

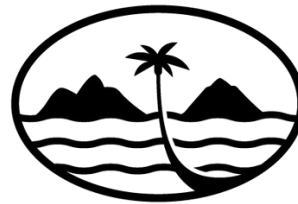
Department of Oceanography Graduate Symposium

**CMORE Moore Conference Center
May 4th & 5th**



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exploring connections
and learning community**

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Department of Oceanography Graduate Student Symposium

CMORE Moore Conference Center

May 4th (Day 1)

8:00

Doors Open

8:30

Dr. Margaret
McManus

Dept. of Oceanography Chair's Welcome

Lightning Talks

8:45

Reece James

High resolution in situ quantification and classification of particles during oligotrophic phytoplankton blooms

8:52

Eleanor Bates

Investigating the sources of lithogenic particles at Station ALOHA using trace metal elemental ratios

1. Chemical Tracers Through Time and Space

9:00

Corinne Hite

Lithium isotope and elemental partitioning in inorganic calcite and aragonite

9:15

Ching-Tsun Chang

Understanding long-distance migration patterns of molids in the western Pacific Ocean using isotopic analysis

9:30

Blake Stoner-
Osbourne

The utility of $\delta^{13}\text{C}$ Essential Amino Acid (EAA) analysis for tracing nearshore primary production through pelagic food webs in Hawaii

9:45

Coffee Break

2. Exploring Communities of the Twilight Zone

10:00

Elizabeth Miller

Transformations of sinking and suspended particulate organic matter and associated microbial communities at two sites in the Northeast Pacific

10:15

Michael Dowd

Seasonal variation of the trophic ecology in the Clarion-Clipperton zone characterized by compound-specific isotope analysis of amino acids of particles and zooplankton

10:30

Alexus Cazares

Spatial and temporal variation in zooplankton biomass and community composition in the eastern clarion-clipperton zone

10:45

Coffee Break

11:00

Victoria Assad

Micronekton community structure in an eastern Clarion-Clipperton Zone (CCZ) mining site, a region with a pronounced oxygen minimum zone

3. From DNA to Ecosystems

11:15

Maria Steadmon

The spatial and temporal distribution of *Staphylococcus aureus* along a tropical Hawaiian watershed

11:30

Anamica Bedi de Silva

Preliminary evidence of small- and large- scale mutations associated with *Micromonas* immune to lytic infection

11:45

Andrian Gajigan

A virus with an exceptionally long tail discovered in the North Pacific Ocean

12:00

Gabrielle Stedman

How much is enough? Environmental DNA baseline surveys prior to deep-sea polymetallic nodule mining

12:15

Lunch

@ CMORE Breezeway and Biomed Courtyard

4. Surviving the Extremes

13:15

Bailey Donaldson

Science and Life in the Arctic Circle on Svalbard

13:30

Lauren Block

Evaluating the effect of a species shift on zooplankton recruitment during the winter-to-spring transition in a high latitude environment

13:45

Michaela Setzer

Assessing the influence of sulfide minerals on prokaryotic nitrogen cyclers from an inactive hydrothermal massive sulfide environment

14:00

Coffee Break

Workshop

14:15

Dr. Craig Nelson

Trade-offs in grant writing: finding balance in narrative, feasibility, novelty, and accessibility

16:00

Pau Hana

@ Biomed Courtyard

Department of Oceanography Graduate Student Symposium

CMORE Moore Conference Center

May 5th (Day 2)

8:00

Doors Open

5. Developing Novel Methodologies

8:30

Ally Morris

Evidence of the Proton Flux Hypothesis: Adaptation of autonomous sensors to monitor Hawaiian corals under various chemical perturbations

8:45

Connor Shea

Embracing Complexity in Mesopelagic Energy Supply: A stable isotope perspective

9:00

Dianne Josephine

Evaluation of the historical conditions at the lateral boundary of the California Current System as represented by Earth System Models

9:15

Kyle Conner

Data from disorder: developing a Raman-based calcifying fluid saturation state proxy for Mg-calcite organisms

9:30

Coffee Break

GES Symposium

GES Symposium

10:00

Come support the graduating GES students as they present their thesis research findings!
@ MSB 114

12:30

Lunch

@ CMORE Breezeway and Biomed Courtyard

6. Connecting Coastal Communities

13:30

Nicolas Storie

Uncovering the Microbial Fingerprints of Coastal Pollution: differentiating wastewater sources using 16s amplicon sequencing

13:45	Christina Comfort	Aspects of the Island Mass Effect near O‘ahu, Hawai‘i: Picoplankton biomass estimates and preliminary assessment of in situ fluorescence to indicate nearshore wastewater pollution
14:00	Lani Musselman	Understanding phytoplankton community and productivity dynamics in a Native Hawaiian fishpond
14:15	Oscar Ramfelt	Using Kāne‘ohe Bay as a model system to study the ecotypic differentiation of SAR86 marine bacteria
14:30	Ryo Dobashi	Air–sea gas exchange in a seagrass ecosystem – results from a ³ He/SF ₆ tracer release experiment
14:45	Coffee Break	
Workshop		
15:00	Reece James	Diversity, Equity, and Inclusion: Awareness and Skills
Closing Remarks		
16:30	Andrea Kealoha	The path forward: Strengthening science through community and culture
17:30	Reconvene for Celebration at TG’s @ MSB Lanai	

High Resolution In Situ Quantification and Classification of Particles during Oligotrophic Phytoplankton Blooms

Reece James, James Allen, Fernanda Hendericx, Daniel Muratore, Angelicque White

Understanding the size, distribution, and identity of oceanic particles is critical to modeling biological processes from particle flux to food web dynamics. The ability to capture sinking and suspended particles, either optically or physically, has been key to tracking carbon cycling in the upper ocean for decades. However, classical methods of particle characterization (e.g. nets, traps, and bottles) are often limited by ex situ analysis and prone to altering particles during collection. High-resolution in situ imaging technologies offer promise to expand our understanding of both living and detrital particles from the sea surface to the sea floor. Here, we utilize the Underwater Vision Profiler (UVP5-DEEP) and EcoTaxa taxonomic classification to analyze the abundance, size, and diversity of particles in the oligotrophic North Pacific Subtropical Gyre. Repeated profiles (n=12) were conducted within an anticyclonic eddy during the demise of a large-scale phytoplankton bloom. Free-floating sediment traps recorded unprecedented rates of particle export ($\sim 50 \text{ mg C m}^{-2} \text{ day}^{-1}$) for the region, while imaging flow cytometry revealed the presence of large diatoms and an array of nitrogen-fixing organisms. Here we present UVP-based estimates of the size, depth-distribution, and abundance of particles over the course of this two-week occupation. We also show the co-occurrence of organisms including foraminifera, copepods, and krill within depth zones of elevated marine snow aggregate concentrations. These results highlight successional patterns of organisms and aggregates along the decline of a mesoscale phytoplankton bloom in the oligotrophic ocean.

Investigating the sources of lithogenic particles at Station ALOHA using trace metal elemental ratios

Eleanor Bates and Nicholas Hawco, University of Hawaii at Manoa

Different sources of lithogenic materials to Station ALOHA can impact the concentrations of particulate trace metals in the upper water column because of their elemental composition. For example, oceanic basalts are enriched in iron compared to bulk continental crust, leading to different contributions of iron to the water column. The lithogenic water column particulates at Station ALOHA are thought to be dominated by continental crustal material, arriving via Asian dust deposition. The Ti:Al ratio of particulate material has been proposed as a good identifier of lithogenic particle sources, in part because Ti is not subject to biological uptake. We collected particulate samples on 14 Hawaii Ocean Time-series cruises to Station ALOHA in the North Pacific Subtropical Gyre. We analyzed the samples for labile and recalcitrant trace metal content, including titanium and aluminum. The majority of particulate samples were enriched in Ti compared to the bulk continental crust (0.037, representative of Asian dust). Sediment trap samples measuring upper ocean particle export were also enriched in Ti relative to Al. Ti enrichment could be due to particle contributions from oceanic island basalts from the Hawaiian Islands (Ti:Al ~ 0.2) or from other unknown non-crustal sources. Multiple lithogenic sources delivering particles to Station ALOHA could result in varying trace metal concentrations due to both the elemental composition of the source and the fractional solubilities of different trace elements from that source. Furthermore, future changes in global atmospheric circulation will likely impact Asian dust supply to the region. Thus, assessing the composition and magnitude of other sources of lithogenic material to Station ALOHA is important for understanding the impact of a changing Asian dust supply on trace metal cycling.

Lithium isotope and elemental partitioning in inorganic calcite and aragonite

Corinne Hite (University of Hawai'i), Joji Uchikawa (University of Hawai'i), Sambuddha Misra (Indian Institute of Science), Richard Zeebe (University of Hawai'i)

Secular changes in the lithium isotopic concentration ($\delta^7\text{Li}$) of seawater are thought to reflect changes in silicate weathering, an important process in sequestering atmospheric CO_2 throughout geologic history. Studies have focused on the $\delta^7\text{Li}$ of marine biogenic CaCO_3 , such as the tests of foraminifera, as a tracer for silicate weathering. However, there is new evidence of additional controls on the $\delta^7\text{Li}$ and abundance of Li (Li/Ca) in the CaCO_3 of foraminifera such as pH and the concentration of dissolved inorganic carbon (DIC). This indicates a need for a better understanding of the physical and chemical controls on lithium incorporation in inorganic CaCO_3 , without the complications of vital effects from a biological system. To this end, I will present results from a set of inorganic CaCO_3 precipitation experiments. The experiments used appropriate seeds to allow precipitation of calcite and aragonite under identical conditions from a parent solution consisting of CaCl_2 , MgCl_2 , LiCl , and Na_2CO_3 . Single-parameter manipulation experiments were varied from a baseline condition to observe the individual effects of chemical parameters (pH, [DIC] and $[\text{Ca}^{2+}]$) on the $\delta^7\text{Li}$ value and Li/Ca of inorganic aragonite and calcite.

Understanding long-distance migration patterns of molids in the western Pacific Ocean using isotopic analysis

Ching-Tsun Chang/Department of Oceanography, University of Hawaii and Eastern Marine Biology Research Center, Fisheries Research Institute, Daniel J. Madigan/Department of Biological Sciences, University of Windsor, Windsor, Aaron B. Carlisle/School of Marine Science and Policy, University of Delaware, Natalie Wallsgrove/Department of Geology and Geophysics, University of Hawaii, Jeffrey C. Drazen/Department of Oceanography, University of Hawaii, Wei-Chuan Chiang/Eastern Marine Biology Research Center, Fisheries Research Institute, Yuan-Hsing Ho/Eastern Marine Biology Research Center, Fisheries Research Institute, Brian N. Popp/Department of Geology and Geophysics, University of Hawaii

Molids comprise a high bycatch in fisheries worldwide and they are expected to decline globally by 30% over the next three decades. Knowing their trophic ecology helps explain how molids interact with the environment under long-distance migrations. Several tagging studies and the spatiotemporal size distributions of *Mola mola* and *M. alexandrini* (*Mola* spp.) suggest they undergo long-distance migration in the Pacific Ocean. However, electronic tagging is limited to studying individual movements. Combining isoscapes with bulk tissue and amino acids stable isotope analyses can provide insights on migration and foraging of fishes at a population level. The aim of this study is to explore migration patterns of *Mola* spp. in the western Pacific Ocean using isoscapes and CSIA-AA. We constructed a nitrogen isotope isoscape estimating $\delta^{15}\text{N}_{\text{phytoplankton}}$ values. We calculated $\delta^{15}\text{N}_{\text{molids}}$ values that are in steady state with the $\delta^{15}\text{N}_{\text{phytoplankton}}$ values. We assume that measured $\delta^{15}\text{N}_{\text{molids}}$ values of residents match the predicted $\delta^{15}\text{N}_{\text{molids}}$ isoscapes; if they do not then there is a possibility of a migrant population. Measured $\delta^{15}\text{N}_{\text{molids}}$ values of fish collected from Taiwan and Japan are here compared to the predicted $\delta^{15}\text{N}_{\text{molids}}$ values. Most of the measured $\delta^{15}\text{N}_{\text{molids}}$ values of large individuals in Japan overlap the predicted $\delta^{15}\text{N}_{\text{molids}}$ values suggesting that they are resident fish. Some large individuals from Japan have high measured $\delta^{15}\text{N}_{\text{molids}}$ values that overlap the predicted $\delta^{15}\text{N}_{\text{molids}}$ values in Taiwan, suggesting they recently migrated to Japan from Taiwan. The measured $\delta^{15}\text{N}_{\text{molids}}$ values from fish collected in waters surrounding Taiwan overlap with predicted values suggesting most are residents. Some individuals from Taiwan have high measured $\delta^{15}\text{N}_{\text{molids}}$ values that are consistent with molids that had recently migrated from the warm pool west of Taiwan. Multivariate cluster analysis based on the source AA $\delta^{15}\text{N}$ values categorized those specimens into three groups, including Japan residents, Taiwan residents, and recent migrants.

The utility of $\delta^{13}\text{C}$ Essential Amino Acid (EAA) analysis for tracing nearshore primary production through pelagic food webs in Hawaii

Blake Stoner-Osborne (Department of Oceanography, University of Hawaii at Manoa, Honolulu, HI 96822), Jeffrey Drazen (Department of Oceanography, University of Hawaii at Manoa, Honolulu, HI 96822), Brian Popp (Department of Earth Sciences, University of Hawaii at Manoa, Honolulu, HI 96822)

Tropical Pacific Islands host productive nearshore ecosystems that show consistently higher phytoplankton biomass over background oceanic conditions in the North Pacific Subtropical Gyre. This near-ubiquitous phenomenon is coined, “The Island Mass Effect,” and is thought to be the primary mechanism responsible for observed increases in zooplankton, micronekton, and pelagic top predator biomass around island flanks. However, we currently lack the analytical techniques to quantify the contribution of island-associated primary production to the diets of pelagic zooplankton, micronekton, and pelagic predators that presumably take advantage of increased nutritional resources around island flanks. In this study, we attempt to use $\delta^{13}\text{C}$ analysis of Essential Amino Acids (EAAs) in zooplankton to establish a distinct isotopic signature for nearshore, island-derived primary production for use in estimating the amount of island-derived nutritional resources in the diets of offshore pelagic organisms around tropical Pacific Islands.

Transformations of sinking and suspended particulate organic matter and associated microbial communities at two sites in the Northeast Pacific

Elizabeth Miller¹, Kenneth Smith², Christine Huffard², Jeffrey Drazen¹, Brian Popp^{1,3},

¹Department of Oceanography, University of Hawai'i at Mānoa

²Monterey Bay Aquarium Research Institute

³Department of Earth Sciences, University of Hawai'i at Mānoa

Particulate organic matter (POM) originating in surface waters is the primary food source for deep-sea organisms. As it sinks to abyssal depths it undergoes reprocessing by microbes, protozoans, and metazoans, decreasing in quantity and quality. We used a combination of compound-specific stable isotope analysis (CSIA) and microbial community barcoding to quantify the trophic transformations and associated microbial communities of POM throughout the water column at two sites in the Northeast Pacific with contrasting productivity. POM was collected in sediment traps at 50 and 600 meters above the bottom, as well as filtered into three size fractions throughout the water column. The $\delta^{15}\text{N}$ values of “source” amino acids (AAs), which are indicative of material at the base of a food web and are not affected by metazoan processing, generally increased with depth due to microbial heterotrophy.

$\delta^{15}\text{N}_{\text{SourceAA}}$ values also varied between different sizes of POM filtered in situ, as well as between filtered particles and sediment traps, suggesting that sediment traps do not capture a representative sample of POM reaching abyssal depths. Sediment trap material instead had similar isotopic signatures to surface POM and high trophic positions, suggesting that fast-sinking POM such as fecal pellets may be preferentially collected while small (<53 μm) particles are undersampled in sediment traps. Different sizes of POM also appear to host distinct microbial communities, which change significantly with depth. By identifying particle-associated microbes, as well as the ways they alter sinking POM, we can better understand the impact of microbes on material at the base of deep-sea food webs.

Seasonal variation of the trophic ecology in the clarion-clipperton zone characterized by compound-specific isotope analysis of amino acids of particles and zooplankton

Michael Dowd¹, Erica Goetze¹, Jeff Drazen¹, Brian Popp¹

¹Department of Oceanography, University of Hawaii at Manoa, Honolulu, HI 96822

A main objective of this study is to characterize zooplankton trophic ecology in the Clarion-Clipperton zone in the eastern tropical North Pacific in order to understand how sediment dewatering plumes (consisting of seafloor sediments) at mesopelagic depths associated with future deep-sea polymetallic nodule mining will impact the ecosystem in this region. We used compound-specific isotope analysis of amino acids, which is a useful tool to understand marine trophic ecology. The $\delta^{15}\text{N}$ values of source amino acids of particles and zooplankton can be used to characterize what forms the base of the food web. Size fractionated particle (0.7-6, 6-53 and >53 μm) and zooplankton (0.2-0.5, 0.5-1, 1-2, and 2-5 mm) samples from 25-1500 m were collected in March and October of 2021 via in situ pumps and 1M2 MOCNESS nets, respectively. The $\delta^{15}\text{N}$ values of source amino acids in the smallest and largest size fractions of particles differ significantly below about 200 m depth, with the smaller size fraction in deeper samples having highest $\delta^{15}\text{N}$ values. These differences in the $\delta^{15}\text{N}$ values of source amino acids can be traced into zooplankton to identify what size fractions of particles form the base of the food web at depth. The $\delta^{15}\text{N}$ values of source amino acids show during the spring, the base of the food web is predominately made up of small particles. However, in the fall, large particles instead form the base of their food web. Identifying the size fraction that forms the base of the food web is important because the sediment dewatering plume produced during deep-sea mining contains small particles and could impact the diet of deep zooplankton.

Spatial and Temporal Variation in Zooplankton Biomass and Community Composition in the eastern Clarion-Clipperton Zone

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Deep-sea mining generates midwater sediment plumes that can have wide-ranging impacts on pelagic communities, including altered ingestion for particle feeders, clogging of respiratory and feeding structures, and population level effects on animal distributions, community structure, and food webs. To establish a baseline for zooplankton communities in a region at near-term risk for mining impacts, we conducted surveys at two sites, a preservation reference zone and a test mining area, during two cruises to the NORI-D exploration area of the eastern Clarion-Clipperton Zone.

Zooplankton biomass was higher in spring, but overall biomass patterns with depth and across oxygen gradients were comparable between cruises. Biomass was structured by oxygen gradients, with high biomass in the well-oxygenated upper 100m, significant reduction across the oxygen minimum zone core (500-700m), and a modest increase at the lower oxycline (700-800m). Migrant biomass, which was predominately comprised of zooplankton in the 2 to >5 mm size fractions, was higher and patterns were more typical during spring. Community composition, as resolved by multigene metabarcoding, was significantly different across both depths and sites. Copepods dominate the assemblage, ostracods and pteropods occur primarily in the epi- and mesopelagic, and siphonophores become increasingly important in the deep mesopelagic and bathypelagic. At the reference site, scyphozoans made up a large portion of the non-copepod assemblage. Results will be discussed in the context of deep-sea mining and expanding OMZs.

Micronekton community structure in an eastern Clarion-Clipperton Zone (CCZ) mining site, a region with a pronounced oxygen minimum zone

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Micronekton, including mesopelagic fishes, are a vital part of midwater food webs and have the potential to be impacted by deep-sea nodule mining (DSM). DSM activities will have a variety of potential impacts on midwater ecosystems including sediment plumes and release of dissolved metals. Micronekton communities in the eastern Clarion-Clipperton Zone (CCZ) region have been studied very little so baseline community descriptions are needed. Utilizing a 10 m Multiple Opening Closing Net and Environmental Sensing System (MOCNESS), fish samples were collected from 0 - 1500 m day and night, at both a control and impact site in the NORI-D claim zone of the CCZ in Spring and Fall 2021. Nets were deployed based upon oxygen patterns because this region has a very pronounced oxygen minimum zone (OMZ). Seasonal differences showed higher springtime densities and biomasses of fishes, crustaceans, and cephalopods; springtime reflected juvenile recruitment, suggesting seasonal mining, particularly fall, may have the least impact. We frequently observed significant site differences suggesting the impact site may not be representative of the control site. The micronekton community in NORI-D is clearly structured by oxygen; the fish community exhibits species with daytime abundance peaks in the OMZ core and strong vertical migration patterns. The fish community displayed high rates of endemism and OMZ specialization, suggesting this site to be unique from other North Pacific regions. A 1200m discharge depth could not only affect the unique community in the 1000–1500m depth zone but additionally impact organisms adapted to extremely low oxygen levels from the input of oxygenated discharge water. Preliminary results on diversity, composition, migration patterns, and control site representation will be discussed.

The spatial and temporal distribution of *Staphylococcus aureus* along a tropical Hawaiian watershed

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(1) University of Hawai 'i at Mānoa, Department of Oceanography

(2) University of Hawai 'i at Mānoa, Pacific Biosciences Research Center

(3) Rowan University School of Osteopathic Medicine

Staphylococcus aureus is the leading source of community-acquired skin infections in the U.S., with Hawai 'i historically leading the country in these infections. Studies have shown that recreational waters are a vector for exposure to *S. aureus*. Unfortunately, knowledge is limited on tracking potential sources and abiotic influences of *S. aureus* in Hawaiian recreational waters. This study investigates the abundance and distribution of *S. aureus* and associated virulence genes through culture and culture-independent techniques with high spatial resolution across the Waimea, O 'ahu watershed, which receives a gradient of human influence. On average, *S. aureus* concentrations were significantly greater by two orders of magnitude when measured by quantitative PCR of the *femA* gene, than culture-based methods with CHROMagar. In the dry season, concentrations of cultured *S. aureus* were consistent across sites; whereas abundances of *femA*, and staphylococci antibiotic resistance and virulence genes (*mecA*, and *etB*) increased downstream likely due to increased human activity, lower streamflow, and higher residence times in wider estuarine sites. In the wet season, streamflow and rainfall rates were greater and *S. aureus* concentrations gradually increased along the watershed peaking at estuarine sites similar to the dry season. However, *mecA* and *etB* genes were highest at upstream sites with no public access, suggesting a potential zoonotic source for virulent *S. aureus* strains. Lastly, models developed in this study will help predict *S. aureus* concentrations along watersheds, enabling land stewards to more effectively apply interventions to mitigate risk and maintain public health in recreational waters.

Preliminary evidence of small- and large- scale mutations associated with *Micromonas* immune to lytic infection

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Marine microbes that are immune to lytic viral infection are commonplace in all ocean basins. However, such immunity appears to come with a fitness cost in certain circumstances. The underlying mechanisms that confer immunity may explain why these fitness costs exist. Past researchers have found, in separate studies, that mutations associated with viral resistance can occur at small- (<100kb) and large-scale (>100kb) regions of the genomes of marine microbes. Our work utilizes short- and long-read technologies to detect small polymorphisms, as well as large-scale structural variants. Thus, we compared the genomes of twenty-two lines of the marine eukaryote *Micromonas*, each genome representing different sensitivities to viral infection. Preliminary results suggest a suite of genes associated with resistant cell lines and implicate specific chromosomes that may be affected when selecting for resistance.

A virus with an exceptionally long tail discovered in the North Pacific Ocean

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and Grieg F. Steward^{1,2}

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³Pacific Biosciences Research Center, University of Hawai'i at Mānoa

Viral infections are a ubiquitous source of mortality for marine plankton, but relatively few viruses that infect phytoplankton in the open ocean have been characterized. Here we describe a novel mimivirus, PelV-1, with unusual morphological and genomic features that infect a dinoflagellate, *Pelagodinium* sp. The virion belongs to a taxonomic group of viruses, the family Mimiviridae, that contains many of the largest viruses ever discovered. The capsid of this virus has a modest capsid size (ca. 200 nm) but an incredibly long tail-like structure ranging from 300 nm to 2.3 μm—which would be the longest virus appendage described to date. Both the host and virus were isolated from the epipelagic zone of Station ALOHA in the North Pacific Ocean. The long virion tail appears to consist of an inner and outer tube but may be fragile, as it is seen on virions in fresh lysates handled gently, but not in virions that have been more aggressively purified. The virions sometimes also display a shorter (60 nm) but thicker and tapered tail, which appears to emerge from a “stargate” opening of the capsid directly opposite the attachment point of the long, thin tail. A draft genome of the virion consisting of four contigs with a total length of 397 kb was assembled and annotated and found to contain some unusual and unexpected genes. Among these are genes similar to those coding for tail fibers of bacteriophages infecting the cyanobacterium *Synechococcus*. PelV-1 also contains auxiliary metabolic genes for amino acid metabolism (e.g., aspartate and glutamine transferases), carbohydrate metabolism (ex., PEP carboxykinase in gluconeogenesis, aconitate hydratase in the TCA cycle), lipid metabolism (ex. phospholipase), and several other noteworthy genes (i.e., sulfite exporter, HSP70, and a light-harvesting complex), among others. What ecological advantages might be conferred by the extraordinarily long tail of PelV-1 and the virus' remarkable suite of metabolic genes is not yet known, but this isolate expands the scope of known morphological and metabolic diversity of viruses and suggests many more unusual marine viruses await discovery.

How much is enough? Environmental DNA baseline surveys prior to deep-sea polymetallic nodule mining

Gabrielle Stedman¹, Oliver Laroche², Lauryn Pisciotto¹, Craig Smith¹, Erica Goetze¹

1. University of Hawai'i at Mānoa, HI USA

2. Cawthorn Institute, Nelson, NZ

Large extents of the abyssal seafloor are currently allocated for mineral extraction, with the primary focus located in the Eastern Tropical Pacific, the Clarion-Clipperton Zone. This region is divided into mining claims and preservation regions, which are intended to safeguard biodiversity that might be impacted by mining. The regulatory agency, the International Seabed Authority (ISA), mandates that mining contractors collect oceanographic data -- including biological community description -- in their respective claim areas by which to document pre-impact conditions, assess preservation region suitability, and to quantify impact over time. The ISA recognizes environmental DNA (eDNA) methods as an appropriate tool for biodiversity monitoring, though eDNA has been little applied across the abyssal ecosystem and no standard of practice is currently in place for targeting metazoans. Robust, reproducible methods are required for eDNA surveys to be used for ecological description, comparison, and monitoring over time. We conducted extensive eDNA surveys in the NORI-D claim of the Clarion-Clipperton Zone from abyssal water, sediment, and the mining target, i.e. nodules. We generated over 5.78 million metazoan reads representing 6,448 species equivalents. This work collectively represents the greatest local sampling effort to date of abyssal metazoan surveyed by eDNA and aims to establish best practices for conducting baseline eDNA ecological surveys prior to human impact. We describe the metazoan community at NORI-D across substrate type and between mining and preservation regions. Our results show that substrate type and choice of genetic marker influence the community captured. Additionally, we show that intensive sampling at local to regional scales is critical for the effective use of this method on metazoans.

Science and Life in the Arctic Circle on Svalbard

Bailey Donaldson

At the start of this year, I lived in Longyearbyen on Svalbard, a Norwegian island at 78°N, to take a course on Arctic climate change at the University Centre in Svalbard. The island has a unique culture of miners, scientists, and tourists living in total darkness for four months each year under the constant threat of polar bears. This presentation shares my experience living in this town and learning how to conduct fieldwork and experiments in Arctic conditions.

Evaluating the effect of a species shift on zooplankton recruitment during the winter-to-spring transition in a high latitude environment

Lauren Block - University of Hawai 'i at Mānoa

The 2014-2016 North Pacific marine heatwave was unusual given its magnitude, longevity, and impact on marine ecosystems. The Northern Gulf of Alaska (NGA) experienced abrupt and substantial species shifts and population collapses across multiple trophic levels—including declines in commercially important fishes, marine mammals, and seabirds. Changes in the zooplankton community have been identified as a possible bottom-up driver contributing to the observed declines in upper trophic level species. Dimensional reduction analysis of eight years of zooplankton community data collected in the NGA suggests that spring zooplankton community composition differed before, during, and after the heatwave. Notably, a species shift occurred between two copepod species, *Neocalanus flemingeri* and *Calanus marshallae*, coinciding with the marine heatwave. While both species serve similar ecosystem functions as lipid-rich prey, they differ in reproductive strategy and timing. A species shift could result in the delayed appearance of nauplii, the early developmental stages. This in turn could impact the availability of winter and early spring prey for first-feeding larval fish. However, copepod nauplii remain poorly studied due to identification challenges and coarse sampling intervals, especially during winter. Biweekly sampling was conducted from early January to late March in Resurrection Bay, Alaska to investigate copepod recruitment and phenology. Zooplankton were collected from three depth strata, corresponding to regions of the water column with distinct physical properties. Nauplii were staged and enumerated for each collection date and depth. Future molecular analysis will evaluate species composition and relative abundance in three size fractions to resolve the vertical and temporal distribution of nauplii over the sampling period, placing quantitative emphasis on *N. flemingeri* and *C. marshallae*.

Assessing the influence of sulfide minerals on prokaryotic nitrogen cyclers from an inactive hydrothermal massive sulfide environment

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Massive sulfide structures provide diverse and long-lasting geochemical sites for endolithic microbes to take advantage of and may represent important habitats for deep-sea nitrogen cyclers. Nitrogen is essential for life and the amount of bioavailable nitrogen in the environment is largely mediated by nitrogen cyclers. In massive sulfide environments, nitrogen cyclers may aid in the dissolution of sulfide minerals by utilizing sulfur species as electron donors in their metabolisms. Here, we address how the composition and concentration of sulfide minerals and sediment geochemistry influence the diversity, functional potential, and distribution of microbial nitrogen cyclers. We assessed the influence of sulfide minerals on nitrogen cycling communities along transects within the Escanaba Trough massive sulfide deposit, located on the Southern Gorda Ridge. Triplicate push cores were collected at five sites along each transect starting from inactive massive sulfides out to pelagic background sediments. Cores were subsampled at 1-2cm horizon depths for microbiology and geochemistry. To characterize the diversity and functional potential of benthic nitrogen cyclers, DNA was extracted for 16s rRNA amplicon sequencing, qPCR (targeting specific N-cycling genes), and metagenomics. Geochemistry analyses included shipboard microprofiling (O, S, and Fe), pore water extractions (nutrients, sulfides, and trace metals), organic geochemistry, mineralogy (bulk and detailed), grain size, and porosity. We expect nitrogen cyler abundance and diversity to be highest in the presence of sulfide minerals. By pairing physiochemical and molecular data we can better link microbial taxonomy with nitrogen cycling functional potential in the context of the environment, thus elucidating the potential importance of massive sulfides in deep-sea nitrogen cycling.

Evidence of the Proton Flux Hypothesis: Adaptation of autonomous sensors to monitor Hawaiian corals under various chemical perturbations.

Ally Morris, Ellen M Briggs, Keisha D Bahr, Christopher L Sabine, Ku'ulei Rodgers

Evidence has shown that the phenomenon of Ocean Acidification (OA) disrupts the ability of calcifying organisms to maintain calcium carbonate shells and more work is required to quantitatively measure how the process of calcification will change under the expected increase of corrosive conditions. To understand the mechanisms of calcification in corals, mesocosm experiments are underway at the Hawai'i Institute of Marine Biology in Kaneohe Bay, O'ahu to (1) assess which aqueous carbon dioxide species corals (specifically, *Montipora capitata*) prefer to uptake during calcification under various chemical conditions and to (2) test the Proton Flux Hypothesis. This leading hypothesis suggests that a coral's rate of calcification is limited by its ability to expel waste hydrogen ions (H^+). Our mesocosms are equipped with an automatic pCO_2 system and acid control system to simultaneously and independently control both AT and pCO_2 to alter seawater chemistry. In order to monitor the coral's responses to this chemical modification, we have adapted a prototype sensor that utilizes modified ion-sensitive field-effect transistor (ISFET) pH-sensing technology to make measurements of both pH and AT. The new in situ pH-AT sensor is now capable of monitoring changes in the carbonate chemistry of the mesocosms at an unprecedented rate (< 60 s) without altering surrounding seawater. The high-frequency pH-AT sensor will provide more detailed insight, which is not possible with discrete bottle samples traditionally used in mesocosm experiments, into the coral's response to changing oceanic chemistry under elevated pressure from OA and provide information to validate or challenge the Proton Flux Hypothesis. Here we present preliminary findings collected with ISFET technology (Honeywell Durafet pH sensor) that provides key information required for future mesocosm experiments.

Embracing Complexity in Mesopelagic Energy Supply: A stable isotope perspective

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Over the past decade, compound specific stable isotope analysis of amino acids has emerged as a unique tool for understanding sources and cycling of organic matter in deep-sea food webs. This work has deepened our understanding of resource supply below the surface ocean, suggesting multiple possible organic matter supply pathways involved in supporting food webs in the mesopelagic zone and below. Yet, this enhanced understanding has led to increasingly complex conceptual models to describe these systems. As a result, the conventional linear-mixing models and trophic position equations previously utilized in such studies are now stretched to the limit of their explanatory power, necessitating the development of new analytical frameworks. In this short talk I will summarize our current state of thinking around organic matter supply pathways in the mesopelagic zone, highlighting the recent work that has contributed to this understanding, and introduce a Bayesian food web model that we are developing to describe this system. I hope to conclude the talk by sharing some reflections on how we grapple with complexity as researchers in a world that encourages certainty.

Evaluation of the historical conditions at the lateral boundary of the California Current System as represented by Earth System Models

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The California Current System (CCS) is one of the most productive upwelling regions in the world, supporting a variety of fisheries along the Northwest Pacific coast. In the region, changes in ocean density, oxygen, and nitrate content have been evident throughout recent decades, where increased transport of low-oxygen waters from the equatorial Pacific have resulted in massive fish die-offs and reduced catch. Similarly, intrusions of cold, relatively fresh water with low-oxygen and high-nitrate levels from the northern Pacific have resulted in hypoxic conditions in the northern CCS. This work analyzes outputs from the 7 standard-resolution CMIP6 Earth System Models (ESMs) that often provide lateral boundary conditions for high-resolution coastal models used to inform adaptation and management decisions in the region. The main goal is to evaluate the representation of remote water masses entering the CCS and their variability in ESMs as compared to observations and reanalysis data, and to determine how biases in the representation of water mass transport could affect projections of productivity in the CCS. Initial results using Empirical Orthogonal Function analyses show that the ESMs capture realistic seasonal variability at the surface layer, while at 300 m, low frequency variability dominates with considerable inter-ESM spread in its characteristics.

Data from disorder: developing a Raman-based calcifying fluid saturation state proxy for Mg-calcite organisms

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Ocean acidification (OA) from continuous anthropogenic carbon emissions negatively impacts calcifying organisms across the world by reducing ocean pH, $[\text{CO}_3^{2-}]$, and thus the calcium carbonate saturation state (Ω). Although end-of-century OA-induced changes in seawater carbonate chemistry are projected to place increased energetic strain on calcifying organisms and severely impede calcification rates, instances of calcifier resilience to acidified conditions have been observed in prior laboratory and field studies. A major factor aiding calcifier resilience lies within the organisms' calcifying fluid, where carbonate system parameters like pH and Ω are biologically upregulated relative to external seawater to promote biogenic calcification. Increasing attention has been directed towards characterizing calcifying fluid chemistry not only to establish baselines for biological modification of calcifying conditions but also understand how such modification behaves under environmental stressors like OA. While calcifying fluid proxies have mostly focused on quantifying pH, a proxy for calcifying fluid saturation state (Ω_{CF}) has also recently been developed using nondestructive Raman spectroscopy applicable to organisms that precipitate aragonite, a polymorph of CaCO_3 (i.e., shallow water corals). However, a Raman-based Ω_{CF} proxy has not been experimentally verified for organisms precipitating Mg-calcite largely due to the complicating effects of Mg on Raman spectral measurements. This talk will focus on the ongoing experimentation required to develop a robust Raman-based calibration for Mg-calcite Ω_{CF} and subsequently apply the proxy to various Mg-calcite organisms like deep sea octocorals, coralline algae, and barnacles.

Uncovering the Microbial Fingerprints of Coastal Pollution: Differentiating Wastewater Sources using 16S Amplicon Sequencing

Nicolas Storie and Craig Nelson

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Leaking on-site sewage disposal systems (OSDS) and failing urban sewage infrastructure release raw sewage, severely threatening human and environmental health globally. Culture-dependent monitoring for sewage pollution does not resolve fecal source, which is central to management strategies and risk assessment. Culture-independent microbial source tracking (MST) includes a suite of host-specific quantitative polymerase chain reaction (qPCR) assays that exploit gut-associated taxa, such as *Bacteroides*, to differentiate between human and non-human fecal pollution, while community analysis MST can be employed to detect community DNA signatures of human wastewater sources in the environment. This study aimed to develop and validate community analysis MST methods to discriminate wastewater pollution sources in Hilo, HI which houses a wastewater treatment plant and over 10,000 cesspools, the highest density in the state. We employed 16S rRNA amplicon sequencing to characterize the microbial communities of OSDS septage, untreated sewage, treated effluent, and marine coastal waters varying in submarine groundwater discharge inputs. Among wastewater sources, distinct microbial communities were identified differentiating septage, sewage, and effluent samples with multiple algorithms identifying indicator bacterial taxa for each of the wastewater sources. Wastewater indicator taxa were found across sites in low prevalence suggesting a mixture of wastewater sources is threatening Hilo's coastal water quality. This study highlights the application of random forest algorithm with 16s rRNA amplicon sequencing to identify non-fecal associated taxa useful in discriminating sources of wastewater pollution in coastal waters.

Aspects of the Island Mass Effect near O'ahu, Hawai'i: Picoplankton biomass estimates and preliminary assessment of in situ fluorescence to indicate nearshore wastewater pollution

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The Island Mass Effect (IME) refers to the enhanced chlorophyll-a concentrations that are commonly observed near islands in the oligotrophic ocean basins. Island bathymetry can cause localized upwelling of nutrients, and additionally, land-based nutrients can enter the marine environment as a result of natural processes or anthropogenic pollution. In this talk, I will be discussing two different aspects of my work related to the IME near O'ahu, Hawai'i. First, I will summarize the spatial distributions of picoplankton at three long-term monitoring stations located 2 km, 7 km, and 100 km from the island of O'ahu over a 7-year time series. The observed abundances and estimated carbon content of *Prochlorococcus*, *Synechococcus*, picoeukaryotes, and heterotrophic bacteria in this dataset will be discussed in the context of the IME. For the second part of my talk, the focus will shift to land-based pollution in coastal waters. New research will focus on assessing the feasibility of using a novel in-situ fluorometer to detect wastewater pollution in marine and estuarine environments in Hawai'i. I will provide a project plan and share preliminary data relating specific fluorescence excitation/emission frequencies to water quality parameters such as salinity, turbidity and fecal indicator bacteria.

Understanding phytoplankton community and productivity dynamics in a Native Hawaiian fishpond

Lani Musselman, Rosanna Alegado, Yoshimi M Rii, Paepae o He 'eia

A comprehensive understanding of the base of the microbial food web in He 'eia Fishpond (O 'ahu, Hawai 'i) is critical knowledge for resource managers. Current knowledge on phytoplankton in the fishpond is lacking productivity rates, a key measurement to help understand biogeochemical processes in a dynamic, estuarine ecosystem. This proposed project will build upon data generated between 2014 to 2019 that examined water biogeochemistry and bacterial and eukaryotic diversity based on the 16S and 18S ribosomal RNA genes within He 'eia Fishpond, which indicated that water characteristic changes during wet and dry seasons influence phytoplankton abundances. Thus, the wet and dry seasons vary in nutrient inputs, which may shift nutrient limitations on the microbial food web. Information on seasonal variation in primary productivity and organic matter production will aid in understanding fishpond health and identifying possible stressors, allowing for development of strategic management plans to predict variations in fish production as a result of changes to primary productivity. In this study, we will perform nutrient amendment experiments with the goal of discovering which nutrient is limiting to phytoplankton and whether it shifts between seasons. We will measure primary productivity rates, biomass, species richness, and follow the drawdown of nutrients in each of the in-situ bioassays. Nutrient concentration additions were determined under the scenario of heavy rainfall causing quick and increased stream flow faster than soil and vegetation can remove nutrients from the water leading to stream water entering the pond at concentrations similar to that of the upper watershed. Non profit organizations such as Paepae o He 'eia and Kāko 'o 'Ōiwi continuously work to remove invasive species such as guinea grass and mangroves; this restoration has opened up a new water flow source into the pond as well as continue to improve existing water flow. Our experimental design is set up so that we help to give insight into how these stream flow improvements can impact the phytoplankton communities. The overarching goal of this research is to create a comprehensive understanding of the phytoplankton community response to shifting nutrient regimes and their impact on primary productivity between the wet and dry seasons.

Using Kāne 'ohe Bay as a model system to study the ecotypic differentiation of SAR86 marine bacteria

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SAR86 is one of the most abundant groups of planktonic bacteria found in the oligotrophic surface ocean. Since its discovery over thirty years ago various aspects of its ecology have come to light. These include an emphasis on lipid metabolism, an expanded repertoire of TonB-dependent transporters, and streamlined genomes. These discoveries have almost exclusively focused on SAR86's role in the open ocean. Early reports on SAR86 clones sequences showed that SAR86 is also present in the coastal environment but this environment has largely been ignored by SAR86 literature. To help rectify this we analyzed metagenomic and amplicon data from within and outside Kāne 'ohe Bay and station ALOHA. Our results indicate that SAR86 populations undergo immense changes across the coastal to offshore environment and between offshore and open ocean environments. These changes present themselves at the family, genus, and sub-genus taxonomic levels. Additionally, by analyzing the presence and absence of individual genomes across the environments we have also been able to identify potential functions that have helped different SAR86 populations succeed in the investigated environment. Overall, our results suggest that there is a wealth of discoveries about SAR86 waiting to be explored beyond the traditional environment that SAR86 research has focused on historically.

Air-sea gas exchange in a seagrass ecosystem – results from a ^3He / SF_6 tracer release experiment

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Seagrass meadows are some of the most productive ecosystems in the world and could help to mitigate the increase of atmospheric CO_2 from human activities. However, understanding the role of seagrasses in the global carbon cycle requires knowledge of air-sea CO_2 fluxes and hence knowledge of the gas transfer velocity. In this study, gas transfer velocities were determined using the ^3He and SF_6 dual tracer technique in a seagrass ecosystem in south Florida, Florida Bay, near Bob Allen Keys (25.02663°N , 80.68137°W) between 1 and 8 April 2015. The observed gas transfer velocity, normalized for CO_2 in freshwater at 20°C , $k(600)$, was $4.8 \pm 1.8 \text{ cm h}^{-1}$, which was lower than that calculated from published wind speed/gas exchange parameterizations. The deviation in $k(600)$ from other coastal and offshore regions was only weakly correlated with tidal motion and air-sea temperature difference, implying that wind is the dominant factor driving gas exchange. The lower gas transfer velocity was most likely due to wave attenuation by seagrass and limited wind fetch in the study area. A new wind speed/gas exchange parameterization is proposed ($k=0.143u^{10^2}$), which might be applicable to other seagrass ecosystems and wind-fetch-limited environments.