5th Global Invertebrate Genomics Alliance Conference 2023

October 31- November 3, 2023
Cartagena, Colombia

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Program at a glance

Time	Tuesday October 31st	Wednesday November 1st	Thursday November 2nd	Friday November 3rd
8:00-9:00		Registration		
9:00-9:30		Introduction	Plenary Speaker **JingChun Li**	Plenary Speaker **Vanessa Yepes-Narváez**
9:30-10:00		Plenary Speaker **Sarah Lemer**		
10:00-10:30		Coffee Break	Professional Practice	
10:30-11:00		Session 1: Population, Ecosystem and Biodiversity Genomics	Coffee Break	Coffee Break
11:00-11:30			Professional Practice (cont)	Business Meeting
11:30-12:00			Session 5: Comparative Genomics and Biodiversity	
12:00-12:30				
12:30-1:00		Lunch	Lunch	
1:00-1:30				
1:30-2:00		Session 2: Whole Genome Sequencing and Comparative Genomics I	Session 6: Metagenomics and Symbiosis II	
2:00-2:30			Session 7: Whole Genome Sequencing II	
2:30-3:00		Session 3: Metagenomics and Symbiosis I		
3:00-3:30		Coffee break	Coffee Break	
3:30-4:00			Session 7: (cont) Whole Genome Sequencing II	
4:00-4:30		Session 3: (cont) Metagenomics and Symbiosis I		
4:30-5:00			Workshops	
5:00-5:30		Poster Lightning Talks	Professional Development Panel	
5:30-6:00				Informal Banquet in Walled City
6:00-6:30		Poster Session		
6:30-7:00				
7:00-7:30	Reception and Registration			
7:30-8:00				
8:00:8:30				
8:30-9:00				

The conference was organized primarily by the GIGA V Organizing Committee (2023): Vanessa Gonzalez (GIGA Conference Director, Smithsonian Institution, USA), Jeffrey Robinson (Robinson Scientifics LLC, USA), Joe Lopez (NOVA Southeastern University, USA), Kate Castellano (Gloucester Marine Genomics Institute, USA), Adelaide Rhodes (USA), and Juan Sanchez (University of Andes, Bogota, Colombia), and the GIGA Governing Board.

7:00-9:00 PM	Reception and Registration Tuesday October 31st	Sunset Terrace

Reception will feature:

- **Halloween invertebrate themed costume party**
- **Raffle for scientific prizes**

and

https://www.youtube.com/watch?v=m24YNqA-4rU

Scientific Program

Time	GIGA V Wednesday November 1st
8:00-9:00 AM	**Registration**
9:00-9:15	**Introduction to Meeting** Todd Oakley, UC Santa Barbara, GIGA President
9:15-10:15	**Plenary Speaker: Sarah Lemer (University of Guam)** Coral Reef Genomics: Exploring the Evolution and Adaptation of Non-model Species
10:15-10:45	**Coffee Break**
10:45-12:15	**Session 1: Population, Ecosystem, Biodiversity Genomics** Chair: Todd Oakley
10:45-11:00	**Natalia Andrade Rodriguez (University of Miami)** Annual transcriptomic characterization of *Orbicella faveolata* genotypes under SCTLD threat
11:00-11:15	**Bassem Allam (Stony Brook University)** Survival of the fittest: Genomic investigations of the bay scallop reveal a shift in population structure through a summer mortality event
11:15-11:30	**Dylan Comb (Gloucester Marine Genomics Institute)** Jonah Crab Population Genomics
11:30-11:45	**JoÃo Gabriel Rodinho Nunes Ferreira (Federal University of Rio de Janeiro)** The genomes of Tubastraea spp. (Dendrophylliidae) as a tool for the study of invasive coral species
11:45-12:00	**Pablo Saenz-Agudelo (Universidad Austral de Chile)** Scurria limpets as a novel model to study seascape genomics and the evolution of genomic divergence.
12:00-12:15	**Adriana Sarmiento (Universidad de los Andes)** Resolving the diversity of the Caribbean candelabrum corals: a phylogenomic approach.
12:15-12:30	**Laura Villegas (University of Cologne)** From samples to genomes: biodiversity and genomics of desert nematodes
12:30-1:30 PM	**Lunch**
1:30-2:45	**Session 2: Whole Genome Sequencing and Comparative Genomics I** Chair: Gonzalo Giribet
1:30-1:45	**JoÃo Gabriel Rodinho Nunes Ferreira (Federal University of Rio de Janeiro)** A chromosome-level assembly supports hemizygosity investigation and genome-wide characterization of the DMRT gene family in the golden mussel (*Limnoperna fortunei*)
1:45-2:00	**J. A. Baeza (Clemson University)** Low coverage sequencing provides insights into the key features of the nuclear and mitochondrial genomes of the deep-water azooxanthellate coral *Madracis myriaster*
2:00-2:15	**Tauana Cunha (Field Museum)** Nematomorph genomes and the loss of universally conserved cilium-related genes

2:15-2:30	**Niklas Dreyer (Harvard University)** Chromosome-level genome assembly of a Neotropical velvet worm
2:30-2:45	**Emily C Giles (Universidad Austral de Chile)** Comparative genomics of three Scurrinid limpets (Patellogastropoda)
2:45-4:30	**Session 3: Metagenomics and Symbiosis I** Chair: Joe Lopez
2:45-3:00	**Marcela Uliano-Silva (Wellcome Sanger Institute)** Intro Talk (Sanger): To sequence all life and revolutionise biology: that is why we are here. The Darwin Tree of Life Project and Earth Biogenome Project
3:00-3:15	**Noah Gettle (Wellcome Sanger Institute)** Advances and Challenges in Symbiotic Systems Genome Assembly
3:15-3:45	**Coffee Break**
3:45-4:00	**Camilla Santos (Wellcome Trust Sanger Institute)** Sponges and their cobionts: main challenges faced by ASG Project
4:00-4:30	**Joe Lopez (Nova Southeastern University)** Characterizing Whole Genomes from Photosymbiotic Organisms and Sponges: Updates from the Aquatic Symbiosis Genome (ASG) Project
4:30-5:00	Poster Lightning talks;
5:00-7:00	Poster session

Time	GIGA V Thursday November 2nd
9:00-10:00 AM	**Plenary Speaker: JingChun Li (University of Colorado, Boulder)** Transcriptomes, nuclear genomes, and mitochondrial genomes: what do they teach us about marine bivalve photosymbiosis
10:00-11:30	**Session 4: Professional Practice in Genome Research** Chair: Joe Lopez
10:00- 10:30	**Sadye Paez and Marcela Uliano-Silva (Earth BioGenome Project)** Justice, Equity, Diversity and Inclusion + (JEDI+): building a global collaborative network of researchers to sequence all life on Earth
10:30 - 11:00	**Coffee Break**
11:00 - 11:30	**Laurie Goodman (GIGA Science Press)** The Future of Publishing: From Open Access to Open Science.
11:30-12:15	**Session 5: Comparative Genomics and Biodiversity** Chair: Kevin Kocot
11:30-11:45	**Dennis V. Lavrov (Iowa State University)** Comparative genomics of mitochondrial tRNA import in sponges
11:45-12:00	**Elizabeth Boville (Pennsylvania State University)** Understanding transcriptional mechanisms for reproductive isolation in the *Orbicella annularis* species complex
12:00-12:15	**Kevin M. Kocot (University of Alabama & Alabama Museum of Natural History)** Scaphopoda is the sister taxon to Bivalvia: evidence of ancient incomplete lineage sorting

12:30-1:30 PM	**Lunch**
1:30-2:15	**Session 6: Metagenomics and Symbiosis II: Photosymbiosis** Chair: Michael Middlebrooks
1:30-1:45	**Lisa Yeter Mesrop (University of California, Santa Barbara)** Gene expression changes and the evolutionary origin of secretory bioluminescence in sea fireflies
1:45-2:00	**Senjie Lin (University of Connecticut)** Comparative metatranscriptomics reveals molecular signatures of different lifestyles in coral symbionts Symbiodiniaceae
2:00-2:15	**Michael Middlebrooks (University of Tampa)** Combining High Throughput Genomic Sequencing and Field Surveys Reveal Cryptic Sources of Chloroplasts for the Solar-Powered Sea Slug *Elysia crispata*
2:15-4:00	**Session 7: Whole Genome sequencing and Assembly II** Chair: Vanessa L. Gonzalez
2:15-2:30	**Vanessa L. González (National Museum of Natural History, Smithsonian Institution)** High-quality genome assemblies of *Verpa penis* (Bivalvia: Anomalodesmata) and *Scintilla philippinensis* (Bivalvia: Galeommatida)
2:30-2:45	**Nickellaus G. Roberts (University of Alabama)** Whole Genome Amplification for de novo Genomics of the Genome of the Gastrotrich, Lepidodermella squamata as a case study
2:45-3:00	**Padmanabhan Mahadevan (University of Tampa)** Evaluation of various short read genome assemblers on sea slug genomic data
3:00-3:30	**Coffee Break**
3:30-3:45	**Arianna Lord (Harvard University)** Covering the bases: Extracting metazoan UCEs from low-coverage whole genome sequencing data
3:45-4:00	**Nadège Guiglielmoni (Universität zu Köln)** Resolving haplotypes in invertebrate genome assemblies: applications to parthenogenetic species
4:00-6:00	**Session 8: Workshop: EBP, GIGA BioProject, and GoaT resources** Chair: Jeffrey Robinson
4:00-4:20	**Caroline Howard (Tree of Life programme, Wellcome Sanger Institute)** The wet-lab processes behind 1000 high quality reference.
4:20-5:00	**Jeffrey Robinson (University of Maryland, Baltimore County)** Practical: Participate with GIGA Community by Registering with the GIGA NCBI BioProject and Genomes on a Tree (GoaT) Resources - A Guided Quickstart.
5:00-6:00	**Kate Castellano (Gloucester Marine Genomics Institute)** Professional Development Panel: Transitioning to your next steps and transferrable skills

Time	GIGA V Friday November 3rd
9:00-10:00 AM	**Plenary Speaker: Vanessa Yepes-Narváez (INVEMAR)** eDNA metabarcoding vs metagenomics: an approach to marine invertebrate monitoring in Colombia
10:30 - 11:00	**Coffee Break**
11:00 – 12:30 PM	Final Roundtable and business meeting
5:30	Informal Banquet in Walled City

Abstracts

PLENARY

Coral Reef Genomics: Exploring the Evolution and Adaptation of Non-model Species

Sarah Lemer, University of Guam

Tropical reef ecosystems are facing increasing threats due to global climate change, and there are troubling signs that the intensity and frequency of environmental disturbances are exceeding the adaptive capabilities of reef ecosystems. These events not only endanger corals but also pose a serious threat to the reef ecosystems they support and the countless species they sustain. In light of these challenges, the need for effective and tailored conservation and management strategies is essential, especially for understudied marine invertebrate groups. Conservation genomic approaches, which combine genomic and environmental data, can be powerful tools for this purpose. In this context, we present three case studies, each showcasing the power of diverse population genomic approaches in elucidating the molecular mechanisms of adaptation and diversification within populations of three interconnected coral reef species: a scleractinian coral, a photosymbiotic bivalve, and a small, often overlooked coral guard crab. Each of these species is directly or indirectly threatened by climate change. The coral *Acropora millepora* is known to be susceptible to bleaching in response to environmental stressors. However, two populations of *A. millepora* are currently surviving in low-pH CO2 seep environments, against all odds. Using a recently sequenced genome and transcriptomic data previously analyzed for gene expression, we demonstrate that these corals display clear signs of genomic adaptation to low-pH conditions. These results highlight the ability of corals not only to acclimate to extreme environments but also to adapt when given sufficient time. Like *A. millepora*, the small giant clams Tridacna maxima have a wide Indo-Pacific distribution and are found in shallow tropical reefs. They are endangered throughout their distribution range mostly because of overfishing. To explore the adaptive capacity of T. maxima populations we combined low-coverage whole-genome sequencing data with environmental information. Our analyses show that genomic signatures of adaptation to specific environmental conditions are involved in the observed genetic differentiation between T. maxima populations in Micronesia. This suggests that any future change in these environmental conditions could potentially have detrimental effects on T. maxima populations. Finally, the coral guard crabs Trapezia bidentata are obligate exosymbionts of corals, living between the branches of their hosts and threatened by habitat destruction. In an effort to characterize the genetic connectivity between endangered populations of T. bidentata throughout the Indo-Pacific, we applied a recently developed genome subsampling method and generated thousands of SNPs from highly degraded museum samples. Analysis of this data revealed that despite their long dispersal ability, some T. bidentata populations are genetically very divergent, suggesting the presence of at least three cryptic species. In light of these results, we reconstructed the phylogenetic relationships of a dozen Trapezia species to help clarify the taxonomy of this group before undertaking more in-depth population genomic studies. The three case studies presented here will highlight how conservation genomic approaches can improve our understanding of species evolution and ecology and provide critical guidance to mitigate future losses and conserve ecosystem functions.

Annual transcriptomic characterization of *Orbicella faveolata* genotypes under SCTLD threat
Natalia Andrade Rodriguez, University of Miami

Stony coral tissue loss disease (SCTLD) has threatened coral reef ecosystems in the Caribbean since 2014. Many research studies have shown that SCTLD affects coral species with different intensities, having coral species that are almost fully resistant to infection and others very susceptible to it. The difference in susceptibility is also seen at an intraspecific level, where some colonies will have more recurrent SCTLD infections than others (e.g. *Orbicella faveolata*). Unfortunately, the cause of SCTLD and variability in susceptibility are still unknown. These knowledge gaps limit the amount of intervention that can be put in place to avoid or control the spread of SCTLD. The SCTLD resistance research consortium put in place a project to tackle these unknowns through a holistic approach to obtain biochemical, physiological and genetic data from 90 O. faveolata colonies on Florida's Coral Reef with different susceptibilities to SCTLD. Tissue samples from these colonies were collected in 3 different sample periods (May/June 2021, August/September 2021, February/March 2022) to capture the seasonal variation. Here, we present the data for the transcriptomic analysis done with the 3' RNAseq protocol. Preliminarily, we identified potential antimicrobial peptides and immune genes differentially expressed when comparing resistant and susceptible colonies. These results give us a better understanding of possible genes and cellular pathways that could make a colony less susceptible to SCTLD.

Survival of the fittest: Genomic investigations of the bay scallop reveal a shift in population structure through a summer mortality event
Bassem Allam, Stony Brook University

The bay scallop Argopecten irradians is a commercially and recreationally important shellfish species found in estuarine and coastal environments from New England to the Gulf of Mexico. In New York, adult bay scallop populations have been decimated every summer since 2019, causing the collapse of the fishery. These mortality events were associated with annual outbreaks of an undescribed apicomplexan parasite recently dubbed Bay Scallop Marosporida (BSM). This presentation summarizes some of our genetic and genomic investigations on bay scallop in New York. First, a chromosome-level assembly of the bay scallop genome was generated and used as a reference for exploring host-pathogen interactions and evaluation of population structure. Data from RNA-Seq, RAD-Seq, and mitochondrial DNA sequencing have been used to identify the population structure of New York bay scallops. Results showed that the New York bay scallop population structure has changed over the past 25 years by increasing the representation of southern lineages of Argopecten irradians. The investigations also allowed the characterization of wild and aquacultured scallops used for stock enhancement in NY and enabled the assessment of changes in population structure throughout a mortality outbreak. Specifically, results enabled the identification of what appears to be a more resilient scallop lineage that seems to better survive the mortality outbreak. While a better understanding of scallop population structure in New York and along the east cost of the United States is highly needed, these results are important for understanding the evolutionary history of bay scallops and for identifying populations with unique genetic makeups that could be important for conservation and restoration efforts.

Jonah Crab Population Genomics
Dylan Comb, Gloucester Marine Genomics Institute

Over the past several years, Jonah crab (Cancer borealis) has transitioned from a bycatch species of the lobster industry to a targeted fishery that is now one of the most lucrative in Massachusetts, valued at $13.4M in 2022. Despite commercial interest in this species, there is scarce biological information regarding life history or abundance of Jonah crab, and under the current Atlantic State Marine Fisheries Commission fisheries management plan, the fishery is managed as a single homogenous stock from Maine to Virginia. The lack of comprehensive biological data creates a high degree of uncertainty regarding the impact of the fishery and any potential for overexploitation. Assessing fish stocks that are spatially mismatched relative to biological reality can bias stock assessment, which may result in depletion of unique spawning components and erroneous estimates of stock productivity leading to reduced biodiversity, destabilized stock dynamics, and a suboptimal utilization of resources. In preparation for the upcoming Jonah crab stock assessment, we conducted a genetic population structure assessment to provide necessary data on spatial structure and connectivity. Over 600 Jonah crab tissue samples were collected from Canada to New Jersey in collaboration with commercial fishers and state biologists and low-coverage whole-genome sequencing was used to generate genotype likelihood data for millions of SNP loci. Preliminary results indicate weak population structure with differentiation between Nova Scotia, New England, and New Jersey populations. Findings will be combined with tagging, life history, and landings data to aid the Jonah Crab Technical Committee in establishing biologically relevant boundaries for stock delineation.

The genomes of Tubastraea spp. (Dendrophylliidae) as a tool for the study of invasive coral species
Name: JoÃo Gabriel Rodinho Nunes Ferreira. Affiliation: Federal University of Rio de Janeiro | Bio Burau Biotechnology

Corals have been attracting huge attention due to the impact of climate change and ocean acidification on reef formation and resilience. Nevertheless, some invasive species like Tubastraea coccinea and *Tubastraea tagusensis* have been spreading very fast replacing the native ones, affecting the local environment and decreasing biodiversity of corals and other organisms associated with them. Despite some focal efforts to understand the biology of these organisms, they remain understudied at the molecular level. In this circumstance, it is expected that genome sequencing would provide powerful insights that could lead to better strategies for prevention, management, and control of this and other invasive species. Here, we present three genomes of Tubastraea spp. in a comprehensive biological study that includes flow cytometry, karyotyping, transcriptomics and genomics. The genome of *T. tagusensis* is organized in 23 chromosome pairs and has 1.1 Gb, the T. coccinea genome is organized in 22 chromosome pairs and is 806 Mb long, and the Tubastraea sp. genome is organized in 21 chromosome pairs and 795 Mb. The coral genomes have been assembled using an hybrid approach combining short and long (PacBio) sequencing reads. We inferred that almost half of the genomes consist of repetitive elements, mostly interspersed repeats. We provide evidence for exclusive Scleractinia and Tubastraea gene content related to adhesion and immunity. The genomes of Tubastraea spp. are references that hold the potential to offer insights not only into the genetic foundation behind the remarkable invasiveness of this specific genus of coral, but to understand the adaptation flaws of some reef corals in the face of anthropic-induced environmental disturbances. We expect the data generated in this study will foster the development of efficient technologies for the management of coral species, whether invasive or threatened.

Scurria limpets as a novel model to study seascape genomics and the evolution of genomic divergence
Pablo Saenz-Agudelo, Universidad Austral de Chile

Genetic divergence is a fundamental process driving speciation and the emergence of new species. However, our understanding of the mechanisms underlying genetic differentiation and its progression during speciation remains limited. Here, we present the key findings from a comprehensive research program on speciation genomics in Scurria, a genus of intertidal gastropods (Patellogastropoda) endemic to the Southern East Pacific (SEP). The SEP is characterized by strong coastal upwellings and sharp environmental discontinuities, providing a diverse ecological landscape in which at least eight Scurria species have evolved. We conducted comparative population genomic analyses on five Scurria species over 20Âº of latitude, employing state-of-the-art sequencing techniques. These species exhibit varying degrees of genetic divergence, different divergence times, distinct geographic distributions, and habitat preferences. Together, we have an excellent scenario to investigate genomic divergence at various stages of speciation within a complex ecological and geographic context. Leveraging a de-novo genome assembly of one species as a reference, we have generated genome-wide maps of genomic diversity for all five species within this environmentally heterogeneous system. Our findings indicate different levels of population genetic structure among species and shed light on the dynamics of genomic divergence as speciation progresses. Moreover, our research uncovers intriguing genomic changes around biogeographic transition zones, unraveling the forces shaping genetic diversity in intertidal marine invertebrates. Our study contributes to the broader knowledge of how genetic divergence facilitates the formation of new species and provides important information about the factors influencing genomic diversity in intertidal marine organisms.

Resolving the diversity of the Caribbean candelabrum corals: a phylogenomic approach
Adriana Sarmiento, Universidad de los Andes

The evolutionary history of the Caribbean Candelabrum corals from the genus *Eunicea* remains unknown, despite its high diversity and abundance in reef environments. Understanding the evolutionary relationships between and within the *Eunicea* species is critical to have accurate measures of the group diversity, which is indispensable to understanding the biology, ecology, and conservation issues of the group. Besides, the group has a high potential to find cryptic diversity and new species, particularly given the existing rich morphological variability, but classical molecular markers have not provided a clear positioning for the species inside the genus. Here, we provide the first phylogenomic reconstruction of candelabrum corals employing a phylogenomic approach, using NextRAD, a reduced-representation sequencing technique to generate thousands of SNPs. We include 13 species and several morphotypes sampled throughout the Caribbean. In general, the phylogeny is well supported and resolved. In total, the group performed 13 well supported clades and just one problematic clade involving three different species *E. mammosa, E. palmeri* and *E. succinea*. We also characterize the cryptic diversity inside the *E. clavigera* clade that performs a high morphological variation with at least one possible new species.

From samples to genomes: biodiversity and genomics of desert nematodes
Laura Villegas - University of Cologne

Nematodes are distributed worldwide and frequently found in extreme environments like the Atacama Desert, the driest non-polar desert on Earth. In this ecosystem, where water is scarce, high salinity patches are frequent, and pronounced changes in temperature occur continuously, only specialized taxa can survive. However, little is known about the distribution, diversity, and frequency of such taxa in the Atacama. Nematodes are particularly challenging to identify using morphological methods, high morphological similarity of genetically distinct species and fast evolution throughout the tree make single-gene barcoding inconclusive. We thus aim to apply an integrative approach combining morphological analysis with multi-marker and whole genome data to identify nematodes and further understand their phylogenetic relationships and evolutionary patterns.
We conducted sampling campaigns across salinity and altitude gradients with variable vegetation coverage across four transects. Using 18S SSU rRNA and classical morphological analysis we preliminarily identified 32 roundworm genera. We then focused on the Panagrolaimidae family, obtaining long-read genome assemblies for one asexual triploid and two diploid sexual Panagrolaimus strains and a diploid asexual Acrobeloides from the desert as outgroup. We used two approaches to estimate phylogenies including these new strains: (i) ultra-conserved elements (UCEs) and (ii) universal single copy orthologues obtained from Nanopore sequencing. For (i) we designed a bait set targeting over 1600 UCEs in the Panagrolaimidae family. In-silico tests showed this approach can retrieve reliable phylogenies for Panagrolaimidae and close relatives. This method can be implemented on newly described/isolated species for cost- and labour-efficient phylogenomics, and population genomics. For (ii) we developed an on-site real time sequencing protocol in the desert using the MinION platform and portable laboratory equipment for the generation of genome skims of freshly isolated nematodes that cannot be kept as laboratory cultures. This allows rapid biodiversity assessment in the field, including in extreme environments.

A chromosome-level assembly supports hemizygosity investigation and genome-wide characterization of the DMRT gene family in the golden mussel (Limnoperna fortunei)
Name: JoÃo Gabriel Rodinho Nunes Ferreira. Affiliation: Federal University of Rio de Janeiro | Bio Burau Biotechnology

The golden mussel (Limnoperna fortunei) is a highly invasive species that causes environmental and socio economic losses in invaded areas. Reference genomes are a valuable resource for studying the biology of invasion, as it allows the identification of molecular mechanisms conferring adaptiveness and of potential genes for biotechnology-based control strategies. While the short-reads-based currently available golden mussel genome has been useful for identifying new genes, its high fragmentation hinders some applications such as populational and comparative genomic studies. Here we present a new golden mussel reference, a chromosome-level genome built using PacBio HiFi, 10X and Hi-C sequencing data. The final assembly contains 99.4% of its total length assembled to the 15 karyotyped chromosomes of the species and a scaffold N50 of 97.05 Mb. A total of 34 862 protein-coding genes were predicted, of which 84.7% were functionally annotated. A significant (6.48%) proportion of the genome was found to be in a hemizygous state, which has been associated with gene presence absence variation (PAV) in other mollusks. Using the new genome, we have performed a genome-wide characterization of the DMRT gene family and identified a DMRT1L ortholog, which is a promising target for future development of population control strategies. This chromosome-level genome supports genome editing efforts aimed at developing biotechnology-based solutions for invasion control. Additionally, it serves as a reference for future resequencing studies, enabling the assessment of genomic variation among different golden mussel populations. These studies unveil potential routes of dispersion and contribute to the establishment of more effective control policies. Finally, it's a substrate for studies of the molecular evolution of Mytilidae and Lophotrochozoa.

Low coverage sequencing provides insights into the key features of the nuclear and mitochondrial genomes of the deep-water azooxanthellate coral Madracis myriaster
J. A. Baeza. Department of Biological Sciences, Clemson University, Clemson, SC, USA

Madracis myriaster is one of the most important reef builder corals in deep-water habitats of the Caribbean Sea, offering refuge to numerous species of fish and invertebrates. In this study, we developed genomic resources for M. myriaster. Using a low-coverage short read sequencing strategy, this study estimated the genome size, repetitive genome content, annotated and quantified repetitive elements, assembled the 45S-rRNA-DNA operon, and characterized in detail the mitochondrial genome of *M. myriaster.* The haploid genome size estimated using a k-mer strategy was 615-697 Mbp, which is within the range reported for scleractinian corals. Repetitive genome content estimates using different word sizes (=k-mers) indicated that 53-65% of the genome of M. myriaster comprised repetitive elements. A relatively large number of the discovered repetitive elements could not be annotated. Taking into account only annotated repetitive elements, the most common were classified as Satellite DNA which were more abundant than Class I-LINE, Class Penelope, and Class II (DNA transposons) Subclass 2 Maverick mobile elements. Less abundant repeat element families included Class I-LTR Ty3-gypsy retrotransposons, Class II-Subclass 2-Helitron mobile elements, Class I-LTR-Bel-Pao, and Class I-DIRS mobile elements. The nuclear ribosomal operon of *M. myriaster* was assembled into a single contig that contains, in the following order: a 5â€² ETS (length = 1200 bp [partially assembled]), ssrDNA (1,800 bp), ITS1 (233 bp), 5.8S rDNA (158 bp), ITS2 (204 bp), lsrDNA (3,616 bp), and 3'ETS (827 bp [partial sequence]). The mitochondrial genome of *M. myriaster* is 17,044 bp long and encodes 13 protein coding genes, 2 transfer RNAs, and two ribosomal genes. Based on protein coding genes, the phylogenetic position of *M. myriaster* was examined. These new genomic resources are of utmost relevance for the development of conservation plans of this remarkable reef-forming deep-water coral.

Nematomorph genomes and the loss of universally conserved cilium-related genes
Tauana Cunha, Field Museum

Members of the phylum Nematomorpha (horsehair worms, hairworms, or Gordian worms) are large endoparasites that affect the behavior of their arthropod hosts. In terrestrial hosts, they cause erratic movements toward bodies of water, where the adult worm emerges from the host to find mates for reproduction. We present a chromosome-level genome assembly for the freshwater Acutogordius australiensis and a draft assembly for one of the few known marine species, Nectonema munidae. The assemblies span 201 Mbp and 213 Mbp in length (N50: 38 Mbp and 716 Kbp), respectively, and reveal four chromosomes in Acutogordius, which are largely rearranged compared to the inferred ancestral condition in animals. Both genomes have a relatively low number of genes (11,114 and 8,717, respectively) and lack a high proportion (~30%) of universal single-copy metazoan orthologs (BUSCO genes). We demonstrate that missing genes are not an artifact of the assembly process, with the majority of missing orthologs being shared by the two independent assemblies. Missing BUSCOs are enriched for Gene Ontology terms associated with the organization of cilia and cell projections in other animals. We show that most cilium-related genes conserved across eukaryotes have been lost in Nematomorpha, providing a molecular basis for the suspected absence of ciliary structures in these animals.

Comparative genomics of three Scurrinid limpets (Patellogastropoda)
Emily C Giles, Universidad Austral de Chile

Despite displaying many interesting developmental, ecological, and physiological attributes, the genomic resources available for Patellogastropoda are limited. This paucity of information challenges our understanding of forces contributing to speciation in intertidal environments and in marine gastropods in general. Here we present genomes and transcriptomes for three species of *Scurria* (*S. scurra, S. viridula*, and *S. zebrina*), and we compare gene content, synteny, collinearity, and orthologous relationships among these species and other Patellogastropoda. Overall, we highlight interesting features of this genus, and suggest that the resources herein presented will be useful for future studies of speciation and reconstructions of deep phylogenetic relationships such as those that currently remain unresolved in gastropods.

Chromosome-level genome assembly of a Neotropical velvet worm
Niklas Dreyer, Museum of Comparative Zoology, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

Onychophora is the last panarthropod group to enter the genomic era. Until recently, only a single and highly fragmented genome was publicly available. An additional more contiguous genome was published in the past few months, yet a general dearth of genome-scale molecular resources has hampered comprehensive resolution of the origins and evolution of (especially) Neotropical velvet worms. This talk will outline directions to rectify this situation from a genomic perspective. We present preliminary data on the first chromosome-level genome assembly of an onychophoran, *Epiperipatus barbadensis*, focusing on the underlying drivers of genome gigantism. As recently done for the E. broadwayi genome, this involves comparing the extent of intron length inflations, repeat contents and gene family expansions to the conditions of other panarthropods. We will also present preliminary results on estimation of past effective population sizes of Barbadian velvet worms, additionally attempting to relate these to major geological events since the origin of the species. The new sequence data will also be used to infer the most comprehensive, time-calibrated, non-â€œUCEâ€ phylogeny of Peripatidae to date by using a rigorous tree-based approach to ortholog identification. This exercise will also place E. barbadensis in the velvet worm Tree of Life with genome-scale data. We will finally discuss how such data may contribute to disentangling the complex evolutionary history of Neotropical velvet worms.

To sequence all life and revolutionize biology: that is why we are here. The Darwin Tree of Life Project and Earth Biogenome Project
Marcela Uliano-Silva, Wellcome Sanger Institute

The Darwin Tree of Life Project (DToL) is part of a global effort under the umbrella of the Earth BioGenome Project to sequence all complex life on Earth. It is delivering at-scale genome sequences of unprecedented quality for all eukaryotes of Britain and Ireland, which holds substantial biodiversity, encompassing over 40% of documented families. DToL is a massive collaborative enterprise with scientists and institutions enabling sample collection, taxonomy assignment, genome sequencing and assembly. As of August 2023, DToL has successfully delivered 1030 high-quality genomes, representing 427 families. More than 2,000 additional species are underway. Among the complete genomes, 823 are invertebrates, with 89% being arthropods, but there are representatives of 6 other phyla. Pacbio HiFi and chromatin conformation capture reads are central to our assembly pipeline, providing long DNA length and distance to scaffold genomes to chromosomes. It allows separation of contamination, and the assembly of cobionts and mitochondria for which we have developed pipelines. Our automated assembly pipeline and manual curation run across taxa, with some clades needing extra manual intervention, such as Hymenoptera with high amounts of heterochromatin and Mollusca with high heterozygosity and typically low BUSCOs. The smallest scaffold N50 for completed arthropods is 1.82 Mb and for Molluscs is 25 Mb. Once finished, our assemblies and raw data are readily released to INSDC databases and Genome Notes are published. Analyses across >200 lepidopterans enabled reconstructions of their ancestral karyotype and showed fusions of sex chromosomes and autosomes shaping their evolution. The systematic presence of large repeats in Hymenoptera mitogenomes was found. Many other avenues of research are being followed by Sanger and DToL partners. DToL is revolutionising biology as it goes along by developing lab and bioinformatics methods to sequence high-quality genomes, and by enabling the study of genome evolution at the finest resolution.

Advances and Challenges in Symbiotic Systems Genome Assembly
Noah Gettle, Wellcome Sanger Institute

Recent advances in long read sequencing technology along with new tools and pipelines have opened the door for major genome assembly project that seek to generate reference quality assemblies for vast numbers of eukaryotic organisms. Many organisms, however, cannot be understood or characterized based on a single genome but, rather, only in conjunction with the symbiotic partners they live, interact, and coevolve with. Moreover, sequencing and assembling complex pools of species is a process that lies largely outside the standard pipelines and many symbiotic systems of particular interest (e.g. corals and Symbiodinium dinoflagellates) are relatively underrepresented in genomic studies. The Aquatic Symbiosis Genome Project, funded by the Gordon and Betty Moore Foundation in conjunction with the Darwin Tree of Life Project, seeks to address these issues by sequencing and assembling over 400 symbiotic systems including lichen, sponges, amoeba, and tube worms. In this talk, I will share our current process for assembling pooled assemblages of organisms and some of the challenges we have encountered.

Sponges and their cobionts: main challenges faced by ASG Project
Camilla Santos, Wellcome Trust Sanger Institute, Cambridge, UK

The Aquatic Symbiosis Genomics Project (ASG) aims to provide the genomic foundations for scientists to answer key questions about the ecology and evolution of symbiosis in marine and freshwater species. ASG species include corals, molluscs, ciliates, algae and sponges, where the last one is among the most challenging groups. Sponge tissue isolation is not easy due to the nature of the tissue and cobionts living along it. Although sponge DNA isolation results in good yields, the material is highly degraded, fragmented, intermixed with holobionts and unsuitable for long-read sequencing. Mainly, the most difficult sponge orders to work have been Clionaida and Haplosclerida, with little success. Additionally, the genome assembly and curation can be laborious due to low PacBio and Hi-C coverage data. However, we now have seven sponge species finalised and publicly available and a further two under submission. Overall, they belong to seven different orders and presented significant improvements in genome contiguity after curation: scaffolds number (309 to 14), N50 (2.9 to 12.4 Mb) and L50 (10 to 4), producing assemblies which are up to 99.98% chromosome level. All public sponge species present symbiont relationships, highlighting Aplysina aerophoba and its producing secondary metabolites cyanobacteria. It links with Tylodina perversa mollusc ASG species, where it is still unclear whether it feeds on both A. aerophoba and cobiont or on cyanobacteria only. Applying the latest genomic resources to hundreds of aquatic species and their symbionts, the data produced through ASG will guide future studies and contribute to vital conservation efforts.

Characterizing Whole Genomes from Photosymbiotic Organisms and Sponges: Updates from the Aquatic Symbiosis Genome (ASG) Project
Jose V. Lopez

This project represents one of ten hubs set up as the Aquatic Symbiosis Genome (ASG) Project supported by the Gordon and Betty Moore Foundation and the Wellcome Sanger Institute to generate high quality whole genome sequences from various symbiotic invertebrates. Ten hubs would focus on characterizing 50 symbiotic pairs composing the holobiont, which adds up to a projected total of 1000 novel whole genomes by the end of the project. Although we know that most organisms live in symbiosis, our hub focused on photosymbiosis, where one partner actively photosynthesizes for the survival or advantage of the holobiont. This distinct phenotypic trait encompasses a wide phylogenetic spectrum including corals, hydra, sponges, acoel worms, mollusks, protists, tunicates and others. The diversity of taxa and natural histories provides multiple opportunities to characterize common mechanisms for symbiont initiation and maintenance. For example kleptoplastic saccoglossans such as *Elysia crispata* or *Costasiella ocellifera* only sporadically incorporate chloroplasts into their tissues from their food. This can be contrasted with multiple coral-Symbiodinium associations which can be disrupted by environmental stresses (high sea surface temperatures). In contrast, cyanobacteria-animal symbioses may be more stable. Sponge hosts provide other technical challenges such as wider symbiont diversity and recalcitrant DNA. As designed, ASG has helped forge a community of diverse symbiosis focused scientists, and offered genomics training to address the large datasets, and long-standing symbiosis questions.

PLENARY

Transcriptomes, nuclear genomes, and mitochondrial genomes: what do they teach us about marine bivalve photosymbiosis

Jingchun Li, University of Colorado, Boulder

Photosymbioses between marine invertebrate hosts and autotrophic symbionts are evolutionarily prevalent and ecologically significant, contributing to diversification of major lineages and stability of ecosystems. However, molecular mechanisms behind such symbioses remain less elucidated, hindering our understanding of their origin and adaptive evolution. This work used genomic tools to examine the molecular evolution of photosymbiosis under three lenses: transcriptome, nuclear genome, and mitochondrial genome. It revealed surprising aspects of gene evolution and genome composition of photosymbiotic bivalves and shed light on molecular evolution in invertebrate photosymbiosis.

The bivalve subfamily Fraginae provides an ideal system to investigate molecular mechanisms of photosymbiosis, because it is composed of two sister clades, one exclusively photosymbiotic and one non-symbiotic. We compared gene expression patterns of a photosymbiotic Fraginae species (*Fragum sueziense*) and a closely related non-symbiotic species (*Trigoniocardia granifera*) under different light conditions. Many immune-related genes in *F. sueziense* mantle were significantly down-regulated in the normal light condition and enriched in the dark. This could mean that the host treated symbionts as pathogenic in prolonged darkness and/or the symbionts had mechanisms to suppress host immune functions under normal light. Some of the photosymbiotic pathways we identified were shared among distantly related host lineages, such as mollusks and cnidarians, indicating that parallel and/or convergent evolution is instrumental in driving host-symbiont adaptations in diverse organisms. In light of the transcriptome work, we further investigated a chromosomal-level genome assembly of a second group of photosymbiotic bivalve – the giant clam *Tridacna maxima*. The genome showed contraction of common immune system Pattern Recognition Receptors (PRR) gene families, expansion of novel PRR families, as well as enriched tandem duplications in immune system functions. All indicate that *T. maxima* has a unique immune system likely shaped by its association with photosymbionts. Lastly, we compared mitogenomes from PacBio long-read assemblies to de novo reference-guided assemblies of Illumina short reads for several photosymbiotic bivalve species. We observed an inability to assemble complete mitogenomes from short reads alone due to elaborate repetitive sequences in the non-coding “control” region (NCR). In particular, NCRs varied drastically in photosymbiotic bivalves from the genera *Fragum*, *Tridacna*, and *Hippopus*. The mitogenomes exceeded 22 kbps in all three genera, much longer than those of non-photosymbiotic bivalves. Some of the NCRs contained large numbers of tRNA copies, as well as open reading frames. We speculated that the high levels of NCR expansion through long repeats in these photosymbiotic species may be associated with elevated levels of reactive oxidative species due to photosymbiotic activities. Taken together, these results indicate that transcriptomic and genomic approaches are highly effective in investigating molecular evolution and ecology of non-model invertebrates, and have great potential in unlocking diverse molecular mechanisms in metazoans.

Justice, Equity, Diversity and Inclusion + (JEDI+): building a global collaborative network of researchers to sequence all life on Earth
Sadye Paez (Earth BioGenome Projecdt) and Marcela Uliano-Silva, Wellcome Sanger Institute

Recent advancements in genomics sparked an unprecedented revolution in biology. To avoid redundancy, optimise resource utilisation, and create reference genomes for scientific progress, global consortia, including GIGA, united under the Earth BioGenome Project to sequence all life on Earth within 10 years. The ramifications are profound, amplifying our comprehension of speciation and adaptation as well as facilitating the emergence of fresh bioeconomies and resources to mitigate impacts of the ongoing sixth mass extinction. However, fulfilling this scientific potential is not possible without addressing systemic global inequalities that limit opportunities for genuine transnational participation. The extent to which the EBP achieves its scientific goals will depend in large part on recognising and removing barriers to equity and inclusion at all stages of the genomics pipeline, from project funding and sample collection through to sequencing, bioinformatics and data release. While many of these issues extrapolate to national and international policies, tackling them to the best of our abilities remains imperative within our scientific enterprise. In 2021, the EBP established a Justice, Equity, Diversity, and Inclusion (JEDI) committee to address these challenges by targeting root causes of structural racism and systemic oppression in biodiversity genomics. The JEDI committee advocates an iterative, transparent, and deliberate approach to restore access and build capacity for diverse epistemologies and ideologies in planning, decision-making, and policy development. Through this approach, EBP aims to include all interested parties in processes by engaging in continuous reflection, reorientation, improvement and action, e.g., who is participating/leading/receiving attribution, how can we foster equitable infrastructure development, etc. Assembling a global collaborative network of all researchers and interested parties is critical to fulfil not only EBP's scientific mission but also its aspiration to lead a paradigm-shift in the current scientific landscape for a just and inclusive ecological future.

The Future of Publishing: From Open Access to Open Science
Laurie Goodman, PhD GigaScience Press

Scientific publishing is finally moving beyond Open Access (a movement that began nearly 30 years ago) to Open Science. Open Science provides the global community with more than just a written narrative about the work done and instead aims to provide all the information that underlies the research, e.g data, source code, workflows etc). With the need for new technology and methods to achieve Open Science, smaller publishers, which are better poised to embrace or build new technologies, are doing far better at achieving this than legacy publishers, which need to jettison 20-year-old publishing technology that was built for print rather than optimized for online content. Here, I will discuss examples that GigaScience Press is taking to break barriers in scientific communication to improve discoverability, access, and reuse of all scientific information we publish. I will also discuss the use of generative AI (such as GPTchat and BingChat), which has the potential to democratize manuscript preparation provided it is used with extreme care and with understanding of the rules publishers are putting in place for its use.

Comparative genomics of mitochondrial tRNA import in sponges
Dennis V. Lavrov, Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, Iowa, USA.

Unlike other animal phyla, sponges, phylum Porifera, display a large variation in the number of tRNAs encoded by their mitochondrial genomes. Surprisingly, a large part of this variation is replicated in a single clade of sponges, so-called Clade B of Haplosclerid Sponges (CBHS). The number of mt-tRNAs within this clade varies from three in an undescribed Haliclona species to 25 in Xestospongia muta. Because 24 tRNAs is the minimal set necessary for mitochondrial translation in demosponges, cytosolic analogs of lost tRNAs have to be imported to mitochondria. While import of cytosolic tRNAs to mitochondria (aka mitochondrial tRNA import) has been studied extensively in some groups of eukaryotes, it is poorly understood in animals. Thus, CBHS can represent a useful model system for the study of this process in the Metazoa. Here we report nuclear genome sequences for three species of CBHS: Haliclona (Haliclona) simulans (Johnston, 1842), Niphates digitalis (Lamarck, 1814), and Xestospongia muta (Schmidt, 1870), which we analyzed together with other available genomes and transcriptomes from this group. In particular, we investigated coevolution between mitochondrial and cytosolic tRNA families as well as changes in aminoacyl-tRNA synthetases and other proteins that interact with tRNAs and may be involved in the import machinery.

Understanding transcriptional mechanisms for reproductive isolation in the *Orbicella annularis* species complex
Elizabeth Boville, Pennsulvania State University

Many scleractinian corals participate in annual mass spawning events, however the timing of these events varies between species, providing a possible mechanism for reproductive isolation. The precise time of gamete release is thought to be based on environmental factors such as light, depth and temperature, as well as genetic differences between species. Here we use a transcriptomic approach to compare the gene expression before, during, and after spawning events in two Caribbean corals, *Orbicella annularis* and *Orbicella franksi*, that are capable of cross-fertilization but differ in spawning times. These two species do not often live at the same depth, with *O. annularis* dwelling shallowly (~5m) and *O. franksi* found deeper (~35m). We also begin to examine the gene expression profile of a third species, *Orbicella faveolata*, that is not known to hybridize with *O. annularis* or *O. franksi* and is commonly seen concurrently with both sister species. These corals generally spawn at the same time as *O. annularis*, several hours after *O. franksi*. Our aim is to explore differences in gene expression between species to identify the genes that impact when these corals spawn, and to elucidate possible sources of reproductive isolation between the three *Orbicella* species. *O. annularis* and *O. franksi* are known to hybridize and exhibit similar spawning behavior, albeit at different times, yet our findings thus far indicate a low degree of similarity in gene expression profiles between during spawning events. However, we do observe differentially expressed genes involved in clock regulation (Krueppel-like 15 factor) and iodothyronine precursors commonly involved in endocrine signaling and embryonic development. Our preliminary results also suggest that genes involved in morphogenesis and fate development of external sensory organs are differentially expressed, which could have an ancestral function involved with light perception and detection of environmental cues.

Scaphopoda is the sister taxon to Bivalvia: evidence of ancient incomplete lineage sorting
Kevin M. Kocot, University of Alabama & Alabama Museum of Natural History

The almost simultaneous emergence of major animal phyla during the early Cambrian shaped modern animal biodiversity. Reconstructing evolutionary relationships among such closely-spaced branches in the animal tree of life has proven to be a major challenge, hindering understanding of early animal evolution and the fossil record. This is particularly true in the species-rich and highly varied Mollusca where dramatic inconsistency among paleontological, morphological and molecular evidence have led to a long-standing debate about the group's phylogeny and the nature of dozens of enigmatic fossil taxa. A critical step needed to overcome this issue is to supplement available genomic data, which is plentiful for well-studied lineages, with genomes from less well-studied but important lineages, such as Scaphopoda. Here, by presenting first chromosome-level genomes from both extant scaphopod orders and leveraging complete genomes spanning Mollusca, we provide strong support for Scaphopoda as the sister taxon of Bivalvia, consistent with the morphology-based Diasoma hypothesis originally proposed 50 years ago. Our molecular clock analysis confidently dates the split between Bivalvia and Scaphopoda at ~520 Ma, prompting a re-interpretation of controversial laterally compressed Early Cambrian fossils, including Anabarella, Watsonella and Mellopegma, as stem diasomes. Moreover, we show that incongruence in the phylogenetic placement of Scaphopoda in previous phylogenomic studies was likely due to ancient incomplete lineage sorting (ILS) that occurred during the rapid radiation of Conchifera. Our findings highlight the need to consider ILS as a potential source of error in deep phylogeny reconstruction, especially in the context of the unique nature of the Cambrian Explosion.

Gene expression changes and the evolutionary origin of secretory bioluminescence in sea fireflies
Lisa Yeter Mesrop, University of California, Santa Barbara

Bioluminescent glands are evolutionary novelties that evolved convergently many times to generate light, often resulting in extensive ecological impacts. Evolutionary novelties often involve changes in the regulation of genes and co-expression networks between ancestral and descendant species. Yet whether novel bioluminescent glands originate mostly through new genes or changes in the expression and interaction of existing genes is unknown. Here, we use an â€œunbiasedâ€ approach to identifying gene co-expression networks, coupled with comparative transcriptomics and phylogenetics, to understand the origin of bioluminescent upper lip glands, a novel phenotype of luminous cypridinid ostracods. Both luminous and non-luminous ostracods have an upper lip gland, but only luminous ostracods possess additional specialized cell types in their upper lip gland to secrete bioluminescent products for anti-predation and courtship displays. Here, we capitalize on a functionally demonstrated gene (c-luciferase) critical to light production to characterize a Bioluminescent Co-Regulatory Network (BCN) of genes co-expressed with c-luciferase in the bioluminescent upper lip. We find the BCN to be an assemblage of primarily conserved housekeeping genes and putatively secreted genes. This represents the first BCN characterized for any luminous animal, which allows us to hypothesize molecular processes associated with light production in Luminini ostracods. In comparison to co-expression networks of a non-luminous relative, we infer highly modified regulatory interactions between genes of the BCN. Additionally, by comparing differentially expressed genes of luminous and non-luminous upper lips compared to eyes and guts, we infer distinct patterns of differential expression from non-homologous gene families in the novel upper lip. Taken together, our results provide an example in which differential expression of mainly conserved genes and modified interactions between conserved genes and c-luciferase promoted the genesis of the novel bioluminescent gland in cypridinid ostracods. Other bioluminescent glands with secretory properties could show similar evolutionary origins.

Comparative metatranscriptomics reveals molecular signatures of different lifestyles in coral symbionts Symbiodiniaceae

Senjie Lin, Department of Marine Sciences, University of Connecticut

Coral reefs are productive and economically important marine ecosystems hosting unsurpassed biodiversity, whose ecological success is mainly driven by the mutualistic endosymbiosis between scleractinian corals and dinoflagellates of the family Symbiodiniaceae. In recent decades, coral bleaching events have occurred frequently around the world. However, the coral-Symbiodiniaceae symbiosis mechanism is extremely complex and has not been clearly understood, and elucidating the symbiotic mechanism will help us understand the mechanism of coral bleaching. The current study was conducted to address the research gap by identifying the molecular signatures of the sympatric in-hospite and free-living Symbiodiniaceae in situ to better understand the mutualistic mechanism. We collected 77 colonies of Pocillopora damicornis and 21 ambient water samples and conducted comparative metatranscriptomics to reveal molecular signatures of different lifestyles in its endosymbiont species from the family Symbiodiniaceae. Our results revealed the gene expression of Symbiodiniaceae was affected by different lifestyles and water depth. Generally, in-hospite Symbiodiniaceae exhibited lower transcriptional activity than free-living counterparts, suggesting energy-saving benefits for endosymbionts. Indeed, many genes related to energy metabolism were up-regulated in the symbiotic populations, indicating that in-hospite Symbiodiniaceae need to generate more energy for corals to maintain the symbiotic relationship. In contrast, cell division-related genes were down-regulated in-hospite, suggesting coral's repressing effects on the endosymbiont cell population growth. Furthermore, free-living Symbiodiniaceae were more sensitive to environmental variables than in-hospite Symbiodiniaceae, evidencing that mutualism benefits both endosymbionts and their coral hosts. Additionally, we found that Symbiodiniaceae with different lifestyles may have different preferences for nitrogen sources. The findings indicate the value of simultaneous analysis of the sympatric in-hospite and free-living Symbiodiniaceae to gain an understanding of the symbiosis (and hence bleaching) mechanism in the changing environments and produce information useful to guide engineering stress-tolerant coral endosymbionts.

Combining High Throughput Genomic Sequencing and Field Surveys Reveal Cryptic Sources of Chloroplasts for the Solar-Powered Sea Slug *Elysia crispata*
Michael Middlebrooks, University of Tampa

Certain sacoglossan sea slugs are capable of maintaining a unique photosymbiosis known as kleptoplasty. These herbivorous slugs typically feed on siphonaceous green algae and then incorporate chloroplasts taken from the algae into specialized cells lining their digestive diverticula. The sacoglossans can then maintain these chloroplasts to the nutritional benefit of the slug for a period of time ranging between several days to many months depending on the species of sacoglossan and the source of algal chloroplasts. The majority of sacoglossans are oligophagous, only feeding a single or very few species of algae. However, a few species are polyphagous and can incorporate chloroplasts from many different algae species. *Elysia crispata* is polyphagous sacoglossan native to the Caribbean which can maintain functional chloroplasts for three to four months post feeding. We conducted a study where we combined traditional ecological field surveys of *E. crispata* and green macroalgae populations on a shallow reef in the Florida Keys with high throughput genomic sequencing to determine the diet and source of sequester chloroplasts in the slugs. We found that macroalgae abundance was a poor indicator for the diet and source of sequestered chloroplasts for *E. crispata*. Instead, the slugs were feeding primarily on minute filamentous algae which are not easily observed or identified using traditional visual surveys. Furthermore, the algal species detected by this study have mostly been ignored by researchers as a significant food source for *E. crispata*. This study highlights the value of combining high throughput genomic sequencing with traditional surveys to yield new insights into sacoglossan ecology.

High-quality genome assemblies of *Verpa penis* (Bivalvia: Anomalodesmata) and *Scintilla philippinensis* (Bivalvia: Galeommatida)
Vanessa L. González, National Museum of Natural History, Smithsonian Institution

Bivalves, an ancient and ubiquitous group of aquatic invertebrates with an estimated 10,000 described living species, are present in almost all aquatic environments and depth ranges, representing a multitude of different life modes and morphologies. Here, we report genome assemblies for *Verpa penis* (Bivalvia: Anomalodesmata) and *Scintilla philippinensis* (Bivalvia: Galeommatida), each with morphological and behavioral adaptations that allow for some unique modes of life. *V. penis*, known as the 'watering pot shell,' lives in a modified shell, that no longer retains the typical bivalved morphology, but instead lives in a tube-shaped shell. *S. phillipinensis*, a galeomatid bivalve known for its crawling behavior, is hypothesized to be mimicking the behavior of nudibranchs or crabs. We generated high-quality high-coverage genome assembles using PacBio high-fidelity (HiFi) read sequencing. In *V. penis*, this approach yielded a 508 Mb assembled genome with an N50 contig length of 27.5Mb. Hi-C scaffolding of the genome resulted in assembly of 19 pseudochromosomes. A total of 25,135 protein-coding genes were predicted (metazoan BUSCOs complete n = 954, single-copy complete = 97.9%, duplicated = 0.7%, fragmented = 0.9%, and missing = 1.2%). The *S. phillipinensis* genome assembly was 1.7Gb with a contig N50 of 116.3 Kb (metazoan BUSCOs complete n = 954, single-copy complete = 94.0%, duplicated = 8.5%, fragmented = 1.7%, and missing = 4.3%).

Whole Genome Amplification for de novo Genomics: the Genome of the Gastrotrich, Lepidodermella squamata as a case study
Nickellaus G. Roberts, Department of Biological Sciences the University of Alabama

Obtaining adequate input material for long-read genome sequencing is a significant problem when aiming to generate high-quality genomes from small-bodied organisms. Multiple displacement amplification (MDA) is an in vitro technique that makes use of phi29 DNA to amplify minute amounts of DNA to micrograms of DNA suitable for long-read sequencing. Combining this technique with the accuracy and length of Pacific Biosciences HiFi reads we can produce complete and contiguous genomes of small-bodied organisms. We demonstrate the efficacy of this approach comparing a genome of the model nematode Caenorhabditis elegans generated from MDA DNA from just one-half specimen (102 Mb assembly; 336 contigs; N50 = 868,123 bp; L50 = 39; BUSCO_nematoda C:94.9%, S:92.2%, D:2.7%) with a genome obtained via sequencing a pool of worms. We demonstrate comparable coverage across regions of varying GC richness and repeat content. Using this technique, we also sequenced the genome of the meiofaunal gastrotrich *Lepidodermella squamata* (122 Mb assembly; 157 contigs; N50 = 3.9 Mb; L50 = 13; BUSCO_metazoa: S: 78.0%, D: 2.8%). The genome of *Lepidodermella squamata*, an emerging model system, gives valuable insight into Gastrotricha's relationship to other lophotrochozoan phyla such as its proposed sister group relationship to Platyhelminthes. As well, recovery of the Hox cluster, analysis of gene family evolution, and characterization of repeat families provides valuable insight into the evolutionary history of the group.

Evaluation of various short read genome assemblers on sea slug genomic data Comparative genomics of three Scurrinid limpets (Patellogastropoda).

Padmanabhan Mahadevan, Dept. of Biology, University of Tampa, Tampa, Florida

Elysia crispata is a photosynthetic sea slug that consumes green algae and then sequesters chloroplasts from the algae in special cells lining the digestive tubules, in a process called kleptoplasty. This sea slug can photosynthesize using stolen chloroplasts for 3-4 months after feeding. We used Illumina short read sequencing to determine the genome of this sea slug and evaluated the performance of various short read genome assemblers on this sea slug genomic data. The short read data was composed of 455 million reads (~150bp length) and 132GB total size. All analyses were performed using a cloud server hosted on Vultr which had 256GB RAM and AMD CPU (2.85GHz, 24 cores). Before the data was fed into the genome assemblers, data cleaning was performed by removing the mitochondrial and chloroplast reads from the main data set using BBMap. The reads were then mapped to a closely related reference genome (Elysia chlorotica) using the BWA short read aligner and the reads that aligned to the reference were kept for downstream analyses. The genome assemblers evaluated were MEGAHIT, SPAdes, ABySS, MaSuRCA, Clover, Platanus allee, Mini SR, Wengan, IDBA, SOAPdenovo, Geneious, GATB-Minia and Discovar denovo. The top 2 genome assembly programs based on BUSCO completeness and total number of contigs were MaSuRCA and MEGAHIT. MaSuRCA reference assisted, MaSuRCA and MEGAHIT produced the assemblies with the highest percent of complete and partial core genes with the sea slug data. However, they are still highly fragmented given the total number of contigs in the final assemblies. The MaSuRCA assemblies took 15 hours, but produced the best assembly compared to MEGAHIT which took 3 hours. MaSuRCA produced the best assembly with reference assisted mode, suggesting that reference assisted assembly may be the best option when a suitable reference genome is available.

Covering the bases: Extracting metazoan UCEs from low-coverage whole genome sequencing data

Arianna Lord, Harvard University

As a result of high throughput sequencing, researchers have several options for generating genome-scale data for phylogenetic inference. One of the less lab intensive of these methods is genome skimming, an approach which typically relies upon capturing high copy number mitochondrial, and in some instances, nuclear genes from low coverage whole genome sequence data. Alternatively, using hybrid capture of ultra-conserved elements (UCEs) is a popular and effective method of generating robust phylogenies and resolving organismal relationships from population level relationships to deep time, especially for many invertebrate taxa. In the standard UCE protocol a target enrichment step in library preparation is used to select DNA fragments containing UCEs for sequencing. However this protocol can be cost-prohibitive. Depending on your organismal group of interest, a probe set will need to be purchased, or if not available, one will also need to be designed and tested. To circumvent these barriers, we test the feasibility of using bioinformatics to capture core metazoan UCEs from low to mid coverage genomic sequencing data. To do this we first designed a UCE probe set from genomes spanning 25 metazoan phyla, then tested the probe set in silico against metazoan genomes. Here we share our work investigating how different variables impact the feasibility of using bioinformatics to extract these UCEs from sequence data, in terms of the number of UCEs retrieved and the generation of informative datasets for phylogenomic inference. Variables we investigate include genome characteristics, such a size, repeat content, and GC content, the position and span of your target group in the metazoan tree, and level of sequencing coverage. We also illustrate how this approach would work in practice with two datasets from the phyla Priapulida and Onychophora.

Resolving haplotypes in invertebrate genome assemblies: applications to parthenogenetic species
Nadège Guiglielmoni, Universität zu Köln

The field of genome assembly has been thriving with the continuous improvement of sequencing methods, and chromosome-level assemblies are now routinely obtained. The current standard for genome assembly is to generate collapsed assemblies, in which homologous chromosomes are represented by a single sequence. While collapsing haplotypes is straightforward for low-heterozygosity genomes, this approach is often suboptimal for non-model invertebrate genomes with higher levels of heterozygosity. The challenge of collapsing haplotypes brings into question whether these assemblies should still be sought for rather than phased assemblies, in which all haplotypes are included. Previously, the error rate of low-accuracy long reads prohibited the discrimination of errors from alternative haplotypes, but highly accurate long reads, such as PacBio HiFi and Oxford Nanopore Q20+ reads, open new possibilities for phased assemblies.
Haplotype assemblies are a crucial resource for the study of parthenogenetic species. Sexual reproduction is the most common form of reproduction among animals, yet obligate asexual species have emerged among many invertebrate branches, including rotifers, arthropods and nematodes. Parthenogenetic species are expected to go extinct rapidly due to the accumulation of deleterious mutations and slower adaptation, but some species subsist in the absence of sex. Asexual species represent a compelling use case for phased assemblies as the lack of recombination is predicted to lead to haplotype divergence which can only be studied in haplotype-resolved assemblies.
We are generating collapsed and phased assemblies for sexual and asexual oribatid mites and nematodes. For oribatid mites, we obtained highly contiguous phased assemblies using PacBio HiFi and TELL-seq linked reads from single individuals. For nematodes, which can be cultivated, we generated highly contiguous and chromosome-level phased assemblies using PacBio, Nanopore and Hi-C reads. These haplotype assemblies will be used to decipher how these species transitioned to asexuality and how they adapt in the absence of sex.

The wet-lab processes behind 1000 high quality reference assemblies: adaptations for Aquatic Symbiotic Genomics
Caroline Howard, Tree of Life programme, Wellcome Sanger Institute, UK

The Tree of Life Core Laboratory team have been systematically developing and applying standardised protocols to thousands of species, with the aim of providing the data required for reference level genome assembly. Having completed and released 1000 genomes, and with thousands more in the pipeline, the protocols developed and the method of their application is detailed and described. A suite of modular processes has been developed to cover sample preparation, homogenization methods and guidelines, High Molecular Weight DNA extraction and processing, subsampling for HiC, and RNA extraction, which are available in protocls.io.
The application of these protocols for the Moore Aquatic Symbiosis Genomics project has proven challenging, aiming to provide data sufficient for reference level genome assembly from host and symbiont(s) in parallel from a broad range of organisms. Many adaptations have been required in order to successfully process samples, not least because the challenges occur at all parts of the pipeline: How to estimate the genome size of a mixed sample? How do you collect aquatic samples and store them under optimal conditions on a boat? Which method will homogenisation corals? How can air dried lichen can be weighed meaningfully and homogenised correctly? How can DNA be extracted from jellyfish and sponges that is sufficient for long read sequencing? Where in this sample does the symbiont reside?

The approaches used in these circumstances will be described, and whether they were in the end successful.

Participate with GIGA Community by Registering with the GIGA NCBI BioProject and Genomes on a Tree (GoaT) Resources - A Guided Quickstart.
Jeffrey Robinson, University of Maryland, Baltimore County

The GIGA community engages in a variety of -Omics projects, with questions ranging from applied fisheries to ecosystem dynamics and population genetics. Given this proliferation of research goals, it is critical to identify potential collaborators, utilize data available from previously published genomes, and avoid duplication of efforts. Proper metadata curation is also critical for data reproducibility. Registration of metadata from individual sequencing efforts facilitates this. The GIGA community is pursuing these goals through its participation as a member of the Earth Bio-Genome Project (EBP) and by linking individual collaborator projects with GIGA's NCBI BioProject (PRJNA649812). Genomes on a Tree (GoaT) is a new resource developed by the Tree of Life Programme. Designed to collate genome metadata for the Darwin Tree of Life (DToL) and Aquatic Symbiosis Genomics projects (both EBP members), GoaT has grown to function as a dashboard for GIGA NCBI BioProject-linked projects and progress tracker for EBP initiatives.

In the first half (30 minutes), we will provide an introduction to GIGA's NCBI BioProject, the Earth BioGenome Project (EBP), and the Genomes on a Tree (GoaT) resources. In the following half (30 minutes), we will show how to submit an NCBI BioProject and link a BioProject to GIGA. Common GoaT use cases will be demonstrated using current GIGA BioProjects. Tasks include: 1) Finding which species on a target list have already been sequenced to the desired standards, and 2) Finding sequencing status of different projects to help coordination between sample collectors and sequencing centres.

For GIGA-V, we encourage all GIGA members to register their own projects with NCBI BioProjects, link their projects to the GIGA BioProject, and how these activities can benefit the entire GIGA community. We will offer online documentation and guides to accompany the session. Bioinformatics Office Hours can be arranged on-site, in conjunction with other bioinformatics presenters as well.

Professional Development Panel: Transitioning to your next steps and transferrable skills
Kate Castellano, Gloucester Marine Genomics Institute

The goal of this panel is to provide scientists from a variety of professional (academia, industry, non-profit etc) and personal backgrounds that will be available to answer questions for graduate students and postdocs. Panel topics will focus on: 1) transitioning to your next steps and 2) transferrable skills that can help make you stand out. However, this panel is meant to support all GIGA students so questions covering all topics are welcome! Panel members include: Vanessa Gonzalez (Smithsonian, Computational Genomics Scientist), Wayra Navia (PacBio, Territory Account Manager), Kevin Kocot (University of Alabama, Associate Professor) and many more!

Additionally, short 2-3 minutes videos will be available on the GIGA slack from professionals not attending the meeting including: Shelly Wannamaker (Gloucester Marine Genomics Institute, Research Scientist I), Zak Swartz (Marine Biological Laboratory, Assistant Scientist), Menchie Ablan (De La Salle University, Professor), Aabha Deshpande (Loopworm, Senior Research Associate, GIGA Ignite Fellow), Manoj Dadlani (CosmosID, CEO) and many more!

PLENARY

eDNA metabarcoding vs metagenomics: an approach to marine invertebrate monitoring in Colombia

Vanessa Yepes-Narváez

Colombia is a megadiverse tropical country with coasts in two of the most conspicuous oceans in the world. Marine biodiversity assessments have demonstrated that in overall we know about 40% of our total diversity, from which 70% correspond to fish from all ecosystems and latitudes. The baseline knowledge of most marine species has been historically provided by visual censuses and traditional monitoring techniques which require a deployment of big research platforms and the expertise from highly trained taxonomists. However, to continue supporting the marine research demands in the country and in order to provide insights of the biological trends and their response to environmental changes in short term, new methods have been tested. From 2019, Colombia started implemented eDNA metabarcoding censuses in offshore and coastal environments, focused mainly on the co-occurrence of marine fish and testing the efficacy of several mitochondrial and ribosomal markers. Results were useful for the generation of an extended species and MOTUs lists, some of them were useful for the declaration of two new MPAs in the Caribbean and Pacific. One limiting factor on the taxonomic delimitations using eDNA metabarcoding was the scarce genetic databases available and the lack of understanding about the species population dynamics, for instance most results were provided to the extent of MOTUs lists.

For this reason, in 2021 the eDNA lab of INVEMAR, started an initiative for the generation of 12S genetic database from fin tissue and ichthyoplankton collected on board of several offshore campaigns as a cost-efficient strategy to gather a larger sample size of coastal and offshore fish. That initiative also led to the creation of the first marine zooplankton genetic database of Colombia in which genomic DNA from several pelagic invertebrate phyla from both Caribbean and Pacific were sequenced, and their taxonomic-level metadata is now publicly available through BoldSystems platforms.

On this later development, we performed an ambitious study in La Guajira (North Caribbean), in which we compared the efficacy of invertebrate eDNA metabarcoding detections from the filtration of over 3000L of seawater and the taxonomic-level inventories, as well as the creation of a larger genomic database from a wide range of zooplankton phyla (crustaceans, cnidarians, bryozoans, equinoderms, molluscs, etc). Our results showed improved metabarcoding detections after the DNA database creation, however, we noticed that most of the MOTUs detected were assigned to specimens at the phylum-level rather than species when samples were analysed using 12S and 18S markers since eDNA metabarcoding relies on PCR amplifications of genes which at times result in vague of ambiguous detections.

Based on those, from June 2023 we have been exploring high-throughput shotgun metagenomic sequencing of the total invertebrate DNA to bypass the PCR-based methods' limitations and improve detection sensitivity at the species-level for our pelagic fauna in coastal and offshore areas. Preliminary results have detected the presence of a wide range of calanoid copepods species, a hydrozoan species from the order Narcomedusae, four new records of planktonic annelids and a new record of bivalve mollusc for northern Colombia.

Although, bioinformatic analysis are still being performed, we already have valuable data that promises a wider understanding on the pelagic composition in the area and undoubtably we can conclude that eDNA metagenomics provide a complete biodiversity assessment, however, is important to highlight the importance of developing genetic databases on marine invertebrates in Colombia as without them, detections will still be undetermined.

Also, we believe that the combination of both eDNA metabarcoding and metagenomics can complement the traditional biological inventories and further studies have to be carried out to reduce metagenomic sequencing costs and bioinformatic time consumption so academia and local stakeholders can also take advantage of it while increasing species lists for the Colombian marine fauna.

Poster Abstracts

P1 Genomic Analysis of Chemosensory Genes in Bees with Different Levels of Social Organization

Felipe Cordeiro Dias, Universidade de São Paulo

Insects, especially those with social behaviors, are valuable model organisms due to their diverse habitats and lifestyles. The chemosensory system and its Chemosensory Related Genes (CRGs) are crucial in biological interactions, detecting and responding to external stimuli. Genetic sequencing advances have enabled comprehensive exploration of CRGs, revealing their structure and evolution. As these genes are vital for communication, variations in their expression or presence are expected across organisms with diverse social behaviors. This study proceeds with a research of CRGs across three bee species: Apis mellifera (highly eusocial), Bombus terrestris (primitively eusocial), and Tetrapedia diversipes (solitary). The aim is to analyze CRG genes in these species, understanding their quantity and composition. Genomic data from public repositories (B. terrestris and A. mellifera) and laboratory data (T. diversipes) are used. The focus is on five chemosensory gene families: odorant receptors (ORs), gustatory receptors (GRs), ionotropic receptors (IRs), odorant-binding proteins (OBPs), and soluble chemosensory proteins (CSPs). A search across Hymenoptera's public genetic data identified these gene families. Datasets were curated for each CRG family, using significant blast hits from genome annotations. A quantitative analysis revealed CRG counts: A. mellifera had 177 ORs, 14 GRs, 10 IRs, 21 OBPs, and 6 CSPs; B. terrestris had 166 ORs, 24 GRs, 11 IRs, 23 OBPs, and 5 CSPs; T. diversipes had 151 ORs, 17 GRs, 14 IRs, 20 OBPs, and 4 CSPs. Though gene count variations existed, significance was insufficient to pinpoint family-species associations with social organization. This suggests similarity in overall gene numbers. Gene preservation likely underscores their roles in essential processes, regardless of social structures, also presenting a pattern within Hymenoptera. The distribution of gene numbers within each CRG family unveiled patterns in the Hymenoptera order, highlighting their importance in bee communication. Future insights from transcriptomic and proteomic data could enrich understanding.

P2 Comparative evaluation of the trophic activity of sea anemones (Cnidaria; Actiniaria): morphology and metabarcoding

Julia Melo Molina, Universidade Estadual Paulista

Studying the feeding habits of marine organisms in their natural habitat is a complex and mysterious task. It presents significant challenges because gaining insights into the dietary preferences and behaviors of these individuals is vital for comprehending the ecology and evolution of the species as a whole, as well as their development, reproduction, and overall trophic performance. Sea anemones, members of the phylum Cnidaria, class Anthozoa and order Actiniaria, are described as opportunistic polyphagous predatory organisms, performing ecologically significant functions in benthic food webs, whose diet represents a singular and intriguing factor for studies that provide information about their trophic role. In this research, individuals of three species of sea anemones, *Actinia bermudensis*, *Anemonia sargassensis* and *Bunodosoma caissarum*, collected in two different locations in Floria polis, Santa Catarina, were morphologically and molecularly analyzed in order to identify, describe and compare their potential feeding behavior patterns. The morphological studies comprised an important and interesting step towards the partial identification of the fragments found in the gastrovascular cavity of the specimens, mainly small crustaceans, such as from the order Amphipoda, and the molecular analysis, through metabarcoding approach, will be responsible for providing a diverse and extensive portion of the ingested organisms, illustrating the feeding variation of the groups regarding the influence of location and the species itself in its trophic performance.

P3 Mind the gap: Peru's invertebrate genomics data as an example of the necessity of more inclusive science

Pedro E. Romero, Universidad Nacional Mayor de San Marcos

Latin American countries display some of the world's highest levels of biodiversity. Peru frequently ranks at the top in terms of vertebrate species diversity, specially, birds, mammals, reptiles, and more. Nevertheless, quantifying the diversity of invertebrate species in Peru has been a challenge, resulting in limited accuracy. The emergence of high-throughput sequencing technologies is revolutionizing biodiversity studies. However, their utilization within biodiverse countries of the Global South is still in an early stage.

In this study, I search into the NCBI BioSample database to obtain the genomic data available for invertebrate species that were possibly collected in Peru. My search yielded over two thousand records across five phyla: Annelida, Arthropoda, Mollusca, Nematoda, and Platyhelminthes. The majority of the records (98%) belonged to Arthropoda. Surprisingly, only one arthropod species (*Penaeus vannamei*) had its genomic resources information submitted by a Peruvian institution.

The generation of genomic information from species collected in Peru is predominantly attributed to research institutions in the USA. For instance, the University of Illinois at Urbana-Champaign (Hemipteroid Insect Assembling the Tree of Life Project), UT Southwestern Medical Center (Genomics-guided refinement of butterfly taxonomy project), and the City College of New York (ButterflyNet initiative). German institutions like the Koening museum and the European Bioinformatics Institute in the UK also contributed with genomic data. Conversely, the involvement of Peruvian researchers and institutions in such initiatives seems limited.

It is imperative to afford invertebrate researchers in the Global South, including Peru, the opportunity to be involved in genomic sequencing projects that use native species. The decreasing costs of sequencing, the proliferation of open and accessible bioinformatics tools, and the establishment of robust North-South and South-South collaborations will foster future invertebrate sequencing projects in Peru and Latin America that considers local researchers.

P4 Genome sequencing of blowflies: new resources for evolutionary studies of trophic specialization

Diniz Lima Ferreira, University of São Paulo

One of the greatest challenges in biology is to understand the genetic basis of complex phenotypes. Blowflies (Diptera: Calliphoridae) represent a unique and important case in evolutionary biology due to their diverse feeding habits and the rapid evolution throughout the group's phylogenetic history. Blowfly larvae exhibit three important feeding behaviors: parasitic (feeding on living tissue of vertebrates), necrophagous (feeding on decaying organic matter), and facultative parasitic (showing both parasitic and non-parasitic habits). Despite the veterinary implications they pose by infesting wounds of domestic animals, and their importance in sanitary and forensic contexts through colonization of carcasses, the origin and evolution of their feeding habits is still vastly understudied. To address this gap in our current knowledge, we sequenced the genome of two facultative parasitic species, *Chrysomya albiceps* and *Lucilia eximia*, alongside two exclusively necrophagous species, *Chrysomya putoria* and *Chrysomya megacephala.* We employed whole genome PacBio HiFi reads for de novo assembly with hifiasm. The sequenced genomes exhibit great quality, with coverage of at least 58x and a minimum N50 of 1.5Mb. For C. albiceps, we assembled a chromosome-scale genome using the HiRise pipeline with data from Dovetail OmniC reads based on a chromatin fixation and proximity ligation methodology. In this case, we were able to assemble a genome with coverage of 78x, six chromosome-length and 297 unplaced scaffolds. The four new genome assemblies of blowfly species greatly advance our knowledge on the genetic architecture and evolution of this complex phenotype. They will also serve as invaluable resources that will be further used for genome-wide variant analysis between populations of the same species, comparative genomics and genotype-phenotype association studies.

P5 A comparison of next generation sequencing technology and PCR for the identification of the algal sources of sequestered chloroplasts in the Sacoglossan Elysia crispate
Nicholas Curtis, Ave Maria University

Elysia crispata is a Sacoglossan sea slug which sequesters, maintains, and utilizes chloroplasts from a range of Ulvophycean algal species. Accurately identifying the source of sequestered chloroplasts is necessary for a variety of studies involving this animal. Most studies have relied on PCR based DNA barcoding techniques combined with plasmid cloning and screening to separate and sequence chloroplast encoded genes (usually rbcL or tufA). Recent studies, however, have utilized next generation sequencing (NGS) technology to broadly sequence total genomic DNA from the animals and then filter out chloroplast sequences from the resulting data to identify the chloroplasts. In this study we compare rbcL data obtained by PCR and NGS from the same animal specimens. Although the PCR method produced longer sequences (562 bp for PCR vs 150-300 bp for the NGS), NGS was able to produce 100x more sequences than PCR at a similar overall cost. The results show that compared to PCR methodology, NGS allows for more chloroplast species to be identified, and for the relative proportions of the chloroplast population to be estimated.

P6 Identifying candidate chromosomal inversions in the genus Mytilus using a linkage-chain analysis
Vanessa Garcia, Pennsylvania State University

Most marine invertebrates have a highly dispersive larval stage, which may create high levels of gene flow across species ranges. This gene flow homogenizes local gene pools thereby mitigating the effects of natural selection; yet physiological studies of near panmictic marine populations often demonstrate local adaptation. This long-standing paradox of local adaptation in highly connected marine populations that exhibit little to no population structure remains unresolved. Chromosomal inversions, in which a segment of a chromosome arm is reversed in orientation, have been implicated in local adaptation at both small scales and at large scales along environmental gradients across a diversity of taxa. This is due to the suppression of recombination in heterozygotes with one copy of the inverted arrangement and one copy of the ancestral arrangement. As a result, large haplotype blocks are maintained and local adaptation becomes possible in the face of high gene flow. Mussels of the genus Mytilus are ideal candidates for this line of inquiry as high quality reference genomes have been published for several species. These sessile, intertidal species are often distributed across environmental gradients both within a single location (tidal zones) and across latitudinal gradients spanning the speciesâ€™ geographic ranges. Additionally, local adaptation to temperature and salinity gradients has been discovered in previous ecophysiological studies. Using a linkage chain analysis approach, based upon genome wide synteny, we present preliminary results from our assessment of disruptions in the conservation of gene order between species of the genus Mytilus to identify candidate inversions for subsequent analysis.

P7 Repeatome evolution in Ceriantharia genomics (Anthozoa:Cnidaria)
Jeferson A. Duran-Fuentes, São Paulo State University

The Ceriantharia clade (Anthozoa:Cnidarai) includes ~55 currently valid species. With a highly debated phylogenetic position within the Anthozoa group, there is a general consensus that ceriathinds are one of the earliest branches of the cnidarian tree of life. Taking into account their peculiar mitochondrial genome (linear and fragmented, one of the biggest in nucleotide size among metazoans), it is of high interest to describe nuclear genomic content as well. This project sequenced five cerianthid species representing representing main phylogenetic clades (Penicillaria and Spirularia): families Arachnactidae (Arachnanthus sarsi) and Cerianthidae (Cerianthomorphe brasiliensis, Cerianthus sp, Ceriantheopsis lineata and Pachycerianthus magnus). Our strategy included general DNA extractions using high-salt precipitation and Illumina© sequencing (short reads, paired-end). From these datasets, we estimated genome sizes using k-mer strategies and analyzed general genome traits using several bioinformatic tools (repetitive content). Genome sizes were estimated in mid-values anthozoan scale (~500 megabases) with repeatome content ~35%. Our initial results indicate a highly stable genomic condition, even for these long-lasting lineages. Subsequent studies will illuminate hypotheses about mechanisms and processes regarding the Ceriantharia genome evolution in particular and Anthozoa-Cnidaria in general.

P8 **A genomic framework for Ceriantharia evolution**
Jeferson A. DurÃ¡n-Fuentes, São Paulo State University

Ceriantharia is an anthozoan clade with a relatively small number of species (~55 extant species) and a relevant evolutionary profile. Because of its alternative phylogenetic affinities, it would be related to ancestral traits and early trends on molecular divergence on main cnidarian clades. To establish a genomic database and related knowledge on this group, we prioritized a list of species to sequence both RNA and DNA sources. We based our approaches to maximize specimen access and phylogenetic representativeness; it included a total of 11 specimens, representing main ceriantharian clades (Spirularia, Penicillaria) from families Arachnactidae (Arachnanthus, Isarachnanthus), Cerianthidae (Ceriantheomorphe, Ceriantheopsis, Cerianthus and Pachycerianthus) and Botrucnidiferidae (Botruanthus mexicanus). Using a short read sequencing strategy, we were able to collect basic data for genomic and transcriptomic studies, taking into account genome size estimation, repeatome analysis, genome skimming (mitogenomics and phylogenomics) and differential expression, among others. Together with phenotypic and historical data (ex., paleoclimatics), we are establishing a well-grounded source for molecular information as well as evolutionary hypotheses. With our approach we expect to enhance biological knowledge for one of the main anemone clades.

P9 **Annotated genome of the sea anemone Actinostella sp. nov. (Le Sueur, 1817) (Cnidaria, Actiniidae) from Western Atlantic Ocean**
Jeferson A. DurÃ¡n-Fuentes, São Paulo State University

The sea anemone Actinostella flosculifera (Le Sueur, 1817) (Actiniaria) is characterized by the presence of a fairly wide marginal ruff that is formed by a number of short or long series of small frond-like papillae, column more or less elongated, usually with adhesive verrucae in its upper part. Currently, A. flosculifera has a wider distribution compared to its nine congeners, it is considered a single, morphologically similar species across West America and East Africa, but with a high chromatic variability. Our preliminary results on genetic and taxonomic comparison between Brazilian and Mexican specimens using three mitochondrial (12S, 16S, and COI) and nuclear (18S and 28S) markers, indicate that these represent different species. Therefore, it suggests that the diversity in form and color within A. flosculifera may hide still unrecognized species diversity. This project aims to facilitate the study of population genetics and systematics of the Atlantic Actinostella complex; we have sequenced, assembled and annotated the whole-genome of a single individual of Actinostella sp. nov. from Saco da Ribeira, Ubatuba (SÃ£o Paulo, Brazil), using two methods (Illumina and Oxford Nanopore) with long and short reads. It is expected that this study will contribute to the knowledge of the species, and to understand its evolutionary history and molecular composition in more detail

P10 The Arachnid mind: Insights into embryonic brain development in Parasteatoda tepidariorum
Jessica Kolbe

Spiders have evolved a huge variety of locomotion and prey capture methods and associated behavioural biology. Little is known how this diversity is reflected in the morphology and development of the central nervous system, especially the brain. The components of the central nervous system of adult spiders are intimately fused and are mainly concentrated in the prosoma. However, during embryonic development the segmental primordia, including those of the anterior brain region and of the opisthosomal segments, are still well separated and can be studied in more detail. Especially the formation and development of the anterior portions of the brain, including its putative integration centres could provide insight in the evolution of central nervous system morphology in relation to the diversification of locomotion and prey capture behaviour.

Limited research has been done on the embryonic and postembryonic brain in our model spider species Parasteatoda tepidariorum. Studies of several key factors of head allocation and head segment development have already shown, that anterior development uses some conserved mechanisms that are also known from other arthropod species, but there are few detailed studies of brain morphology and development of embryonic and postembryonic stages. Therefore, I would like to study embryonic brain development in P. tepidariorum, at the morphological as well as at the molecular genetic levels.

The aim of the project is to identify molecular genetic factors that influence brain development and its specific substructure. Does a divergent structuring of the brain/central nervous system already take place in the embryos of different spider species? For this purpose, candidate genes/marker genes known in the model organism Drosophila melanogaster to be involved in the formation of brain anatomy will be studied in P. tepidariorum. Using molecular cloning, in situ hybridisation, immunocytochemistry and histological sections, candidate genes and their role in brain development will be studied.

P11 The microbiome of the Tampa Bay sponge, Chondrilla nucula, sheds light on early metazoan holobionts.
Haydn Rubelmann, University of Tampa

Increasingly, sponges have been studied due to the natural products isolated from their microbial communities. These studies primarily focus on the bacterial portions of their communities while ignoring other members such as fungi and viruses. Additionally, they tend to rely solely on DNA sequencing in their quest. Here, we describe the prokaryotic and fungal diversity of the Tampa Bay sponge, Chondrilla nucula, using fungal cultivation techniques, First Generation Sequencing (FGS) and Next Generation Sequencing (NGS). A total of 18 sponges and 6 water column samples from 3 different sites produced 46 cultivated fungal isolates of which, when sequenced, clustered into 16 unique Operational Taxonomic Units (OTUs) with Penicillium, an Ascomycete, being the most represented genus. An additional 48 fungal OTUs were found through NGS with the taxa in highest relative abundance being a Basidiomycete from the genus Malassezia. Only one OTU was shared between the cultivated isolates and NGS features, showing the need to perform both methods (cultivation and sequencing) when describing a microbiome. 16s rRNA NGS produced 258 OTUs, with the most abundant OTU belonging to a marine group of uncultured Gammaproteobacteria followed by two Cyanobacteria: Cyanobium and Synechococcus. The sponge-specific Bacteria phylum Poribacteria are also represented but are much less abundant. Among the 3 populations of sponges collected, core symbionts are found and remain distinct from the surrounding water columns. Of the abiotic factors measured, depth had the largest impact on community structure with a decrease in abundance of photoautotrophs in sponges sampled from lower depths. This study is the first to describe both fungal and prokaryotic communities of C. nucula from Tampa Bay, highlighting the polyphony of interactions within the most basal animal phylum and providing insights into the evolution of metazoan holobionts.

P12 Into the shadows: Functional genetics of the spider molting gene cascade (Parasteatoda tepidariorum)

Denise KlinkenbuÃŸ, University of Giessen

Molting controlled by ecdysteroid hormones is a key process in the lifecycle of all ecdysozoans, and is essential for growth or metamorphosis. In both Pancrustacea and Arachnida, the 'Halloween genes' (HG) are conserved components of the ecdysteroid synthesis pathway. HGs encode cytochrome P450 enzymes and, along with other genes involved, are expressed in the prothoracic gland of Drosophila or the Y-organ of crustaceans.

To study the role of the HGs in the spider model organism Parasteatoda tepidariorum, the mRNA expression of the HG homologs was localized using WISH on late-stage embryos and vibratome sections of subadults. Knockdown experiments with parental RNAi were performed to establish the function of shadow in embryonic development. Additionally, subadult males were injected with dsRNA of the detectable HGs to elucidate the function during postembryonic development.

Embryonic expression of HGs shows a consistent and distinct pattern in a medial stripe close to the dorsal opisthosomal surface, which resembles the migrating pericardial cells during dorsal closure, suggesting a role in heart development. In addition, gene expression is detected in a symmetrical expression pattern in the developing brain of P. tepidariorum. Genes displaying embryonic expression are also detectable in Drosophila embryos, whereas genes without pattern are not expressed in the fly either.

Knockdown of shadow resulted in increased embryonic lethality or fatal molting complications in hatchlings during the first ecdysis. Surviving spiders showed delayed molting cycles and remained smaller than the control. Likewise, the phenotype of injected subadult males included delayed molting cycles, incomplete molts and behavioral abnormalities if ecdysis did not occur within a predetermined time. The observed molting defects in RNAi knockdown animals demonstrate that at least shadow is involved in spider molting and suggests a conserved role in the spider ecdysteroid synthesis pathway.

P13 Comparative Analyses of Mitogenomes from Ligia Isopod Species

Carlos A. Santamaria, The University of Tampa

The mitochondrial genomes of isopods are known to exhibit unique gene patterns and gene rearrangements that differ from the pan-crustacean ground gene arrangement. Distantly related isopod genera have been shown to differ in their mitochondrial gene patterns, with rearrangements such as the translocation of genes such as NAD1 and the 12S rDNA gene, and the loss of tRNA genes being common. To our knowledge, previous work been limited to comparisons of the mitochondrial genomes of species across genera and families, leaving unclear whether mitochondrial gene rearrangements occur amongst closely related species. Herein, we examine whether species in the isopod genus Ligia exhibit mitochondrial gene rearrangements and whether any such events are shared by closely related species. Ligia comprises âˆ¼50 species, most of which inhabit the supralittoral zone of rocky intertidal habitats. In this study, we used genome skimming approaches based on Illumina reads to de novo assemble the mitochondrial genomes of 15 Ligia species from around the world. Mitogenomes were annotated using the MITOS Web Server and examined for gene rearrangement events (e.g., gene losses/gains). Gene rearrangement events were then plotted on a maximum likelihood phylogeny of Ligia isopods reconstructed in RAxML v8.0.0 using ribosomal and protein coding mitochondrial genes. We report not only the occurrence of several mitochondrial gene arrangements amongst Ligia species, but also patterns that suggest these events exhibit phylogenetic signal.

P14 The complete mitochondrial genome of the coral Madracis aurentera
Sofia Giordani, Clemson University

Madracis aurentera is a reef builder coral in shallow-water habitats of the Caribbean Sea that provides refuge to invertebrates and fishes. In this study, we assembled and characterized in detail the mitochondrial genome of M. aurentera. The program GetOrganelle assembled and circulared the mitochondrial genome of M. aurentera with a coverage equal to 47x and 102x per kmer (=151 bp) and nucleotide. The mitochondrial genome of M. aurentera is 16,997 bp long and encodes 13 protein coding genes, 2 transfer RNAs, and two ribosomal genes. Based on protein coding genes, the phylogenetic position of M. myriaster among hard corals (Scleractinia) was examined. Madracis aurentera and its congener M. myriaster formed a well-supported clade sister to other corals belonging to the genus Pocillopora. Our analysis supported the monophyletic status of the family Pocilloporidae to which the genus Madracis belongs. This new genomic resource will support bioprospecting and biomonitoring activities focusing on M. myriaster using state-of-the-art environmental DNA that, in turn, is needed to support the development and implementation of conservation plans targeting this reef-formingcoral.

P15 Kill it with venom: Embryonic development of venom glands in the spider Parasteatoda tepodariorum
Franziska WÃ¶hrmann-Zipf, Justus-Liebig-University Giessen

Spiders are a morphologically diverse group of arthropods, adapted to a wide range of habitats and lifestyles. One reason for their evolutionary success is their prey-hunting strategy - they incapacitate or kill their prey with venom. The venoms are often of interest because of their composition and potential application in medicine. Recently, interest has focused on the venom producing organ - the venom gland. The origin and relationships of spider venom glands are currently the subject of controversy. Spider venom glands are hypothesized to have evolved from salivary or silk glands precursors in early chelicerates.

The spider Parasteatoda tepidariorum will be used to study the embryonic origin and postembryonic development of the venom glands in more detail. Comparisons with other glands, e.g. silk glands, will reveal developmental and histological similarities or differences, in order to asses the possible serial homologies and evolutionary origin of the venom glands. To gain a better understanding of gland morphology and development of venom glands, high-resolution nano-CT scans will be used to construct a 3D model across all developmental stages. In addition, homologs of genes with known functions in e.g. salivary gland development in insects will be isolated from P. tepidariorum. The expression of these candidate genes in the spider will be studied on whole body preparations and vibratome sections. Furthermore, the potential role of the candidate genes in venom gland development and function will be determined by knockdown of genes with parental RNAi.

These studies will reveal the allocation and further development of the venom gland in spiders and will provide insights into both serial homology of venom glands with other spider glandular structures and direct homology with similar gland types in other arthropods.

P16 The role of large-scale gene duplications in phenotypic diversity of spiders
Chetan Munegowda, Justus-Liebig-University Giessen

Spiders are a large group of animals with more than 51,000 identified species. They are very diverse in size, colouration, web-building behaviour, venom composition, silk production, and prey catching behaviour. Chromosome-level genome assemblies are only available for about 10 species. This lack of genomic data limits our understanding of the genetic underpinnings of the evolution and diversification of these fascinating eight-legged creatures. In our study we aim to generate chromosome level assemblies for spiders occupying interesting phylogenetic positions including the mygalomorph spiders (Acanthoscurria geniculata and Ischnothele caudata) and Mesothelae trapdoor spider (Liphistius).

Previous studies have suggested that a whole genome duplication event occurred in the common ancestor of spiders and scorpions. They have also speculated that multiple duplication events took place in their descendants. Gene duplication events provide a source for new gene functions which might lead to the development of morphological novelties. Several studies also show that gene duplications in spiders have contributed to phenotypic novelties like the diversification of venom arsenal, varying silk compositions, as well as developmental processes like leg-patterning. Using the chromosome level genomes, we will systematically identify duplicate and single copy genes common for all spiders, as well as those of specific lineages. Comparative analyses across arthropods will allow us to test whether these duplications may also be involved in the evolution of phenotypic novelties.

P17 Developing a field-based soil-ecosystem health assessment based on invertebrate genome data
Lucy Jimenez, University of Cologne

Global change demands understanding soil-ecosystem health and stability, particularly for agriculture and re-cultivation sectors. The state of an ecosystem is encoded in the genes and metabolic interactions of the species living in it. In soils, these are mostly tiny invertebrates and their associated protists and prokaryotes.

The rapid progress in genomic and computational technologies and methods has opened up new opportunities for understanding and evaluating the health of ecosystems. Here, we present a novel approach using machine learning and network analysis techniques to assess soil-ecosystem health comprehensively based on genomic data and geochemical soil properties.

To train our system, we will first functionally and metabolically categorize genome skimming data from batch sequencing of soil invertebrates, associated protists, and prokaryotes from diverse geographical locations (Chile, Namibia, Germany, Sweden, and Australia). For this, high-quality reference genomes generated by the Biodiversity Genomics Center Cologne (BioC2) and under the umbrella of the Earth BioGenome project will allow us to assign predicted genes to species. Physical and geochemical measurements of soil properties will be additional data points in our networks and classification system.

Secondly, several machine-learning techniques will be employed to analyze genomic and environmental data and generate predictive models and classifiers capable of evaluating soil-ecosystem health accurately. These techniques include classification algorithms, deep learning methods, and network analysis tools.

Ultimately, our system will assess soil ecosystems' status based on cross-species genetic networks and geo-biochemical interactions in real-world field-based applications. Thus, the system will have substantial value in applied agricultural settings and biodiversity conservation and management scenarios, safeguarding the delicate balance of our planet's ecosystems.

P18 Detecting putative probiotics for corals: physiological and genomic-based approaches
Jordan Steven Ruiz Toquica

Customized probiotics represent a promising solution to sustain coral health under climate change. Here, we isolated 132 bacterial strains associated with the Caribbean coral Madracis auretenra from urban environments. Using 16S rRNA amplicon sequencing, we determined that these bacteria are affiliated with 11 genera, including Vibrio, Shewanella, Bacillus, Exiguobacterium, Priestia, Fictibacillus, Niallia, and others. We established cultures from some of these bacteria and ran a series of physiological screenings to detect traits with potential benefits for coral hosts such as catalase, pigments, antimicrobial, and the production of siderophores activities. From the 32 selected isolates, we excluded those exhibiting low growth, close relationship to coral pathogens, and redundant morphology. Seven remaining bacterial strains were used to establish a putative probiotic consortium that was tested for antagonism and assembled at a concentration of 10E+7 UFC per mL. We generated high-quality genome assemblies for these bacteria, and analyses to search for biosynthetic gene clusters related to detoxification, photo-protection, energy metabolism pathways, and biogeochemical cycling are ongoing. Preliminary assays show an improved resistance of a different coral species (Porites sp.) subjected to heat stress and treated with our customized consortium, implying ample applicability of our bacterial strains as probiotics for distressed Caribbean corals. We foresee the successful implementation of our probiotic consortium, and other consortia derived with the same approach, for coral active restoration.

P19 Histology and Cell Culture of Octocoral, *Antillogorgia americana,* to Enhance their Potential for Genomics and Conservation
Rachel Hannah Bacaner, NSU

Cnidarians have been used as model organisms in the field of developmental and molecular biology for decades. An excellent way to study the cellular biology of organisms is through cell culture. Generating continuous cell lines for rare or threatened organisms can also advance conservation goals (Ryder and Onuma 2018). However, establishing cnidarian cell cultures has been a major challenge due to the difficulty in determining the most beneficial media, antibiotics, and dissociation methods that yield viable cell types, stave off contamination, and maximize cell growth. Many questions still surround the cnidarian *holobiont*, which includes the cnidarian host, its microbiome, and algal symbionts. Culture methods require antibiotic treatments to fend off contamination that may destroy or compete with eukaryotic cell types, yet the natural microbiomes can also benefit the holobiont. Few studies address the interactions of multiple cells or how these antibiotics may be affecting the cnidarian microbiome in cnidarian cell culture. Additionally, characterizing the dominant taxa in cnidarian cultures has not been well studied. Using the cnidarian model organism *Aiptasia pallida* and octocoral species *Antillogorgia americana*, this study will explore how cnidarian primary cell cultures interact with natural or contaminating microbiomes. This octocoral species is common on the Florida Reef Tract and has been placed in the whole genome pipeline of the Aquatic Symbiosis Genome (ASG) Project (https://www.sanger.ac.uk/collaboration/aquatic-symbiosis-genomics-project/). Specifically, I will aim to investigate and manipulate various cell culture methods to enhance cnidarian cell growth as well as characterize the dominant contaminating taxa or bacteria and other microbes the cnidarians have within their natural microbiome using 16S High Throughput Sequencing (HTS).

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