweitzer CE
Kent State University

In the 1960s, Richard Raymond acquired 36 specimens of the Pennsylvanian horseshoe crab Euproops danae (Meek and Worthen, 1865) originally collected from an abandoned strip mine south of Windber, Pennsylvania, USA. Morphological features common in E. danae, including a transverse bar across the intercardiophthalmic area, were missing from many well-preserved specimens. Raymond suggested this was a sexually dimorphic character based on statistical analyses, and that individuals with a transverse bar were male due to their location corresponding to male grasping appendages in modern species. However, transverse bars are more apparent among small specimens than those that are larger. Ophthalmic spines were also present in larger specimens but naturally truncated in those that were small. Raymond began a manuscript describing E. danae from this locality, which would have been the first documented occurrence of the species from the Mercer Shale; however, the manuscript never made it to print. His unpublished interpretations were analyzed herein, and new interpretations have been made. Using discriminant function analysis and other statistical approaches, it was determined that this small population is comprised of juveniles or sub-adults across five instar stages. It is proposed that the absence of ophthalmic spines and presence of transverse bars is associated with small prosomal size and therefore, early ontogenetic stages, while transverse bars become less pronounced as ophthalmic spines become longer in larger, older specimens.

Decapod Crustacea from the Remote Oceanic Archipelago Trindade & Martin Vaz, South Atlantic Ocean

Tavares M
University of Sao Paulo

The oceanic islands Trindade and Martin Vaz (TMV) are the aerial parts (3–3.5 and 1–1.5 my, respectively) of a submarine volcanic chain, and thus much younger than the South American and African shores, which originated some 130–120 mya. TMV are 1200 km away from Brazil and 4200 km from Africa. Therefore, the benthic invertebrates of TMV appears to be mainly a result of dispersal of larvae, which may travel across wide distances and establish local populations. Determining patterns of species distribution and faunistic composition is central to the understanding of the relationships and connections between TMV, the WA and EA shelves and other South Atlantic oceanic islands, and their possible causes. Six campaigns conducted between 2012–2017 resulted in vast material of decapod crustaceans. Sampling consisted of 222 scuba diving down to 30 m and numerous snorkeling dives and intertidal collecting. Specimens were collected by flipping and breaking up clumps of coralline algae and coral rocks, from soft and mixed sediments and from marine invertebrates and algae, and from artificial reef substrates placed for 12-15 months between 10–20 m. Based on current taxonomic knowledge, the decapod fauna of TMV appears to be a mosaic of WA, EA, amphi-Atlantic, central Atlantic (insular), endemic and circumtropical species. The benthic decapods of TMV are chiefly derived from the tropical WA edges, despite the dominance of the westward flowing trans-Atlantic South Equatorial Current, which brings warm waters from west Africa and should therefore facilitate the migration of EA species westward.

Rhythms and Reproduction

Thiel M
Universidad Catolica del Norte

Reproductive rhythms are common in many crustacean species. In this chapter we review the temporal scales of rhythms and how these are entrained and maintained by external cues and endogenous clocks. The occurrence and synchrony of rhythms varies along latitudinal and depth gradients, which may depend on the availability of zeitgeber cues such as temperature and photoperiod, on changing selective pressures such as predation risk, and on changing variability of temperature and larval development rates that affect the predictability of synchronized reproductive rhythms. Commonly observed reproductive rhythms are spawning migrations and synchronized larval release, which are often timed to reduce predation risk for newly hatched larvae. In crustaceans, reproductive rhythms rarely evolve under pure density-dependent selection for synchrony. Pure density dependence is common in marine broadcast spawning invertebrates like corals, which rely on swamping predators through massive accumulation of offspring in time and space. Instead, (density-independent) selection for synchrony with environmental cycles that track changes in fitness-relevant factors such as energy expenditure, predation risk or food availability seems to be the rule, although some exceptions may exist. In contrast to natural selection, sexual selection has rarely been considered as a mediator of reproductive rhythms. Reproductive synchrony between the sexes should favor mating possibilities, but deviations from synchrony are supposed to affect the operational sex ratio and thereby will also influence sexual selection. Finally, we discuss the possibility of sexual conflict over reproductive timing between males and females and explore circumstances under which synchronous reproductive rhythms might be abandoned.

Citizen Science: Crustacean Research for Everybody

Thiel M
Universidad Catolica del Norte

Walter Koch is a dentist - and Hyalella kochi is a small amphipod that lives in permanent streams in the Atacama Desert. Walter found it there without suspecting that it was still unknown. He handed over his find to a crustacean researcher, who then gave Walter’s name to this little amphipod. How did that happen? Walter and the crustacean researcher (Exequiel Gonzalez) are friends and when Walter told Exequiel that he wanted to travel to the Atacama Desert, Exequiel gave him many jars to collect freshwater amphipods wherever he could. Among these finds was also the then nameless H. kochi. Since then this species has become one of the most cited crustaceans from South America (13,000 Google entries). There are many examples of this kind. Citizen participation in science is currently experiencing a new spring and this development is also being addressed by research on crustaceans. The fascinating range of research projects on crustaceans, in which citizens actively participate, is briefly presented. These examples show the great potential of these projects. Citizens love to participate in natural science research projects on crustaceans. In particular, projects with a high level of observation effort (in terms of space and time) can benefit from the active participation of citizens. Communicating and working together with citizens also poses challenges for scientists. Carefully planned and carried out, the long-term social benefits of these collaborations can be far greater than those of many high-impact publications. And last but not least: it's all great fun!

Phylogenetic Revision of the Semi-Terrestrial Crab Species, Genus Gecarcinus Leach, 1814 (Brachyura: Grapsoidea: Gecarcinidae) from Mexico

Toledano Carrasco IA, Villalobos Hiriart JL
Institute of Biology of Universidad Nacional Autónoma De México

The geographical isolation caused by the emersion of the Isthmus of Panama has favored the speciation process of many species. Within the populations that were separated are those of the genus Gecarcinus Leach, 1814: G. lateralis (Freminville, 1835), G. nobilii Perger and Wall, 2014, G. quadratusDeSaussure, 1853 and G. ruricola (Linnaeus, 1758). Taxonomically, several authors have tried to differentiate these species, using morphologic characters that show a high intra-population variability, which has made its identification difficult, that is why some of them were considered synonymous. In this work, a molecular analysis was performed with G. lateralis and G. quadratus, comparing specimens from the Mexican coasts,Pacific and the Atlantic.Mitochondrial genes COI and 16S were used, to corroborate the presence of two different lineages that morphologically are very similar. The results showed the separation of two clades strongly supported, one for the population of the Gulf of Mexico and in another to the Pacific coast. Also, it was obtained a high interspecific genetic distance in comparison with the intraspecific one, confirming the existence of G. quadratus as a valid species and not as a synonym of G. lateralis.Regarding the morphological revision, there are populations that present high variability in different characters, including sexual appendages. No characters that can clearly differentiate these species have been found.

Reconstructing the Phylogeny of Mantis Shrimps (Stomatopoda): Are Rates of Molecular and Morphological Evolution Correlated?

Van Der Wal C, Ahyong ST, Ho SYW, Lo N
University of Sydney, Marine Invertebrates, Australian Museum

Mantis shrimps (Crustacea: Stomatopoda) are ecologically and economically significant crustaceans, acting as dominant predators in many coastal ecosystems and serving as an important fisheries resource. Phylogenetically they are important as they are thought to represent one of the earliest branching eumalacostracans, and in being a highly specialized rather than a highly diversified lineage. Despite these unique attributes and their charismatic nature, much remains unknown about stomatopod systematics, evolution and phylogeny. The aims of this project were to generate a robust phylogeny of Stomatopoda, understand their evolutionary history and compare the rates of morphological and molecular evolution within the group. We inferred a dated phylogeny of the group using mitochondrial genomes, nuclear ribosomal fragments and fossil calibrations. Additionally, using a matrix of morphological characters we will test for correlations between rates of morphological and molecular evolution. This is the first comparison of evolutionary rates across Stomatopoda, and our study presents the most comprehensive phylogeny of the group. Our results significantly expand our understanding of stomatopod evolution and, in combination with previous studies, provides a comprehensive picture of this remarkable and important group.

Clawed Lobster Genus Oncopareia and Its Convoluted Taxonomic History

Tshudy D, Hyžný M, Jagt J, Veselská MK
Edinboro University, Comenius University, Natuurhistorisch Museum Maastricht, Charles University

Oncopareia (Turonian–Paleocene) is a clawed lobster genus, representatives of which have short, quadrate pleonal pleura and a major claw with a bulb-like palm and very long, slender fingers bearing acicular dentition. The fossil record of Oncopareia consists of five species from shallow water deposits of northwestern and central Europe. Morphologically, this genus is similar to the extant, deep-dwelling genera, Thaumastocheles (Miocene–Recent), Thaumastochelopsis (Recent) and Dinochelus (Eocene–Recent) currently inhabiting aphotic depths mostly in the Indo-Pacific; eight Recent "thaumastocheliform" species are known. These extinct and modern lobsters are morphologically so similar to each other, and collectively so different from other lobsters, that there can be no doubt about their close evolutionary relationship. The taxonomic history of Oncopareia, erected in 1854 by Bosquet for a single late Maastrichtian species, O. bredai, is complex and convoluted, beginning with a type species that is an accidental composite of two lobsters that differ at the generic level – one resembling modern thaumastocheliforms and the other a mainstream-looking nephropid. Mertin (1941) redefined Oncopareia to include Thaumastocheles-like characteristics; most notably, the pleon and major claw with acicular dentition. He did this because some Thaumastocheles-like species had them, and some of these, in turn, had a spiny rostrum, a generic character for Oncopareia. Thus, on the basis of the shared possession of a spiny rostrum, the Thaumastocheles-like extinct species were allied with O. bredai. With this, Mertin asserted that Oncopareia is an ancient relative of Thaumastocheles, a view that has persisted to the present day. Importantly, Mertin never recognized that Bosquet's type series was an accidental composite. He transferred to Oncopareia also some other genera, namely Nymphaeops, Ischnodactylus and Stenocheles, and a few other species from other genera. His synonomies were too extensive; most cannot be referred to Oncopareia and are, instead, claws of other decapods showing convergence, whereas others are of uncertain affinity.

Assessing the Conservation Status and Genetic Diversity of the Giant Sydney Crayfish, Euastacus spinifer Using Molecular Approaches

Van Der Wal C, Ahyong ST, Ho SYW
University of Sydney, Marine Invertebrates, Australian Museum

Freshwater crayfish (Decapoda: Parastacidae) are experiencing significant human-mediated impacts, and are ranked among the five most endangered animal groups. Australia is home to approximately 140 species of crayfish, of which the genus Euastacus is one of the largest. Euastacus are of significant conservation concern owing to a number of key threats including climate change, habitat loss and illegal harvesting. Previous morphological studies have highlighted the difficulties associated with species delimitation in Euastacus. For example, it is unclear whether differences in colour and morphology reflect intraspecific or interspecific variation. In order to assess their biodiversity and conservation status within New South Wales we investigated the genetic diversity, population structure and phylogeny of Euastacus spinifer using mitochondrial and ddRAD nuclear SNP data. We hypothesise that the currently recognised distribution of E. spinifer is inaccurate, and predict that this species represents a species-complex with numerous populations in fragmented habitats. Our analyses of mitochondrial and nuclear data revealed strong clustering of individuals on the basis of their geography, with little evidence for gene flow between members of the 5 populations examined. Our results suggest that E. spinifer in its current form likely represents at least 4 distinct species. We are now examining morphological variation among members of the group to explore this possibility in more detail.

Distribution and Abundance of Nephropidae and Polychelidae of the Southern Gulf of Mexico (Tamaulipas to Yucatán)

Vázquez-Bader AR, Gracia A, Briones-Fourzán PD, Lozano-Alvarez E
Instituto de Ciencias Ddel Mar y Limnología

A systematic study along the Mexican continental slope (300-1200 m depth) of the Gulf of Mexico (Tamaulipas-Yucatán) was conducted on board the R/V JUSTO SIERRA of the Universidad Nacional Autónoma de México, to study crustacean biodiversity and potential fishery resources. The benthic fauna was sampled day and night using a semi-commercial shrimp trawling net with a 18 m mouth and 4.5 cm mesh. We collected a total of 900 individuals belonging to Families Nephropidae (Acanthacaris caeca, Neprhropsis aculeta, N. rosaea, and Thaumastocheles zaleucus), and Polychelidae (Cardus crucifer, Polycheles perarmatus, Polycheles typhlops, and Stereomastis sculpta). We analyzed the bathymetrical and geographical distribution of the species in the southern part of Gulf of Mexico, also we made ANOVA analysis to compare the density by species, sex, depth, and Gulf of Mexico sector. For the entire southern area, N. aculeata, presented the great abundance, following by N. rosea, whereas C. crucifer and T. zaleucus were the less abundant. Highest abundance for all species was observed in a narrow bathymetrical range (500-599 m). N. aculeata size increases with depth, whereas N. rosea showed the opposite.

Biodiversity of Decapod Crustaceans in the Continental Slope of the Southern of Gulf of Mexico

Vázquez-Bader AR, Gracia A
Instituto de Ciencias Ddel Mar y Limnología

A systematic study along the Mexican continental slope (300-1200 m depth) of the Gulf of Mexico (Tamaulipas-Yucatán) was conducted on board the R/V JUSTO SIERRA of the Universidad Nacional Autónoma de México, to study crustacean biodiversity and potential fishery resources. The benthic fauna was sampled day and night using a semi-commercial shrimp trawling net with a 18 m mouth and 4.5 cm mesh. One hundred and thirty-four species belonging to 38 families of deep water decapod crustaceans were collected throughout of 11 oceanographic cruises in a depth range of 300 -1,200 m. The families Munidopsidae, Muninidae, Nephropidae and Pandalidae were the most speciose. We also found, that the NE and SE were the Gulf sectors with more species, while few species were registered in Caribbean Sea and South Atlantic. We found two new species, and also several species were extended in its bathymetrical and geographical range.

Marching to a Different Drummer –the Female Reproductive System of Dorippid Crabs

Vehof J, Scholtz G, Becker C
Humboldt-Universität Zu Berlin, Queen's University

Two fundamentally different types of sperm storage organs are present within brachyuran crabs. The early diverging lineages (formerly "Podotremata") possess sternal spermathecae which are separated from the coxal gonopores, and therefore, fertilisation is external. In contrast, seminal receptacles of Eubrachyura have direct connections with the ovaries and the first contact of oocytes and spermatozoa occurs internally. This pattern has been interpreted as an apomorphy of Eubrachyura. Species within the family Dorippidae depict an enormous morphological varitey of female reproductive systems different from other eubrachyurans. Here, Paradorippe granulata which shows one of the most peculiar female reproductive systems is used to highlight conceptual shortcomings about evolution of sperm storage. Histological investigations revealed that the female reproductive system of P. granulata consists of paired ovaries and four cuticle-lined bursae, two on each side of the oviducts. Oviducts and bursae have no internal connection and open into the vulva via separated pores and the first contact of spermatozoa and oocytes seems to occur externally in the vulva opening. Thus, the reproductive systems of dorippids challenge several common concepts on eubrachyuran seminal receptacles and give rise to several questions: (i) Is the reproductive system of P. granulata the result of increasing reduction of originally well developed seminal receptacles or (ii) is a twin sperm storage system with external fertilisation the plesiomorphic form of the dorippid reproductive system? (iii) Is the characteristic eubrachyuran seminal receptacle with an internal connection to the oviduct may not an apomorphy of the Eubrachyura?

Spatial Distribution of Hermit Crabs Associated with Deep-Water Shrimp Fishing in the Pacific Coast of Costa Rica, Central America

Villalobos-Rojas F, Wehrtmann IS, Azofeifa-Solano JC, Romero-Chaves R*
Universidad De Costa Rica

One of the greatest threats for deep-water ecosystems are fisheries with non-selective fishing gear such as bottom trawling, which cause serious ecological impacts on the associated fauna. The number of studies on bycatch of deep-water fisheries has increased significantly in the last decades, indicating an increase in discard rates in recent years. In Costa Rica, deep-water fisheries (> 100 m) focused on Heterocarpus vicarius ("camello"; Pandalidae) and Solenocera agassizii ("fidel"; Solenoceridae), which present discard rates of up to 80%. Nineteen species of hermit crabs have been reported in waters deeper than 50 m, and in 2007 two species were reported from shrimp trawls carried out in the Costa Rican Pacific (Paguristes bakeri and Petrochirus californiensis). The taxonomy of this group is under constant review and a large number of new species have been described for the Eastern Tropical Pacific. The present work enlists the hermit crab species present in samples from a deep-water shrimp fishery monitoring program during the period 2010-2012, as well as the geographical and bathymetric distribution of these hermit crabs along the Costa Rican Pacific. The number of hermit crabs present in deep-water shrimp fisheries is extended to six species: Paguristes cf. holmesi, Areopaguristes praedator, Tomopagurus mericulatus, Dardanus stimpsoni, Dardanus nudus and Xylopagurus cancellarius. Paguristes cf. holmesi was the most abundant species (n = 65), while Dardanus stimpsoni (n = 10) is a new record for the collection of the Museum of Zoology of the University of Costa Rica.

Ghost Crabbing: a Stressful Touristic Activity For Ocypode quadrata

*Vogt EL, Lima MV, Model JFA, Souza SK, Rocha DS, Fabres RB, Vinagre AS**
Federal University of Rio Grande Do Sul

The ghost crab, Ocypode quadrata, found in sandy beaches along the western Atlantic coast, is considered a bioindicator of human impact on sandy beaches. In some beaches, ghost crabbing is considered a familiar nocturnal touristic activity, therefore the aim of this study was to identify the effects of a handling stress protocol on metabolic and physiological parameters. The crabs (n=66), were collected at Quintão (-30.39, -50.29, Brazil) and kept in terrariums (natural photoperiod, 25±2°C, food every other day) for 14 days. After, the crabs were submitted to a handling stress protocol (5 minutes) and recovery (0, 30 or 60 minutes). After each time, haemolymph and tissues samples were collected. Data homogeneity was analyzed with Levene test, and afterwards, the data were submitted to Student´s t, 2 way ANOVA or Kruskal-Wallis tests. Stressed crabs immediately increased hemolymph lactate, returning to basal levels after 60-min recovery. Hemolymph glucose levels increased after 30 and 60-min recovery. Triglycerides levels in the hemolymph decreased after 30 min. The levels of glycogen increased in the muscle after 30 min. CHH and HSP70 expression were not altered. A glucose-sparing effect is suggested as the sum of muscular glyconeogenesis and the use of hemolymph triglycerides. New investigations as to the fate of lactate formed during intense muscle work with longer recovery times are required, as well as gene expression under these new conditions. This work may contribute to the development of new strategies to raise the awareness of the antropogenic activities at the beaches.

Effects of Organotins On Crustaceans: Update and Perspectives

*Vogt EL, Model JFA, Vinagre AS**
Federal University of Rio Grande Do Sul

Organotins (OTs) are considered some of the most toxic chemicals introduced into aquatic environments by anthropogenic activities. They are widely used for agricultural and industrial purposes and as antifouling additives on boat hull's paints. Even though the use of OTs was banned in 2008, elevated levels of OTs can still be detected in aquatic environments. OTs' deleterious effects upon wildlife and experimental animals are well documented and include endocrine disruption, immunotoxicity, neurotoxicity, genotoxicity and metabolic dysfunction. Crustaceans are key members of zooplankton and benthonic communities and have vital roles in food chains, so the endocrine disrupting effects of TBT (Tributyltin) on crustaceans can affect other organisms. Crustaceans are also important fisheries worldwide and its consumption can pose risks to human health. This work aimed to update information about the effects of OTs on the metabolism, growth and reproduction of crustaceans, compare with known effects in mammals, and point aspects that still needs to be addressed in future studies. TBT can disrupt carbohydrate and lipid homeostasis of crustaceans by interacting with Retinoid X Receptor (RXR) and Crustacean Hyperglycaemic Hormone (CHH) signaling. Moreover, it can also interact with other nuclear receptors, disrupting MF (Metyl Farnesoate) and ecdysteroid signaling, thereby altering growth and sexual maturity, respectively. This compound also interferes in Cytochrome P450 system disrupting steroid synthesis and therefore, reproduction. However, some questions remain unanswered. Since both macro and microcrustaceans are good models to study the effects of sub lethal TBT contamination, novel studies should be developed using multibiomarkers and omics technology.

Influence of Particle Size on Shrimp Nutrient Digestibility and Particle Movement Through the Digestive System

Wade NM, Bourne N, Simon CJ
Queensland Biosciences Precinct

A range of inert digestibility markers, such as yttrium (Y) and ytterbium (Yb) oxides, are used to indirectly calculate the digestibility of nutrients in aquafeeds. Gross over-estimations of nutrient digestibility can be encountered if several assumptions are not met, including that nutrients move through the digestive system at the same rate as the markers. The present study assessed the effect of particle size on apparent nutrient digestibility or relative particle absorption, and traced the movement of several inert metal markers (Y, Yb and gold) of various sizes (>3 µm, 400 nm, 100 nm, 50 nm and 5 nm) through the shrimp digestive tract (1, 2, 3, 5, 10 and 18 hours) after a set ration. This work showed that particle size significantly effected nutrient digestibility, and that 50 nm and 5 nm gold particles had relative particle absorption coefficients of 37.3 ± 2.7% and 48.9 ± 1.8%, respectively. Gold particles were detected in the hepatopancreas of animals fed 5 nm gold for more than 18 hours, despite that the shrimp evacuation rate was calculated at 22.1% h-1. Large Y and Yb particles (>3 µm) found within the animal 1-hour after feeding showed that true feed intake was lower than measured feed intake by 15-25%, and provided an estimate of manipulative losses. Overall, this study showed that the shrimp filter press was highly efficient at excluding small indigestible particles, to below 400 nm, and that extremely high rates of nutrient digestion were maintained despite rapid movement through the digestive system.

De Novo Assembly, Characterization, Functional Annotation and Expression Patterns of the Black Tiger Shrimp (Penaeus monodon) Transcriptome

Wade NM, Huerlimann R, Gordon L, Montenegro JD, Goodall J, McWilliam S, Siemering K, Giardina E, Donovan D, Sellars M, Cowley JA, Condon K, Coman GJ, Khatkar M, Raadsma H, Maes G, Zenger KR, Jerry DR
ARC Research Hub for Advanced Prawn Breeding, a collaborative partnership between James Cook University, CSIRO, University of Sydney, Australian Genome Research Facility, Seafarms Group Pty Ltd, Australia

The black tiger shrimp (Penaeus monodon) remains the second most widely cultured shrimp species globally. However, issues with disease and domestication have seen production levels stagnate over the past two decades. To help identify innovative solutions to resolve bottlenecks hampering the culture of this species, we produced the most complete publicly available P. monodon transcriptome database to date. The assembly was carried out in multiple assemblers using 2x125 bp HiSeq data from PolyA selected, ribo-depleted RNA from nine adult tissues and eight early life-history stages. In total, approximately 700 million high-quality sequence reads were assembled into 99,203 adult tissue and 58,678 early life-history stage clusters. The final transcriptome had a high TransRate score of 0.37, with 88% of all reads successfully mapping back to the transcriptome. BUSCO statistics showed the assembly to be highly complete with low fragmentation, few genes missing but higher duplication (C: 98.2%, F: 0.8%, M: 1.0%, D: 51.3%), which greatly exceed the completeness of existing P. monodon transcriptomes. While annotation rates were low (20-25%), as is typical for a non-model organisms, annotated transcript clusters were successfully mapped to several hundred functional KEGG pathways. To help address the lack of annotation, transcripts were clustered into groups within tissues and early life-history stages, providing initial evidence for their roles in specific tissue functions or developmental transitions. We expect this high-quality de novo assembled transcriptome to provide an essential publicly available resource to investigate the molecular basis of commercially relevant-significant traits in P. monodon and other shrimp species.

Approaching the True Diversity of Mantis Shrimps Beyond Taxonomy: Morphological Heterogeneity of Larval Forms

Wagner P, Braig F
Ludwig-Maximilians-University Munich

Mantis shrimps (Stomatopoda) are marine predators with four pairs of raptorial appendages; the most prominent first pair arises from the 7th post-ocular segment. Mantis shrimps form an ingroup of Malacostraca with about 500 extant species. They occupy a broad range of marine habitats, from shore to 1500 m depth. Their ontogeny features several free-living larval stages, occupying pelagic habitats in contrast to the benthic adults. Most of these larvae already show the prominent raptorial appendages, however slightly differing in shape compared to those of adult stomatopods. Among adults two principal methods of capturing prey are generally differentiated: "Smashers" possess a proximally bulged outer margin on their most distal appendage element (dactylus), which they use for a powerful punch-like movement towards the prey. In contrast, "spearers" stab the prey with their dactylus, which in most cases bears spines along the inner edge. In contrast to this, most larvae exhibit a spineless, more dagger- or scythe-shaped dactylus. To quantify this morphological diversity, a morphospace approach was applied. A morphospace is a multi-dimensional graphical representation of the variability of an organism or a specific structure of that organism. This allows a comparison of morphological diversity of structures not only between different adult forms, but also between different ontogenetic stages. In addition to the dactylus, we also investigated the morphological diversity of other structures of stomatopods for which significant morphological differences have been observed. Our results indicate an unexpectedly large morphological diversity of larval forms, a possible indicator for a large impact of larvae for their ecosystem.

Morphology of the Cumacean Male: the Importance of Being Sleek, Or Not

Watling L, Gerken S, Boudrias M
University of Hawaii At Manoa, University of Alaska, Anchorage, University of San Diego

Cumaceans are peracarid crustaceans that undergo a terminal male molt. As juveniles and early subadults, males and females are nearly identical in their general morphology. As the male develops, the antenna and pleopods begin to change shape, but the carapace morphology remains similar to that of the female. For most males, the molt to the mature form results in an overall change in the body to one that is more hydrodynamically smooth, with strong swimming setae on the pleopods and thoracic exopods. These changes may be so dramatic, especially in the features of the carapace, that it can be difficult to align a mature male with the immature males and females of the same species. In a few families, however, the male has forsaken the swimming mode and modified its antennae and other appendages to be able to grasp the female. In this case the male is usually smaller than the female. We examine the mature male characters with a view to understanding those that change in concert in both the swimming and grasping males. We hypothesize that the swimming male is the primitive condition and that various pressures have driven the evolution from swimming form to the grasping form.

New Insights Into the Proboscis of Pantopoda: a Comparative Approach Based on Morphology

Wagner P, Doemel J, Hofmann M, Huebner J, Leese F, Melzer RR
Ludwig-Maximilians-University Munich, University Duisburg-Essen, Bavarian State Collection of Zoology

The primary organ for food uptake in pantopods is their prominent proboscis. The shape of the proboscis is very variable: thin and elongated forms (e.g., in Austrodecus glaciale) occur as well as short and stout forms (e.g., in Pigrogromitus timsanus). The highly differentiated inner structures comprise a filter apparatus and an armature made of denticles. We used a comparative approach, including representatives of all major pantopod lineages, to analyse the inner surface of the proboscis with its different structures. In this study we bisected the proboscides of Achelia langi (Ammotheidae), Anopodactylus californicus (Phoxichilidiidae), Ascorhynchus castellioides (Ascorhynchidae), Austrodecus glaciale (Austrodecidae), Callipallene margarita (Callipallenidae), Colossendeis macerrima (Colossendeidae), Endeis spinosa (Endeidae), Nymphon macronyx (Nymphonidae), Pallenopsis patagonica (Pallenopsidae), Pantopipetta sp. (Austrodecidae), Pigrogromitus timsanus (Ascorhynchoidea incertae sedis) and Pycnogonum litorale (Pycnogonidae). These were subsequently analysed with Scanning EM, µCT and fluorescence microscopy. Results were used to establish sets of "inner trunk" characters that vary between species. These traits included length and width of proboscis, shape of the mouth opening, borders and armature of the three antimeres forming the proboscis, shape and position of denticles arrays, length of filter apparatus, and structure of the filter bristles. Analyses of these characters indicate a high variability of structures on the inner surface of the pycnogonid proboscis, probably related to different modes of food uptake.

Freshwater Decapod Research in Central America: Past – Present – Future

Wehrtmann IS
Universidad de Costa Rica

Studies on the freshwater decapod fauna of Central America started in the late 1800 by scientists based outside of the region. Mary Jane Rathbun was the first author to describe species of freshwater crabs from Central America. Later on, Otto Pesta published the results of an Austrian expedition to Costa Rica, including freshwater decapods. The second period of freshwater decapod research started with the description of Archaeatya chacei from Isla del Coco by Alejandro Villalobos F.. Subsequent important contributions were published by Alfred Smalley, Richard Bott, Horton Hobbs III, and Gilberto Rodríguez. Carlos Villalobos was the first carcinologist from Central America to publish on freshwater decapods in the 1970s. During the last two decades, different authors continued publishing on taxonomic aspects of freshwater decapods: Célio Magalhães and co-workers described a new freshwater crab species from Costa Rica and provided recently a review of the freshwater crabs from Costa Rica with a revision of the genus Ptychophallus. Recent studies included also ecological and molecular aspects, mainly related to Macrobrachium species from Costa Rica. Another current focus has been the study of parasites in pseudothelphusid crabs. Future studies should investigate the impact of the large diversity of anthropogenic activities on (migratory) freshwater decapods. Also, freshwater decapods are widely used as a fishery resource in the region, and information for adequate management measures is urgently needed. Finally, basic information about most freshwater decapod species is still missing.

Deep Discoverer Gives a New View of Deep Decapods

Wicksten MK
Texas A&M University

The NOAA research ship Okeanos Explorer conducts exploration of deep hard ecosystems in U.S. waters and western Atlantic-Caribbean areas with emphasis on geology and deep coral communities. The ship deploys a large remotely operated vehicle, the Deep Discoverer (DD2), which can operate to depths as much as 4000 m. It is capable of viewing animals as small as gammarid amphipods with scale and producing high definition video and still views. Live commentary and footage can be beamed by satellite to distant observers who can comment by telephone or a chat room. Every photo file is available with data on depth and exact location. The DD2 cannot collect fragile, small or agile species, but the photos are of great value. Among the many recent findings are the first in-situ views of feeding in an intact Bathystylodactylus, consistent associations of certain species of Chirostylidae with gorgonians or antipatharians, associations of shrimps (Lebbeus) with hexactinellid sponges while Bathypalaemonella tend to associate with a variety of octocorals, blind lobsters (Acanthocaris) seem to be ambush predators, anemone-carrying hermit crabs (Parapagurus) move by "pacing", and parasitic rhizocephalans occur on carideans at 1642 m.

Crayfish Symbiont Reponse to Invasion in the Northwestern United States

Williams BW, Weaver PG, Woodson A, Lukas L, Egly R, Larson ER
North Carolina Museum of Natural Sciences, Meredith College, University of Illinois at Urbana-Champaign

Astacoidean crayfishes are known hosts for two groups of obligate ectosymbionts, branchiobdellidan worms and entocytherid ostracods. Recent surveys of crayfishes in the northwestern United States suggest that the decline of the Pilose Crayfish, Pacifastacus gambelii, native to areas of Wyoming, Idaho, and Utah, is in large part coincident with introduction and spread of the Northern Crayfish, Faxonius virilis, native to much of the Interior Plains and Great Lakes regions. In this study, we examine specimens of both species of crayfish within the historic native range of P. gambelii to gain insight into host-symbiont response to invasion. We hypothesize three possible scenarios: full community replacement, where F. virilis and its symbionts completely replace P. gambelii and its symbionts; partial replacement, where F. virilis does not carry its symbionts with it, replaces P. gambelii and picks up the native's symbionts, or; host replacement with symbiont extirpation, where F. virilis does not carry its symbionts with it, and replaces P. gambelii with no symbiont transfer. Preliminary results show the latter scenario at the majority of sites where crayfishes were recovered; however, we did observe full or partial community replacement at several sites, including at a single locality where we found F. virilis and P. gambelii codistributed. Our results provide important insight into development and maintenance of short- and long-term host-symbiont associations, and ultimately host and symbiont conservation.

Cryptic Diversity of Endoparasitic Isopods Associated with Brachyuran Hosts Along the East Coast of the United States

Williams JD, McDermott JJ, Boyko CB, Blakeslee AMH, Tepolt CK
Hofstra University, Franklin and Marshall College, American Museum of Natural History, East Carolina University, Woods Hole Oceanographic Institution

Entoniscid isopods are endoparasitic in a variety of anomuran and brachyuran decapods and caridean shrimp. However, due to their enigmatic nature, many undescribed species of entoniscids remain to be discovered, even along the east coast of the United States where such hosts have been relatively well-studied. Work in our labs has revealed a new entoniscid species from the pea crab Pinnixa chaeopterana, a polychaete symbiont, collected in New Jersey, North Carolina and Florida. This represents only the third entoniscid species described from a pinnotherid host. Prevalence of the parasite in hosts from North Carolina ranged from 22 to 42%. Mature females occupied nearly all available space within the crab's hemocoel and larvae were liberated via a pore in the wall of the host's branchial chamber. In contrast to some other entoniscid species, mature females of the new species did not inhibit breeding or molting in the host. In addition to the pinnixid parasite, we document the first record of an entoniscid from the mud crab Rhithropanopeus harrisii collected from New Hampshire to Florida. Based on light and scanning electron microscope investigations, this entoniscid is morphologically indistinguishable from Cancrion carolinus, a parasite of the mud crab Panopeus herbstii. However, molecular evidence from these samples indicates the presence of two distinct clades along the Atlantic coast. The parasite was found to reach up to 40% prevalence in some localities; however, its impacts on hosts are poorly known. Details on the natural history and morphology of these entoniscids will be presented.

Conservation Challenges for a Species Flock of Eophreatoicus (Isopoda; Phreatoicidea) in Australia's Northern Territory

Wilson GDF, Humphrey CL
Saugatuck Natural History Laboratory, Environmental Research Institute of the Supervising Scientist

Conservation of a species flock in the genus Eophreatoicus Nicholls, 1926 presents problems that may be typical for extreme narrow range endemic freshwater crustaceans. Species of Eophreatoicus and a related new genus, identified using morphology and genetic corroboration, are found in springs and emerging streams at the base of sandstone plateaus and outliers in Kakadu and Arnhem Land (Northern Territory, Australia). Geographically small (less than 1 km in length) sites may include up to 3 distinct species with separation from different species sites of only a few kilometers in some cases. Because of their extreme narrow range endemism, these isopods are highly vulnerable to localized aquifer loss caused by mining, agriculture or direct modification of the habitat. We analyze the cost of species loss using Phylogenetic Diversity (PD), which is derived from a summation of branch-wise distance between phylogenetic tree nodes, using both genetic and morphological data. Although the cost of single species losses are largely identical, loss of multispecies sites or loss of uniquely divergent taxa would accrue a larger PD cost. Whether or not losses of these species, which currently do not have any obvious threats or commercial uses, are acceptable depends on a consideration of societal values.

Taxonomic Status and Identity of the Commercially Important Portunid Crab, Monomia haanii (Stimpson, 1858) and Resolution of the Portunus gladiator Species Complex

Windsor AM, Mendoza JCE, Warner KA, Choudhuri A, Deeds JR
US Food Drug Administration, National University of Singapore, OCEANA, Newport International

Species substitution of brachyuran crabs in food products is an ongoing issue in the US resulting in the addition of blue and king crabs to the list of at-risk species by the Presidential Task Force on Illegal Unreported and Unregulated Fishing and Seafood Fraud in 2015. Recent DNA testing of retail Callinectes sapidus Rathbun, 1896 crabmeat "locally sourced" from Maryland and Virginia revealed DNA barcode matches to the western Pacific species Portunus (Monomia) pseudoargentatus Stephenson, 1961. This species is not generally regarded as commercially important, but is closely related to, or possibly synonymous with, Portunus haanii (Stimpson, 1858), a highly exploited species imported to the US as "Portunus haanii" or "red swimming crab." However, P. haanii has been synonymized under Portunus (Monomia) gladiator Fabricius, 1798, and is therefore not an appropriate name for commercial crabmeat. Analysis of additional DNA barcode sequences from cans of crabmeat labeled as "Portunus haanii" were also identified as P. pseudoargentatus. These three species comprise the Portunus gladiator complex, which we investigated with the aim to resolve the taxonomic status of each putative species and to confirm the identity of crabmeat imported into the United States as "Portunus haanii". We undertook a two-pronged approach utilizing independent morphological and molecular phylogenetic analyses to resolve the taxonomic status of the species in the P. gladiator complex. Pairwise comparisons of DNA barcodes generated from the taxonomic study to commercial products sold in the US as "Portunus haanii" were then used to identify the species present in those products.

Ultrastructure of Spermatozoa of Aegla Sp. (Crustacea, Decapoda, Aeglidae): Description of Morphological Patterns, Comparison of the Potential Cryptic Taxon Aegla castro Schmitt, 1942 and Information for Conservation

Wolf MR, Zara FZ, Tudge CC, Bueno SLS, Castilho AL
Universidade Estadual Paulista, American University, Universidade de São Paulo

The diversity of the endemic South American genus Aegla has been increased since the current taxonomy revisions and the advance of genetic analysis. The existence of hidden diversity, reflected as a cryptic species complex with a wide geographic distribution, is investigated here for A. castro. The ultrastructure of spermatozoa is described for three supposed “A. castro” species, for one potential new species of Aegla and for two external taxa, A. parana and A. quilombola. Two general spermatozoal formats are identified: the spherical and the irregular cell shape with the two hemispheres (cytoplasm and nucleus) separated by a membrane. We did not find a distinctly different spermatozoal morphology for each species; however, we can determine at least three patterns of spermatozoal morphology 1) spherical cell with short acrosome 2) irregular cell with long and lobulated acrosome and 3) irregular cell with short acrosome. These results show that different species can share a similar pattern of spermatozoa morphology. Our results also support the exclusion of Aeglidae from the superfamily Galatheoidea and agree with the previous information of no evidence of distinct spermatophores in this group. Remarkably we observe scant spermatozoal production in all the species studied here and this matches information from literature, which leads us to think what the implications for future population recovery are. These species are very sensitive to environmental changes and currently at least 31 species are threatened. Key words: threatened, freshwater, conservation, sperm transfer.

Morphological Comparison Between Aegla Castro Schmitt, 1942 (Decapoda, Anomura, Aeglidae) Populations as an Important Source of Information for Conservation Status

Wolf MR, Bueno SLS, Moraes JCB, Tudge CC, Teixeira GM, Castilho AL
Universidade Estadual Paulista, Universidade de São Paulo, American University, Universidade Estadual de Londrina

The Aegla species are very similar in relation to their morphological characters and species identification always has been problematic. Indeed, it has been observed that a complex of cryptic species often reveals hidden diversity in this taxon. This has serious implications for the true geographic distribution of the species and consequently their validation as vulnerable, endangered or extinct species. The family Aeglidae currently represents the most threatened freshwater taxon in South America. For this reason, the goal of this research was to investigate Aegla castro and verify if they are in fact a complex of cryptic species or not. With a wide geographic distribution, this species were collected using traps or manual collection from three regions that they were identified previously as A. castro (including the holotype): Ponta Grossa, Castro and Mauá da Serra (Paraná state) and Itatinga (São Paulo state) and in three new regions in Tibagi (Paraná state). Two characters are very conservative on the holotypes and paratypes: the subrostral process with proximal half well developed, high, broad, triangular, and oriented downward and the third thoracic sternite that is tapered. Comparing these characteristics with the other species, only Aegla sp. from Castro shared the same pattern indicating that there are more than one species identified as A. castro or that they vary in relation to this character. Key words: cryptic species, taxonomy, endangered and threatened species, freshwater.

What Defines Crustaceans? Insights from the Cambrian Fossil Record and from Phylogenomics

Wolfe JM
Massachusetts Institute of Technology

The inclusion of insects within a newly defined Pancrustacea has challenged traditional morphological synapomorphies for crustaceans. Exceptionally preserved fossils from the Cambrian (542-485 million years ago), the time when major pancrustacean lineages are inferred to have diverged, complicate the situation. Previously proposed ladder-like patterns of character evolution leading up the putative stem-lineage make inadequate assumptions about the developmental expression of morphology in fossils. Trunk tagmosis, among other characters, may be quite evolutionarily labile. Micro-CT study of new bivalved arthropod material from the Chengjiang biota reveals the putative pancrustacean stem-group bears previously believed crown-group synapomorphies, such as tritocerebral (second) antennae and epipodites on the basipodal or coxal trunk limb segment. A complex evolutionary history, with substantial character loss in the crown-group of early diverging lineages (e.g. the less-studied Oligostraca), is proposed in the context of recent phylogenomic hypotheses.

The Remarkable Remipedia

Yager J

National Museum of Natural History, Smithsonian

This presentation will be a very general look at the exciting history of the crustacean class Remipedia, from discovering them in a water-filled cave in the Bahamas in 1979 to today. Because the session is in honor of the life work of Horton Hobbs lll, ardent caver and friend, I will begin with an introduction to the beautiful remipede cave habitat. We will explore where these fascinating animals live and what other cave crustaceans inhabit their community. I will recap remipede research since publishing their description in the first volume of the Journal of Crustacean Biology in 1981 through 37 years of research. Several interesting rem

Revisiting the Phylogeny and Classification of Penaeus Sensu Lato (Decapoda, Dendrobranchiata, Penaeidae)

Yang CH, Ma KY, Chu KH, Chan TY

National Taiwan Ocean University, the Chinese University of Hong Kong

Penaeus sensu lato Fabricius, 1798 consists of 33 species and is the most commercially important group in the family Penaeidae Rafinesque, 1815. Recently this genus was divided into six genera based on morphological characters. However, many molecular phylogenetic analyses suggested that some of these recently established genera may not be monophyletic. Therefore, Penaeus sensu lato (i.e. in a broad sense) is used to refer to these shrimps for avoiding the arguments of the validity of these recently established genera. The present study attempts to add more molecular markers, including 3 genes of mitochondrial DNA (COI, 16S rRNA and 12S rRNA) and 5 genes of nuclear DNA (28S rRNA, histone 3, NaK, PEPCK and AK), as well as increase the taxonomic coverage to 28 species in order to have an interpretation on the phylogenetic relationships among these shrimps for revising their higher classification. Furthermore, Ancestral State Reconstruction (ASR) analysis will be performed to elucidate the character evolution in Penaeus sensu lato.

Population Genetic Structure and Connectivity of Squat Lobsters in Vulnerable Marine Ecosystems

Yan RJ, Schnabel KE, Rowden AA, Guo XZ, Gardner JPA

Victoria University of Wellington, National Institute of Water & Atmospheric Research, New Zealand

Vulnerable marine ecosystems (VMEs) are at significant risk from fishing activity and other kinds of disturbance because VME species are usually long lived, late to reproduce, delicate and vulnerable to damage, and slow to recover, if they recover at all. VME species and associated species or taxonomic groups can act as indicators of the presence of VMEs for specific ocean regions, even if the VME itself is not identifed. Squat lobsters, Munida isos, Munida endeavourae and Munida gracilis, are widely distributed across the New Zealand Exclusive Economic Zone (EEZ) and south Australian EEZ region. M. isos and M. endeavourae are primarily associated with seamounts, while M. gracilis is found on both seamount and non-seamount habitats. A genomic library was obtained based on an Illumina paired-end shotgun sequencing platform to develop microsatellite loci for M. isos. Cross-amplification was attempted for the two other species. Novel polymorphic microsatellite markers and mitochondrial Cytochrome Oxidase I sequencing were employed to evaluate genetic variability and genetic connectivity of three Munida species sampled in the New Zealand EEZ and the Tasman Sea. High genetic diversity, weak genetic differentiation and moderate levels of gene flow were detected for all three species. Evaluation of connectivity within and among habitats for the three New Zealand Munida species will help provide information for the effective management of the deep-sea and its VMEs.

Investigating the Connectivity of the Florida Spiny Lobster Recruit Using Microsatellites

Yao N, Zhang Y

Florida International University

The Caribbean spiny lobster (Panulirus argus) provides many ecological and economic benefits to the Southeast US, and Caribbean countries. However, the limited knowledge on the recruitment dynamics of the Caribbean spiny lobster has long been an issue for biologists, as well as fishery scientists, in the study of this species. The long pelagic larval stage and the dynamic physical oceanographic processes in the Caribbean Sea have led many researchers to hypothesize that Caribbean lobster stocks are demographically open, implying the potential straying connectivity among stocks. Over the past two decades, genetic markers have been proven to be useful in investigating the connectivity among populations, including the P. argus stocks in the Caribbean region. However, most of the previous research ignored the temporal scale. In this project, we applied 12 microsatellite markers on the postlarvae arrived in the Florida Keys monthly from August 2014 to July 2016 to explore the dynamics of the recruit connectivity. The connectivity results derived from microsatellite analysis are also compared with those derived from stable isotope analysis and biophysical modeling. The results suggest that the genetic differentiation exists among the monthly samples and also varies temporally. Our study reveals the possibility that the Florida spiny lobster stock receives recruits from multiple source populations.

Transcriptome Analysis For Molting Process in Litopenaeus vannamei

Yi G, Fuhua L, Jianhai X
Chinese Academy of Sciences

Molting is one of the most important biological processes in shrimp growth and development. All shrimp undergo cyclic molting periodically to shed and replace their exoskeletons. This process is essential for growth, metamorphosis, and reproduction in shrimp. However, the molecular mechanisms underlying shrimp molting remain poorly understood. We investigated global expression changes in the transcriptomes of the Pacific white shrimp, Litopenaeus vannamei, the most commonly cultured shrimp species worldwide. The transcriptome of whole L. vannamei was investigated by RNA-sequencing (RNA-seq) throughout the molting cycle, including the inter-molt (C), pre-molt (D0, D1, D2, D3, D4), and post-molt (P1 and P2) stages, and 93,756 unigenes were identified. Among these genes, we identified 5,117 genes differentially expressed (log2ratio _1 and FDR _0.001) in adjacent molt stages. The results were compared against the National Center for Biotechnology Information (NCBI) non-redundant protein/nucleotide sequence database, Swiss- Prot, PFAM database, the Gene Ontology database, and the Kyoto Encyclopedia of Genes and Genomes database in order to annotate gene descriptions, associate them with gene ontology terms, and assign them to pathways. The expression patterns for genes involved in several molecular events critical for molting, such as hormone regulation, triggering events, implementation phases, skelemin, immune responses were characterized and considered as mechanisms underlying molting in L. vannamei. Comparisons with transcriptomic analyses in other arthropods were also performed. The characterization of major transcriptional changes in genes involved in the molting cycle provides candidates for future investigation of the molecular mechanisms.

Seasonal Catch, Size, Color, and Assessment of Trapping Variables for the European Green Crab Carcinus maenas (Linnaeus, 1758) (Brachyura: Portunoidea: Carcinidae), a Nonindigenous Species in Massachusetts, USA

Young AM, Elliott JA, Incatasciato JM, Taylor ML*
Salem State University, University of Maine

The population of the nonindigenous green crab Carcinus maenas (Linnaeus, 1758) in Salem Sound, Massachusetts, USA, was studied over a three-year period (July 2013 - June 2016) using baited traps deployed monthly at five sites. Seasonal catch per unit effort, sex, size, and color were determined and the role of temperature, salinity, water depth, and substrate, were evaluated. Seasonal CPUE was highest in the fall (October-December), followed by summer (July-September), spring (April-June) and winter (January-March). Crabs captured at sites with very fine sand were larger than those captured on other sediment types. Females comprised 73% of the total catch of 7,822 crabs. Green-phase crabs comprised 56.8% and red-phase crabs 43.2% of the catch. Green-phase crabs were significantly smaller (mean = 48.1 mm) than red-phase crabs (mean = 53.6 mm). Red-phase females were most common in the spring and green-phase in the fall, whereas red-phase males were most common in the spring and fall and green-phase in the summer. A yellow-phase category is proposed as a distinct intermediate between red and green phases. Merits of various types of traps and bait were evaluated based on different trapping requirements and goals. This is the first investigation of multiple aspects of a population of C. maenas in Massachusetts. The findings should prove useful for researchers studying other populations of C. maenas, as well as for commercial crab fishers or others trapping green crabs for bait, or in efforts to reduce population numbers of this destructive invasive species.

How to Walk and Settle On a Bed of Nails? Extreme Variation of Antennular Structure, Settlement, Process and Metamorphosis of Sponge-Inhabiting Barnacle

Yu MC, Liu JCW, Kolbasov GA, Chan BKK
Marine Biotechnology National Sun Yat-Sen University Academia Sinica, National Taiwan University, Moscow State University, Biodiversity Research Center

Sponges are important component in the coral reef ecosystem and host a large number of symbiotic organisms within the sponge tissue. Sponge-inhabiting barnacles are classified in the subfamilies Acastinae and Bryozobiinae, also two genera Membranobalanus and Conopea in the subfamily Archaeobalaninae. They are obligatory symbionts of poriferans, alcyonaceans and antipatharians. The key objective of the present study is to examine how do the sponge barnacle larvae settle on the sponge tissue and start their symbiotic life. Similar to the other free-living barnacle species, sponge barnacles also composed of naupliar and cyprids stages in the larval cycle. The cyprids stage is specialized to settle and a process to metamorphose to juvenile and adult stages. Barnacle cyprids use its paired antennules to explore and walk on substratum searching for settlement site. We used SEM to investigate the extreme morphological diversity in the attachment disc of sponge barnacle, which include shoe-shaped, hook-shaped and spear-shaped attachment discs. We are the first to use microscopy video recording how the sponge barnacles Euacasta dofleini and Membranobalanus brachialis explore and settle in their sponge host (Petrosia sp. and Sphaeciospongia sp.). They display two diverging settlement process patterns (epibiotic and embedding) and the settlement and metamorphosis process are comprised six distinct phases.

Why Be Androdioecious?: the Barnacle Case

Yusa Y, Dreyer N, Høeg JT
Nara Women's University, University of Copenhagen

Androdioecy (coexistence of males and hermaphrodites in a population) is unlikely to occur theoretically because males must have twice as high reproductive success as male-acting hermaphrodites to attain equal fitness if other things being equal. Androdioecy is in fact very rare in the animal kingdom, known only in 120 or so species. Yet, it is an important sexual system linking between hermaphroditism and dioecy (gonochorism). Barnacles are worth studying because about one third of known cases of androdioecy are included, as found by Darwin. Here we overview the theory, distribution within barnacles, and detailed empirical studies, addressing the question why androdioecy does occur in barnacles. The key findings are as follows. First, the theoretical assumptions that "other things being equal" or "equal fitness" may be violated in the case of barnacles with dwarf males. Second, the distribution of androdioecy in barnacles suggests that there is little phylogenetic constraint and the evolution of androdioecy from hermaphroditism is relatively easy by a shift in resource allocation of some individuals from growth and female function to male function. Third, studies in Scalpellum scalpellum show that shift in sex allocation of hermaphroditic individuals occurs and the proportion of males may vary according to population parameters such as group size, but these are not extreme enough to render the sexual system to dioecy or hermaphroditism. In conclusion, androdioecy in barnacles is a special case that escaped theoretical attention until recently, but such androdioecy may be found also in other hermaphroditic animals.

Ensemble Forecasting of the Global Potential Distribution of the Invasive Chinese Mitten Crab, Eriocheir sinensis

Zhang Z, Capinha C, Weterings R, Xi D, Lü HJ, Yu L
Tokyo University of Marine Science Technology, Universidade do Porto, Cat Drop Foundation, Universities of Shandong, Weifang University, Pearl River Fisheries Research Institute of Chinese Academy of Fishery Sciences

Invasive alien species have posed substantial threats to freshwater ecosystems and are always difficult and cost-intensive to eradicate once established. Therefore, it is of great importance to identify their potential distribution and take preventive actions. Species distribution modelling has been regarded as a powerful tool to identify areas that provide suitable environmental conditions for the establishment of invaders. In this study, we developed an ensemble species distribution model for the Chinese mitten crab (Eriocheir sinensis H. Milne-Edwards, 1853) by using 188 worldwide occurrence records and 11 environmental variables to predict its global potential distribution in freshwater habitats. The ensemble model showed high predictive performance and indicated that annual mean temperature was the most important environmental variable that limits the distribution of this invasive crustacean. The model successfully predicted the known distribution of this crab in its native range and invasive range and suggests that this pest has not fully realised its potential distributions in Europe and North America. Our model also predicted some additional suitable areas (Japan, part of South America, Australia, and New Zealand) where this crab has not yet been observed. We propose several management strategies to control this invasive crab. Eradication programmes should be performed in the known distribution in Europe and North America. Precautionary preventative management measures should be implemented in the unoccupied suitable areas. In addition, appropriate ballast water management strategies should be developed to prevent the further introduction of this pest via ballast water discharge.

Phylogeography of Aegla uruguayana (Anomura, Aeglidae) Reveals Cryptic Diversity

*Zimmermann BL, Buzatto I, Crivellaro MS, Bartholomei-Santos ML, Santos S**
Universidade Federal De Santa Maria

Phylogeographic studies have revealed the presence of cryptic species in a variety of taxa, especially when morphological diagnostic characters are few and exhibit little variation among related species. This is the case of the freshwater crabs of genus Aegla. In this context, A. uruguayana is a species with one of the broadest distribution among the genus, occurring in Brazil, Argentina and Uruguay. Besides that, populations of this species exhibit clinal variation in carapace shape, which can be amplified by the geographical isolation and the weak dispersal abilities of individuals. The aim of this study was to use phylogeographic methods to test the hypothesis that A. uruguayana encompasses a complex of cryptic species. Sixteen populations of A. uruguayana from Brazil were analyzed. Three molecular markers (one nuclear and two mitochondrial) were used for the construction of Bayesian phylogenies. According to our expectations, A. uruguayana represents an assemblage of cryptic species. Ten of the analyzed populations formed a well-supported clade together with previously sequenced specimens of A. uruguayana. However, individuals from five populations formed distinct clades, which did not cluster with any other previously described Aegla species. In addition, one population has some representatives that belong to A. uruguayana and others that correspond to a potential new species. Our results reinforce the fact that classical taxonomy does not provide clear-cut species resolution in Aegla. Thus, extensive molecular analysis is required to verify the actual number of species and to identify the potential cryptic diversity present in this threatened and peculiar genus.

Potential Competitive Impacts of the Invasive Chinese Mitten Crab On Native Japanese Mitten Crab

Zhang Z, Yokota MDS
Tokyo University of Marine Science Technology

The Chinese mitten crab Eriocheir sinensis is an invasive species outside native range and represents a substantial threat to recipient ecosystems. It has been recently discovered in Japan, but little is known about its possible impacts on native species, especially on its congener, the Japanese mitten crab Eriocheir japonica. In this study, we examined shelter competition between E. sinensis and E. japonica under laboratory conditions. Shelter competition trials were conducted in pairs of one male native and one male invasive crab in different size combinations. Our results suggested competition between two species was size-dependent: E. japonica successfully defended shelter when competing with size-matched or slightly larger E. sinensis; E. sinensis only evicted E. japonica from shelter when having a considerable size advantage. Fight duration between two species had an inverted-U shape relationship with relative size difference of carapace width, and reached maximum when two opponents had similar winning probability. Our results suggest that native E. japonica is competitively dominant over invasive E. sinensis, and E. sinensis is unlikely to exclude native E. japonica from its habitat by direct competition for shelter. Our results highlight the important role of biotic resistance in controlling invasion success and absence of strong native competitors may favour the establishment of E. sinensis in Europe and North America.

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