National Shellfisheries Association

Program and Abstracts
of the
115th Annual Meeting

March 26–30, 2023
Baltimore, Maryland

Follow on Social Media: #shellfish23

The National Shellfisheries Association would like to recognize and thank our publishing partners

KGL KnowledgeWorks Global Ltd.

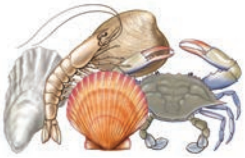
CJK GROUP

and

Sheridan

CJK GROUP

for 36 years (and counting) of service and dedication to providing outstanding publishing services to the National Shellfisheries Association.



NSA 115th ANNUAL MEETING
National Shellfisheries Association
Baltimore Marriott Inner Harbor at Camden Yards - Baltimore, Maryland
March 26 – 30, 2023

SUNDAY, MARCH 26, 2023

8:30 AM-4:00 PM	**Annual Meeting Northeast Coordinating Committee (USDA sponsored) on shellfish genetics** **Chesapeake**
6:30 PM	**STUDENT ORIENTATION** **Chesapeake**
7:00 PM	**PRESIDENT'S RECEPTION** **Grand Ballroom**

MONDAY, MARCH 27, 2023

6:30-8:00 AM	**STUDENT MONTOR-MENTEE BREAKFAST (students only – advanced sign-up required)** **Chesapeake**
8:00-8:50 AM	**PLENARY LECTURE: Marisa Bass (Yale University)** **Grand Ballroom**

	Grand D/E/F	Grand East	Grand West	Grand A/B/C	University 1/2
9:00-10:30 AM	ECOSYSTEM SERVICES	SHELLFISH GENETICS AND GENOMICS	BLUE CRAB ECOLOGY AND FISHERIES	BIRDS AND SANITATION	ONE HEALTH EPIGENOMICS
10:30-11:00 AM	MORNING BREAK				
11:00-12:30 PM	UNDERGRADUATE RESEARCH COLLOQUIUM	SHELLFISH GENETICS AND GENOMICS	BLUE CRAB ECOLOGY AND FISHERIES	BIRDS AND SANITATION	ONE HEALTH EPIGENOMICS
12:30-1:30 PM	LUNCH BREAK				
1:30-2:45 PM	DIVERSITY AND INCLUSION	SHELLFISH GENETICS AND GENOMICS	BLUE CRAB ECOLOGY AND FISHERIES	ROBOTICS AND EMERGING TECHNOLOGY	ONE HEALTH EPIGENOMICS
3:00-3:30 PM	AFTERNOON BREAK				
3:30-5:00 PM	PUBLIC SCIENCE ENGAGEMENT WORKSHOP	SHELLFISH GENETICS AND GENOMICS	BLUE CRAB ECOLOGY AND FISHERIES	GENERAL CONTRIBUTED I	ONE HEALTH EPIGENOMICS

TUESDAY, MARCH 28, 2023

	Grand D/E/F	Grand East	Grand West	Grand A/B/C	University 1/2	University 3/4
8:00-8:50 AM	**PLENARY LECTURE: Patricia Glibert (University of Maryland)** **Grand Ballroom**					
9:00-10:00 AM	**ECHINODERMS**	**OsHV-1 NOROVIRUS**	**NUTRIENTS AND SHELLFISH**	**MUSSELS**	**SHRIMPENCODE**	
10:00-10:30 AM		**OsHV-1 NOROVIRUS**	**DOWN ON THE FARM**	**MUSSELS**	**SHRIMPENCODE**	
10:30-11:00 AM	**MORNING BREAK**					
11:00-12:30 PM	**SHELLFISH AND SEAGRASS INTERACTIONS**	**DISEASE**	**DOWN ON THE FARM**	**MUSSELS**	**SHRIMPENCODE**	
12:30-1:30 PM	**LUNCH BREAK**					
1:30-3:00 PM	**COMMERICAL SHELLFISHERIES**	**DISEASE**	**HARMFUL ALGAL BLOOMS**	**REMOTE SENSING AND SHELLFISH**	**SHRIMPENCODE**	**MEET THE AGENCIES**
3:00-4:30 PM	**COMMERICAL SHELLFISHERIES**	**DISEASE**	**GENERAL CONTRIBUTED II**	**REMOTE SENSING AND SHELLFISH**	**SHRIMPENCODE**	**MEET THE AGENCIES**
4:30-6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Stadium Ballroom – 2nd floor**					
7:00 – 10:00 PM	**STUDENT ENDOWMENT FUND AUCTION** **Grand Ballroom**					

WEDNESDAY, MARCH 29, 2023

8:00-8:50 AM	**PLENARY LECTURE: Vic Kennedy (*Emeritus*, University of Maryland) Grand Ballroom**				
	University 1/2	**University 3/4**	**Grand A/B/C**	**Harbor I**	**Chesapeake**
9:00-10:00 AM	**FRESHWATER MUSSELS**	**SHELLFISH RESTORATION & CONSERVATION**	***VIBRIO***	**EDNA APPLICATIONS FOR SHELLFISH**	**CLAM SELECTIVE BREEDING WORKSHOP**
10:00-10:30 AM	**HATCHERIES**	**SHELLFISH RESTORATION & CONSERVATION**	***VIBRIO***	**EDNA APPLICATIONS FOR SHELLFISH**	**CLAM SELECTIVE BREEDING WORKSHOP**
10:30-11:00 AM	**MORNING BREAK**				
11:00-12:30 PM	**HATCHERIES**	**SHELLFISH RESTORATION & CONSERVATION**	***VIBRIO***	**MODELLING AND CLIMATE CHANGE**	**CLAM SELECTIVE BREEDING WORKSHOP**
12:30-2:00 PM	**NSA BUSINESS LUNCHEON Grand Ballroom**				
2:00-4:30 PM	**SCALLOP GALLOP EXPLORE BALTIMORE!! Solar Oyster Production System Tour (advance sign-up required)**				**CLAM HUB PROJECT TEAM MEETING**
4:30-6:00 PM	**POSTER SESSION AND HAPPY HOUR Stadium Ballroom – 2nd floor**				

THURSDAY, MARCH 30, 2023

8:00-8:50 AM			**PLENARY LECTURE: Ximing Guo (Rutgers University)** **Grand Ballroom**		
	Grand A/B/C	**Grand D/E/F**	**Grand East**	**Grand West**	**University 1/2**
9:00-10:15 AM	**OYSTERS**	**SCALLOPS**	**CLAMS**	**CONTAMINANTS OF EMERGING CONCERN**	**MANGROVE SHELLFISH**
10:15-10:45 AM			**MORNING BREAK**		
10:45-12:00 PM	**OYSTERS**	**SCALLOPS**		**CONTAMINANTS OF EMERGING CONCERN**	**MANGROVE SHELLFISH**
12:00-1:00 PM			**LUNCH BREAK**		
1:00- 3:30 PM	**OYSTERS**	**MACROALGAE-SHELLFISH CO-CULTURE**	**HORSESHOE CRABS**	**GENERAL CONTRIBUTED III**	**MANGROVE SHELLFISH**
3:30-6:30 PM			**CLOSING HAPPY HOUR** **Stadium Ballroom – 2nd floor**		

POSTERS and All BREAKS are in the Stadium Ballroom on the 2nd floor.

NSA AT THE MOVIES - FILM FESTIVAL will be showing on a continuous loop all day for each day of the conference (Promenade)

In addition to the scheduled Poster Sessions, posters will be available for viewing in the Stadium Ballroom from Monday, 9 a.m. through Thursday noon.

PLEASE REMOVE YOUR POSTERS BY NOON ON THURSDAY

MONDAY March 27, 2023					
6:30-8:00AM	**STUDENT MENTOR-MENTEE BREAKFAST (STUDENTS ONLY - *Advanced sign up will be required*)** **Chesapeake**				
8:00-8:50AM	**PLENARY: Marisa Bass (Yale University) - *More than just a shell: collecting and conchophilia in the Dutch Golden Age*** **Grand Ballroom**				
	NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Promenade**				
ROOM	**Grand D/E/F**	**Grand East**	**Grand West**	**Grand A/B/C**	**University 1/2**
SESSION TITLE	**ECOSYSTEM SERVICES** **Suzanne Bricker & Matt Parker**	**SHELLFISH GENETICS & GENOMICS** **Louis Plough**	**BLUE CRAB ECOLOGY & FISHERIES** **Rom Lipcius, Rochelle Seitz & Matt Ogburn**	**BIRDS & SHELLFISH SANITATION** **Bob Rheault**	**ONE HEALTH EPIGENOMICS** **Acacia Alcivar-Warren**
9:00AM	Determining feeding rates in eastern oysters (*Crassostrea virginica*) using natural seston flow-through system **Wiltsee*, Gray**	The Molluscan Broodstock Program: a retrospective on 25+ years of improving West Coast oyster stocks **Langdon, Schoolfield, Durland, De Melo, Divilov**	Putting the *Callinectes sapidus* genome into the context of decapod genomics **Bachvaroff, Chung**	Bird interactions with shellfish aquaculture **Rheault**	ONE HEALTH Epigenomics: from *Vibrios* to transgenerational epigenetic inheritance - recognition of students and 'Outstanding ONE HEALTH Researchers' awardees **Alcivar-Warren, Tang**
9:15AM	Examining phytoplankton-related ecosystem services of sessile suspension feeders in Inner Harbor, Baltimore, Maryland **Kido*, Stewart, Adaranijo, Geba, Schott**	Toward understanding sex-specific gene expression patterns during the conditioning process in eastern oyster, *Crassostrea virginica* **Proestou, Sullivan, Delomas, Lundgren, Hart, Satkowski**	Testosterone and steroidogenic genes in the male blue crab *Callinectes sapidus* and their relationship with insulin-like androgenic gland factor (IAG) and crustacean female sex hormone (CFSH) **Wang*, He, Blaney, Chung**	Seasonal patterns of distribution and abundance of waterbirds in relation to oyster aquaculture in coastal Rhode Island **Muller, Paton, McWilliams^{p}**	Tracking ecosystem contaminants to protect public health **Jones**
9:30AM	Spatially-explicit oyster filtration services in the Hudson River Estuary: research to help guide restoration and public understanding **Gray, Brady, Fraioli, Hare, Kramer, Schreiber**	Polyploid breeding strategies for *Crassostrea virginica* **Small, Kube, Allen Jr.**	Developing and validating novel microsatellite markers in the red deep-sea crab, *Chaceon quinquedens* **Green, Plough, Chung**	Birds and shellfish sanitation - the New York experience **Rivara, Byrnes, Carden, Finora**	
9:45AM	Fish production and use of oyster aquaculture gear in comparison to natural habitats north and south of Cape Cod **Schultz*, Hughes, Kimbro, Kirk, Rose, Mercaldo-Allen, Clark, Phillips, Redman, Grabowski**	Genetic parameters for heat and salinity stress tolerance in northern Gulf of Mexico eastern oyster, *Crassostrea virginica* **McDonald*, Saillant**	Transcriptomic analysis of the hemocyte response to a virus infection **Chung, Bachvaroff**	Observations on the use of bird kites at an oyster farm in southern Mobile Bay, Alabama **Supan, Wilson, Bradley**	Analysis of the expression and inhibition of the PirAB^{VP} toxin in *Vibrio* and non-*Vibrio* strains: the case of the pVA1 plasmid **Victorio-De Los Santos*, Vázquez-Reyes, Ayón-Pérez, Zambrano-Zaragoza, Agraz-Cibrián, Gutiérrez-Franco**
10:00AM	Integrating information on beneficial services provided by shellfish aquaculture into the aquaculture permitting and review process **Schillaci, Rose, Mercaldo-Allen, Gordon, Clark, Kirk, Milke, Munroe, Phillips, Redman, Schultz, Shinn**	Comparing genotyping technologies for estimating genetic diversity and genomic selection in eastern oyster (*Crassostrea virginica*) broodstock **Varney, Wilbur**	Investigating the interstate movement of blue crab viruses and the implications for fishery biosecurity **Herrera*, Zhao, Bachvaroff, Mohammed Geba, Schott**	Small-scale investigations of bird deterrent methods on and around Massachusetts shellfish farms using floating gear **Reitsma, Archer, Booth**	
10:15AM		Segregation distortion and null alleles in the eastern oyster (*Crassostrea virginica*) **Wang*, Guo**	Parasitic dinoflagellate *Hematodinium perezi* prevalence in *Callinectes* spp. in a tropical urban estuary **Pares*, Schott**	Comparing available deterrent methods to reduce Double-crested cormorant attempts to roost on floating oyster cages **Cunningham, Wang, Burr, Tappa, Redd, Glover, Dorr**	Repetitive sequence composition in two assemblies of Pacific oyster, *Crassostrea gigas* **Alcivar-Warren, Bao**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**UNDERGRADUATE RESEARCH COLLOQUIUM** **Ed Catapane & Margaret Carroll**	**SHELLFISH GENETICS & GENOMICS** **Louis Plough**	**BLUE CRAB ECOLOGY & FISHERIES** **Rom Lipcius, Rochelle Seitz & Matt Ogburn**	**BIRDS & SHELLFISH SANITATION** **Bob Rheault**	**ONE HEALTH EPIGENOMICS** **Acacia Alcivar-Warren**
11:00 AM	Effects of manganese on dopamine D2R signal transduction pathway L-type calcium channels and control of lateral cell cilia response and membrane potential in gill of *Crassostrea virginica* **Small*, Ulumbelashvili, Catapane, Carroll**	Three cryptic surfclam taxa in southern New England: genetic differences, biogeography, and relevance for aquaculture **Hare, Hartung**	Ecological aspects of the transmission of *Hematodinium perezi* to blue crabs **Shields, Chen**	A *Campylobacter* illness outbreak associated with oysters contaminated by seabirds roosting on floating aquaculture gear **Borkman, Slaten, Miller, Goetsch**	Overview of transposable element identification, classification, and annotation for a better epigenetic landscape generation in non-model eukaryotic genomes **Rodriguez, Arkhipova**
11:15 AM	Western blot study of GABA and histamine receptors in peripheral tissues of *Crassostrea virginica* **Mansfield*, Wallach, Foster, Pierce, Souffrant, Carroll, Catapane**	Challenges and opportunities for genomics-informed selective breeding of highly divergent eastern oyster populations in Texas **Hollenbeck, Matt, Portnoy**	Aspects of the feeding ecology of *Carcinonemertes carcinophila* and its effect on *Callinectes sapidus* reproductive output **Schneider, Pomroy*^{p}, Shields**	The prevalence of birds as sources of fecal contamination in the shellfish waters of the northeast U.S. **Jones, Howell, Foxall, Howell**	
11:30 AM	Effects of stimulation of mantle rim sensory tentacles by algae on gill cilia beating in the bivalve mollusc, *Crassostrea virginica* **Obianke*, McFarlane, Allam, Espinosa, Carroll, Catapane**	Genomic selection models for the growth and survival traits of the eastern oyster in low salinity water **Liu, Wolf-Bryant, Farrington**	Blue crab, *Callinectes sapidus*, reproductive phenology in Chesapeake Bay **Schneider*, Fabrizio, Lipcius**	Addressing data gaps in the consideration of bird-based pathogen introduction in shellfish aquaculture **Noble, Ciesielski**	Portions of a *Homo sapiens* LINE 1 (L1) sequence are present in Penaeid shrimp genomes **Alcivar-Warren**
11:45 AM	GABA inhibits serotonergic innervation to the gill from the visceral ganglia in the bivalve mollusc, *Crassostrea virginica* **Chery*, Chery, Catapane, Carroll**	Strategies for cost-effective genomic breeding of *Crassostrea virginica* in Texas **Matt, Portnoy, Hollenbeck**	Relating climate change to abundance and reproductive dynamics of Atlantic blue crab (*Callinectes sapidus*) in South Carolina, USA **Kendrick, Brunson**	Developing strategies for managers and industry to address public health concerns related to bird congregations on floating aquaculture gear **Schillaci, Rheault**	One Health approach to study the impact of Antimicrobial Resistance in shrimp aquaculture **Rodulfo, De Donato^{p}, Alcivar-Warren**
12:00 NOON		Improving low salinity tolerance in Louisiana populations of the eastern oyster, *Crassostrea virginica*, using genomic selection **Schwartz, Plough, Lavaud, LaPeyre, Pandelides, Comba, Stauffer**	Habitat-specific abundance and mortality of juvenile blue crab, *Callinectes sapidus*, with Bayesian inference: influences of post-larval abundance, seasonality, and turbidity **Hyman*, Chiu, Seebo, Saluta, Smith, Knick, Lipcius**	Birds on floating culture, oh my! **Hudson**	Epigenetic mechanisms reported in fish and shellfish exposed to glyphosate-based herbicides (GBH) **Alcivar-Warren, Warren**
12:15 PM		Using only low-density marker panels for genomic selection can lead to declining genomic estimated breeding value accuracy over time **Delomas, Hollenbeck, Matt, Thompson**	Test of treatment-specific bias in simulated marsh with juvenile blue crab, *Callinectes sapidus* **Miller*, Hyman, Shi, Lipcius**		
12:30-1:30 PM	**LUNCH BREAK**				

* denotes student presenter ^{p} denotes non first-author presenter

MONDAY
March 27, 2023

NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Promenade

ROOM	Grand D/E/F	Grand East	Grand West	Grand A/B/C	University 1/2
SESSION TITLE	**DIVERSITY AND INCLUSION** **Angela Caporelli** **Aswani Volety**	**SHELLFISH GENETICS & GENOMICS** **Louis Plough**	**BLUE CRAB ECOLOGY & FISHERIES** **Rom Lipcius, Rochelle Seitz & Matt Ogburn**	**ROBOTICS AND EMERGING TECHNOLOGY** **Yang Tao, Miao Yu & Allen Patillo**	**ONE HEALTH EPIGENOMICS** **Acacia Alcivar-Warren**
1:30 PM	Aquaculture in the midst of social change **Caporelli**	Evaluation of three non-lethal biopsy methods for SNP array genotyping in the eastern oyster, *Crassostrea virginica* **Plough, Schwartz**	Relationships between community structure and juvenile blue crab abundance in structurally complex nursery habitats in the York River, Chesapeake Bay **Guennouni*, Hyman, Smith, Seebo, Saluta, Lipcius**	Seabed classification of oyster farms using a single beam scanning sonar with machine learning **Xu*, Rajasekaran, William, Pattillo, Gray, Miao Yu**	Reverse transcriptase-related genes and their possible role in the host cell response to transition metal pollution **Yushenova, Rodriguez, Arkhipova**
1:45 PM		Opportunity for genomic selection to increase survival against an OsHV-1 microvariant from San Diego Bay (California, USA) **Thompson, Agnew, Calla, Burge**	Ontogenetic variation in blue crab (*Callinectes sapidus*) use of seagrass nurseries: survival and abundance vary by microhabitat **Lipcius, Farrar, Bromilow, Orth**	Mechanized Manila clam farming in northern Puget Sound, Washington, USA **Dewey**	
2:00 PM	Does the past shape the future?: The future of increasing diversity in aquaculture **Black**	The effects of probe and gDNA insert length on the de novo assembly and capture efficiency of Expressed Exome Capture sequencing (EecSeq) **Green*, Puritz**	Spatial variation in nursery habitat use by juvenile blue crabs in a shallow, wind-driven estuary **Voigt, Eggleston^{p}**	Automating oyster aquaculture with solar energy **Caffrey, Pattison, Rice, Summers**	Are metals endocrine-disrupting chemicals (EDC) in shellfish? **Warren*, Hernandez, Alcivar-Arteaga, Alcivar-Warren**
2:15 PM	Discussion: This session will cover different perspectives from organizations, businesses, and institutions wading through the issue of Diversity and Inclusion and some initiatives in motion to address it.	Investigating the effects of coastal stressors on the genomic variation of oyster populations in Narragansett Bay, Rhode Island **Zyck*, Stevick, Gomez-Chiarri, Puritz**	Blue crab and forage fish abundances are reduced with subestuary shoreline and upland development **Seitz, Lipcius, Saluta, Kornis, Breitburg, Jordan, Weller**	Developing the OysterBot for oyster cage retrieval **Curran, Leavitt^{p}**	Taxonomy of shellfish follows the classification by the World Register of Marine Species (WORMS): for *Penaeus* species, only *Penaeus vannamei* Boone, 1931 is accepted (*Litopenaeus vannamei* is not accepted) **Alcivar-Warren**
2:30 PM		Early life exposure to hypoxia and warming alters the microbiome and DNA methylation in the eastern oyster **Gignoux-Wolfsohn, Donelan**	Female blue crab spawning migration revealed by carapace biogeochemistry **Ogburn, Gilmour, Aguilar, Johnson, Richie, Hines**	Incorporating a decade of water quality data around Washington State within a regional smart aquaculture framework **Page, Booth, Suhrbier, Hudson**	
2:45 PM		Nucleotide and structural polymorphisms of the eastern oyster genome paint a mosaic of divergence, selection, and human impacts **Puritz, Zhao, Guo, Hare, He, LaPeyre, Lotterhos, Lundgren, Modak, Proestou, Rawson, Robledo, Weedop, Witkop, Gomez-Chiarri**	Is the high exploitation rate resulting in the declining reproductive output of blue crab (*Callinectes sapidus*) in the Chesapeake Bay? **Fujaya, Aguilar, Bardelli, Richie, Ogburn^{p}**	Shellevator™: Automating oyster production on submersible and mobile watercraft **DePaola**	Is glyphosate and endocrine disrupting chemical (EDC) in people and shrimp? - A literature review **Warren*, Hernandez, Alcivar-Arteaga, Alcivar-Warren**
3:00 – 3:30 PM	**AFTERNOON BREAK**				
ROOM	**University 3/4**	**Grand East**	**Grand West**	**Grand A/B/C**	**University 1/2**
SESSION TITLE	**PUBLIC SCIENCE ENGAGEMENT WORKSHOP** **David Shiffman**	**SHELLFISH GENETICS & GENOMICS** **Louis Plough**	**BLUE CRAB ECOLOGY & FISHERIES** **Rom Lipcius, Rochelle Seitz & Matt Ogburn**	**GENERAL CONTRIBUTED I** **Matt Parker**	**ONE HEALTH EPIGENOMICS** **Acacia Alcivar-Warren**
3:30 PM	How to use social media to communicate your science to the public, and why you should A hands-on workshop to learn basic principles and advanced tips and tricks for public science engagement, focusing on crafting your message and using some social media tools to share it with the world	Genomic and genetic investigations of the bay scallop population in the Peconic Bay, New York **Grouzdev, Espinosa, Muehl, Farhat, Boutet, Tanguy, Tettelbach, Tobi, Allam**	An ecological threat and an economic resource: the Atlantic blue crab in Mediterranean waters **Mancinelli**	Aquaculture regulations: why the complexity? **Zajicek**	From BPA to phthalates to PFAS: how environmental chemicals are harming shellfish and human health and what we can do about it **Vandenberg**
3:45 PM		Combining physiological assays, high-throughput sequencing, and functional genomics to understand costs and mechanisms associated with resilience to acidification in marine bivalves **Schwaner*, Barbosa, Farhat, Boutet, Tanguy, Haley, Espinosa, Allam**	Evidence for a male bias in blue crab (*Callinectes sapidus*) pot-based sampling **Brunson, Sitta, Kendrick, Kingsley-Smith**	Collaboratively tracking shellfish aquaculture production data in Washington State **Hudson, Eardley, Toepelt, Butler**	
4:00 PM		DeNovo transcriptome assembly and analysis of the flat oyster pathogenic protozoa, *Bonamia ostreae* **Chevignon, Dotto-Maurel, Serpin, Chollet, Arzul**	Assessing northeast Florida offshore blue crab fishing effort within Florida State waters **Ehnert-Russo, Crowley, Becker**	Maine Nearshore Marine Resources Program: a new name and focus **Leach, White, Kanwit**	
4:15 PM		A novel and rapid qPCR probe assay for the detection of the roseovarius oyster disease (ROD) bacterium, *Aliiroseovarius crassostreae*, in the eastern oyster (*Crassostrea virginica*) **Yong, Carnegie, Kingsley-Smith, Darden**	Density-dependent matrix-based modeling of blue crab, *Callinectes sapidus*, population dynamics in the Chesapeake Bay **Li*, Hyman, Shi, Lipcius**	University of Maryland online economic spreadsheet tool for oyster aquaculture: a shellfish odyssey **Parker**	
4:30 PM		Genetic basis of abnormal mussel mortality in France using a field and experimental infection investigations **Munusamy*, Lillehammer, Travers, Maurouard, Aslam, Dégremont**	Ranking ecosystem impacts of the Chesapeake Bay blue crab (*Callinectes sapidus*) using empirical Gaussian graphical models **Liang, Miller, Nesslage, Wilberg**	Detecting the multiple states of oyster activity and orientation using deep learning image processing and computer vision algorithms **Jin, Comfort, Rudy**	
4:45 PM					

* denotes student presenter ^{p} denotes non first-author presenter

TUESDAY
March 28, 2023

8:00-8:50AM	**PLENARY: Patricia Glibert (University of Maryland) – *Harmful algal blooms and oysters: harm is multifaceted*** **Grand Ballroom**				
	NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Promenade**				
ROOM	**Grand D/E/F**	**Grand East**	**Grand West**	**Grand A/B/C**	**University 1/2**
SESSION TITLE	**ECHINODERMS** **Chris Pearce & Andrew Suhrbier**	**OsHV-1 Norovirus** **Colleen Burge**	**NUTRIENTS & SHELLFISH** **Lisa Kellogg**	**MUSSELS** **Luc Comeau**	**ShrimpENCODE** **Acacia-Alcivar Warren & Kathy Tang**
9:00AM	Expanding northeastern US green sea urchin aquaculture production and their potential to reduce biofouling of shellfish **Suckling, Plee, Morse, Eddy**	Genetic diversity of the Ostreid Herpesvirus type 1 **Pelletier*, Chevignon, Jacquot, Heurtebise, Faury, Degremont, Escoubas, Delmotte, Maurouard, Renault, Morga**	Developing default denitrification enhancement estimates for restored oyster reefs: a Chesapeake Bay example **Kellogg, Cornwell, Owens**	Seasonal variability of *Mytilus* sp. feeding activity: the role of environmental conditions and food characteristics **Aguera, Strohmeier, Krogness, Rastrick, Strand**	Shrimp Genomes and Epigenomes (ShrimpENCODE): recognition to students and "Outstanding ONE HEALTH Researchers" Awardees **Alcivar-Warren, Tang**
9:15AM	Thermal priming juvenile green sea urchins (*Strongylocentrotus droebachiensis*) to increase tolerance to extreme field heterogeneity **Plee*, Suckling**	Evaluation of tangential flow filtration coupled to long-read sequencing for Ostreid Herpesvirus type 1 genome assembly **Dotto-Maurel*, Pelletier, Morga, Jacquot, Faury, Dégremont, Bereszczynki, Delmotte, Escoubas, Chevignon**	Cryopreservation of *Tetraselmis striata* through systematic evaluation of multiple parameters **Yee*, Yang**	The role of galactosamine in mediating capture efficiency in mussels and ascidians **Capriotti, Holohan, Rosa, Yahel, Shumway, Ward**	Penaeid shrimp genomics and post-genomics: whole reference genomes needed for the economically important *Penaeus* species **Alcivar-Warren, Li**
9:30AM	Biological biofouling control of salmon net pens using the giant red sea cucumber, *Apostichopus californicus* **Montgomery, Cannon, Pearce**	Viral shedding rates of tolerant and susceptible *Crassostrea gigas* infected with multiple OsHV-1 variants **Agnew*, Burge, Parikh**	Estimating oyster larval development and success at metamorphosis in the western Mississippi Sound **Klein*, Powell, Zhang, Kreeger, Wissing**	A multi-study analysis of gut microbiome data from the blue mussel (*Mytilus edulis*) emphasizes the methodological impact of gut voidance on biological interpretation **Griffin*, Darsan, Collins, Holohan, Ward**	
9:45AM		Susceptibility of shellfish aquaculture species in the Chesapeake Bay and Maryland coastal bays to Ostreid herpesvirus-1 microvariants **Kachmar*, Reece, Agnew, Schreier, Burge**	Quantifying farm-scale ecosystem services associated with eastern oyster aquaculture in the Mid-Atlantic and creating a regional oyster farm filtration calculator **Barr*, Munroe, Calvo, Steeves, Kreeger, Cheng, Rose, Bayer**	Initiating mussel (*Mytilus* sp.) monitoring in Norway and baseline for 2021 and 2022 **Strohmeier, Aguera, Strand**	Making sense of the taxonomy of the most commercially important shrimp *Penaeus fabricius*, 1798 s.l. (Crustacea: Decapoda: Penaeidae): a way forward **Yang, Ma, Chu, Chan^{P}**
SESSION TITLE		**OsHV-1 Norovirus** **Colleen Burge**	**DOWN ON THE FARM** **Bill Walton & Leslie Sturmer**	**MUSSELS** **Luc Comeau**	
10:00AM		Microbiome of the Pacific oyster before, during, and after an OsHV-1 outbreak **Burge, Chu, Grimm, Shen, Dayal, Prado-Zapata, Evans, Dumbauld**	Got the fuzz?: a conversation about the effect of stalked ciliates on oyster nursery culture **Congrove, Glover^{P}, Allen Jr., Snyder**	Impact of sound intensity related to maritime transport on the embryogenesis and metamorphosis of the blue mussel, *Mytilus edulis* **Veillard*, Beauclercq, Olivier, Laurent, Genard, Marcotte, Tremblay**	
10:15AM		Laboratory studies on the impact of an OsHV-1 microvariant on *Crassostrea virginica* families and lines **Burge, Small, Agnew, MacIntyre, Reece^{P}**	Can a fish finder find more than fish? **Leavitt**	Mussels in hot water: the behavioural ecology of temperate mussels under ocean warming and acidification **Clements, Ramesh, Nysveen, Dupont, Jutfelt, Hicks, Tremblay, Comeau**	Using genomes and transcriptome datasets for functional annotation of the immune response of Penaeid shrimp to pathogens **De Donato, Rodulfo, Fajardo, Alcivar-Warren**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**SHELLFISH & SEAGRASS INTERACTIONS** **Brett Dumbauld & Kay McGraw**	**DISEASE** **Ryan Carnegie & Tal Ben Horin**	**DOWN ON THE FARM** **Bill Walton & Leslie Sturmer**	**MUSSELS** **Luc Comeau**	**ShrimpENCODE** **Acacia-Alcivar Warren & Kathy Tang**
11:00 AM	Juvenile Pacific oyster growth and food resources in eelgrass habitat of variable shoot density in a US West Coast Estuary **Merrill*, Dumbauld, McIntyre, Nash, Waldbusser**	Pathology associated with recurring summer oyster mortalities **Ben-Horin, Audemard, Ciesielski, Katsuki, Lucas, Noble, Reece, Small, Wilbur**	Oyster Farming Resilience Index **Grice, Swann, Sempier, Sempier, Deal**	Ocean acidification and bivalve byssus: explaining variable responses using meta-analysis **Clements, George**	A novel virus of Flaviviridae associated with sexual precocity in Macrobrachium rosenbergii **Tang, Dong, Wang, Hu, Li, Li, Cao, Shi, Wang, Zou, Song, Gao, Meng, Yang, Li, Shi, Huang**
11:15 AM	Assessing interactions between shellfish and seagrass beds and macroalgae to promote sustainable aquaculture in the Delaware Inland Bays **Ozbay, Attarwala, Parsaeimehr**	Characterizing drivers of oyster mortality using molecular tools **Ciesielski*, Lucas, Ben-Horin, Noble**	Building a benchmarking program for market oysters **Walton, Lynch**	Ocean acidification, hypoxia, and warming impair digestive parameters and antioxidant responses of marine mussels **Pan*, Khan, Hu, Wang**	
11:30 AM	Effect of oyster density on the biofiltration of the pathogen, *Labyrinthula zosterae* **Bergman*, Groner, Schreier, Burge**	Co-occurrence patterns of oyster parasites across natural and anthropogenic conditions in Chesapeake Bay **Tracy, Lohan, Carnegie, McCollough, Southworth, Ogburn**	The Auburn University Shellfish Lab: Twenty years of industry-driven research **Tarnecki, Rikard, Grice, Walton**	Exploring adaptation and plasticity to ocean warming in blue mussels (*Mytilus edulis*) from Atlantic Canada **Clarke*, Hori, Comeau, Filgueira**	Endogenous virus elements (EVE) of Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV-EVE) in the genomes of *Penaeus vannamei* and *P. monodon*: interactions with transposable elements **Asuncion, Tang, Alcivar-Warren**
11:45 AM	Multi-year assessment of the impacts of oyster aquaculture on submerged aquatic vegetation **Kellogg, Shields, Dreyer**	Are triploid oysters more tolerant to *Perkinsus marinus* than diploids? **Brianik*, Lee, Allam**	The collaborative benefits of the NEFSC sea grant connection: an example investigating poor growth of hard clams in New Jersey **Gordon, Parikh, Parsons, Robillard, Dacanay, Schuster, Wasserman, Wikfors**	Mussel farming in Galicia (NW Iberian Peninsula): new perspectives in a global change scenario **Babarro, Silva, Padín, Gilcoto**	White Spot Syndrome Virus (WSSV) genomes from China, Ecuador, Mexico and other countries are not integrated in the genomes of five Penaeid shrimp species, but endogenous viral elements (EVE) of WSSV (WSSV-EVE) are found in the transcriptome of the first specific pathogen-free (SPF) *Penaeus vannamei* domesticated in the United States **Galindo*, Asuncion, Alday-Sanz, Alcivar-Warren**
12:00 NOON	Nekton associations in mosaic of oyster aquaculture, seagrass, and mudflat habitats **Boardman*, Subbotin, Ruesink**	Visualization of environmental *Perkinsus marinus* cell forms and implications for its transmission dynamics **Poslednik*, Carnegie**	New Hampshire Shellfish Farmers Initiative: the importance of outreach in the aquaculture industry **Meyer***	Commercial performance of blue mussel (*Mytilus edulis*) stocks at a microgeographic scale **Tremblay, Guillou, Cyr, Laplante, Bourque, Toupoint**	
12:15 PM	Nekton use of oyster (*Crassostrea gigas*) flip-bag farms within and adjacent to native eelgrass (*Zostera marina*) habitat **Houle, Page, Boardman, Ruesink**	*Perkinsus marinus* infection of *Crassostrea virginica* with a changing climate in the Chesapeake Bay: a meta-analysis **Kachmar*, Bergman, Gignoux-Wolfsohn, Feild, Schreier, Lohan, Carnegie, Burge**	Outcomes and future directions of the Supporting Oyster Aquaculture and Restoration Program **Hancock, Jones, Kornbluth, Greenberg, Rheault, Barley*^{P}, Borgert, Popolizio**	A fully-phased genome assembly for *Mytilus edulis* unveils a high degree of presence-absence variance between mussel populations **Hori**	A retrotransposon putatively associated with Abdominal Segment Deformity Disease (ASDD) of farmed *Penaeus vannamei* from Thailand is part of NonLTR-1_LVa retrotransposon isolated from the first specific pathogen-free shrimp domesticated in the United States **Alcivar-Warren, Yuan, Karoonuthaisiri, Uengwetwanit, Sittikankaew, Asuncion^{P}**
12:30 PM		The role of tropodithietic acid (TDA) in Phaeobacter inhibens (S4) role as probiont **Coppersmith*, Charette, Ovalles, Bernabe, Nelson, Rowley, Gomez-Chiarri**	The tough people behind the tender shellfish: non-fatal injuries associated with oyster and clam aquaculture in Panacea and Cedar Key, Florida **Kane, Brooks, Myers, Durborow, Dunleavy**	Triploid mussels with better attachment may act as improved extractive species **Osterheld*, Davidson, Comeau, Audet, Hori, Tremblay**	
12:30-1:30 PM	**LUNCH BREAK**				

* denotes student presenter ^{p} denotes non first-author presenter

TUESDAY March 28, 2023						
	NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY Promenade					
ROOM	**Grand D/E/F**	**Grand East**	**Grand West**	**Grand A/B/C**	**University 3/4**	**University 1/2**
SESSION TITLE	**COMMERCIAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**	**DISEASE** **Ryan Carnegie & Tal Ben Horin**	**HARMFUL ALGAL BLOOMS** **Steve Morton**	**REMOTE SENSING & SHELLFISH** **Michelle Tomlinson & Suzanne Bricker**	**MEET THE AGENCIES** **Sandra Shumway**	**ShrimpENCODE** **Acacia-Alcivar Warren & Kathy Tang**
1:30 PM	Bridging research and practice to improve the future sustainability and growth of the Irish bivalve industry (BIVALVE Project) **Hlordzi, Lynch^{P}, Culloty**	The effect of ploidy on the formation and antimicrobial efficacy of extracellular traps in the eastern oyster **Brianik*, Bouallagui, Allam**	Applying environmental DNA techniques for early detection of rust tide caused by *Margalefidinium polykrikoides* around aquaculture farms **Scro, Pilate, Osinski, Bayer, Smolowitz**	The NOAA Aquaculture Program – ecological forecasting data needs **Schillaci, Otoshi, Wesyby**	An opportunity to meet the leaders of agencies and organizations (PSI, ECSGA, NOAA, NAA, USDA, NRAC, PCSGA, APHIS, SeaGrant) that support shellfish research and industry – and to ask questions!	Genomic selection of healthy shrimp: a new, continuous, whole reference genome for specific pathogen-free (SPF) *Penaeus vannamei* is needed **Alcivar-Warren**
1:45 PM	Improving shellfish harvest data in Maryland through daily electronic reporting **Amrhein, Walters, Caretti, Slacum Jr., Coleman, Baxter, Richards, Kennedy, Stevenson, Mole, Corbin**	Life history and impacts of an undescribed parasite on its first intermediate host, the bay scallop **Boggess*, Andrade, Ben-Horin, Wilbur, Buck**	Differential activation of subcellular and molecular mechanisms by the Amnesic Shellfish Poisoning toxin, domoic acid, between the slow-depurator *Pecten maximus* and the fast-depurator *Mytilus edulis* **García-Corona*^{P}, Blanco, Hegaret, Fleury, Bidault, Calvo, Fabioux**	Extending the reach of quasi-operational harmful algal bloom forecasts to estuarine shellfish harvesting in coastal California **Anderson, Kudela, Bjorkstedt, Free**		Genomic assisted breeding: perspectives for genomic selection in shrimp **Isidro y Sanchez**
2:00 PM	A comparison of survey design techniques for scallop, *Placopecten magellanicus*, camera sampling **Delargy, Cassidy, Stokesbury**	An undescribed apicomplexan parasite as a major driver of the collapse of the bay scallop population in New York: a side effect of climate change? **Espinosa, Bouallegui, Grouzdev, Brianik, Czaja, Geraci-Yee, Kristmundsson, Muehl, Schwaner, Tettelbach, Tobi, Allam**	Buoys and autonomous surface vehicles for aquaculture: an inexpensive harmful algal bloom monitoring approach **Levin, Morton, Lantham**	PhytO-ARM, an open source/open design toolkit for automated and adaptive HAB monitoring and response **Brosnahan, Govostes, Lucke, Batchelder, Pathare, Petitt, Ward, Villac, Hubbard, Anderson, Doucette**		
2:15 PM	Evaluating whether a modification to commercial sea scallop dredges can reduce bycatch and increase catch efficiency **Gius, Morson, Bochenek, Zemeckis, O'Brien**	Time series analysis of Abalone Withering Syndrome: tracking responses in microbiome and host health **Kunselman*, Marshman, Souza, Moore, Aquilino, Allard, Gilbert**	Nanobubble ozone technology (NBOT) for scalable emerging algae/toxin mitigation and remediation **Moeller, Lee, Janech, Beauchesne, Bland, Schanke**	Remote sensing for shellfish management: efforts toward early warning, tool development and training for harmful algal blooms in Chesapeake Bay **Tomlinson, Yu, Staugler, Abecassis, Wilson, Morton, Fuquay, Stumpf**		Preliminary survey of transposable elements from specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, domesticated in the United States **Alcivar-Warren, Bao**
2:30 PM	Monitoring surfclams at offshore wind energy projects **Munroe, Morson, Saba**	Invasive crayfish as potential vectors of white spot syndrome virus (WSSV) to native crustaceans of South Carolina, USA **Rothman*, Allen, Kingsley-Smith, Beers, Welch, Kendrick**	Mobile lab utilized in monitoring phytoplankton dynamics for safe shellfish harvest in southcentral Alaska **Jarosz*, DeMaster, Branson**	Satellite sea surface temperature guidance for reducing *Vibrio parahaemolyticus* in shellfish **Daniels, Ransibrahmanakul, Ellett, Jacobs**		The genome of *Penaeus vannamei* solinvivirus (PvSV) identified in diseased shrimp from Brazil is identical to Wenzhou shrimp virus 8 and *P. vannamei* picornavirus in wild shrimp from China - portions of these viruses are present in one (ASM373033v1) of the two genome assemblies available for *P. vannamei* **Zuniga, Alcivar-Warren**
2:45 PM	Economic impacts of offshore wind energy development on the commercial sea scallop fishery **Borsetti, Scheld, Rudders, Munroe, Powell, Hofmann, Klinck**	Natural transmission of *Hematodinium perezi* in juvenile blue crabs (*Callinectes sapidus*) in the laboratory **Chen*, Reece, Shields**	Aquaculture Phytoplankton Monitoring Network: a citizen science approach to monitor harmful algal blooms and changes in environmental conditions with the aquaculture industry **Rene, Maucher-Fuquay, Shuler, Morton**	Can satellite products or state monitoring data substitute for on-farm data for oyster aquaculture modeling? **Bricker, Ransibrahmanakul, Okada, Davenport, Karrh, Vogel, Briggs, Tomlinson**		
SESSION TITLE	**COMMERCIAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**	**DISEASE** **Ryan Carnegie & Tal Ben Horin**	**GENERAL CONTRIBUTED II** **Cathy Liu**	**REMOTE SENSING & SHELLFISH** **Michelle Tomlinson & Suzanne Bricker**	**MEET THE AGENCIES** **Sandra Shumway**	
3:00 PM	Understanding reproductive development in female white shrimp, *Penaeus setiferus* in support of sustainable fisheries management **Mitchell*, Kingsley-Smith, Brunson, Wagner, Kendrick**	Regional Shellfish Seed Biosecurity Program (RSSBP) Forum: The RSSBP was established to improve shellfish health management in the context of interstate commerce in aquaculture products along US coasts. This open forum will include an update on progress toward RSSBP development and discussion of emerging issues of concern to the shellfish aquaculture industry and regulatory community.	Staging of channeled whelk (*Busycotypus canaliculatus*) female gonads using gross and histological analyses **Towne, Cameron, Scro, Angell, Smolowitz**	Improving oyster aquaculture site selection with high resolution satellite imagery **Kiffney*, Jiang, Hesketh, Lavaud, Boss, Brady**	An opportunity to meet the leaders of agencies and organizations (PSI, ECSGA, NOAA, NAA, USDA, NRAC, PCSGA, APHIS, SeaGrant) that support shellfish research and industry – and to ask questions!	
3:15PM	Rotational management of oyster harvest in the Rappahannock River, Virginia: 15 years onward **Southworth, Wesson, Button, Mann, Marquardt, Scheld**		Recovery from estivation in the apple snail, *Pomacea maculata*: nitrogen excretion **Deaton**			
3:30 PM	A vignette on the evolution of oyster management: the search for a triumvirate of reference points simultaneously defining biomass-maximum-sustainable yield (Bmsy), fishing mortality rate at MSY (Fmsy), and cultch content at MSY **Powell, Solinger, Hemeon, Pace**		Growth of the banded tulip (*Cinctura hunteria*) in Tampa Bay, Florida **Levine, Geiger**			
3:45 PM	How accurately can sea scallops be aged? **Roman, Rudders, Clark, Southworth, Mann**		Comparisons of wild and farmed seafood: nutrition profiles and safety attributes **Liu**			
4:00 PM	Atlantic surfclam (*Spisula solidissima*) population demographics through the decades **Díaz*, Hofmann, Klinck, Munroe, Powell, Scheld**					
4:15 PM						
4:30 – 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Stadium Ballroom – 2nd floor**					
7:00 -10:00 PM	**STUDENT ENDOWMENT FUND AUCTION** **Grand Ballroom**					

* denotes student presenter ^{p} denotes non first-author presenter

WEDNESDAY
March 29, 2023

8:00-8:50AM	**PLENARY: Vic Kennedy (*Emeritus*, University of Maryland) – *Depleting the immense protein factory that was Chesapeake Bay*** **Grand Ballroom**				
	NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Promenade**				
ROOM	**University 1/2**	**University 3/4**	**Grand A/B/C**	**Harbor I**	**Chesapeake**
SESSION TITLE	**FRESHWATER MUSSELS** **Dee Kreeger**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**VIBRIO** **Steve Jones**	**eDNA APPLICATIONS FOR SHELLFISH** **Phoebe Jekielek**	**CLAM SELECTIVE BREEDING: RESEARCH ADVANCEMENT & OPERATIONALIZING GENOMIC RESEARCH** **Dina Proestou & Rebecca Shuford**
9:00AM	Reefense: DARPA and a multi-disciplinary team of scientists join forces to develop oyster reefs for coastal protection **Bushek, Cebrian, Goad, Guo, Jin, Kibler, Kreeger, La Peyre, Lowe, Moody, Morris, Nassif, Rikard, Riman, San Nicolas, Sparks, Temple**	Estuarine shoreline conservation and restoration in the urbanized watershed of Charleston County, South Carolina, USA **Kingsley-Smith, Sundin, Wagner, Dyar, Hodges, Bell, Prochaska, Morganello**	*Vibrio parahaemolyticus* population in native and cultured oysters in New Hampshire **Whistler, Foxall, Wasson, Jones**	Environmental DNA (eDNA): What is it and how does it work? **Jekielek***	An Overview of the Sea Grant Hard Clam Selective Breeding Collaborative (Hub) **Clemetson**
9:15AM	Implementation of a regional "Mussels for Clean Water Initiative" for the upper mid-Atlantic region **Morgan, Kreeger, Cheng, Gentry**	Location and reef size drive oyster restoration success **Caretti*, Eggleston, Bohnenstiehl, Puckett**	Understanding the influence of the oyster on levels of human-pathogenic *Vibrio* spp. **Audemard, Reece, Latour, Bienlien, Carnegie**	Developing eDNA as a tool for monitoring cultured and wild populations of sea scallops (*Placopecten magellanicus*) in Maine, USA **Jekielek*, Leslie, Price**	Updates from the East Coast Hard Clam Selective Breeding Collaborative **Allam, Espinosa, Grouzdev, Tanguy, Reece, Yang, Rivara, Reitsma, Clemetson, Guo**
9:30AM	Incidence and restoration prioritization of rare and common species of freshwater mussels in the tidal Delaware River, USA **Kreeger, Cheng, Gentry, Morgan**	Comparison of artificial substrates with oyster shell for oyster recruitment and biomass in the York River, Virginia **Patel*, Knick, Saluta, Lipcius, Seitz**	Studying *Vibrio parahaemolyticus*-eastern oyster (*Crassostrea virginica*) interactions, including the oyster-associated bacterial community **Stevens, Hines, Madanick, Smith, Kuhn**	Proactive and non-invasive pathogen diagnostics to prevent the spread of *Bonamia ostreae* **Regan, Vythalingam, Bean^{P}**	Population genetic structure and transcriptomic response to low salinity in *Mercenaria mercenaria* **McDowell, Youtsey, Ropp, Snyder, Biesack, Reece**
9:45AM	Freshwater mussel grow out techniques: linking modern aquaculture practices with restoration goals **Cheng, Gentry, Kreeger, Butler, Thomas**	Successful eastern oyster (*Crassostrea virginica*) recruitment on two alternative settlement substrates in Virginia tributaries **Seitz, Knick, Pysher, Suchonic**	Hitching a ride or taking advantage? How phytoplankton and host microbiomes influence *Vibrio* spp. accumulation in oysters **Diner, Zimmer-Faust, Griffith, Gilbert**	Environmental DNA based detection of *Polydora* species on oyster beds in Chesapeake Bay **Biesack, Hudson, Fisher, McDowell**	Challenge of heat shock on northern quahogs for genome-wide association study **Yang, Yee, Zeng, Bently, Bell**
SESSION TITLE	**HATCHERIES** **Don Webster**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**VIBRIO** **Steve Jones**	**eDNA APPLICATIONS FOR SHELLFISH** **Phoebe Jekielek**	**CLAM SELECTIVE BREEDING: RESEARCH ADVANCEMENT & OPERATIONALIZING GENOMIC RESEARCH** **Dina Proestou & Rebecca Shuford**
10:00AM	Chinese "nature and grower-centered" oyster hatchery technology: is it sustainable? **Thiyagarajan, Yu, Xiao, Li, You, Wang, Chung**	Advancing alternatives to shell for oyster restoration **Moffat, Slacum Jr., Caretti**	Probiotic-induced disease resistance of Pacific oyster larvae **Hesser*, Mueller, Langdon, Schubiger**	Developing larva-specific environmental RNA (eRNA) tools for the blue mussel aquaculture industry **Ernst, Beal, Grey, Pepperman, Whitney, Price**	Selection for growth in hatchery-reared soft-shell clams, *Mya arenaria* L.: a series of field investigations **Beal**
10:15AM		Seven years of monitoring shellfish on a constructed, intertidal reef in the Delaware Bay, New Jersey **Shinn, Bushek**	Prevalence of *Vibrio parahaemolyticus* and *V. vulnificus* in blue crabs (*Callinectes sapidus*) and seawater collected from the Maryland coastal bays **Smalls*, Jacobs, Townsend, Chigbu, Parveen**		A coastwide perspective on production, challenges and needs in stock improvement of *Mercenaria mercenaria* **Rheault, Reitsma, Sturmer, Clemetson**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**HATCHERIES** **Don Webster**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**VIBRIO** **Steve Jones**	**MODELLING & CLIMATE CHANGE** **Eric Powell**	**CLAM SELECTIVE BREEDING: RESEARCH ADVANCEMENT & OPERATIONALIZING GENOMIC RESEARCH** **Dina Proestou & Rebecca Shuford**
11:00 AM	Low temperature storage of bivalve larvae - a new management tool for shellfish hatcheries **Rivara, Patricio, Allen**	The impact of vessel noise pollution on the early recruitment of benthic invertebrates in two distinct sites in Saint-Pierre and Miquelon, France **Gauthier*, Uboldi, Tremblay, Meziane, Olivier, Chauvaud, Winkler**	Nested spatial and temporal modeling of environmental conditions associated with genetic markers of *Vibrio parahaemolyticus* in *Crassostrea gigas* in Washington State **Fries, Davis^{P}, Corrigan, DePaola, Curriero**	Temporal and spatial comparisons of ocean quahog (*Arctica islandica*) growth on the mid-Atlantic continental shelf: from the Neoglacial through the twentieth century **LeClaire, Powell^{P}, Mann, Hemeon, Pace, Saba, du Pontavice, Sower**	Panel Discussion: Perspectives and experiences in the development of genomic technology and application in broodstock programs Moderator: Rebecca Shuford
11:15 AM	On track to optimize the bottle upweller system (BUPSY): testing four bottle configurations **Benitz, Leavitt^{P}**	Rebuilding a collapsed *Mercenaria mercenaria* population, restoring seagrass meadows, and eradicating harmful algal blooms in a temperate lagoon using spawner sanctuaries **Doall, Peterson, Gobler**	In-house *Vibrio parahaemolyticus* enumeration in oysters by industry to manage risk **DePaola, Kim, Tarnecki, Dewey**	Physiological and behavioural response of eastern oysters (*Crassostrea virginica*) and soft-shell clams (*Mya arenaria*) to hypoxia and heatwaves **Talevi*, Clarke, Coffin, Comeau, Sakamaki, Filgueira**	
11:30 AM	Optimizing a low-volume flow-through system for rearing Pacific oyster (*Crassostrea gigas*) larvae **Fleener, Thompson, Langdon^{P}**	Restoration oyster reefs do not provide settlement and early nursery habitat for the blue crab, *Callinectes sapidus* **Lipcius**	Pilot-scale depuration demonstrates the suitability of non-pathogenic *Vibrio parahaemolyticus* as a surrogate for commercial-scale validation studies **Lunda*, Kilgore, Hesser, Waite-Cusic, Schubiger**	Evaluation of the degree of co-occurrence of surfclams and ocean quahogs at fishable concentrations **Stromp*, Powell, Mann**	
11:45 AM	Evaluating abiotic and biotic factors influencing hard clam production in Florida, USA **Laramore, Getter^{P}*, Sturmer, Anderson, Collins, Philps, Baker**	Oyster reef control of carbonate chemistry – implications for restoration in estuaries subject to coastal ocean acidification **Tomasetti, Doall, Kraemer Jr., Hallinan, Gobler**	Effects of aquaculture practices on *Vibrio* and the microbiome of the eastern oyster (*Crassostrea virginica*) **Parveen, Almuhaideb, Rashed, Hassan**	Climate-induced warming on the MAB seafloor: modeling future distributions of the Atlantic surfclam (*Spisula solidissima*) **Spencer*, Powell, Klinck, Munroe, LeClair, Scheld, Hofmann, Curchitser, Alexander**	
12:00 NOON	Commercial trials with RAS for oyster (*Crassostrea virginica*) larvae **Congrove, Glover^{P}, Ovissipour, van Senten, Bentley, Snyder, Schwarz**	Supporting Oyster Aquaculture and Restoration (SOAR) in Maryland: an adaptive strategy to support oyster farmers and restore oyster reefs during Covid-19 **Walters, Slacum Jr., Bryer, Hancock, Caretti, Wills, Amrhein**	The responses of total and potentially pathogenic *Vibrio parahaemolyticus* in resubmerged oysters in the Northeast U.S. **Jones, Howell, Petitpas, Whistler, Foxall, Regan, Madden, Howell, Shanks, Nash**	What shellfish farmers want the government to do to reduce climate impacts on their businesses **McGee, Dewey**	
12:15 PM	Industry update: developing a pilot scale hatchery in Delaware **Campbell, Hale, McIntosh, Blank**	Integrating a Rapid Assessment Protocol (RAP) into monitoring of subtidal oyster reefs **Tracy, Aguilar, Ritter, Ogburn**		Taking an energetic approach to predicting habitat suitability: the interactive roles of temperature and food availability in bivalve development **Czaja*, Jr, Allam, Espinosa, Beal, Pepperman**	
12:30-2:00 PM	**NSA BUSINESS LUNCHEON** **Grand Ballroom**				
2:00 - 4:30 PM	**SCALLOP GALLOP** **EXPLORE BALTIMORE!!**				**CLAM HUB TEAM PROJECT MEETING**
4:30 - 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Stadium Ballroom – 2nd floor**				

* denotes student presenter ^{P} denotes non first-author presenter

THURSDAY
March 30, 2023

8:00-8:50AM	**PLENARY: Ximing Guo (Rutgers University) – *Shellfish aquaculture in the genome era* Grand Ballroom**				
	NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY Promenade				
ROOM	**Grand A/B/C**	**Grand D/E/F**	**Grand East**	**Grand West**	**University 1/2**
SESSION TITLE	**OYSTERS Bill Fisher**	**SCALLOPS Steve Geiger**	**CLAMS Brian Beal**	**CONTAMINANTS OF EMERGING CONCERN Kayla Mladinich & J. Evan Ward**	**MANGROVE SHELLFISH Acacia Alcivar-Warren & Kathy Tang**
9:00AM	Triploid Pacific oysters experience enhanced mortality following marine heatwaves **George, Cattau, Middleton, Lawson, Vadopalas, Gavery, Roberts**	Wild scallop population resilience: using multigenerational studies to estimate robustness and adaptive potential to rapidly changing ocean acidification **McFarland, Gurr, Bernatchez, Padilla, Dixon, Guy, Milke, Poach, Novara, Hart, Plough, Redman, Sennefelder, Stiles, Wikfors, Meseck**	Evaluation of immunological responses to environmental salinity change in northern quahogs, *Mercenaria mercenaria*, using flow cytometry **Zeng*, Yang**	Sex-dependent toxicity of aquatic contaminants and their impact on blue mussels, *Mytilus edulis* **Ciocan, Koagouw, Minier, Bucca, Hesketh, Stewart**	Mangrove Shellfish: pollutants, ONE HEALTH, and epigenetics – recognition of students and outstanding researchers **Alcivar-Warren, Tang**
9:15AM	Citrate-synthase response and multiple-stress in Pacific oysters, *Crassostrea gigas* **Cattau, George, Roberts**	A dynamic pathway to transition from vulnerable to resilient fisheries social ecological systems: a transdisciplinary case study of the U.S. Atlantic sea scallop fishery **Berger*, Colburn, Meseck, Siedlecki, Matassa, Hart, Bethoney, Inglis, Alves**	Optimizing hatchery conditioning for sunray venus clam spawning **Cerino, Ben-Horin^p, Lucas, Synder, Wilbur**	Understanding and leveraging the response of shellfish microbiomes to coastal pollution **Diner, Wiggin, Gilbert**	Molluscs, microplastics, and the misinformation highway **Shumway, Mladinich, Ward, Holohan, Blaschik**
9:30AM	Can we eat them to save them? Farming the West Coast native oyster, *Ostrea lurida*, for market and restoration values in Tomales Bay, California **Fleener, Rintoul, Maguire**	Predicting larval dispersal and population connectivity of sea scallops (*Placopecten magellanicus*) in coastal Maine through computer modeling and population genomics **Ward*, Rawson, Xue**	A soft-shell clam recruitment monitoring network: a tool for the coastal communities of Maine **Beal, Randall**	Effects of elevated temperature and TiO_2 nanoparticles on the gut microbiota and byssus performance of the thick shell mussel, *Mytilus coruscus* **Gao*, Li, Li, Wang**	
9:45AM	Investigation of the *Ostrea edulis* larval microbiome throughout a natural spawning event **Farley, Regan, Warr, Batista, Bass, Bean**	Brant Point Shellfish Hatchery: a municipal shellfish restoration initiative striving to save one of the last commercial bay scallop fisheries on Nantucket Island, Massachusetts **Riley, Hill, Minella, Berry**	Intertidal mudflats as nursery sites for cultured, juvenile soft-shell clams, *Mya arenaria* L. **Beal, Coffin**	Future ocean acidification and warming will increase the physiological impact and bioavailability of metals from historic mine deposits on commercial bivalve species **Rastrick, Bank, Garcia, Krogness, Kutti, van der Meeren, Rastrick**	Environmental epigenomics and transgenerational epigenetic inheritance in livestock and shellfish species **Khatib**
10:00AM	A comparative study of the biodiversity associated with fallow, actively fished and non-fished European oyster (*Ostrea edulis*) beds **Medlar, Graves, Culloty, Lynch^p**	Patterns and processes underlying spatiotemporal variation in bay scallop density and size-structure within and among three Sounds of North Carolina **LaCroce, Brooks, Eggleston**	Pilot-scale studies to examine reproductive output in soft-shell clams, *Mya arenaria* L. **Beal, Randall**	Effects of underwater noise associated with the installation of offshore wind turbines on the larval development of eastern North Atlantic commercial bivalves **Olivier, Gigot, Bonnel, Mathias, Meziane, Tremblay, Chauvaud**	
10:15AM			Three centuries of increasing growth rates of a long-lived clam (*Arctica islandica*) on the western mid-Atlantic Continental Shelf (US) **Hemeon, Powell, Klinck, Mann^p, Pace**	Microplastic accumulation kinetics and effects on the energy condition of giant scallop (*Placopecten magenallicus*) **Faraut*, Soubaneh, Tremblay, Rouleau, Pelletier**	Status of mangrove forests in Ecuador **Galindo, Alcívar-Arteaga^p, Hernández, Diaz, Asunción, Saltos, Figueroa, Espinoza, Villota, Calvache, Jaen, Valarezo, Romero, Mejía, Aveiga, Mendoza, Alcívar-Warren**
10:15-10:45AM	**MORNING BREAK**				
SESSION TITLE	**OYSTERS Bill Fisher**	**SCALLOPS Steve Geiger**		**CONTAMINANTS OF EMERGING CONCERN Kayla Mladinich & J. Evan Ward**	**MANGROVE SHELLFISH Acacia Alcivar-Warren & Kathy Tang**
10:45AM	Assessing dredge gear versus diver-based surveys in support of a fishery-independent monitoring program for sub-tidal oyster reefs **Bowling, Eggleston, Boutin**	Comparison and calibration of trawls to diver surveys for monitoring Florida bay scallop (*Argopecten irradians concentricus*) populations **Granneman, Levine**		Determination of the upper size limit of microplastic particles that can be ingested by the Quagga mussel, *Dreissena bugensis* **Collins*, Holohan, Ward**	Cytochrome P450-dependent mixed function oxidases (MFO) system dynamics during the polyaromatic hydrocarbon (PAH) metabolism in the green mussel, *Perna viridis* (Linnaeus, 1758) **Amutha**
11:00 AM	Dose-dependent effects of exposure to polyunsaturated aldehydes on embryos of early larval stages of the bivalves, *Crassostrea virginica* and *Mytilus edulis* **Peterson, Rawson**	The effect of population density on oocyte development in Atlantic sea scallops (*Placopecten magellanicus*) **Clark*, Roman, Mann, Rudders**		Smaller microplastics accumulate with age in the Philippine cockle, *Anadara antiquata* **Bucol*, Vasig, Watanabe, Kataoka**	The Mangrove Epigenome (MangroveENCODE) Project of the FUCOBI Foundation of Ecuador: A ONE HEALTH approach to conservation of healthy mangroves, to produce healthy shellfish, and protect people's long-term health **Alcivar-Arteaga, Warren, Galindo, Hernandez, Díaz, Espinoza, Figueroa, Mejia, Romero, Asunción, Zuniga, Aveiga, Mendoza, Alcivar-Warren**
11:15 AM	Energetic physiology of *Crassostrea virginica* oyster spat from the acclimation period to the dormancy phase: implications for their survival during cold winters **Bridier, Clements, Comeau, Mallet, Mallet, Carver, Tremblay**	Testing the transfer of fecal and digestive gland microbiotas between mussels (*Mytilus edulis*) and the King scallop (*Pecten maximus*) for accelerated depuration of domoic acid **Deléglise*, Noël, Barnouin, Corona, Offret, Lassudrie, Hegaret, Bidault, Fabioux**		Ecotoxicological effects of microplastics on mussels: insights from immune defense, oxidative stress, and energy metabolism **Wei*, Gu, Wang**	Future direction of the FUCOBI Mangrove Shellfish Research Project in Ecuador through a Rotary Foundation Global Grant - interested in joining us? **Alcivar-Arteaga, Alcivar-Warren^p**
11:30 AM	Revisiting the Newell number: estimating pre-colonial oyster abundance and ecological services in the Chesapeake Bay **Mann, Southworth, Tarnowski, Wesson, Marquardt, Harding, Rudnicky**	Observation of boring clams in calico scallops from Cape Canaveral, Florida, USA **Geiger, Adams, Kiryu, Luba, Leal**		Microplastics as vectors of *Vibrio parahaemolyticus* to the Pacific oyster **Wiggin*, Allard, Gilbert**	
11:45 AM	Analysis of stress associated to inter-site transport of the eastern oyster production **Gravel-Brunet, Gilmore-Solomon, Tremblay**			Microplastics and oyster aquaculture **Mladinich*, Holohan, Ward, Shumway**	
12:00-1:00 PM	**LUNCH BREAK**				

* denotes student presenter ^{p} denotes non first-author presenter

THURSDAY
March 30, 2023

NSA AT THE MOVIES - FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Promenade

ROOM	**Grand A/B/C**	**Grand D/E/F**	**Grand East**	**Grand West**
SESSION TITLE	**OYSTERS** **Bill Fisher**	**MACROALGAE-SHELLFISH CO-CULTURE** **Michael Doall**	**HORSESHOE CRABS** **Elizabeth Bouchard & Daniel Sasson**	**GENERAL CONTRIBUTED III** **Daphne Munroe & Emily Fuqua**
1:00 PM	Gender ratios of oysters in stressed estuaries in southern Florida **Geiger**	Mapping the growth and quality of farmed sugar kelp (*Saccharina latissimi*) in the estuaries surrounding Long Island, New York **Doall, Curtin, Morrell, Provost, Eckstein, Chen, Gobler**	A method for estimating horseshoe crab abundance in the Delaware Bay, USA **Anstead, Sweka, Barry, Hallerman, Smith, Wong**	Off-shore aquaculture potential for the Atlantic surfclam, *Spisula solidissima*: field observations and multi-stressor laboratory experiments **Steeves, Munroe, Meseck, Guo, Towers, Myers, Martin, Dameron**
1:15 PM	Effects of shifts in salinity and parasite loading in the eastern oyster, *Crassostrea virginica* **Kirby, Geiger**	Use of seaweeds to protect aquacultured bivalves against climate change co-stressors and harmful algal blooms **Gobler, Sylvers, Doall**	Using epibiont diversity and carapace condition in American horseshoe crabs (*Limulus polyphemus* L.) as tools to distinguish between populations and elucidate age-structure **Botton, Colón, Jean-Baptiste, Zaw, Loveland**	Revisiting ecological carrying capacity indices for bivalve culture **Comeau, Guyondet, Drolet, Sonier, Clements, Tremblay, Filgueira**
1:30 PM	Transcriptomic responses to low salinity in eastern oyster adults and larvae **Bhandari, Purnell, Yeboah, Butt, Liu**	Can integrated multi-trophic aquaculture help mitigate the effects of climate change on economically important filter feeders **Rastrick, Jiang, Wang, Graham, Collier, Whiteley, Strohmeier, Fang, Strand**	Mitigation strategy for horseshoe crab impingement by a Florida power plant **Heres, Brockmann, Crowley, Gandy**	Food webs supporting crab production in estuaries with expanding coastal urbanisation **Waltham, Connolly**
1:45 PM	Survival and growth of tetraploid eastern oyster, *Crassostrea virginica*, in differing salinities within the northeastern Gulf of Mexico **Capps, Rikard, Spellman, Chaplin**	Enhancing marine aquaculture in the tropical U.S.: methods for sustainable commercial co-cultivation of shellfish and seaweed in Florida **Welch, Roberson**	Distribution of horseshoe crab eggs and infauna around intertidal oyster farms in Delaware Bay **Bouchard*, Munroe, Maslo, Bushek**	Potential trophic niches overlap of native and non-indigenous species: who eats what and who eats more? **Cabral*, Costa, Chainho, Comeau, Tremblay**
2:00 PM	Effects of desiccation practices on eastern oyster (*Crassostrea virginica*) condition index, growth rate, and parasite load **Thomas, Buck, Wilbur**	The GreenWave Ocean Farming Hub: a platform for seaweed farmer training and collaboration **Olsen**	Horseshoe crab interactions within a newly-restored fringing marsh in Stratford Point, Connecticut **Kasinak**	How does recruitment contribute to recent shifts in long-term trajectories of burrowing shrimp populations and their effect on shellfish aquaculture in Willapa Bay, Washington? **Dumbauld, McIntyre, Lewis, Ruesink, Hull**
2:15 PM	Mechanisms of mortality in *Crassostrea virginica* during severe hypoxia: effects of endogenous and exogenous bacteria, and temperature **Steeves, Winterburn, Filgueira, Comeau, Guyondet, Maillet, Babarro, Clements, Mallet, Haché, Poirier, Deb, Coffin**	Incorporating kelp and oyster co-culture at scale **Grindle**	Comparing embryonic development in beach and marsh habitats for the American horseshoe crab, *Limulus polyphemus*, in South Carolina, USA **Scott, Sasson, Kendrick, Brunson, Kingsley-Smith**	Sensitivity of the grooved carpet shell clam, *Ruditapes decussatus*, to ocean acidification **El-Wazzan, Shaltout, Madkour, Abu El-Regal, El Shazly, Awad**
2:30 PM	Effect of biofouling control and stocking density on microclimate in off-bottom oyster culture grow-out bags: oyster performance **Grenn, Walton**	Leveraging the shared resources of oyster co-operative to support kelp production **Sparta, Foote, Sparta**	The use of non-sandy beach habitats by spawning horseshoe crabs: a conversation about its implications and future research priorities **Sasson, Brunson, Scott, Kendrick**	Ontogenetic shifts in salinity tolerance in the eastern oyster, *Crassostrea virginica*: implications for restoration and recovery in Apalachicola Bay, Florida **Fuqua*, Brooke**
2:45PM		Co-culture of bay scallops and kelp in Chincoteague Bay, Maryland **Rush, Holloway**		Effects of hypoxia and acidification on early-stage bivalves under natural and artificial cycling conditions **Kraemer Jr.*, Gobler**
3:00 PM				Transgenerational inheritance of ocean acidification-induced feminization in the Portuguese oyster **Dang*, Thiyagarajan**
3:30 – 6:00 PM	**CLOSING HAPPY HOUR** **Stadium Ballroom – 2nd floor**			

* denotes student presenter ^{p} denotes non first-author presenter

CONTENTS

ORAL PRESENTATIONS

POSTER PRESENTATIONS

VIRAL SHEDDING RATES OF TOLERANT AND SUSCEPTIBLE *CRASSOSTREA GIGAS* INFECTED WITH MULTIPLE OSHV-1 VARIANTS

M. Victoria Agnew*[1], Colleen A. Burge[2], and Meghana P. Parikh[3]

[1]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, 701 E Pratt St, Baltimore MD 21224

[2]California Department of Fish and Wildlife, UC Davis Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, CA 94923

[3]NOAA Fisheries, Northeast Fisheries Science Center, 212 Rogers Ave, Milford, CT 06460

magnew1@umbc.edu

The emergence of a new variant of Ostreid herepesvirus-1 (OsHV-1) in San Diego, California, USA elicits concern for the livelihood of its host, *Crassostrea gigas*, on the west coast of the USA. OsHV-1 variants are associated with mass mortalities of *C. gigas* globally, and the microvariant detected in San Diego Bay has been associated with die-offs of *C. gigas* in 2018 and 2020. The rapid spread of OsHV-1 in other parts of the world indicates that spread of OsHV-1 in the USA is plausible. Understanding the risk of spread of OsHV-1 from San Diego Bay, or other areas of introduction, is valuable for mitigating disease outbreaks in the future. An important aspect to understanding viral transmission is viral shedding rate, and the shedding rate of OsHV-1 is largely unknown. The viral shedding rate of two-family lines of OsHV-1 produced by the Molluscan Broodstock Program were tested. In a previous challenge with an OsHV-1 microvariant from France, these families had an average survival of 62% (tolerant) and 26% (susceptible). Each line was exposed to an OsHV-1 microvariant isolated in France and the microvariant isolated from San Diego, California. Oysters were injected with virus and placed in individual containers for 6 days. Water samples were taken every ~24hrs and assessed via qPCR for total OsHV-1 DNA copies shed into the water. Data from this experiment will be presented. These results will be directly applied to a geospatial model assessing the risk of OsHV-1 spread along the west coast of the USA.

SEASONAL VARIABILITY OF *MYTILUS* SP. FEEDING ACTIVITY: THE ROLE OF ENVIRONMENTAL CONDITIONS AND FOOD CHARACTERISTICS

Antonio Aguera*, Tore Strohmeier, Cathinka Krogness, Helen Rastrick, and Øivind Strand

Institute of Marine Research, Nordnesgaten 50, N-5020 Bergen, Norway

antonio.aguera@hi.no

Blue mussels are an important natural and cultured resource in coastal areas around the world. As such, there has been a wide interest in describing their feeding response in varying environments. Increased frequency measurements of mussel feeding activity is necessary to gain further insight on the sensitivity to natural changes, the potential adaptations to different seasons or the variability of individually physiological performance. Growth and feeding activity (clearance, retention rates and ingestion rates) of the same 10 mussels exposed to the natural variation of food, temperature and salinity were observed and measured every 2 hours for a year. The data set comprises more than 40000 measurements of feeding activity over a year. Seston characteristics (inorganic and organic content, energy density, phytoplankton community and fatty acids composition) were sampled on a monthly basis. Preliminary results show that mussels exhibit a wide response in feeding activity that reflects in their growth and performance. Individuals could not be classified as either slow or fast growers/feeders but a continuous range of performance was observed. Food was the main driver of feeding activity during the year, with little effect of temperature in modulating these within the observed temperature range (5 - 18°C).

FUTURE DIRECTION OF THE FUCOBI MANGROVE SHELLFISH RESEARCH PROJECT IN ECUADOR THROUGH A ROTARY FOUNDATION GLOBAL GRANT - INTERESTED IN JOINING US?

Miriam Alcivar-Arteaga[1] and Acacia Alcivar-Warren[1,2]*

[1]Foundation for Conservation of Aquatic and Terrestrial Biodiversity (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Environmental Genomics Inc., ONE HEALTH Epigenomics Educational Initiative, Southborough, MA, 01772, USA

fucobi@gmail.com

This presentation will inform about the current mangrove shellfish research being undertaken with collaborators of the FUCOBI Foundation of Ecuador, and future direction of our ONE HEALTH program. It is hopeful that researchers with expertise on epigenetics and generational inheritance of animals and people will join the project to collaborate. The project would like to study the potential health effects to shrimp and oysters from five coastal provinces and the Galapagos Islands of Ecuador caused by the exposure to microplastics, glyphosate-based herbicides, and other pesticides, and metals chelated by glyphosate. Please attend the session to discuss a potential collaboration for the next 10 years.

THE MANGROVE EPIGENOME (MANGROVEENCODE) PROJECT OF THE FUCOBI FOUNDATION OF ECUADOR: A ONE HEALTH APPROACH TO CONSERVATION OF HEALTHY MANGROVES, TO PRODUCE HEALTHY SHELLFISH, AND PROTECT PEOPLE'S LONG-TERM HEALTH

Miriam Alcivar-Arteaga*, Caroline Warren, Mayra Galindo, Iris Hernandez, César Díaz, Daniela Espinoza, Sofia Figueroa, Carlos Mejia, Jorge Romero, Gober Asunción, Gladys Zuniga, Freddy Aveiga, Marcela Mendoza, and Acacia Alcivar-Warren

Fundación para la Conservación de la Biodiversidad Acuática y Terrestre (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Edén, Quito, Ecuador

fucobi@gmail.com

The long-term goal of the Mangrove Epigenome (MangroveENCODE) project of the FUCOBI Foundation of Ecuador is to help conserve healthy mangroves ecosystems through education and research, by (1) promoting replanting of new trees to address both the community needs and the underlying ecological causes of mangrove degradation; (2) understanding mangrove resilience to climate change by studying their genomes, epigenomes, microbiomes, transposable elements (TEs), and (3) educating about wastewater-based epidemiology and association of antimicrobial resistance (AMR) and contaminants of concern (COC) in emerging resistant pathogens of shellfish and zoonosis of public health concern.

The short-term goal is to examine the interactions between greenhouse gas fluxes and carbon sequestration (blue carbon) and microbial communities (microbiome) with AMR and COC [microbial transgene *Bacillus thuringiensis*; endocrine disrupting chemicals (EDC) like glyphosate-based herbicides, metals chelated by glyphosate, BPA, DEPH, PFAS, organophosphates, PCB, PAH] in mangrove sediment, considering adaptation to climate change.

Baseline information is being obtained for future studies to test mechanism-driven hypotheses to examine the transgenerational epigenetic inheritance mechanisms involved in the interactions of CO_2 with EDC and the microbiome of mangrove sediment, using ecological, toxicological, 'omics' technologies, and computational tools. Preliminary results will be presented about (a) literature review about mangroves genomes and transcriptomes, TE like Gypsy LTR retrotransposons, epigenetic components (DNA-histone methylation, non-coding RNA) involved in salt and temperature stress adaptation of mangroves to global change, (b) protocol to collect 1-meter sediment cores for CO_2 and EDC analyses; (c) metal concentrations in mangrove sediment, shellfish, and people from estuaries of Ecuador.

GENOMIC SELECTION OF HEALTHY SHRIMP: A NEW, CONTINUOUS, WHOLE REFERENCE GENOME FOR SPECIFIC PATHOGEN-FREE (SPF) *PENAEUS VANNAMEI* IS NEEDED

Acacia Alcivar-Warren

ONE HEALTH Epigenomics Educational Initiative, Environmental Genomics Inc. (EGI), P.O. Box 196, Southborough, MA 01772

environmentalgenomics.warren@gmail.com

The estimated genome size (Gb) for specific pathogen-free (SPF) *Penaeus vannamei* is ~2.89Gb. The current draft of *P. vannamei* genome assembly (ASM378908v1) is ~1.80Gb, prepared with DNA from a male *P. vannamei* farmed in China (breed Kehai No. 1), stocks potentially originating from SPF lines produced by American breeding companies supported by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP) maintained at the Oceanic Institute in Hawaii, funded by the U.S. Department of Agriculture. As a member of the Technical Committee of the USMSFP representing Tufts University, I stored frozen DNA and tissue samples from the founder broodstocks and offspring of all lines developed by the USMSFP.

Initial efforts to sequence a BAC library using DNA from the Kona Line (high growth) were unsuccessful. In collaboration with Amplicon Express and Dr. Weidong Bao, Genetics Information Research Institute, CA, a pilot genome sequence was initiated, and 438 transposable elements (TE) have been characterized and deposited in Repbase (www.girinst.org). Preliminary information on endogenous viral elements (EVE) and repetitive sequences/TE will be presented.

Putative EVE of Infectious hypodermal and hematopoietic necrosis virus (IHHNV), White spot syndrome virus (WSSV), nimavirus *Nimav-1_LVa*, *P. vannamei* solinvivirus, Wenzhou shrimp virus8, and *P. vannamei* picornavirus are present in shrimp genomes. High percentage of repeats were identified in ASM378908v1, but information on chromosomal location is not available. For genomic selection, a new, continuous, complete whole reference genome sequence from SPF founders is first needed to clearly identify all repetitive sequences and TE from USMSFP shrimp.

PORTIONS OF A *HOMO SAPIENS* LINE 1 (L1) SEQUENCE ARE PRESENT IN PENAEID SHRIMP GENOMES

Acacia Alcivar-Warren

Environmental Genomics Inc, P.O. Box 196, Southborough, MA 01772

environmentalgenomics.warren@gmail.com

Long Interspersed Nuclear Element-1 (LINE-1 or L1) is an autonomous, non-long terminal repeat retrotransposon comprising approximately 17% of the human genome. Identification of transposable elements (TEs) in *Penaeus vannamei* from the United States showed 438 different TEs, but no L1 element has been reported. Twelve whole genome sequence (WGS) and 35 transcriptome shotgun assembly (TSA) databases available for Penaeoidea were used to determine if a human L1-like sequence (AF148856.1, 6019bp) was present in Penaeid shrimp.

WGS searches identified a large fragment (nucleotides 1291-6019) homologous to *Homo sapiens* L1 retrotransposon (AF148856.1, 6019bp) with 96% identity to nucleotides 4788-64 of *P. japonicus* Ginoza2017 DNA, scaffold_15245 (BOPN01015245.1 4788bp). Smaller fragments were also identified in *P. monodon*.

TSA searches revealed highest homology to *P. vannamei* transcript (GGKO01014538.1, 6259bp, 2 matches) isolated from populations of a breeding program from Brazil evaluated for growth performance and exposed to White Spot Syndrome Virus (WSSV). Nucleotides 1-781 of AF148856.1 showed 97% identity to nucleotides 5443-6226 of GGKO01014538.1. Nucleotides 779-6019 of AF148856.1 were 98% identical to nucleotides 82-5317 of GGKO01014538.1, which was also found in BOPN01015245.1.

Results based on BLASTP showed that L1 reverse transcriptase is present in current drafts of Penaeid shrimp genome assemblies (1.6-1.8Gb in *P. vannamei* and *P. japonicus*; 2.3Gb in *P. monodon*) but the expected size for *P. vannamei* is ~2.83Gb. Availability of new, continuous whole reference genome for *P. vannamei* will help confirm if L1 is present in the shrimp genome.

TAXONOMY OF SHELLFISH FOLLOWS THE CLASSIFICATION BY THE WORLD REGISTER OF MARINE SPECIES (WoRMS): FOR *PENAEUS* SPECIES, ONLY *PENAEUS VANNAMEI* BOONE, 1931 IS ACCEPTED (*LITOPENAEUS VANNAMEI* IS NOT ACCEPTED)

Acacia Alcivar-Warren

ONE HEALTH Epigenomics Educational Initiative, Environmental Genomics Inc, P.O. Box 196, Southborough, MA 01772

environmentalgenomics.warren@gmail.com

Information on Penaeidoa shrimp and marine molluscan species listed in the MolluscaBase database (www.molluscabase.org/) is displayed in the World Register of Marine Species (WoRMS, 2023). This paper reviews the literature on the taxonomy of *Penaeus sensu latu* (*s.l.*) genus (*Penaeus* Fabricius, 1798) which includes economically important penaeids. The genus was separated into six subgenera raised to the genus level (Pérez-Farfante and Kensley, 1997). Recent phylogenetic analyses have clearly demonstrated monophyletic status of single genus nomenclature for *Penaeus s.l.*, favoring reinstating genus *Penaeus*. Therefore, only the taxonomy classification accepted by WoRMS should be used for *Penaeus vannamei* Boone, 1931. *Litopenaeus vannamei* is no longer accepted and journal Editors should not accept it (https://www.marinespecies.org/aphia.php?p=taxdetails&id=106822).

The accepted classifications for other *Penaeus* species are *P. aztecus* Ives, 1891; *P. brasiliensis* Latreille, 1817; *P. brevirostris* Kingsley, 1878; *P. californiensis* Holmes, 1900; *P. canaliculatus* (Olivier, 1811); *P. chinensis* (Osbeck, 1765); *P. duorarum* Burkenroad, 1939; *P. esculentus* Haswell, 1879; *P. hathor* Burkenroad, 1959; *P. indicus* H. Milne Edwards, 1837; *P. isabelae* (Tavares & Guzmão, 2016); *P. japonicus* Spence Bate, 1888; *P. kerathurus* (Forskål, 1775); *P. konkani* (Chandra & Bhattacharya, 2003); *P. latisulcatus* Kishinouye, 1896; *P. longistylus* Kubo, 1943; *P. marginatus* Randall, 1840; *P. merguiensis* De Man, 1888; *P. monodon* Fabricius, 1798; *P. notialis* Pérez Farfante, 1967; *P. occidentalis* Streets, 1871; *P. paulensis* Pérez Farfante, 1967; *P. penicillatus* Alcock, 1905; *P. plebejus* Hess, 1865; *P. pulchricaudatus* Stebbing, 1914; *P. schmitti* Burkenroad, 1936; *P. semisulcatus* De Haan, 1844; *P. setiferus* (Linnaeus, 1767); *P. silasi* Muthu & Motoh, 1979; *P. similis* (Chanda & Bhattacharya, 2002); *P. simplex* Chan, Muchlisin & Hurzaid, 2021; *P. stylirostris* Stimpson, 1871; *P. subtilis* Pérez Farfante, 1967.

PRELIMINARY SURVEY OF TRANSPOSABLE ELEMENTS FROM SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS VANNAMEI*, DOMESTICATED IN THE UNITED STATES

Acacia Alcivar-Warren[1,2]* and Weidong Bao[3]

[1]Fundación para la Conservation de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada Casa 17, El Eden, Quito, Ecuador

[3]Environmental Genomics, Inc., P.O. Box 196, Southborough, MA 01772 USA

[3]Genetics Information Research Institute, 20380 Town Center Lane, Suite 240, Cupertino, CA 95014 USA

environmentalgenomics.warren@gmail.com

As part of the efforts to understand the epigenetic mechanisms associated with the susceptibility of *Penaeus vannamei* to bacterial and viral diseases, genomic structural and methylation variation, mediated by the activity of transposable elements (TE), particularly horizontal transfer (HT), is proposed to play a fundamental role in determining susceptibility to several marine diseases such as Acute Hepatopancreatic Necrosis Disease (AHPND), White Spot Syndrome Virus (WSSV), and Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV). To test this hypothesis, access to another *P. vannamei* genome assembly, a fully-assembled one (expected size ~2.8 Gb), is needed instead of the current ~1.8 Gb assembly from GCA_003789085.1.

A pilot sequencing project of the original SPF strain *P. vannamei*, domesticated by the U.S. Marine Shrimp Farming Program (USMSFP) breeding program in Hawaii, has generated a small (~470 Mb) portion of its genome sequence. To date, this initial project has resulted in the discovery of a total of 438 TE families deposited in Repbase (https://www.girinst.org/repbase/). These include 126 DNA transposons [DNA(42), DNAV(7), EnSpm(1), Harbinger(11), hAT(13), Kolobok(2), Mariner/Tc1(10), Merlin(12), MuDR(1), P(1), piggyBac(8), Polinton(3), Transib(2), Sat(5), TE(8)]; 237 LTR retrotransposons [BEL(25), Copia(2), Gypsy(200), LTR(10)], 75 non-LTR retrotransposons [CR1(7), Daphne(7), Ingi(4), Jockey(3), Neptune(2), Nimb(7), NonLTR(11), Penelope(16), Proto2(2), RTE(9), R4(2), SINE2(3), Vingi(2)]. Undoubtedly, the vast complexity of the Shrimp mobilome is far from being fully explored. At this stage, one more new, well-assembled reference genome will certainly facilitate this process and is highly demanded in various areas of shrimp research, including shrimp breeding and disease susceptibility or tolerance, ecological and environmental studies. Based on its biological specialty, such a genome could be the original SPF *P. vannamei*, optionally followed by another wild shrimp.

REPETITIVE SEQUENCE COMPOSITION IN TWO ASSEMBLIES OF PACIFIC OYSTER, *CRASSOSTREA GIGAS*

Acacia Alcivar-Warren[1]* and Weidong Bao[2]

[1]Environmental Genomics Inc., ONE HEALTH Epigenomics Educational Initiative, P.O. Box 196, Southborough, MA 01772

[2]Genetic Information Research Institute, 20380 Town Center Lane, Cupertino, CA 95014

weidong@girinst.org

The Pacific oyster, *Crassostrea gigas,* with its genome ranging from 545 Mb to 637 Mb, is an ideal model for investigating adaptation to environmental challenges. This species exhibits enormous intraspecific polymorphism or variation. Nearly half of its genome is composed of repetitive sequences. Most of these repetitive sequences are accounted by transposons. A large number of transposon families are currently active in transposition. From the assemblies of two Pacific oyster species varieties, including oyster_v9 and NWPU_Cgig_v2 (the black-shelled Pacific oyster), more than one thousand transposon families were categorized. The genomic transposon landscapes are compared in the two genomes. This thoroughly characterized repository of transposons will greatly facilitate the understanding of how these transposons shaped the genome, and the potential adaptive merit conveyed by these transposons.

PENAEID SHRIMP GENOMICS AND POST-GENOMICS: WHOLE REFERENCE GENOMES NEEDED FOR THE ECONOMICALLY IMPORTANT *PENAEUS* SPECIES

Acacia Alcivar-Warren*[1] and Fuhua Li[2]

[1]Fundación para la Conservation de la Biodiversidad Acuática y Terrestre (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Institute of Oceanology, Chinese Academy of Sciences, 7 Nanhai Road, Qingdao 266071, China

fucobi@gmail.com; fhli@qdio.ac.cn

Shrimp is the most important internationally traded fishery commodity in terms of value, with a global market valued at USD 37.6 billion in 2021. Despite its economic importance, research on penaeid shrimp genomics and epigenomics is lacking. So far, twelve draft genome assemblies are available in GenBank for only five penaeid species: *Penaeus monodon*, *P. vannamei*, *P. japonicus*, *P. chinensis*, and *P. indicus*. The *P. monodon* genome size is 2.39-Gb, the only sequence approximating the expected size of ~2.83-Gb of specific pathogen-free (SPF) *P. vannamei* domesticated in the United States, the most cultured species worldwide. The genome size of *P. vannamei* assembly ASM378908v1 is ~1.8-Gb. Research is needed to fill the gaps in the genome assemblies to address susceptibility to diseases caused by viral and bacterial pathogens, growth performance, and environmental contamination, and further for application of molecular genetic breeding techniques in shrimp.

The journal *Genes* is planning a special issue on 'Penaeid Shrimp Genomics and Post-genomics' and will welcome reviews or original articles covering genomic, epigenomic, or post-genomic profiling of penaeid shrimp that may provide the clues to solve the mechanisms of pathogenesis, evolution, and resilience to environmental change. For example, whole exomes, genomes and gene–environment susceptible microbiomes, metabolomes, proteomes, transcriptomes, and methylomes can individually and/or collectively inform specific molecular mechanisms, leading to the potential identification of factors or simple sequence repeats, transposable elements, and epigenetic marks to study transgenerational epigenetic inheritance of disease tolerance. This will eventually identify the most effective genomic selection approaches and precise treatments for emerging diseases.

MANGROVE SHELLFISH: POLLUTANTS, ONE HEALTH, AND EPIGENETICS – RECOGNITION OF STUDENTS AND OUTSTANDING RESEARCHERS

Acacia Alcivar-Warren[1,2]* and Kathy F. Tang[2]

[1]Fundación para la Conservation de la Biodiversidad Acuática y Terrestre (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Environmental Genomics Inc., ONE HEALTH Epigenomics Educational Initiative, P.O. Box 196, Southborough, MA 01772, USA

[3]Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, 106 Nanjing Road, Qingdao 266071, China

fucobi@gmail.com

The speakers of the Mangrove Shellfish will address the following topics, among others: molluscs, microplastics, and the misinformation highway (Shumway et al.), environmental epigenomics and transgenerational epigenetic inheritance in livestock and shellfish species (Khatib), status of mangroves forests of Ecuador (Miriam Alcivar-Arteaga et al.), cytochrome P450-dependent mixed function oxidases (MFO) system dynamics during the polyaromatic hydrocarbon (PAH) metabolism in green mussel *Perna viridis* (Linneaus, 1758) (Amutha et al.), the Mangrove Epigenome (MangroveENCODE) Project of the FUCOBI Foundation of Ecuador: a ONE HEALTH approach to conservation of healthy mangroves, to produce healthy shellfish, and protect people's health long-term (Alcivar-Warren et al.), Shrimp Scampi: A Citizens Science Project - educating about hormone disruptors like metals and glyphosate using foldscopes (Warren et al.), future direction of the FUCOBI mangrove shellfish research project in Ecuador through a Rotary Foundation Global Grant - interested in joining us? (Alcivar-Arteaga et al.).

Two researchers will be recognized as "Outstanding ONE HEALTH Researchers in Aquaculture" by the FUCOBI Foundation: Dr. Sandra Shumway, University of Connecticut, for her pioneering research on closing the reproductive cycle of the northern shrimp *Pandalus borealis*, microplastics research, and helping to educate about the holistic concept of ONE HEALTH for conservation of healthy shellfish biodiversity; and Dr. Hasan Khatib, University of Wisconsin, Madison, for his pioneering research on environmental epigenomics and transgenerational epigenetic inheritance in livestock and shellfish species.

Twelve students, postdocs and research associates will be recognized as winners of the 2023 'Johnnie Castro Montealegre Travel Awards' of the FUCOBI Foundation, representing four countries: Ecuador (7), India (1), Taiwan (1) and United States (4).

ONE HEALTH EPIGENOMICS: FROM *VIBRIOS* TO TRANSGENERATIONAL EPIGENETIC INHERITANCE - RECOGNITION OF STUDENTS AND 'OUTSTANDING ONE HEALTH RESEARCHERS' AWARDEES

Acacia Alcivar-Warren[1]* and Kathy F.J. Tang[2]

[1]Environmental Genomics Inc., P.O. Box 196, Southborough, MA 01772, USA

[2]Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, 106 Nanjing Road, Qingdao 266071, China

environmentalgenomics.warren@gmail.com

At the ONE HEALTH session, speakers will address topics that addresses the holistic concept of ONE HEALTH including: tracking ecosystem contaminants to protect public health (Jones), analysis of the expression and inhibition of the PirAB_{vp} toxin in *Vibrio* and non-*Vibrio* strains: the case of the *p*VA1 plasmid (Victorio-De Los Santos et al.), environmental epigenetics and transgenerational epigenetic inheritance in shrimp: research needed (Alcivar-Warren et al.), transposable element identification, classification, and annotation in non-model eukaryotic genomes like shrimp (Fernandez et al.), antimicrobial resistance in shrimp aquaculture (De Donato), epigenetic mechanisms reported in shellfish exposed to glyphosate- (Alcivar-Warren and Warren), reverse transcriptase-related genes and their possible role in the host cell response to transition metal pollution (Yushenova et al.), metals and glyphosate as endocrine disrupting chemicals in shellfish (Warren et al.), and taxonomy of Penaeus shrimp following the classification by the World Register of Marine Species (WORMS) (Alcivar-Warren), among others.

Three researchers will be recognized as "Outstanding ONE HEALTH Researcher in Aquaculture" by the FUCOBI Foundation: Dr. Stephen Jones, University of New Hampshire, for his research on *Vibrios* in oysters, microbial cycling of mercury in estuarine and marine environments, and monitoring for toxic chemicals in the marine environment; Dr. Hasan Khatib, University of Wisconsin-Madison, for his research on environmental epigenetics and the influence of diet on intergenerational and transgenerational epigenetic inheritance; and Dr. Laura Vandenberg, University of Massachusetts-Amherst for her research on endocrine disrupting chemicals.

Eighteen students, postdocs and research associates will be recognized as winners of the 2023 'Johnnie Castro Montealegre Travel Awards' of the FUCOBI Foundation, representing eight countries: China (1), Ecuador (6), India (2), Mexico (2), Spain (1), Taiwan (1), Venezuela (1), and United States (4).

SHRIMP GENOMES AND EPIGENOMES (SHRIMPENCODE): RECOGNITION TO STUDENTS AND 'OUTSTANDING ONE HEALTH RESEARCHERS' AWARDEES

Acacia Alcivar-Warren[1]* and Kathy F.J. Tang[2]

[1]Environmental Genomics Inc., P.O. Box 196, Southborough, MA 01772, USA

[2]Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, 106 Nanjing Road, Qingdao 266071, China

environmentalgenomics.warren@gmail.com

Speakers of the ShrimpENCODE session will address topics that support development of a sustainable shrimp aquaculture industry including: advances on Penaeid shrimp genomics and epigenomics (Alcivar-Warren and Li); taxonomy of commercially important shrimps (Chan et al.); annotation of immune response of shrimp to pathogens (De Donato et al.); a novel virus of Flaviviridae associated with sexual precocity in *Macrobrachium rosenbergii* (Tang et al); endogenous virus elements (EVE) of Infectious Hypodermal and Hematopoietic Necrosis Virus (Asuncion et al.) and White Spot Syndrome Virus in SPF *P. vannamei* (Galindo et al.); *NonLTR-1_LVa* retrotransposon associated with Abdominal Segment Deformity Disease of *P. vannamei* from Thailand (Asuncion et al.); perspectives for genomic selection in shrimp (Sanchez); and 438 transposable elements from SPF *P. vannamei* (Alcivar-Warren and Bao), among others.

Three researchers will be recognized as 'Outstanding ONE HEALTH Researchers in Shrimp Aquaculture' by the FUCOBI Foundation: Dr. Fuhua Li (China) for her efforts to sequence the complex genomes of *Penaeus vannamei* and other Penaeid species, and studies on sex determination and differentiation in shrimp; and Drs. Timothy Flegel and Kallaya Sritunyalucksana from Thailand for their research on shrimp pathogens and endogenous virus elements in IHHNV and WSSV viruses.

Eighteen students, postdocs, and research associates will be recognized as winners of the 2023 'Johnnie Castro Montealegre Travel Awards' of the FUCOBI Foundation, representing eight countries: China (1), Ecuador (6), India (2), Mexico (2), Spain (1), Taiwan (1), Venezuela (1), and United States (4).

EPIGENETIC MECHANISMS REPORTED IN FISH AND SHELLFISH EXPOSED TO GLYPHOSATE-BASED HERBICIDES (GBH)

Acacia Alcivar-Warren* and Caroline Warren

ONE HEALTH Epigenomics Educational Initiative, Environmental Genomics Inc, P.O. Box 196, Southborough, MA 01772

environmentalgenomics.warren@gmail.com

Glyphosate, a broad-spectrum organophosphorus herbicide, is the most widely used pesticide worldwide, and has raised many scientific, political, and public debates for its classifications as a potential carcinogen, endocrine disruptor, and lack of data about potential epigenetic generational effects (intergenerational and transgenerational) associated with exposure to low levels of glyphosate, its metabolite AMPA, and glyphosate-based herbicides (GBH). In Ecuador, many GBH products are sold without proper government regulation to register them and protect public health. In the Galapagos Islands, Roundup™ has been used since 2000 to control invasive species or pests in banana plantations near shrimp farms, and in feeds used for aquaculture and other agricultural commodities. Currently, research is not being conducted on the potential long-term health effects to shrimp, fish, and people caused by exposure to low levels of GBH and metals chelated by glyphosate, and potential for transgenerational epigenetic inheritance. Epigenetic mechanisms include DNA methylation, histone acetylation and non-coding RNA, but research on epigenetic regulation of aquaculture traits is still at an early stage.

Information will be presented of results obtained from an in-depth review of the scientific literature about epigenetic mechanisms associated with exposure of fish and shellfish to GBH using the PubMed and PubMed Central (PMC) databases and the terms: ‘glyphosate’, ‘glyphosate AND fish’ AND shellfish’, ‘glyphosate AND epigenetics’, ‘glyphosate AND epigenetics AND shellfish’ AND fish’, among others for crustaceans and molluscs. Results showed that most of epigenetic studies have been performed in fish and oyster species, but only a few used GBH. No generational epigenetic information is available for *Penaeus vannamei*, the most important commodity worldwide, or other Penaeid shrimp species.

A RETROTRANSPOSON PUTATIVELY ASSOCIATED WITH ABDOMINAL SEGMENT DEFORMITY DISEASE (ASDD) OF FARMED *PENAEUS VANNAMEI* FROM THAILAND IS PART OF *NONLTR-1_LVA* RETROTRANSPOSON ISOLATED FROM THE FIRST SPECIFIC PATHOGEN-FREE SHRIMP DOMESTICATED IN THE UNITED STATES

Acacia Alcivar-Warren[1,2], Jianbo Yuan[3], Nitsara Karoonuthaisiri[4], Tanaporn Uengwetwanit[4], Kanchana Sittikankaew[4], and Gober Asuncion*[1]

[1]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]ONE HEALTH Epigenomics Educational Initiative, P.O. Box 196, Southborough, MA 01772

[3]Institute of Oceanology, Chinese Academy of Sciences, No. 7 Nanhai Road, 266071, Qingdao, China

[4]National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Pathum Thani, 12120, Thailand

fucobi@gmail.com

Abdominal Segment Deformity Disease (ASDD) of farmed *Penaeus vannamei* from Thailand was suggested associated with a partial non-long terminal repeat (non-LTR) retrotransposon sequence (NLRS) (KC179708, 4,101bp). Using the NLRS probe, *in situ* hybridization signals were detected only in abdominal-ganglion neurons of ASDD distorted abdominal muscles of the shrimp. ASDD appeared related to inbreeding and long-term use of eyestalk-ablated female broodstock used in commercial hatcheries, and increased prevalence in mysis stage offspring from those broodstock.

A search in Rebpase database (www.girinst.org) revealed that KC179708 is part of *NonLTR-1_LVa* [Bao 2015, Repbase Reports 15(4), 1579]. Nucleotides 3-4101 of KC179708 shows 96.9% identity to nucleotides 1974-6062 of *NonLTR-1_LVa* (6,180bp) characterized in the genome of SPF *P. vannamei* domesticated by the US Marine Shrimp Farming Program maintained in Kona, Hawaii. *NonLTR-1_LVa* contains two ORF and conserved protein domains like R1-I-EN from superfamily EEP (exonuclease/endonuclease/phosphatase) and reverse transcriptase (RT, RNA-dependent DNA polymerase) from RT-like superfamily.

Homology searches using the 12 whole genome sequence databases in Genbank identified multiple copies of *NonLTR-1_LVa* in five penaeid species, comprising a significant part of the genome assembly. In the genome sequence of muscle DNA from *P. vannamei* farmed in China, (ASM378908v1, ~1.88Gb), more than 250 loci are found inserted with relatively young copies of *NonLTR-1_LV*a. It was also found in *P. vannamei* transcriptomes from various developmental stages (nauplii, mysis, post-larvae) and adult tissues, with no major increase in expression in ovaries after eyestalk ablation. It remains to be determined if the expression of *nonLTR-1_LVa* increases the incidence rate of ASDD.

UPDATES FROM THE EAST COAST HARD CLAM SELECTIVE BREEDING COLLABORATIVE

Bassem Allam[1]*, Emmanuelle Pales Espinosa[1], Denis Grouzdev[1], Arnaud Tanguy[2], Kimberly Reece[3], Huiping Yang[4], Gregg Rivara[5], Joshua Reitsma[6], Antoinette Clemetson[7], and Ximing Guo[8]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 149 Dana Hall, Stony Brook, NY 11794-5000

[2]Sorbonne Université, Station Biologique de Roscoff, Place Georges Teissier, 29688 Roscoff, France

[3]Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, VA 23062

[4]University of Florida, 7922 NW 71st street, Gainesville, FL 32653

[5]Cornell University Cooperative Extension, 3690 Cedar Beach Road, Southold, NY 11971

[6]Cape Cod Cooperative Extension, 3195 Main Street, Barnstable, MA 02630

[7]New York Sea Grant, 146 Suffolk Hall, Stony Brook University, Stony Brook, NY 11794-5002

[8]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

Bassem.Allam@stonybrook.edu

The northern quahog (= hard clam), *Mercenaria mercenaria*, is among the most economically valuable bivalve species in the United States, representing the most important marine resource in several Atlantic states. The species is extensively cultured from Massachusetts to Florida. Maintenance and growth of this aquaculture industry relies on hatchery production of seed, and billions of seed clams are produced annually to fulfill aquaculture and restoration needs. In this context, the production of quality seed able to survive under harsh biological and environmental conditions represents a major priority for the aquaculture community. This collaborative project builds on partnerships between Sea Grant programs, scientists, and extension teams in five Atlantic states to develop hard clam selective breeding programs using state of the art genomic tools. In this framework, the team produced a chromosome-level assembly of the clam genome and used that resource as a reference for the characterization of the species genetic diversity across its range. Clams from nine populations ranging from Maine to Florida were collected and submitted to genome re-sequencing. Through a series of stringent selection criteria, single nucleotide polymorphisms (SNP) identified in this dataset were filtered and a subset of 66,644 probes (including 66,543 probes targeting clam SNPs and 101 probes targeting the parasite *Mucochytrium quahogii,* a.k.a. QPX) were generated and used for the production of arrays for 3,456 samples. The arrays are currently being used for the identification of SNP associated with field survivorship and clam resistance to QPX disease and heat stress.

IMPROVING SHELLFISH HARVEST DATA IN MARYLAND THROUGH DAILY ELECTRONIC REPORTING

Eric Amrhein[1]*, Jennifer Walters[1], Olivia Caretti[1], H. Ward Slacum Jr.[1], Kaycee E. Coleman[1], Jodi Baxter[2], Stephanie Richards[2], Carrie Kennedy[2], Bryan Stevenson[3], Marc Mole[4], and Ryan Corbin[4]

[1]Oyster Recovery Partnership, 1805A Virginia St. Annapolis, MD 21401

[2]Fishing and Boating Services, Maryland Department of Natural Resources, 580 Taylor Ave., B-2, Annapolis, MD 21401

[3]Electric Edge Systems Group Inc., 3016 Orillia St, Victoria, BC V9A 1Y8, Canada

[4]Versar Inc., 9200 Rumsey Rd #100, Columbia, MD 21045

eamrhein@oysterrecovery.org

Commercial shellfish harvesters in Maryland are required to submit monthly harvest reports summarizing their fishing activity. Harvest data from these reports are essential for fishery management but are delayed from the harvest date and unverifiable. To increase the timeliness and accuracy of these data and improve industry accountability, the pre-existing electronic reporting system in Maryland, Fishing Activity and Catch Tracking System (FACTS™), was expanded to include reporting specific to the commercial oyster and clam fisheries. Stakeholders were involved in development to ensure that the system met the needs of fishery managers and the industry. The reporting system consists of trip-level reporting, allowing managers to view harvest in real time. Industry members were recruited to advise and provide feedback during system development, as well as identify functionality errors throughout the project. Harvest verification is key for improving industry accountability and ensuring that harvest is reported accurately; therefore, dockside monitors were employed to conduct harvest checks at shellfish landing locations throughout Maryland. The pilot launched at the start of the commercial oyster season in October 2021 and ended in November 2022. During this time, 2,848 shellfish trips were reported with FACTS and 171 trips were verified by dockside monitors. Trip-level electronic reporting allows for real-time shellfish fishery management action, such as oyster bar closures, when necessary. Shellfish reporting is now fully integrated into FACTS and is a reporting option for the entire Maryland shellfish fishery. Future outreach efforts and long-term monitoring are recommended to continue to identify misreporting errors and further improve reporting.

CYTOCHROME P450-DEPENDENT MIXED FUNCTION OXIDASES (MFO) SYSTEM DYNAMICS DURING THE POLYAROMATIC HYDROCARBON (PAH) METABOLISM IN THE GREEN MUSSEL, *PERNA VIRIDIS* (LINNAEUS, 1758)

Chinnaiah Amutha

School of Biological Sciences, Department of Animal Behaviour and Physiology, Madurai Kamaraj University, Madurai-625021, TN, India

amuthaji@gmail.com; amutha.biological@mkuniversity.org

Polyaromatic hydrocarbons (PAH) are the prominent and most common pollutants in aquatic environments, particularly in marine water. The discharge of hydrocarbons into the sea might be of great concern for marine species living close to dumping sites. Therefore, toxicological properties of hydrocarbons released into marine environments need to be evaluated. PAH pollution potential may be predicted by assessing the induction of hepatic cytochrome P450-associated enzyme activity. The inducibility and activity of phase I reduction nicotinamide adenine dinucleotide phosphate, reduced (NADPH) cytochrome c reductase (CCR), cytochrome c oxidase (COX) and three CYP450 isoforms (benzyloxyresorufin - O-dealkylase [BROD], ethoxyresorufin-O-dealkylase [EROD] and methoxyresorufin-O-dealkylase [MROD]) enzymes were measured in the hepatic S9 fraction prepared from *Perna viridis* collected from three sites: a highly oil-polluted site (Kasimedu fishing harbor, Rayapuram, Chennai [Station1]); a moderately polluted off-shore site, about 3 Km away from this area [Station 2]; and the least oil-polluted site (Vellar estuary, Parangipettai [Station 3], which was a reference site.) The levels of BROD (CYP2B6), MROD (CYP1A2) and EROD (CYP1A1) in the tissues of green mussel were measured using Spectro-Fluorometer SL-174, (ELICO, India). All the MFO enzymes exhibited a hierarchical dose-dependent activity in response to oil pollution in these study areas. Samples from the heavily oil-polluted (Kasimedu Station-1 and Station-2) areas exhibited greater activity of all enzymes than the least oil-polluted (Vellar estuary) reference area. Among the enzymes analyzed, the MROD activity was best correlated with the level of hydrocarbon contamination ($P < 0.05$). Therefore, MROD can be considered as a robust biomarker for petroleum hydrocarbons in *P. viridis*.

EXTENDING THE REACH OF QUASI-OPERATIONAL HARMFUL ALGAL BLOOM FORECASTS TO ESTUARINE SHELLFISH HARVESTING IN COASTAL CALIFORNIA

Clarissa Anderson[1]*, Raphael Kudela[2], Eric Bjorkstedt[3], and Chris Free[4]

[1]Scripps Institution of Oceanography, Southern California Coastal Ocean Observing System, 8622 Kennel Way, La Jolla, CA 92037

[2]University of California, Santa Cruz, 1156 High St., Santa Cruz, CA 95064

[3]Cal Poly Humboldt, 1 Harpst St., Arcata, CA 95521

[4]University of California Santa Barbara, 2400 Bren Hall, Santa Barbara, CA 93106

clrander@ucsd.edu

Blooms of the toxic diatom *Pseudo-nitzschia* have become commonplace in coastal California, with routine shellfish advisories and annual stranding events of protected marine mammals and seabirds. The largest shellfish disaster was in 2015 with an unprecedented HAB that closed the Dungeness and rock crab fishery in California for the entire season and resulted in $60M dollars in losses. A fundamental question affecting the mitigation of HAB events is how well the coastal oceanographic conditions that nurture these blooms explain the risk to estuarine environments where much of the commercial and recreational shellfish harvesting occurs. With the introduction of the California Harmful Algae Risk Mapping (C-HARM) System, coastal conditions conducive to toxic HAB can be monitored in real-time. This kind of advanced warning has proven valuable to marine mammal resource managers given the tight connection between offshore toxins and animal stranding events. Where C-HARM provides less information is in major inlets, such as Humboldt Bay, a site known for commercial oyster production. While this breakdown in the model-observation relationship is in part due to the limitations of spatial resolution of the C-HARM, there are also knowledge gaps when translating in-water HAB properties to shellfish toxicity, particularly in semi-enclosed systems. Using a combination of satellite remote sensing, particle tracking simulations, and machine learning models, how to extend the reach of C-HARM to better understand shellfish contamination and to meet the needs of fisheries currently underserved by routine HAB forecasts will discussed.

A METHOD FOR ESTIMATING HORSESHOE CRAB ABUNDANCE IN THE DELAWARE BAY, USA

Kristen A. Anstead[1]*, John A. Sweka[2], Linda Barry[3], Eric M. Hallerman[4], David R. Smith[5], and Richard A. Wong[6]

[1]Atlantic States Marine Fisheries Commission, 1050 N. Highland Street, Suite 200 A-N, Arlington, Virginia, 22201

[2]U.S. Fish and Wildlife Service, Northeast Fishery Center, 308 Washington Avenue, Lamar, Pennsylvania, 16848

[3]New Jersey Fish and Wildlife, 360 North New York Road, Port Republic, New Jersey, 08250

[4]Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, 310 West Campus Drive, Blacksburg, Virginia, 24061

[5]U.S. Geological Survey, Leetown Science Center, 11649 Leetown Road, Kearneysville, West Virginia, 25430

[6]Delaware Division of Fish and Wildlife, 89 Kings Highway SW, Dover, Delaware, 19901

kanstead@asmfc.org

Horseshoe crabs, *Limulus polyphemus,* are used as bait for commercial American eel and whelk fisheries and their blood is used by the biomedical industry to produce Limulus Amoebocyte Lysate, an agent used to detect pathogens in injectable drugs and implantable medical devices. In addition to these commercial uses, horseshoe crabs play an important ecological role because their eggs provide forage for migrating shorebirds, particularly in Delaware Bay. Due to their importance in the region, the Atlantic States Marine Fisheries Commission adopted the use of the Adaptive Resource Management (ARM) Framework for setting harvest levels for horseshoe crabs in the Delaware Bay area. The Framework considers the abundance levels of horseshoe crabs and red knots in determining the optimal harvest level in the region. Since its implementation, the ARM Framework has used a trawl survey's swept area-based population estimates and a simplified population model. Now, with more data and modeling techniques available, a catch multiple survey model was developed to provide population estimates for the ARM Framework. The model indicates that the population was stable from 2003-2013 and then began to increase through 2017, a result consistent with stock rebuilding following the restricted harvest recommendations from the ARM. Estimates were lower in recent years, with approximately 6 million mature females and nearly 16 million mature male horseshoe crabs in the region for 2021. The model provides the best and most comprehensive estimates of horseshoe crabs in Delaware Bay and will improve modeling efforts within the ARM Framework going forward.

ENDOGENOUS VIRUS ELEMENTS (EVE) OF INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS (IHHNV-EVE) IN THE GENOMES OF *PENAEUS VANNAMEI* AND *P. MONODON*: INTERACTIONS WITH TRANSPOSABLE ELEMENTS

Gober Asuncion[1]*, Kathy F. Tang[2], and Acacia Alcivar-Warren[3]

[1]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Shangdong, P.R. China

[3]Environmental Genomics Inc., P.O. Box, Southborough, MA 01772, USA

environmentalgenomics.warren@gmail.com

Viral diseases cause major economic losses to the shrimp industry, including White Spot Syndrome Virus (WSSV), Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV; renamed *Decapod penstylhamaparvovirus 1*), among others. Endogenous virus elements (EVE) of IHHNV and WSSV have been reported. IHHNV is lethal to *P. stylirostris* but is less virulent in *P. vannamei* and *P. monodon* and does not typically cause mortality.

IHHNV (AF218266.2, 3909bp) is integrated in *P. monodon* genome from Thailand, (GCA_015228065.1, chromosome7; JABERT010000007.1, 8 fragments; and chromosome35, JABERT010000035.1, 49 fragments). AF218266.2 is also integrated in *P. vannamei* farmed in China (GCA_003789085.1, *P. vannamei* breed Kehai No.1 LVANscaffold_759). IHHNV from *P. vannamei* of Ecuador (AY362548.1, OL598344.2, OM728642.1) is also integrated in the genomes of *P. monodon* from Thailand and *P. vannamei* from China.

From the genome assembly of *P. monodon* from Thailand, a young non-LTR retrotransposon family *RTE-2_PMon* (3,656-bp), encoding a single 1143-aa ORFp, was identified and deposited in Repbase. Around 200 members of this family show only 0.5-2% sequence divergency to the *RTE-2_PMon* consensus sequence, indicating its current translocation activity. Previously, from the African(Madagascar)-originated *P. monodon* genome, an integrated Type-A IHHNV was identified flanked by a 1.39-Kb genomic sequence at the 3'-end, corresponding to nucleotides 3,262-4,655 of DQ228358 (4,655bp) containing a partial sequence of retrotransposon reverse transcriptase (RT) gene of *P. monodon*. This flanking sequence shows 98% nucleotide identity to nucleotides 1,531-2,924 of *RTE-2_PMon* consensus sequence, suggesting IHHNV was recently integrated into a young *RTE-2_PMon* in the genome from Africa. Such integration, as examined by the sequence continuity of DQ228358, is absent in the 2.39-Gb *P. monodon* assembly from Thailand, consistent with the previous PCR results showing the absence of DQ228358 in several Asian-originated *P. monodon*, even though endogenous IHHNV were detected in these Asian populations.

UNDERSTANDING THE INFLUENCE OF THE OYSTER ON LEVELS OF HUMAN-PATHOGENIC *VIBRIO* SPP.

Corinne Audemard*, Kimberly S. Reece, Robert J. Latour, Lydia M. Bienlien, and Ryan B. Carnegie

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062, United States

audemard@vims.edu

Risks associated with human-pathogenic *Vibrio* bacteria occurring in oysters are managed through broad measures that fail to account for the wide range of *Vibrio* spp. concentrations observed among individual oysters within a population. The objectives of this study were to better understand how variations in the oyster habitat may influence concentrations of these pathogens in oyster tissues. More specifically, the influence of parasitism and oyster sex, but also of oyster ploidy and oyster genetics, were examined in the eastern oyster, *Crassostrea virginica*. Data were analyzed through generalized mixed-effects models and identified *oyster line* as a consistent predictor of *Vibrio* levels across the human-pathogenic *Vibrio* species and strains analyzed. Interestingly, the oyster line associated with both higher parasite infection levels and higher mortality tended to harbor higher concentrations of these bacteria. This observation raised the question of the influence of oyster health or stress on levels of these human pathogens, similar to what has been observed with regard to *Vibrio* spp. known as shellfish pathogens. This study suggests that the influence of oyster genetics and oyster health status on levels of human-pathogenic *Vibrio* spp. observed in individual oysters should be further investigated.

MUSSEL FARMING IN GALICIA (NW IBERIAN PENINSULA): NEW PERSPECTIVES IN A GLOBAL CHANGE SCENARIO

Jose M.F. Babarro*, Elsa Silva, Xose Antón Padín, and Miguel Gilcoto

Instituto de Investigaciones Marinas (IIM-CSIC), Eduardo Cabello 6, 36208, Vigo, Spain

jbabarro@iim.csic.es

Mussel cultivation in Galicia (NW Spain) represents an extraordinary activity in terms of the volume of biomass cultivated and the economic impact generates. In the last five years, Galicia produced 1.2 million tons of this marine resource, generating 516.10^6 €(Source: Ministry of Agriculture and Fisheries, Food and Environment). Global change scenario may disrupt the environment in which the cultivation is developed affecting both the acquisition of mussel seed, that sustains the culture, as well as the responses of the adult individuals in their cultivation ropes disposition. The whole cultivation system is supported by the fact that mussels can attach themselves to cultivation ropes and filter natural seawater; however, physico-chemical changes in the environment (ocean acidification, seawater warming, frequency and magnitude of wave-driven storms etc) and management changes linked to new market opportunities may threaten the optimal developing of the culture. Besides, biological factors regarding proliferation of other species or communities (fouling organisms) that benefit from the clustering of the mussels on cultivation ropes may negatively affect the mussel maintenance in the cultivation ropes e.g., deriving in dislodgements events.

The most relevant aspects for better understanding the effects associated to global change on mussel culture regarding the protection and survival structures (calcium carbonate shells and byssus filaments) will be discussed. Depending on the environmental characteristics, secretion of both protective tissues may have significant energetic consequences for other vital structures (somatic and gametogenic soft tissues) impacting the overall energetic balance.

PUTTING THE *CALLINECTES SAPIDUS* GENOME INTO THE CONTEXT OF DECAPOD GENOMICS

Tsvetan R. Bachvaroff* and J. Sook Chung

University of Maryland Center for Environmental Science, Institute of Marine and Environmental Biology, 701 E Pratt St, Baltimore, MD 21202

bachvarofft@umces.edu

The genome of the *Callinectes sapidus* was obtained to better understand this important Maryland fishery. Overall, within the decapod genomes sequenced to date there is a high chromosome number ~40 combined with large genome sizes of over a billion bases, and roughly 50% repeat content have all been found within the brachyran, lobster, and paneaid genomes. The gene families of six decapod genomes were determined in this genomic context using orthofinder. The results directly link physical location on the genome, gene duplication, and phylogeny for each of the >20 thousand genes within the genomes. Approximately 600 gene families are found in tandemly repeated clusters of gene copies in *C. sapidus*. The expression patterns in *C. sapidus* during development including zoea, megalope, and juveniles were then used as a test case for describing the overall expression patterns for several of these tandemly repeated gene families. Examples of hemocyanin and eye opsin expression demonstrate striking differences in overall expression as well as the specific individual most highly expressed genes within a set of tandemly repeated genes. These analyses are readily transferred between species or datasets and provide a more comprehensive, complete, and simpler analysis than either transcriptomic or individual gene family analyses.

QUANTIFYING FARM-SCALE ECOSYSTEM SERVICES ASSOCIATED WITH EASTERN OYSTER AQUACULTURE IN THE MID-ATLANTIC AND CREATING A REGIONAL OYSTER FARM FILTRATION CALCULATOR

Janine M. Barr[1]*, Daphne Munroe[1], Lisa Calvo[1], Laura Steeves[1], Danielle Kreeger[2], Kurt M. Cheng[2], Julie M. Rose[3], and Skylar Bayer[4]

[1]Rutgers, The State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

[2]Partnership for the Delaware rAEstuary, 110 South Poplar Street, Suite 202, Wilmington, DE 19801

[3]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford, CT 06460

[4]NOAA Fisheries, Alaska Regional Office, 709 W 9th Street, Juneau, AK 99801

barrjanine@gmail.com

The eastern oyster (*Crassostrea virginica*) is a commercially important aquaculture species along the Atlantic and Gulf coasts of the United States. In addition to its commercial value, oyster aquaculture has ecological value through provisioning services such as water quality improvement; however, the scale at which oyster farms provide this important ecosystem service is not adequately understood. This project aims to (1) estimate farm-level year-round filtration occurring at three oyster farms in the Mid-Atlantic to quantify their contributions to improved water quality and (2) use these data to create an online calculator so oyster farmers in the Mid-Atlantic can estimate annual water quality benefits on the farm. One goal of the latter is for farmers to use calculator outputs as an outreach tool to attract customers to their product. To achieve these goals, oyster filtration data were collected seasonally between July 2020 and September 2021 at three farms in the Mid-Atlantic using a flow-through filtration chamber with ambient water. During each field experiment oysters were placed in the chamber, from which oyster biodeposits were retrieved to calculate filtration, clearance, and rejection rates of each oyster. An increase in physiological activity across all farms was associated with an increase in salinity and temperature, while physiological activity at each farm was associated with a different suite of environmental variables. These experiments provide a robust dataset of oyster filtration observed under natural conditions and may be used in a broader framework to inform potential oyster aquaculture contributions to water quality management in the Mid-Atlantic.

MORE THAN JUST A SHELL: COLLECTING AND CONCHOPHILIA IN THE DUTCH GOLDEN AGE

Marisa Anne Bass

Yale University, Department of the History of Art, Loria Room 752, 190 York St, New Haven, CT 06511

marisa.bass@yale.edu

The predominant view on shells in the seventeenth-century Netherlands was the more exotic, the better. The collector's cabinets of the Dutch Republic were filled with shells that had been imported from distant seas via the channels of the East and West India Companies. Collectors met to compare their rarest specimens, posed for portraits with prized shells in their hands or on tables before them, and competed in the acquisition of the most beautiful and costly examples. According to Georg Eberhard Rumphius (1627–1702), a naturalist employed by the East India Company and based in what is now Indonesia, these collectors scarcely appreciated the effort that went into harvesting and polishing shells abroad—let alone the artistry of the mollusks who created them. Shells arrived in European hands, empty, pristine, ready for consumption, and bearing little trace of how they got there.

Rumphius was mostly right, but not entirely. There were shells to be found on the shores of the Netherlands too, and they too were collected, studied, and valued in ways both related and distinct from their coveted exotic counterparts. Every shell, however modest, poses questions of origin to the individual who holds it. As this talks explores, the shells that were gathered on local beaches or discovered in local excavations during the seventeenth century mattered precisely because they offered spaces for reflection that were untethered from commodity culture and transnational trade. The world of the Dutch Republic was global and interconnected, but it began at home and with the sand beneath one's feet. For artists, collectors, poets, and naturalists alike, it began with a love of shells.

SELECTION FOR GROWTH IN HATCHERY-REARED SOFT-SHELL CLAMS, *MYA ARENARIA* L.: A SERIES OF FIELD INVESTIGATIONS

Brian F. Beal[1,2]

[1]University of Maine at Machias, Division of Environmental & Biological Sciences, 116 O'Brien Avenue, Machias, ME 04654

[2]Downeast Institute, 37 Wildflower Lane, P.O. Box 83, Beals, ME 04611

bbeal@maine.edu

Cultured soft-shell clam seed are used to enhance wild stocks in some coastal communities in Maine as part of their shellfish management program. During their first year, both hatchery-reared and wild *Mya* juveniles can suffer high losses due mainly to invertebrate predators (e.g., green crabs, *Carcinus maenas*; moon snails, *Euspira heros* and *E. triseriata*; ribbon worms, *Cerebratulus lacteus*). Survival can be enhanced using predator netting, but results are highly variable depending on habitat, predator density, and the specific suite of predators present. As with many infaunal bivalves, survival is a function of size (shell length), and for *Mya*, burrowing depth. Fast growth, then, becomes an important strategy for survival.

Field trials conducted in eastern Maine examined interactive effects of selecting for fast growth, predator exclusion, and intraspecific stocking density. In 2009 & 2010, fate and growth of F1 (control) and F3 (selected) cultured juveniles (9-12 mm SL @ 1,320 ind. m^{-2}) was examined in netted and unnetted units containing ambient sediments for 201 and 174 days (spring to fall). Trials demonstrated that F1 individuals increased 70-84% in mean SL vs. 101-123% for F3 clams, and survival was significantly higher in the selected individuals by ~70-125%. In 2014, stocking density was added to the experimental design as a third factor over five levels (330-2,640 ind. m^{-2}) for 459 days. Survival and final mean SL was 32% and 15% higher for F3 individuals. Negative effects due to density on absolute and relative growth were observed equally across both groups.

INTERTIDAL MUDFLATS AS NURSERY SITES FOR CULTURED, JUVENILE SOFT-SHELL CLAMS, *MYA ARENARIA* L.

Brian F. Beal[1,2]* **and Chad R. Coffin**[3]

[1]University of Maine at Machias, Division of Environmental & Biological Sciences, 116 O'Brien Avenue, Machias, ME 04654

[2]Downeast Institute, 37 Wildflower Lane, P.O. Box 83, Beals, ME 04611

[3]Maine Clammers Association, 26 Litchfield Road, Freeport, ME 04032

bbeal@maine.edu

Soft-shell clam, *Mya arenaria* L., juveniles have been cultured annually for public stock enhancement in Maine – first at the Beals Island Regional Shellfish Hatchery (1987-2002) and, since 2003, at the Downeast Institute. Juveniles (2.5-3 mm SL) are moved to a field-based nursery in eastern Maine where they reside in floating trays from mid-May to November reaching 10-15 mm SL. In November, clams are removed from trays and stored in high-density, flow-through bags (2-3 kg/bag) receiving ambient seawater until the following spring when they are planted in coastal towns. These post-hatchery activities, designed to produce the largest clams possible for enhancement efforts, are necessary because most participating communities have no access to field-based nurseries or land-based upwellers; however, they increase seed cost and risk incurred in maintaining millions juvenile clams held over the winter.

Whether communities could use parts of the soft-bottom intertidal zone as a bivalve nursery was tested. Currently, the mid- and low intertidal lack commercial densities of clams due to the interactive effects of warming seawater temperatures that have led to a population explosion of green crabs and other clam predators and predator behavior that allows them to be more effective in soft bottoms during tidal inundation.

Growth and survival results will be discussed from a short-term field experiment (20 June to 5 November 2022 – 138 days) carried out in the mid-intertidal zone on three mudflats in South Freeport, Maine where cultured seed (1.9-2.5 mm SL) were added to nursery units over five densities (range = 1,667-33,333/m^2).

A SOFT-SHELL CLAM RECRUITMENT MONITORING NETWORK: A TOOL FOR THE COASTAL COMMUNITIES OF MAINE

Brian F. Beal[1,2]* and Sara F. Randall[2]

[1]University of Maine at Machias, Division of Environmental and Biological Sciences, 116 O'Brien Avenue, Machias, ME 04654

[2]Downeast Institute, 37 Wildflower Lane, P.O. Box 83, Beals, ME 04611

bbeal@maine.edu

Commercial soft-shell clam, *Mya arenaria* L., landings in Maine historically rank second or third behind lobster. In 2021, 7.5 million pounds were landed worth $25.2 million. Those landings represent an 80% decline since 1977 (38.4 million pounds). Some suggest the decline relates to the lack of clammers (number of statewide clam licenses has dropped by ~70% over the same period to 1,500), our fisheries-independent data suggests otherwise. That is, thousands of benthic cores taken during the past decade from spring and fall sampling of flats from eastern to southern Maine demonstrates that many clammers have had to move from the intertidal flats to other occupations due to the lack of commercial quantities of clams. In fact, in many of tens of thousands of acres of mudflats in Maine, clams are now restricted to a small strip of the intertidal bordering the uppermost tidal areas close to shore, leaving mid- and lower intertidal areas essentially devoid of clams.

This pattern could result from the lack of clams settling from the plankton due to widespread reproductive failure or an increase in planktonic mortality, or recruitment limitation related to differential mortality along the tidal gradient sometime after settlement. To examine the latter hypothesis, we established a soft-shell clam recruitment monitoring network in 2020 at two intertidal flats in each of three communities located in the southwest, mid-coast and downeast region. Results from three years of monitoring indicate that current levels of recruitment are insufficient to swamp out predators, especially at mid- and lower shore levels.

PILOT-SCALE STUDIES TO EXAMINE REPRODUCTIVE OUTPUT IN SOFT-SHELL CLAMS, *MYA ARENARIA* L.

Brian F. Beal[1,2]* and Sara F. Randall[2]

[1]University of Maine at Machias, Division of Environmental & Biological Sciences, 116 O'Brien Avenue, Machias, ME 04654

[2]Downeast Institute, 37 Wildflower Lane, P.O. Box 83, Beals, ME 04611

bbeal@maine.edu

In Maine, management of the soft-shell clam fishery assumes successful recruitment of 0-yr class individuals. Commercial landings have declined by ~80% since the mid-1970s, and experimental work during the last decade has indicated both indirect (a 40-year warming trend in seawater temperatures) and direct (increased predation, especially from green crabs that are undergoing a coastwide population explosion associated with the warming trend) effects are mainly responsible. It may be possible to increase number of settlers by allowing clams to spawn prior to harvesting (spawning closures) and/or by placing an upper size limit on the largest/oldest individuals in the population; however, no recent information about clam reproductive output exists. Clams (35-90 mm SL) were collected weekly from three tidal levels at an intertidal flat in eastern Maine (colder waters) and southern Maine (warmer waters) from May-August 2020, and induced to spawn via thermal shock (ambient to 25 °C).

Southern Maine clams began spawning (37% of individuals) during the last week of May (seawater temperature: 11 °C), peaked by the second week of June (13 °C; ~70% of clams spawned), and occurred in only 3.2% and 2.8% of animals by the third and fourth week of June. Spawning was more protracted in eastern Maine beginning (16% of individuals) the first week of June (9 °C), peaking by 7 July (62.5%; 12 °C), and continuing into the first week of August (5.6%; 13 °C). At both locations, tidal height did not play a significant role in percent spawning, nor did the largest clams display reproductive senility.

PATHOLOGY ASSOCIATED WITH RECURRING SUMMER OYSTER MORTALITIES

Tal Ben-Horin[1]*, Corinne Audemard[2], Mark Ciesielski[3], Shelley Katsuki[2], Jonathan Lucas[1], Rachel T. Noble[3], Kimberly S. Reece[2], Jessica Small[2], and Ami E. Wilbur[4]

[1]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

[2]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[3]University of North Carolina Chapel Hill, Institute of Marine Science, 3431 Arendell Street, Morehead City, NC 28557

[4]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, NC 28409

tbenhor@ncsu.edu

Oyster aquaculture across the southeastern United States has seen frequent mortality events in recent years. These are common during warm months, particularly in high salinity coastal sounds. In the triploid oysters that represent the bulk of regional production, these events often lack clear etiology and are left to be described simply as summer or triploid mortality. To investigate pathology associated with these events, as well as causal links with ploidy, diploid and triploid oyster lines from Virginia- and North Carolina-derived broodstock were deployed to eight field sites across North Carolina and Virginia in the fall 2021 and monitored biweekly from the spring through fall 2022. In line with widespread reports of mortality at commercial oyster farms across North Carolina in the summer 2022, two of the North Carolina field sites experienced near complete mortality (> 90%) with another experiencing more moderate mortality (> 50%). Neither ploidy nor the geographic origin of broodstock were associated with mortality. Instead, mortality appeared to be site specific and restricted to high salinity (>35) coastal sounds. Across the lines, the pathology observed in oysters at impacted sites was similar to that observed through summer mortality events in past years, highlighted by persistent sloughing of absorptive cells within digestive tubules preceding mortality by two to three weeks. Coastal sounds, which have seen widespread recent aquaculture expansion, have seen disproportionately acute responses to regional climatic shifts relative to their broader estuaries. The results here will therefore be discussed in the context of regional aquaculture industry growth and environmental change.

ON TRACK TO OPTIMIZE THE BOTTLE UPWELLER SYSTEM (BUPSY): TESTING FOUR BOTTLE CONFIGURATIONS

Maija Benitz[1] and Dale Leavitt[2]*

[1]Roger Williams University, School of Engineering, 1 Old Ferry Road, Bristol, RI 02809

[2]Blue Stream Shellfish, 53 Goulart Memorial Drive, Fairhaven, MA 02719

dale@bluestreamaquaculture.com

The bottle upweller system (BUPSY) is becoming a popular tool for the early nursery phase of shellfish production. Entraining small shellfish seed in an upward flowing water current contained within a vessel provides excellent growing conditions for the seed; however, there are numerous designs of the containment vessel currently being used with little knowledge as to the impact vessel shape may have on the dynamics of the seed within the fluidized bed. Moreover, questions remain about the ideal flow rates for growing seed most efficiently.

An open-source computational fluid dynamics model was selected and adapted for modeling various BUPSY configurations. Numerical meshes for four different BUPSY geometries were created. Initial testing indicates that the model will provide robust three-dimensional, time-varying predictions of seed motion.

Preliminary assessment of the flow dynamics of four different BUPSY configurations has been completed. Dramatic differences in the fluidized bed dynamics were observed across the four vessels suggesting that the manipulation of flow within specific vessel configurations may be fine-tuned to optimize bed fluidization. Bottle shape is a significant factor in the dynamics of the seed fluidization.

A DYNAMIC PATHWAY TO TRANSITION FROM VULNERABLE TO RESILIENT FISHERIES SOCIAL ECOLOGICAL SYSTEMS: A TRANSDISCIPLINARY CASE STUDY OF THE U.S. ATLANTIC SEA SCALLOP FISHERY

Halle Berger[1]*, Lisa L. Colburn[2], Shannon L. Meseck[3], Samantha A. Siedlecki[1], Catherine Matassa[1], Dvora Hart[4], David Bethoney[5], Susan Inglis[5], and Catherine L. Alves[6]

[1]University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Rd., Groton, CT 06340

[2]NOAA Fisheries, Office of Science and Technology, 28 Tarzwell Dr., Narragansett, RI 02882

[3]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Ave, Milford, CT 06460

[4]NOAA Fisheries, Northeast Fisheries Science Center, 166 Water St., Woods Hole, MA 02543

[5]Commercial Fisheries Research Foundation, 61B East Farm Rd., Kingston, RI 02881

[6]ECS Federal, LLC, in support of NOAA Fisheries, 28 Tarzwell Dr., Narragansett, RI 02882

halle.berger@uconn.edu

Dynamic social ecological systems (SES) built around fishing stocks with potential for sustainable catch and flexibility to respond to environmental change are key to achieving multiple U.N. Sustainable Development Goals. Atlantic sea scallops have demonstrated the potential for sustainable yield but are increasingly threatened by effects of ocean acidification (OA) and warming. As calcifiers with limited mobility and high revenue potential, this fishery is particularly suited to a transdisciplinary approach combining coastal fishing community assessments with ocean models, sea scallop physiological response, and population dynamics. The vulnerability and resilience of fishing communities to the effects of OA and warming is dependent on their adaptive capacity in relation to social and environmental exposure and sensitivity factors. In the Northeast U.S., the contribution of sea scallops to total regional landed value has steadily increased over recent decades to more than $500 million per year. As a result, the dependence of the regional fisheries SES has shifted to this species. This dependence, and the predicted shift in sea scallop distribution and biomass decline, make this study particularly relevant. Here, regional projections of changes within sea scallop fishing zones based on ocean models and physiological assessment are provided. These projections have been combined with social indicators of fishing community vulnerability and reliance to structure workshops with fishery managers and fishing-dependent communities. The workshops assist stakeholders to explore scenarios and become more resilient to future change. Challenges, lessons learned, and next steps toward achieving a transdisciplinary understanding of SES vulnerability in this fishery are explored.

EFFECT OF OYSTER DENSITY ON THE BIOFILTRATION OF THE PATHOGEN, *LABYRINTHULA ZOSTERAE*

Chelsea N. Bergman[1]*, Maya L. Groner[2], Harold J. Schreier[1,3], and Colleen A. Burge[4]

[1]University of Maryland Baltimore County, Department of Marine Biotechnology, Institute of Marine and Environmental Technology, 701 E Pratt St, Baltimore, MD 21202

[2]Bigelow Laboratory for Ocean Sciences, 60 Bigelow Dr, East Boothbay, ME 04544

[3]University of Maryland Baltimore County, Department of Biological Sciences, 1000 Hilltop Circle, Baltimore, MD 21250

[4]California Department of Fish and Wildlife, University of California Davis Bodega Marine Laboratory, 2099 Westside Road, Bodega Bay, CA 94923

cbergma2@umbc.edu

Eelgrass (*Zostera marina*) is an ecologically important seagrass that provides numerous ecosystem services to coastal habitats. There is a universal decline in *Z. marina* due to multiple factors, including increased water temperature, eutrophication, reduced water quality, and disease. One disease commonly found in *Z. marina* beds is seagrass wasting disease (SWD) caused by the protist *Labyrinthula zosterae*. SWD can be visually characterized by the presence of dark, necrotic lesions. Oysters (*Crassostrea gigas*), which are frequently farmed near *Z. marina* beds, have previously been found to reduce, and transmit SWD in *Z. marina* during laboratory trials; however, the density threshold of *C. gigas* needed to significantly reduce SWD is still unknown. Optimizing *C. gigas* densities for SWD control can inform aquaculture planning and *Z. marina* management. A mesocosm experiment was conducted at Friday Harbor Laboratories with *Z. marina* exposed to two *C. gigas* densities (15 and 60 oysters) and two concentrations of pathogen (1000 cells mL^{-1} and 10 cells mL^{-1}). After 14 days, blade growth and the proportion of blades infected was measured. The intensity of infection in *Z. marina* blades and the concentration of pathogen in the water were determined using quantitative PCR. Results will be presented on the interactions between *C. gigas* density and pathogen concentration on SWD severity, *L. zosterae* infection intensity, and blade growth. Results from this experiment confirm that bivalves can reduce disease in co-occurring pathogens and pave the way for integrated disease management. Future field testing is required to validate oyster filtration as a viable method for pathogen control in situ.

TRANSCRIPTOMIC RESPONSES TO LOW SALINITY IN EASTERN OYSTER ADULTS AND LARVAE

Shivish Bhandari[1,2]*, Maya Purnell[1], Kojo Yeboah[1], Pakeeza Butt[1], and Ming Liu[2]

[1]Morgan State University, 1700 E Cold Spring Ln, Baltimore, MD 21251

[2]Morgan State University, Patuxent Environmental and Aquatic Research Laboratory, 10545 Mackall Road, Saint Leonard, MD 20685

shbha4@morgan.edu

Studies on the transcriptomes of oysters in low salinity water (typically salinity of 10) can aid in understanding the molecular mechanisms that respond to low salinity and the development of genetic markers to aid in selective breeding. To investigate the transcriptome response to low salinity in adult oysters, wild adult oysters were collected from the Patuxent River (Maryland, USA), then were split into three groups evenly and challenged in three tanks with different salinities: 20, 5, and 1. After the challenge, gill tissues from four oysters per group were sampled for 24 hours. RNA from the same group were pooled into one sample based on equal RNA amounts. In the sample with salinity of 5, there were 2,399 genes found to be significantly up- or down-regulated when compared to the gene expression in the sample with salinity of 20, while 2,083 were found to be up- or down-regulated in the sample of salinity of 1. In this study, 786 genes were found to be co-up- or down-regulated in 5- and 1-phosphate samples. The eastern oyster genome was used to annotate 26% of these genes. Similarly, fertilized eggs were split evenly and cultured in two 200-liter tanks with salinities of 15 and 7, respectively, to investigate the transcriptome response in larvae. After 36 hours of fertilization, D-larvae were collected from each tank. Transcriptome sequencing and differential expression analyses revealed 277 significantly up-regulated and 500 down-regulated genes. Only 21 of these genes were also found in the differentially expressed genes identified in adult oysters.

ENVIRONMENTAL DNA-BASED DETECTION OF *POLYDORA* SPECIES ON OYSTER BEDS IN CHESAPEAKE BAY

Ellen E. Biesack[1]*, Karen L. Hudson[2], Robert Fisher[2], and Jan R. McDowell[1]

[1]Virginia Institute of Marine Science, Fisheries Department, 1355 Greate Road, Gloucester Point, VA 23062

[2]Virginia Institute of Marine Science, Marine Advisory Program, 7539 Spencer Road, Gloucester Point, VA 23062

eebiesack@vims.edu

The Virginia oyster aquaculture industry has raised concerns about pests that impact “shuckability” and, consequently, market value. Common fouling pests are *Polydora* mud worms and mitigation strategies, including brining and air exposure, are often undertaken when fouling is already extensive. This study combined manual inspection of oysters and targeted quantitative PCR (qPCR) assays to detect *Polydora* on an experimental farm on the York River, Virginia. A subset of oysters was collected from the farm weekly from March - August and examined for blister coverage and the presence of worms. Replicate water samples were also collected from the farm and a control site and filtered to capture environmental DNA (eDNA). Novel qPCR assays amplifying the COI gene region were designed to target the two commonly observed *Polydora* species, *P. websteri* and *P. cornuta*. At both the farm and control sites, eDNA from *P. cornuta* was abundant throughout the summer, dropping in late July, while eDNA from *P. websteri* was barely detectable in March - April and rose to match the levels of *P. cornuta* by early June. New worm blisters emerged in early summer, and all worms taken directly from blisters were identified as *P. websteri*. Both species were found on the external surfaces of shells throughout the experiment. The qPCR assays were sensitive enough to detect changes in *Polydora* eDNA levels even with no oysters in the immediate vicinity and could serve as effective detection tools for two fouling organisms that have recently experienced range expansion and introductions.

NEKTON ASSOCIATIONS IN MOSAIC OF OYSTER AQUACULTURE, SEAGRASS, AND MUDFLAT HABITATS

Fiona Boardman*, Elena Subbotin, and Jennifer Ruesink

University of Washington, Department of Biology, Box 351800, Seattle, Washington, 98195-1800

fcboard@uw.edu

In southwestern Washington State, the intertidal flats of Willapa Bay provide a mosaic of structured and unstructured habitat for nekton. Structured habitats consist of eelgrass and/or oyster culture, grown as bottom or suspended culture. These habitats can provide resources such as food and shelter for a variety of nekton taxa across life-history stages and are particularly important as nursery habitat. Previous work has shown significantly different nekton community composition found in eelgrass and various oyster culture habitats in Willapa Bay. To further understand the differences in community composition due to habitat structure, taxa associations among eelgrass and oyster culture habitats were investigated. Using two sampling methods (GoPros and seining) and a Bayesian approach to analysis, this work reveals taxa that contribute to differences in community composition across habitat types. Findings here suggest that each of the habitat types support distinct and abundant nekton taxa, and that maintaining a mosaic of intertidal habitat types in Willapa Bay is beneficial for continued ecosystem functioning. Furthermore, this study demonstrates the benefits of using multiple field sampling methods and outlines the pros and cons of the two methods used.

LIFE HISTORY AND IMPACTS OF AN UNDESCRIBED PARASITE ON ITS FIRST INTERMEDIATE HOST, THE BAY SCALLOP

Hailea F.H. Boggess[1,2]*, Ciera Benefield Andrade[1,2], Tal Ben-Horin[3], Ami E. Wilbur[1,2], and Julia C. Buck[1,2]

[1]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, NC 28409

[2]University of North Carolina Wilmington, Department of Biology and Marine Biology, 601 College Rd, Wilmington, NC 28403

[3]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

hfh4639@uncw.edu

Since 2012, infections of bay scallops (*Argopecten irradians*) by an undescribed trematode parasite in North Carolina and the west coast of Florida have been observed. Phylogenetic analysis of the 28S region of rDNA indicates that the parasite belongs to family Didymozoidae and forms a well-supported clade with *Saccularina magnacetabula* from Australia. The undescribed didymozoid uses the bay scallop as a first intermediate host, infecting and greatly distorting the afferent vessels of the host's gill filaments. Condition analysis indicates that infected scallops have a higher proportion of body mass in the viscera (including parasitized gills) and a lower proportion of body mass in the muscle and gonad, indicating possible impacts on scallop fecundity. Results of spawning experiments to investigate the impact of trematode infection on fecundity and early larval development will be presented. Efforts to monitor infection prevalence in wild and cultured scallop populations across temporal and spatial gradients along the North Carolina coast will also be discussed. That the parasite infects a commercially important bivalve and yet has never been described suggests that it may have been recently introduced or recently adapted to the scallop host, and thus merits further investigation.

A *CAMPYLOBACTER* ILLNESS OUTBREAK ASSOCIATED WITH OYSTERS CONTAMINATED BY SEABIRDS ROOSTING ON FLOATING AQUACULTURE GEAR

David Borkman[1]*, Christopher Slaten[2], Adam Miller[3], and Benjamin Goetsch[4]

[1]Rhode Island Department of Environmental Management, Office of Water Resources, Shellfish Water Quality Program, 235 Promenade Street, Providence, RI 02908

[2]Rhode Island Department of Health, Center for Food Protection, 3 Capitol Hill, Providence, RI 02908

[3]Rhode Island Department of Health, State Health Laboratory, 50 Orms Street, Providence, RI 02908

[4]Rhode Island Coastal Resources Management Council, Oliver Stedman Government Center

4808 Tower Hill Road, Wakefield, RI 02879

david.borkman@dem.ri.gov

A *Campylobacter* illness outbreak associated with consumption of oysters contaminated by seabirds roosting on floating aquaculture gear is described. Eight ill individuals consumed raw oysters grown at a single Rhode Island coastal pond location. Campylobacteriosis was confirmed in three cases (as *C. jejuni*) and was identified as the probable agent in five cases.

An environmental assessment showed that growing area fecal coliform concentrations were well-below NSSP criteria and there were no probable *Campylobacter* pollution sources (failed septic systems, agricultural operations) in the watershed. Fecal coliform and *Campylobacter* were monitored in oysters at approximately weekly intervals. Elevated levels of *Campylobacter lari* (8 of 26 samples; 31%), *C. jejuni* (1 of 26 samples; 4%), and fecal coliform were detected in oysters. While both *C. lari* and *C. jejuni* were identified in aquaculture oysters, only *C. jejuni* was confirmed in ill patients. Field observations and detection of *Campylobacter lari* suggested that seabirds (gulls, cormorants), which were frequently observed roosting on aquaculture floats were a probable, but unquantified, source of oyster contamination.

Floating gear was removed, and oyster cages were sunk to the bottom to abate roosting birds. *Campylobacter* and fecal coliform in oysters declined to acceptable levels in less than 18 days (maximum time due to coarse sampling schedule) after roosting birds were abated. The illness outbreak investigation and depuration period resulted in the shellfish area being closed for 52 days. Information on the prevalence of *Campylobacter* in seabirds and quantitative *Campylobacter* depuration studies will help inform future management decisions.

ECONOMIC IMPACTS OF OFFSHORE WIND ENERGY DEVELOPMENT ON THE COMMERCIAL SEA SCALLOP FISHERY

Sarah Borsetti[1]*, Andrew S. Scheld[1], David Rudders[1], Daphne M. Munroe[2], Eric N. Powell[3], Eileen E. Hofmann[4], and John M. Klinck[4]

[1]Virginia Institute of Marine Science, William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

[2]Rutgers the State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Ave, Port Norris, NJ 08349

[3]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Dr, Ocean Springs, MS 39564

[4]Old Dominion University, Center for Coastal Physical Oceanography, 4111 Monarch Way, Norfolk, VA 23508

seborsetti@vims.edu

The Atlantic sea scallop (*Placopecten magellanicus*) fishery on the Northeast U.S. continental shelf has been identified as being at high risk from offshore wind energy development due to the overlap of fishing grounds and wind lease areas and the fishing gear and vessels used. Understanding the scale of potential economic impacts of wind farms on this fishery is critical to management of the fishery; however, previous estimates of impact have been based on generalizations across a suite of commercial and recreational fisheries and have not allowed for route changes or shifts in fishing locations due to wind farms, and thereby may underestimate economic consequences to the fisheries. The complex interactions among wind farm arrays, stock biology, fishers' decision-making, transit routes, and costs must be holistically considered to address potential impacts fully. An agent-based modeling framework that integrates spatial dynamics in stock biology, fishery captain and fleet behavior, federal management decisions, and fishery economics was implemented to investigate how offshore wind energy infrastructure may directly affect the economics of the Atlantic sea scallop fishery. Understanding the costs of displacement or changes in fishing activity due to wind energy will give the industry and fishery managers a quantitative basis for managing future expectations relative to the interaction between the fishery and the wind industry. Test model simulations show little influence of offshore wind farms on catch and effort characteristics of the present-day fishery. Preliminary simulations with currently leased wind farms show some displacement of fishing effort off New Jersey and Long Island.

USING EPIBIONT DIVERSITY AND CARAPACE CONDITION IN AMERICAN HORSESHOE CRABS (*LIMULUS POLYPHEMUS* L.) AS TOOLS TO DISTINGUISH BETWEEN POPULATIONS AND ELUCIDATE AGE-STRUCTURE

Mark L. Botton[1]*, Christina P. Colón[2], Shiva Jean-Baptiste[2], Kelvin Zaw[3], and Robert E. Loveland[4]

[1]Fordham University, Department of Natural Sciences, 113 West 60th Street, New York, NY 10023

[2]Kingsborough Community College, Department of Biological Sciences, 2001 Oriental Boulevard, Brooklyn, NY 11235

[3]Hunter College, City University of New York, 695 Park Avenue, New York, NY 10065

[4]Rutgers University, Department of Ecology, Evolution & Natural Resources, New Brunswick, NJ 08903

botton@fordham.edu

The presence of epibionts on adult horseshoe crabs from Delaware Bay, New Jersey (1,978 males and 1,332 females) and Jamaica Bay, New York (1,963 males and 699 females) was quantified during the peak of the spawning season, mid-May through mid-June from 1997-2003 and 2012-2021. Twenty taxa of epibionts were found on horseshoe crabs from Delaware Bay, 14 of which were also found from Jamaica Bay. Acorn barnacles, bryozoans, slipper snails (*Crepidula fornicata*), sand tube polychaetes (*Sabellaria vulgaris*), and blue mussels (*Mytilus edulis*) were the five most frequently occurring epibionts in both populations. Barnacles, *Crepidula*, and *Mytilus* were more common in the Jamaica Bay population, whereas bryozoans and *Sabellaria* were more common in Delaware Bay. The largest diversity of epibionts was found among molluscs (eight taxa). Male horseshoe crabs in both populations were more heavily encrusted than females; this may relate to their mating behavior, in which the attached male partially blankets the female opisthosoma. Jamaica Bay horseshoe crabs were more heavily fouled than Delaware Bay animals, and the carapace condition index, an indicator of post-molt age, was significantly worse for Jamaica Bay animals. The principal conclusions from this study are that epibionts are insufficiently distinctive between Delaware Bay and Jamaica Bay to be useful as biological tags, and that the preponderance of older aged adults in Jamaica Bay may be indicative of poor recruitment into this population and/or emigration of younger adults from Jamaica Bay to other embayments.

DISTRIBUTION OF HORSESHOE CRAB EGGS AND INFAUNA AROUND INTERTIDAL OYSTER FARMS IN DELAWARE BAY

Elizabeth H. Bouchard[1]*, Daphne Munroe[1], Brooke Maslo[2], and David Bushek[1]

[1]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Ave., Port Norris, NJ 08349

[2]Rutgers University, Department of Ecology, Evolution and Natural Resources, 14 College Farm Road, New Brunswick, NJ 08901

ehb52@hsrl.rutgers.edu

Delaware Bay hosts the largest spawning population of horseshoe crabs in the world (*Limulus polyphemus*, HSC). Their abundant eggs are a critical food resource for many animals, including fish, gulls, and migratory shorebirds. Other marine infauna (*e.g.,* bivalves, polychaete worms) are also important prey for these animals and the adult horseshoe crabs as well. The resurgent eastern oyster (*Crassostrea virginica*) aquaculture industry in Delaware Bay may alter prey availability by influencing local infauna. Research shows that oyster farms do not impact HSC access to spawning beaches; however, they may impact the distribution of eggs or other infauna. In Spring 2021 and 2022, infauna surveys were conducted in four paired farm-control plots (90-m x 180-m) across a 3.5-km stretch of tidal flats in Delaware Bay. Sediment cores determined the relative abundance of surficial HSC eggs and other infauna across each plot.

AIC model selection of generalized linear mixed effects models on samples processed to date clearly indicated that infauna vary across the intertidal zone, but the effect of farms was inconsistent among infauna types. Horseshoe crab eggs were most abundant, and they were highly concentrated on the beach as expected from prior studies. Bivalves, gastropods, and polychaete worms were often more abundant on the tidal flats than the beach. Updated analyses of all collected samples will be presented, including the association of oyster farms with the infauna distribution.

ASSESSING DREDGE GEAR VERSUS DIVER-BASED SURVEYS IN SUPPORT OF A FISHERY-INDEPENDENT MONITORING PROGRAM FOR SUB-TIDAL OYSTER REEFS

D. Bowling*[1,2], D.B. Eggleston[1,2], and B. Boutin[3]

[1]North Carolina State University, Department of Marine, Earth and Atmospheric Sciences, 2800 Faucette Drive, Jordan Hall, Raleigh, North Carolina 27695-8208

[2]Center for Marine Sciences and Technology, 303 College Circle, Morehead City, North Carolina 28557

[3]The Nature Conservancy, 701 W Ocean Acres Drive, Kill Devil Hills, NC, 27948

Djbowlin@ncsu.edu

Oyster populations in North Carolina (NC) are at 5-15% of historic levels. Although oyster restoration efforts in NC have steadily increased over the past decade, natural oyster reefs still represent the large majority of the sub-tidal oyster habitat and support a multi-million-dollar annual harvest. Insufficient data, however, exists to fully understand the status of the harvestable oyster stock NC due, in large part, to the lack of a fisheries-independent stock assessment. The goal of this study was to assess the performance of dredge gear as a fishery-independent tool for assessing the status of the oyster population by comparing dredge estimates with *in situ* excavations of oysters by divers at different reef locations in Pamlico Sound. Mean total oyster densities collected by divers ranged from 55-171 oysters/m^2, whereas densities from the dredge ranged from 2-10 oysters/m^2. The efficiency of the dredge compared to diver excavations ranged from 3-14% for sub-legal and market-sized oysters, to 3-40% for oyster recruits. Despite the low catch efficiency and high variation associated with dredge gear, there was a positive and highly significant relationship between diver- and dredge-based samples for market- and sub-legal-sized oysters, but not for recruits. The information from this study is being integrated into a sampling design for a fisheries-independent survey program conducted by the NC Division of Marine Fisheries.

THE EFFECT OF PLOIDY ON THE FORMATION AND ANTIMICROBIAL EFFICACY OF EXTRACELLULAR TRAPS IN THE EASTERN OYSTER

Christopher J. Brianik*, Younes Bouallagui, and Bassem Allam

Stony Brook University, School of Marine and Atmospheric Sciences, 100 Nicolls Rd, Stony Brook, NY 11794

Christopher.Brianik@stonybrook.edu

DNA-derived extracellular traps (ET) are a highly conserved antimicrobial feature of the innate immune system recently discovered across multiple taxa including bivalves. In response to pathogens, DNA in immune cells is decondensed and released, forming complex meshes decorated with antimicrobial products to both physically capture and biologically neutralize pathogens. As such, the increased DNA content in triploid oysters might enhance the ability of ET to eliminate pathogens.

After a series of trials aimed at optimizing ET formation, triploid and diploid half-sibling oysters were assessed for their ability to produce ET. ET formation was evaluated using a combination of fluorescent microscopy with the DNA binding stain SYTOX green and bacterial neutralization assays with corresponding DNAse controls. Bacterial viability and visual assessment both confirmed that priming oysters by inflicting a puncture wound significantly increased the rate of ET formation as compared to previously published methods (exposure to LPS, live bacteria, calcium ionophore). Bacterial neutralization assays demonstrated that both the production of reactive oxygen species and the percentage of agranulocytes were positively correlated with ET efficacy. ImageJ analysis revealed that triploid oysters produced more ET than their diploid counterparts (higher frequency of ET-producing cells and larger ET nets), however, there was no significant difference in bacterial neutralization between diploid and triploid hemocytes.

Overall, this study demonstrates a new method to induce ET in reliably individual oysters, while also identifying host variables that are important for ET formation allowing further exploration of the role of this conserved mechanism in oyster immunity.

ARE TRIPLOID OYSTERS MORE TOLERANT TO *PERKINSUS MARINUS* THAN DIPLOIDS?

Christopher J. Brianik*, Joshua Lee, and Bassem Allam

Stony Brook University, School of Marine and Atmospheric Sciences, 100 Nicolls Rd, Stony Brook, NY 11794

Christopher.brianik@stonybrook.edu

Disease tolerance is a host defense strategy in which reducing the fitness costs of infection is prioritized over pathogen elimination. Previous studies have shown that triploid and diploid oysters generally display similar resistance with both equally likely to harbor an infection; however, some trends suggest that triploid oysters may display higher tolerance. Using a lab-based approach, this study sought to understand if triploid oysters display greater tolerance to the parasite *Perkinsus marinus* (Dermo), and how immunological features change throughout an infection. Adult half-sibling diploid and triploid oysters were collected in April 2022, and a subset was immediately sacrificed to assess the immunological status and Dermo prevalence. The remaining oysters were then injected with *P. marinus* (experimental) or saline water (controls), maintained in a common garden setup, and monitored daily for mortality. Upon death, oysters were removed and assessed for Dermo body burden and energy reserves. A subset of oysters was censored after eight weeks to evaluate immunological changes and parasite loads. Results generated throughout the 171 days of the study showed that triploid oysters survive significantly longer than diploids (34 days longer on average), although parasite body burdens accumulated at the same rate in both stocks irrespective of ploidy, suggesting that triploid oysters have a higher tolerance to Dermo disease than their half-sibling diploids. Immune trends from censored oysters showed neither cell viability nor reactive oxygen species production was influenced by ploidy, although phagocytosis was consistently greater in triploids. Understanding factors that influence tolerance may aid future disease management strategies.

CAN SATELLITE PRODUCTS OR STATE MONITORING DATA SUBSTITUTE FOR ON-FARM DATA FOR OYSTER AQUACULTURE MODELING?

Suzanne Bricker[1]*, Varis Ransibrahmanakul[2], Katherine Okada[3], Erik Davenport[2], Renee Karrh[4], Ronald L. Vogel[5,6], Travis Briggs[2], and Michelle Tomlinson[2]

[1]NOAA, National Centers for Coastal Ocean Science, Cooperative Oxford Laboratory, 904 S. Morris Street, Oxford, MD 21654

[2]NOAA, National Centers for Coastal Ocean Science, 1305 East-West Highway, Silver Spring, MD 20910

[3]Walter Reed Army Institute of Research, 503 Robert Grant Avenue, Silver Spring, MD 20910

[4]Maryland Department of Natural Resources, 580 Taylor Avenue, Annapolis, MD 21401

[5]University of Maryland, Earth System Science Interdisciplinary Center, 5825 University Research Court, College Park, MD 20740

[6]NOAA, Center for Satellite Applications and Research, 5830 University Research Court, College Park, MD 20740

suzanne.bricker@noaa.gov

Chesapeake Bay and its tributaries have experienced moderate to severe eutrophication impacts from nutrient inputs (nitrogen, phosphorus) from wastewater, urban and agricultural runoff, and atmospheric deposition. Oyster aquaculture is a promising innovative nutrient management strategy, in combination with traditional strategies, because bivalves remove nutrients from the water as they feed. Models are used to estimate nutrients removed by oysters; requirements include monthly water quality data for at least one year. Field sampling and lab analyses are time and resource intensive. Alternative less costly methods of data collection or use of data collected for other purposes was investigated.

Existing satellite-derived chlorophyll-*a* (Chl) products, and monthly water quality data at the closest long-term monitoring station collected by Maryland Department of Natural Resources (MD DNR) were compared with *on-farm* data sampled from two oyster farms in MD Chesapeake Bay (Chester and Honga Rivers). Satellite Chl*,* and MD DNR and *on-farm* data compared well. Model estimated oyster production (harvest) using MD DNR and *on-farm* data as model inputs from a Chester River farm show no significant difference in results (metric tons oysters: 18±4.5 *on-farm*, 20.7±3.5 MD DNR). Results with substitution of *on-farm* Chl with satellite Chl were also not different (16.7±5.3). The analysis suggests that MD DNR data and satellite Chl can be substituted for *on-farm* data, saving time and resources, for a value-added benefit of ~$2,412 station^{-1} year^{-1}, while providing needed information for resource managers and the shellfish industry on potential harvest and nutrient removal.

ENERGETIC PHYSIOLOGY OF *CRASSOSTREA VIRGINICA* OYSTER SPAT FROM THE ACCLIMATION PERIOD TO THE DORMANCY PHASE: IMPLICATIONS FOR THEIR SURVIVAL DURING COLD WINTERS

Guillaume Bridier[1]*, Jeff C. Clements[2], Luc Comeau[2], Martin Mallet[3], André L. Mallet[3], Claire E. Carver[3], and Réjean Tremblay[1]

[1]Institut des sciences de la mer, Université du Québec à Rimouski, 310 Allée des Ursulines, Rimouski, QC, G5L 3A1, Canada

[2]Aquaculture and Coastal Ecosystems, Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Avenue, Moncton, NB, E1C 9B6, Canada

[3]L'Étang Ruisseau Bar Ltée., Chemin des Huîtres, P.O. Box 3332, 111 rue Pointe Brulée Street, Shippagan, NB E8S 3H9

guillaume.bridier@live.ie

The eastern oyster, *Crassostrea virginica,* is economically important species that extends from the Gulf of Mexico to the Gulf of St. Lawrence where it experiences negative temperatures for 3-4 months in winter. In response to these low temperatures, adult oysters decrease the unsaturation index of their polar lipids during the fall to adjust the fluidity of their cell membranes and progressively reduce their metabolism to a near standstill in winter. During this dormant phase, oysters stop feeding and mobilizes their energy reserves to maintain their vital physiological functions; however, the metabolic strategies of oyster spats are still little studied, although they represent a crucial stage determining the production of adults and the economic performance of hatcheries. To better understand the spat energetic physiology, we conducted an experiment between September 2021 and May 2022 to follow the seasonal lipid dynamics and energy reserves of *C. virginica* spats from fall acclimation to the end of winter dormancy. During this period, we analyzed the energy reserves and fatty acid composition of polar lipids of 4- and 6-mm juveniles of hatchery and wild origins. The results showed an interruption in the homeoviscous adaptation and a stabilization of energy reserves around the month of October, suggesting that spats entered dormancy during this period. This quiescence at such an early stage of winter, occurring about two to three months earlier than in adult oysters, could explain in part the oyster mortalities observed at the end of winter when they leave their dormant state.

PHYTO-ARM, AN OPEN SOURCE/OPEN DESIGN TOOLKIT FOR AUTOMATED AND ADAPTIVE HAB MONITORING AND RESPONSE

Mike Brosnahan*[1], Ryan Govostes[1], Verena Lucke[2], Sidney Batchelder[1], Mrun Pathare[1], Bob Petitt[1], Dan Ward[3], Celia Villac[4], Kate Hubbard[4], Don Anderson[1], and Greg Doucette[5]

[1]Woods Hole Oceanographic Institution, 266 Woods Hole Rd., Woods Hole, MA 02543

[2]Georgetown University, Box 571229 Reiss Science Building, 37th and O Streets, NW Washington, DC 20057

[3]Ward Aquafarms, LLC, 51 N. Falmouth Highway, N. Falmouth, MA 02556

[4]Florida Fish and Wildlife Conservation Commission-Fish and Wildlife Research Institute (FWC-FWRI), 100 Eighth Avenue SE, St. Petersburg, FL 33701

[5]National Centers for Coastal Ocean Science, NOAA/National Ocean Service, Hollings Marine Laboratory, 331 Fort Johnson Rd., Charleston, SC, 29412

mbrosnahan@whoi.edu

Systems that automate sensing and response to harmful algal blooms (HAB) are needed to protect vulnerable animals and other resources. To this end, an open source, open design toolkit that is built has been developed around the Imaging FlowCytobot (IFCB), a phytoplankton sensor that acts an automated, submersible microscope. Called PhytO-ARM, the system is easily customized to serve a wide range of needs and sensor configurations. Most hardware is available from commercial vendors, making it easier to replace, maintain, and share the system with other potential users. All software is open source and has been developed as a containerized ROS system, making it easy to adapt and deploy across a wide range computer hosts and networks. Through collaboration with McLane Research Laboratories, the IFCB sensor has been updated so that it can classify its images onboard using convolutional neural network (CNN) models. Many PhytO-ARM systems are deployed within HABON-NE, a region-scale HAB monitoring network that serves the northeast U.S. These include sensor installations aboard trailerable barges, ships of opportunity, and autonomous surface vehicles. Systems specifically for aquaculture have also been developed that send alerts and take automated actions at nurseries when HAB species are detected. Ongoing development is expanding PhytO-ARM capabilities to integrate new nutrient and carbonate system sensors. These ongoing efforts aim to better characterize how increasing stratification, eutrophication, and acidification of coastal oceans may promote the expansion and intensification of HAB and their associated ecosystem impacts.

EVIDENCE FOR A MALE BIAS IN BLUE CRAB (*CALLINECTES SAPIDUS*) POT-BASED SAMPLING

Jeff F. Brunson*, Kimberly A. Sitta, Michael R. Kendrick, and Peter R. Kingsley-Smith

Crustacean Research and Monitoring Section, Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston, SC 29422

brunsonj@dnr.sc.gov

Demographic characterizations of populations can be influenced by sampling gear related biases. The Atlantic blue crab, *Callinectes sapidus,* is a commercially- and recreationally-important species throughout its geographic range and consistently supports one of the highest valued commercial fisheries in South Carolina, USA. Researchers at South Carolina Department of Natural Resources conduct multiple surveys to monitor the status of the blue crab population using a variety of gear configurations, but it is unclear how demographic characterizations may differ across gears. This study compared blue crab sex composition between active, trawl-based sampling and passive, pot-based sampling. Using long-term fisheries-independent monitoring data (1990-2021), the percentages of male crabs in pots and trawls were compared spatially (across three estuaries in the fall) and temporally (in one estuary throughout the year). Significant relative male bias of 20.1% was observed for fall pot-based sampling and of between 12.8% to 26.7% for individual estuaries. Furthermore, an overall relative male sex bias of 22.7% was observed for year-round sampling; however, this bias was only significant in certain months when examined at higher temporal resolution. These findings suggest that while different sampling gears may offer their own advantages, such as reduced costs or greater flexibility in the habitats that can be effectively sampled, the resulting characterizations of the demographics of populations can differ across surveys. Recognizing gear related biases is important for representative assessments of blue crab populations, particularly for those that use sex-specific modeling approaches as part of stock assessments to determine population status.

LABORATORY STUDIES ON THE IMPACT OF AN OSHV-1 MICROVARIANT ON *CRASSOSTREA VIRGINICA* FAMILIES AND LINES

Colleen A. Burge[1], Jessica M. Small[2], M. Victoria Agnew[3], Alanna MacIntyre[2], and Kimberly S. Reece[2]*

[1]University of California Davis, Bodega Marine Laboratory, California Department of Fish and Wildlife, 2099 Westshore Road, Bodega Bay, CA 94923

[2]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[3]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, 701 E Pratt Street, Baltimore, MD 21202

kreece@vims.edu

Oyster herpes viruses (OsHV-1) are primarily known to affect Pacific oysters, *Crassostrea gigas*. There is concern, however, over potential impacts of the spread of OsHV-1, particularly the highly virulent OsHV-1 microvariants, to the US East and Gulf Coasts. Given the lack of host specificity, there is potential for OsHV-1 to infect native molluscan shellfish including targets of the expanding aquaculture industry, eastern oysters and hard clams, *C. virginica* and *Mercenaria mercenaria*. Laboratory trials were conducted exposing spat of 30 eastern oyster families and two lines, as well as two *C. gigas* families as positive controls to a French variant of the OsHV-1 microvariants through a bath challenge for seven days in a salinity of 20 and at 22°C. Mortalities among the *C. virginica* families and lines ranged from 0-50% with a mean mortality of 15%. Juveniles from the high and low surviving families will be subsequently subjected to a challenge. Viral DNA copy numbers (as a proxy for viral loads) in the tissues of surviving and dead oysters, as well as controls from the challenge are being determined by quantitative PCR. These early results suggest that although some *C. virginica* lines and families are susceptible at the early life stage, breeding for tolerance to this virus is likely to be successful, as many demonstrated very low mortality. Results, however, also re-emphasize the importance of biosecurity. It is critical that all measures are taken to reduce the risk of introducing the virus to the East and Gulf coasts.

MICROBIOME OF THE PACIFIC OYSTER BEFORE, DURING, AND AFTER AN OSHV-1 OUTBREAK

Colleen A. Burge[1]*, Annie Chu[2], Jaime Grimm[3], Jonathan Shen[4], Sukanya Dayal[5], Marcela Prado-Zapata[6], Ford Evans[7], and Brett Dumbauld[8]

[1]University of California Davis, California Department of Fish and Wildlife, Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, CA 94923

[2]San Francisco State University, Estuarine and Ocean Science Center and Biology Department, Romberg Tiburon Campus, 3150 Paradise Drive, Tiburon, CA 94920

[3]University of Toronto, Department of Ecology and Evolution, 25 Willcocks Street, Toronto, ON, M5S 3B2 Canada

[4]University of Washington, Friday Harbor Laboratories, 620 University Road, Friday Harbor, WA 98250

[5]University of North Carolina Wilmington, Department of Biology and Marine Biology, 601 S. College Road, Dobo Hall 1010, Wilmington, NC 28403

[6]University of California Davis Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, CA, 94923

[7]Oregon State University, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, Oregon 97365

[8]USDA-ARS, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, Oregon 97365

colleen.burge@wildlife.ca.gov

The Pacific oyster (*Crassostrea gigas*), an important aquaculture species globally, has been the target of disease and mass mortalities caused by the Ostreid herpesvirus 1. Studies indicate that OsHV-1 is needed to initiate mortalities but secondary infection by bacteria may play a role in overall disease outcomes. In the US, OsHV-1 is present only in two growing areas in California. OsHV-1 causes mass mortalities of juvenile oysters (~60% losses) yearly in Tomales Bay, California. In 2020, the US West Coast Sentinel Monitoring program was initiated as an early warning system for OsHV-1 detection and to study pathogenesis of disease where OsHV-1 is detected. One aspect of particular interest is the role that bacteria play in the disease process. Changes to the Pacific oyster microbiome *in situ,* before, during and after an outbreak of OsHV-1 in Tomales Bay were investigated. A family of Pacific oysters produced by the Molluscan Broodstock Program were planted in Tomales Bay, California (and four other sites on the US West Coast) in June 2020 and monitored every two weeks as sentinels for survival, OsHV-1 infection, and growth every two weeks through October 2020. A total of twenty-four individuals at four time points (before, during, and after mortalities) were sequenced using tagged sequencing (Illumina Mi-Seq) of the V4 hypervariable region of the 16S gene. Data will be presented describing the diversity of bacterial communities and how they vary based on both OsHV-1 infection intensity and sample month.

REEFENSE: DARPA AND A MULTI-DISCIPLINARY TEAM OF SCIENTISTS JOIN FORCES TO DEVELOP OYSTER REEFS FOR COASTAL PROTECTION

David Bushek[1]*, Just Cebrian[2], Alex Goad[3], Ximing Guo[1], Hongyue Jin[4], Kelly Kibler[5], Danielle Kreeger[6], Jerome La Peyre[7], Ryan Lowe[8], Joshua Moody[6], Rebecca Morris[9], Hani Nassif[10], Scott Rikard[11], Richard Riman[10], Rackel San Nicolas[9], Eric Sparks[12], and Nigel Temple[13]

[1]Rutgers, The State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

[2]Mississippi State University, Northern Gulf Institute, 1021 Balch Bvld, Stennis Space Center, MS 39529

[3]Reef Design Lab, 61 Southern Rd, Mentone VIC 3194, Australia

[4]University of Arizona, 1127 E. James E. Rogers Way, Tuscon, AZ 85721

[5]University of Central Florida, Civil, Environmental and Construction Engineering, 12800 Pegasus Dr #211, Orlando, FL 32816

[6]Partnership for the Delaware Estuary, 110 S Poplar St, Wilmington, DE 19801

[7]Louisianna State University, Agriculture Center, 39 Forestry Ln, Baton Rouge, LA 70803

[8]University of Western Australia, 35 Stirling Highway, 6009 Perth, Australia

[9]University of Melbourne, 147 Royal Parade, 3010 Victoria, Australia

[10]Rutgers, The State University of New Jersey, Scholl of Civil and Environmental Engineering, 500 Bartholomew Road, Piscataway, NJ 08854

[11]Auburn University, Auburn University Shellfish Laboratory, 150 Agassiz St. Dauphin Island, AL 36528

[12]Mississippi State University, Coastal Research and Extension Center, 1815 Popps Ferry Road, Biloxi, MS 39532

[13]WSP USA, 11 N Water Street, Mobile, AL, 36602

bushek@hsrl.rutgers.edu

The Defense Advanced Research Projects Agency (DARPA) Biological Technologies Office recently funded a program called Reefense that "seeks to develop self-healing, hybrid biological, and engineered reef-mimicking structures to mitigate the coastal flooding, erosion, and storm damage that increasingly threaten civilian and Department of Defense infrastructure and personnel". Reefense is framed by three technical areas (TA): (1) structure, (2) ecosystem engineering and (3) adaptive biology. Rutgers University was selected to lead a team to create a Mosaic Oyster Habitat (MOH) for coastal defense. Reefense metrics include building a reef with innovative materials and a macro-scale topology that provides 70-90% wave attenuation (TA1), provides features that significantly reduce predation and enhances oyster recruitment by a factor of four (TA2), while also enhancing oyster resilience to disease and improve growth by 20 and 15%, respectively (TA3). The proposed MOH will be constructed from resorptive and non-resorptive concretes that will promote the development of a subtidal oyster reef extending into the intertidal zone supported by complimentary, interspersed habitats. Macro- and micro-scale features are being designed to reduce predation and increase recruitment, while genomic selection is being used to increase disease resistance and growth. This presentation will briefly describe the Reefense program objectives, describe the MOH team working to meet those metrics, progress to date and some preliminary experimental results.

POTENTIAL TROPHIC NICHES OVERLAP OF NATIVE AND NON-INDIGENOUS SPECIES: WHO EATS WHAT AND WHO EATS MORE?

Sara Cabral[1]*, José Lino Costa[1,2], Paula Chainho[1,2], Luc A. Comeau[3], and Réjean Tremblay[4]

[1]MARE – Centro de Ciências do Mar e do Ambiente, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal

[2]Universidade de Lisboa, Departamento de Biologia Animal, Faculdade de Ciências, Campo Grande, 1749-016 Lisboa, Portugal

[3]Aquaculture and Coastal Ecosystems, Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Avenue, Moncton, NB, E1C 9B6, Canada

[4]Institut des sciences de la mer, Université du Québec à Rimouski, 310 Allée des Ursulines, Rimouski, QC, G5L 3A1, Canada

sdcabral@fc.ul.pt

The introduction of non-indigenous species (NIS) is threatening the world oceans by acting as one of the main drivers of biodiversity loss. The co-occurrence of NIS and native species in the same habitats may lead to competition for food resources, and consequently to a potential overlap of their trophic niche. Therefore, it is essential to evaluate these feeding interactions to assess the impacts of NIS on the physiological health of native species.

Fatty acids are considered one of the most suitable techniques to study diet composition, since specific lipid markers of primary producers remain mostly unchanged along trophic food webs, and hence can be detected in consumers. In this study, fatty acid trophic markers were used to address the potential trophic niche overlap between the NIS Manila clam (*Ruditapes philippinarum*), the NIS pleated sea squirt (*Styela plicata*), the native cockle (*Cerastoderma* spp.), and the native blue mussel (*Mytilus edulis*). Samples were collected in the Albufeira coastal lagoon (Portugal), where although the cockles are the most important shellfish, the Manila clam harvesting has increased in the last ten years. Since 2017 mussel farmers in this coastal lagoon have been facing significant production losses due to fouling tunicates. Interspecific food competition was assessed on a seasonal basis by comparing the fatty acids contained in the targeted organisms with potential food sources present in the lagoon (fatty acids and flow cytometry). It is concluded that fatty acids represent promising markers to guide NIS management measures.

AUTOMATING OYSTER AQUACULTURE WITH SOLAR ENERGY

Emily Caffrey*, Stephen Pattison, Mark Rice, and Robert Summers

Solar Oysters LLC, 1850 Frankfurst Avenue, Baltimore, MD 21226

ecaffrey@mapcorp.com

Little advancement in oyster aquaculture technology has occurred in an industry needing development to meet global protein demand and advance restoration. Meeting these demands incurs challenges including high employee turnover, limited shallow leasing sites, stakeholder conflicts, and permitting challenges. Without new technology and access to deep-water growing sites, industry growth remains stagnant. The goal of this effort is to introduce an innovative prototype technology, the Solar Oysters Production System (SOPS) and discuss its current state, successes, and future improvements to support advancement within the oyster aquaculture industry.

The SOPS was developed and deployed in Baltimore, Maryland to maximize oyster production while minimizing labor inputs. The 40’ x 25’ system is equipped with five rotatable ladders supporting a series of oyster cages to a 20’ water depth and out of water positions. The depth requirement of the system aims to employ offshore sites untapped by other growers and minimize stakeholder conflicts associated with near-shore leases. All power to the system is provided by (12) 375-Watt roof-mounted solar panels. Rotation of oyster cages facilitates even exposure to dissolved oxygen, salinity, and temperature within the water column, desiccation upon out-of-water positions, and *in-situ* tumbling within cages to provide high-quality oysters. An estimated 200,000 oysters can be grown from seed on one 40’ x 25’ SOPS; a large, 90’ x 67’ SOPS has been designed to produce over 2,000,000 oysters annually. The system can be utilized for both seed (market) and spat-on-shell (restoration) oysters, with other potential applications (nursery system, other species).

INDUSTRY UPDATE: DEVELOPING A PILOT SCALE HATCHERY IN DELAWARE

Alyssa Campbell[1]*, Edward Hale[1], Dennis McIntosh[2], and Grant Blank[2]

[1]University of Delaware, Delaware Sea Grant, School of Marine Science and Policy, 700 Pilottown Rd, Lewes DE 19958

[2]Delaware State University, Delaware Sea Grant, 1200 N. Dupont Hwy, Dover DE 19901

alcamp@udel.edu

Oyster aquaculture is an emerging industry in Delaware, with the first commercial harvest recorded in 2018. Those who sought to get into oyster farming have faced many hurdles in getting established, such as high startup costs, regulatory controls, and COVID setbacks. As the pandemic stalled much of the industry’s progress shortly after it began, the need for critical support infrastructure became apparent to support industry growth. Importing seed from out of state is costly and time consuming, as growers pay out of pocket expenses for disease testing and permitting. In order to help accelerate industry expansion, the University of Delaware in collaboration with Delaware Sea Grant and Delaware State University, established the first pilot scale shellfish hatchery of Delaware at the UD Hugh R. Sharp campus in Lewes. Construction was completed after five months, creating a functional hatchery space equipped with a multistage seawater filtration system, five 160-gallon cone tanks, two 180-gallon raceways, and an algae culture system in development. As of now it is on schedule to be fully operational and producing oyster larvae in the 2023 growing season. The pilot hatchery aims to develop into an industrial scale facility that will support the aquaculture industry regionally through seed production as well as research and development. The hatchery team has also begun working with partners from local schools, including the Indian River School District and the Delaware Technical Community College to develop and implement aquaculture themed curriculum, using the new facility as an education and extension component.

SURVIVAL AND GROWTH OF TETRAPLOID EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, IN DIFFERING SALINITIES WITHIN THE NORTHEASTERN GULF OF MEXICO

Meghan Capps*, Scott Rikard, Sarah Spellman, and Glen Chaplin

Auburn University, Auburn University Shellfish Laboratory, 150 Agassiz Street, Dauphin Island, AL 36528

mec0172@auburn.edu

Triploid oysters, the predominant choice in commercial off-bottom oyster farming, are relatively reproductively sterile and often exhibit faster growth and higher meat yield than diploid oysters, especially during spawning season. The mating of male tetraploid broodstock with female diploid broodstock yields 100% triploid oysters. Understanding how different environmental variables may influence the survival and growth of tetraploids is crucial in producing a more resilient triploid oyster.

Two tetraploid broodstock lines maintained at the Auburn University Shellfish Laboratory (AUSL), 4MGNL20 (Louisiana origin) and 4MAPCK20 (Florida origin), were spawned to produce four experimental cohorts: two pure lines (4MGNL22 and 4M3APCK22) and two reciprocal crosses between the lines (4MAPCKGNL22 and 4MGNLAPCK22). The tetraploid lines are produced in conjunction with 4Cs Breeding Technologies, Inc with the GNL line originating from the Oyster Research Laboratory at Grand Isle, LA of the Louisiana Sea Grant Program and the APCK line originating from AUSL. Four replicates (n=400) of each experimental cohort were deployed at three differing salinity sites in Alabama: Mobile Bay (low salinity), Grand Bay (moderate/high salinity), and Dauphin Island (high salinity). Mortality and size metrics were assessed monthly. Preliminary data suggest a significant effect of site and tetraploid line on survival and shell height, and a higher mortality of 4MGNL at the low salinity site ($p < 0.05$). This is an ongoing experiment and data will be collected over 12 months. Trends will be reassessed to determine next steps in selecting a more resilient tetraploid broodstock for triploid production in the northern Gulf of Mexico.

THE ROLE OF GALACTOSAMINE IN MEDIATING CAPTURE EFFICIENCY IN MUSSELS AND ASCIDIANS

Martina Capriotti[1]*, Bridget A. Holohan[1], Maria Rosa[2], Gitai Yahel[3], Sandra E. Shumway[1], and J. Evan Ward[1]

[1]University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Rd, Groton CT, 06340

[2]Connecticut College, 270 Mohegan Ave, New London, CT 06320

[3]Ruppin Academic Center, Michmoret, 402979, Israel

martina.capriotti@uconn.edu

Suspension feeders have previously been assumed to capture particles based solely on particle size; however, recent studies indicate that similar-sized submicron particles may be captured at different efficiencies, and that surface interactions between cells and particles and the feeding organ may have a significant effect on this efficiency. There is, however, a dearth of information regarding the types of microorganisms that are captured and the factors that determine the capturability of these cells. Considering that surface interactions are an important but understudied factor in suspension feeding, this work focused on understanding the role of epicellular molecules in mediating capture efficiency, in two groups of suspension feeders: mussels (*Mytilus edulis* and *Geukensia demissa*) and benthic ascidians (*Ciona intestinalis* and *Styela clava*). Although these species can capture particles > 2-3µm efficiently, particles and cells <1 µm and of the same size may differentially evade the feeding apparatus. To examine some of the factors responsible for the differential capture efficiency, the four species were exposed to 0.3, 0.5 and 1 µm polystyrene spheres that were either uncoated or coated with the surfactant Poloxamer 188 (Pol) or the glycoconjugate galactosamine (Gal). Galactosamine is highly abundant on microalgal cell walls and interacts with SF mucus lectins during filtration. While no differences have been detected in removal efficiency by ascidians, results indicate that Gal coated spheres were more efficiently captured by mussels than uncoated or Pol coated spheres. Overall, and as expected, ribbed mussels were more efficient in capturing submicron particles than blue mussels.

LOCATION AND REEF SIZE DRIVE OYSTER RESTORATION SUCCESS

Olivia N. Caretti*[1,2,3], David B. Eggleston[2,3], DelWayne R. Bohnenstiehl[2,4], and Brandon J. Puckett[5]

[1]Oyster Recovery Partnership, 1805A Virginia Street, Annapolis, MD

[2]North Carolina State University, Department of Marine, Earth, & Atmospheric Sciences, 2800 Faucette Drive, 1131 Jordan Hall, Campus Box 8208, Raleigh, NC 27695

[3]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

[4]North Carolina State University, Center for Geospatial Analytics, 2800 Faucette Dr., Campus Box 7106, Raleigh, NC 27695

[5]National Centers for Coastal Ocean Science, NOAA National Ocean Service, Beaufort Lab, 101 Pivers Island Rd, Beaufort, NC 28516

OCaretti@oysterrecovery.org

Optimizing restoration success requires understanding how restoration location and design enhance the persistence and function of a restored habitat. Particular attention to the configuration of structure and its interaction with landscape-scale processes is critical for enhancing the habitat value of restored areas. Six subtidal restored oyster reefs in Pamlico Sound, North Carolina were monitored to identify how oyster demographics responded to initial habitat characteristics and how changes in habitat over time altered suitability for oysters. Habitat was characterized by repeated mapping using high-resolution bathymetric and side-scan sonar data. All reefs provided habitat for the settlement and growth of oysters, but this role changed as reefs underwent varying degrees of sedimentation and fragmentation. Within two years, relative differences in oyster recruitment and survival emerged and were related to variations in reef location and two-dimensional habitat characteristics among reefs, namely area and perimeter-to-area ratio. Larger reefs were less fragmented, resisted burial, and enhanced oyster densities and biomass relative to smaller, more fragmented reefs that became heavily sedimented and ultimately failed to provide suitable oyster habitat. Positive feedback mechanisms between habitat characteristics and oyster recruitment and survival were established within one year of restoration and were likely driven by landscape-scale processes such as sediment dynamics and larval settlement. To improve restoration success, we recommend creating relatively large reefs with low perimeter-to-area ratios in areas that promote habitat persistence. Sites in high-energy environments prone to sedimentation may have limited long-term economic and ecosystem benefits.

CITRATE-SYNTHASE RESPONSE AND MULTIPLE-STRESS IN PACIFIC OYSTERS, *CRASSOSTREA GIGAS*

Olivia Cattau*, Matt George, and Steven Roberts

University of Washington, School of Aquatic and Fisheries Sciences, 1122 NE Boat St, Box 355020, Seattle, WA 98195

ocattau@uw.edu

Pacific oysters (*Crassostrea gigas*) are experiencing heat stress due to hotter and dryer summers in addition to polyploidy stress due to the induction of triploidy for commercial stocks. The more troubling of these concerns is the increase in summer daytime low tide temperatures which leads to heat and desiccation stress as the oysters are exposed to open air and direct sunlight. A new way to predict stress tolerance in Pacific oysters is to measure maximum aerobic capacity by direct measurement of citrate synthase (CS) enzyme activity. CS is commonly used as a quantitative enzyme marker for the presence of intact mitochondria. In this study, it was important to determine how the CS response changes with multiple increasing stressors (heat, desiccation, and polyploidy). Six groups were evaluated for CS response under three unique stressors: high water temperature (heat), high air temperature (desiccation), and ploidy status (diploid/triploid). As CS response increases, the cellular respiration rate will increase and therefore thermal tolerance will decrease. There was no significant evidence that triploids had higher CS levels than diploids. The only significant result was that the triploid desiccated population experienced significantly different CS levels than all the other conditions. This leads to the conclusion that it is not heat or ploidy status alone that is causing mass mortality events rather, a combination of multiple factors.

OPTIMIZING HATCHERY CONDITIONING FOR SUNRAY VENUS CLAM SPAWNING

David Cerino[1], Tal Ben-Horin*[2], Jonathan Lucas[2], Bryan Synder[1], and Ami E. Wilbur[3]

[1]Carteret Community College, Aquaculture Technology Program, 3505 Arendell Street, Morehead City, NC 28557

[2]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

[3]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, NC 28409

tbenhor@ncsu.edu

Renewed interest in sunray venus clam (*Macrocallista nimbosa*) aquaculture has necessitated a critical examination of hatchery conditioning for reliable spawning. A series of conditioning trials at two research hatcheries tested how widely used conditioning tanks (open racks vs. sand-filled containers) and the concentration and types of microalgal feeds influenced reproductive staging and spawning success measured as the number of embryos produced. Across all conditioning trials and regardless of treatment, observations of gonad follicles confirmed our previous observations and observations from other investigators that *M. nimbosa* are continuous spawners. Also following previous observations, *M. nimbosa* was confirmed to be an unreliable spawner, although several successful spawns (defined as yielding > 5,000,000 embryos per spawn) did occur across the various conditioning trials. No single treatment was associated with spawning success; spawning was observed in clams held in both open racks and sand-filled containers. Similarly, spawning was observed in clams conditioned on all types of microalgal feeds at both low and high rations. Taken all together, these results highlight that hatcheries should plan for unreliable *M. nimbosa* spawning by focusing on conditioning the largest feasible broodstock cohort, with hatchery variables such as holding strategies and ration being secondary to maintaining this largest feasible cohort.

NATURAL TRANSMISSION OF *HEMATODINIUM PEREZI* IN JUVENILE BLUE CRABS (*CALLINECTES SAPIDUS*) IN THE LABORATORY

Xuqing Chen*, Kimberly S. Reece, and Jeffrey D. Shields

Virginia Institute of Marine Science, P.O. Box 1346, 1375 Greate Road, Gloucester Point, VA 23062-1346, USA

xchen@vims.edu

In high salinity areas of the Chesapeake Bay, juvenile blue crabs, *Callinectes sapidus*, are highly susceptible to the parasitic dinoflagellate, *Hematodinium perezi*. High prevalence levels and severe pathogenic effects in this host may affect blue crab recruitment through high mortality. *Hematodinium perezi* is endoparasitic in marine crustaceans, primarily decapods. The life history outside the host has not been experimentally investigated and, until now, transmission using dinospores has not been successful. The natural transmission dynamics of *H. perezi* was investigated in the laboratory using small juvenile crabs, which are highly susceptible to infection in the field, particularly under elevated temperatures, which are known to stimulate dinospore production. Natural water-borne transmission to naïve crabs varied between 7-100% and was not correlated with dinospore densities measured from their aquaria water. Infections appeared to develop quickly in naïve hosts at 25°C, suggesting that elevated temperatures as seen in the late summer and early autumn have a strong influence on the transmission of *H. perezi* in natural systems.

FRESHWATER MUSSEL GROW OUT TECHNIQUES: LINKING MODERN AQUACULTURE PRACTICES WITH RESTORATION GOALS

Kurt M. Cheng[1]*, Matthew J. Gentry[1], Danielle A. Kreeger[1], Lance H. Butler[2], and Roger L. Thomas[3]

[1]Partnership for the Delaware Estuary, 110 South Poplar Street Suite 202 Wilmington, DE 19801

[2]Philadelphia Water Department, 1101 Market St., 4th Floor, Philadelphia, PA, 19107

[3]The Academy of Natural Sciences of Drexel University, 1900 Benjamin Franklin Parkway Philadelphia, PA 19103

kcheng@delawareestuary.org

Freshwater mussels (Unionida) are filter-feeding bivalves that can serve as ecosystem engineers in the freshwater environments they inhabit. Mussel populations have experienced historical declines in their range and abundance nationally and locally in the Delaware River Basin. While conservation efforts are focused on avoiding extinction of rare species, the water quality and habitat services provided by freshwater mussel populations have also declined. Most provisioning and supporting services are furnished by the relatively more common species that dominate natural mussel beds. Hence, mussel restoration projects motivated by water quality goals should maximize the range and population biomass of these functional dominant species.

Hatchery propagation and rearing technology for freshwater mussels has improved considerably, but challenges remain with regard to increasing production to address the scale needed for larger restoration projects. This study in the Delaware Estuary tested whether modern aquaculture practices and gear developed for commercial marine bivalves can improve the growth and survival of large numbers of hatchery-produced freshwater mussels. Juvenile alewife floaters (*Utterbackiana implicata*) and eastern pondmussels (*Sagittunio nasutus*) were stocked at different densities in multiple types of floating oyster gear, with and without various substrates. Growth and survivorship were monitored over 2 years. Mortality ranged between 76 – 98%, and shell lengths increased >10 mm (>25%). Alewife floaters grew faster but had greater mortality compared to eastern pondmussels. Lessons learned are being used to improve yields and manage expectations for expanding mussel restoration programs in the upper mid-Atlantic region.

GABA INHIBITS SEROTONERGIC INNERVATION TO THE GILL FROM THE VISCERAL GANGLIA IN THE BIVALVE MOLLUSC, *CRASSOSTREA VIRGINICA*

Jennipher Chery*, Patricia Chery, Edward J. Catapane, and Margaret A. Carroll

Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

jennipher.chery@student.mec.cuny.edu

Gill lateral cells (GLC) in *Crassostrea virginica* and *Mytilus edulis* are innervated by excitation serotonin and inhibitory dopamine nerves from visceral ganglia (VG). GABA, an inhibitory neurotransmitter in molluscs and other animals, has not been well studied in bivalves. To test if GABA is an inhibitory neurotransmitter to serotonin neurons in VG of *C. virginica* the effects of applying GABA and a GABA agonist to VG on GLC cilia beating were studied. Cilia beating was measured by stroboscopic microscopy in preparations with VG innervation via the branchial nerve to gills intact. Preparations were positioned in observation chambers separating VG from gill so drugs could be applied to VG or gill without leakage to other tissues. Applying serotonin to VG caused a dose-dependent increase in cilia beating. Applying GABA to VG prior to serotonin reduced the increase. Cutting the branchial nerve that innervates the gill prevented the response of serotonin, with or without GABA. Applying the GABAb agonist SKF 97541 (3-Aminopropylmethyl phosphinic acid) to VG also blocked serotonin, demonstrating GABA is working as an inhibitory neurotransmitter to serotonin nerves in VG. The study provides evidence that the GABA receptor may be a GABAb type G protein-coupled receptor that mediates slow and prolonged inhibitory action, via activation of Gai/o-type proteins. More experiments with other agonists/antagonists need to be done to verify this. Bivalve gill is a useful model to study cilia activity as well as pharmacology of drugs affecting biogenic amines. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP, and PSC-CUNY 62344-0050 and 62344-0051.

DENOVO TRANSCRIPTOME ASSEMBLY AND ANALYSIS OF THE FLAT OYSTER PATHOGENIC PROTOZOA, *BONAMIA OSTREAE*

Germain Chevignon*, Aurélie Dotto-Maurel, Delphine Serpin, Bruno Chollet, and Isabelle Arzul

Ifremer, Unité Adaptation Santé des Invertébrés Marins, Avenue du Mus de Loup 17390 La Tremblade, France

germain.chevignon@ifremer.fr

The flat oyster, *Ostrea edulis,* is native to the European coast. It has declined to functional extinction in many areas of the northeast Atlantic for several decades. Factors explaining this decline include over-exploitation of natural populations and diseases like bonamiosis, regulated across both the European Union and the wider world. This disease is caused by the intracellular protozoan parasite, *Bonamia ostreae*. To date, very limited sequence data are available for this Haplosporidian species. The first transcriptome of *B. ostreae* will be presented. As this protozoan is not yet culturable, it remains extremely challenging to obtain high-quality -omic data. Thanks to a specific parasite isolation protocol and a dedicated bioinformatic pipeline, a high-quality transcriptome for an intracellular marine micro-eukaryote was obtained, which will be very helpful to better understand its biology and to consider the development of new relevant diagnostic tools.

TRANSCRIPTOMIC ANALYSIS OF THE HEMOCYTE RESPONSE TO A VIRUS INFECTION

J. Sook Chung* and Tsvetan R. Bachvaroff

University of Maryland Center for Environmental Science, Institute of Marine and Environmental Biology, 701 E. Pratt St, Baltimore, MD 21202

chungt@umces.edu

The hemocytes play the primary defense role in infection and wound hearing in invertebrates. In the blue crab, *Callinectes sapidus*, the total hemocyte numbers reflect the physiological conditions such as molt stage, infection stage, and the adult females infected with high levels of a double-stranded RNA virus (CsRV1) show changes in the population structure of hemocytes, with fewer semi- and granulocytes. Viral replication depends on host translational machinery. Hence, CsRV1 infection causes changes in the transcripts of the Eukaryotic Translation Initiation Factor 4E (eIF4E) family, varying by the degree of CsRV1 levels. Intriguingly, the CsRV1-infected animals show the highest CsRV1 transcripts in the digestive system and neuronal tissues, while the hemocytes contain the least virus transcripts. This fact confirms the defensive role of hemocytes in this virus infection. The current study aimed to address how the hemocytes respond to early CsRV1 infection using RNA sequence technology. The transcriptomic data of the hemocytes at the early CsRV1 infection stage are compared to the data from naïve animals and the late CsRV1 infection stage.

CHARACTERIZING DRIVERS OF OYSTER MORTALITY USING MOLECULAR TOOLS

Mark Ciesielski[1]*, Jonathon Lucas[2], Tal Ben-Horin[2], and Rachel Noble[1]

[1]University of North Carolina at Chapel Hill, Department of Earth, Marine and Environmental Sciences, 3431 Arendell Street, Morehead City, NC 28557

[2]North Carolina State University, Department of Clinical Sciences, 202 College Circle, Morehead City, NC 28557

mciesi3@live.unc.edu

Over the past decade, the incidence rate of mortality events in the oyster aquaculture industry has been steadily increasing throughout North Carolina. To unveil the primary factors contributing to the progression of oyster mortality, environmental parameters, water, and oyster samples were collected weekly from a local lease in North Carolina for five months throughout the growing season of 2021. A multifaceted approach combining a variety of analyses was employed by coupling histological data with droplet digital PCR (ddPCR) to identify specific pathogens and quantify *Vibrio* sp. in both oyster tissue and the surrounding water column, respectively. Additionally, high power liquid chromatography (HPLC) was performed to track pigment concentrations and distinguish which dominant algal species were present within the system. In early August of the sampling period, this site experienced a mortality event that compromised approximately 95% of the oyster product. The acute mortality event began following a moderate decrease in salinity (Δ10 within 9 days) with a simultaneous increase in both *Vibrio* sp. and total Chl-*a* within the water column. The shifts in environmental conditions and pathogen concentrations also coincided with an increase in degradation of digestive tubules as determined via histopathology. By integrating the data, a stress framework was constructed to describe the progression of mortality and offer predictive power for future monitoring efforts. Extrapolation of the patterns for observed mortality events requires additional work to validate the proposed framework in order to apply it to broader geographic scales.

SEX-DEPENDENT TOXICITY OF AQUATIC CONTAMINANTS AND THEIR IMPACT ON BLUE MUSSELS, *MYTILUS EDULIS*

Corina Ciocan[1]*, Wulan Koagouw[1,2], Christophe Minier[3], Giselda Bucca[1], Andrew Hesketh[1], and Nicolas Stewart[1]

[1]University of Brighton, School of Applied Sciences, Lewes Road, BN1 4GJ, United Kingdom

[2]National Research and Innovation Agency, Gedung B.J. Habibie, Jl. M.H. Thamrin No. 8, Jakarta Pusat 10340, Republic of Indonesia

[3]Universite du Havre, SEBIO, 25 rue Philippe Lebon - BP 1123, 76063, France

C.Ciocan@brighton.ac.uk

The presence of contaminants of emerging concern (CEC) in the aquatic environment is a global issue. The large number of CEC reported in the literature makes it difficult to interpret potential risks, especially because of the variety of biological responses recorded in sentinel organisms and the lack of knowledge surrounding the molecular pathways involved. An overlooked factor that can modulate the pollutant induced responses in aquatic animals is the organism sex. This study explored the role of sex in the reproductive toxicity of CEC, with focus on endocrine disruptors (EDC).

Histopathological and molecular alterations resulting from the exposure of marine bivalves to EDC include abnormalities in reproductive development, with negative impact on fertilization success and survival of the population. Different approaches were employed to investigate the action and impact of EDC, largely dependent on the type of chemical and the gonad development of the organism. Bivalves were exposed to these chemicals in the wild, for either short or prolonged periods as larvae, adults, or both, during gonad development or at the peak of their spawning period.

Sex dependant effects of selected EDC (xenoestrogens, pharmaceuticals, pesticides) on the blue mussel, *Mytilus edulis,* exposed to environmentally relevant concentrations under laboratory conditions will be reported. It was found that the selected stressors, at environmentally relevant magnitudes, have different consequences in male and female mussels, with the potential to impact the timing and breeding events. Therefore, future ecotoxicological studies should avoid interpretation of the results without considering the sex of animals.

THE EFFECT OF POPULATION DENSITY ON OOCYTE DEVELOPMENT IN ATLANTIC SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*)

Kaitlyn R. Clark*, Sally Roman, Roger Mann, and David B. Rudders

Virginia Institute of Marine Science, William & Mary, 1370 Greate Rd, Gloucester Point, VA 23062

krclark@vims.edu

The Atlantic sea scallop fishery employs a rotational closed area strategy designed to increase yield-per-recruit and allow sea scallops to spawn multiple times before they are susceptible to the fishery. Though generally successful, this strategy was challenged by two high-density recruitment events that occurred in the Nantucket Lightship Closed Area in 2012 and the Elephant Trunk Flex Area in 2013. The sea scallops at these sites persisted at high densities and initially exhibited varying degrees of impacted performance. The effect of sea scallop population density on growth, yield, and reproduction was investigated through quarterly sampling trips from 2018–2020 with sampling at 21 random stations divided among high, medium, and low-density sea scallop beds. In previous work on this objective, sea scallop density was identified as an important factor in predicting reproductive effort, with sea scallops at the extreme densities observed in the Nantucket Lightship allocating less energy to gamete production than sea scallops at more typical population densities. Sea scallops in the high-density beds of Nantucket Lightship also exhibited reduced reproductive activity, with fewer sea scallops staged as mature or spawning. A subset of female sea scallop gonads retained during at-sea sampling are being examined using histological methods to directly investigate the effects of density on oocyte development, particularly the volume fraction of developing, mature, and resorbing oocytes. A secondary goal is to assess the agreement between reproductive stages assigned through gross examination at sea with those assigned through histological examination to improve future sea scallop survey efforts.

EXPLORING ADAPTATION AND PLASTICITY TO OCEAN WARMING IN BLUE MUSSELS (*MYTILUS EDULIS*) FROM ATLANTIC CANADA

Shelby B. Clarke*[1], Tiago Hori[2], Luc Comeau[3], and Ramon Filgueira[4]

[1]Dalhousie University, Department of Biology, 1355 Oxford St, Halifax, Nova Scotia, B3H 4R2 Canada

[2]Atlantic Aqua Farms Ltd., 918 Brush Wharf Rd, Vernon Bridge, Prince Edward Island, C0A 2E0, Canada

[3]Department of Fisheries and Oceans, 343 Université Ave, Moncton, New Brunswick, E1C 5K4, Canada

[4]Dalhousie University, Marine Affairs Program, 1355 Oxford St, Halifax, Nova Scotia, B3H 4R2 Canada

shelby.clarke@dal.ca

As waters are progressively warming with climate change, the aquaculture industry will need to identify sources of mussels that are able to perform well under elevated temperatures. Sober Island Pond in Nova Scotia (NS), Canada, is a shallow inlet that experiences limited water exchange between the pond and the open ocean, exposing wild mussels to anomalously high summer temperatures. These environmental conditions could trigger local adaptation on mussels from this area, making them more adept at coping with and responding to climate change induced thermal stress. The objective of this study was to investigate and compare the thermal biology of two sources of mussels from Atlantic Canada, Sober Island Pond, NS and Georgetown, Prince Edward Island (PEI). Mussels were held under four temperatures (20, 25, 30 and 35°C), and four metrics were used to characterize their thermal biology: (1) lethal thermal thresholds (LT_{50}), (2) valve gaping behaviours, (3) RNA sequencing (RNA-seq), and (4) thermal performance curves. The results showed differences between the mussel sources in the four metrics, suggesting that individuals from Sober Island Pond, NS outperform individuals from Georgetown, PEI under elevated temperatures. The RNA-seq identified putative markers of temperature resilience and generated over 5000 differentially expressed genes to characterize the response of heat stress in mussels. This information could have important applications to breeding programs for mussel hatcheries and the aquaculture industry in Atlantic Canada.

OCEAN ACIDIFICATION AND BIVALVE BYSSUS: EXPLAINING VARIABLE RESPONSES USING META-ANALYSIS

Jeff C. Clements[1]* and Matthew N. George[2]

[1]Fisheries and Oceans Canada, 343 Université Avenue, PO Box 5030 Moncton, NB E1C 9B6, Canada

[2]University of Washington, School of Aquatic and Fishery Sciences, 1122 NE Boat St, Box 355020, Seattle, WA 98195-5020

jeffery.clements@dfo-mpo.gc.ca

Numerous studies have documented weakened byssal attachment strength under ocean acidification (OA); however, a comparable number have reported no effect, even within the same species. This study used meta-analysis to explore factors that could potentially explain observed effect size variation in byssal attachment strength following OA exposure. A systematic literature search identified 20 studies that experimentally tested the impact of OA on byssal attachment strength. Meta-analysis revealed body size (mean shell length) best explained the variation in effect sizes, and there was a negative linear relationship observed between body size and effect size. Despite this relationship, no single study or experiment included body size as a variable of interest. That byssal strength in larger bivalves is more susceptible to negative OA effects runs counter to prevailing wisdom that larger animals of a given species are typically more robust to stressors than smaller ones. This result highlights that body size may be an important factor in moderating OA sensitivity in adult calcifiers, which could influence population and community-level responses to OA. In stress response studies, however, variation in animal size is typically standardized methodologically rather than embraced. Empirical studies would thus benefit from better understanding the role of body size in species' responses to stressors for other taxa and biological traits. Future ecological meta-analyses should also consider body size as a moderating variable of species responses to both natural and anthropogenic stressors.

MUSSELS IN HOT WATER: THE BEHAVIOURAL ECOLOGY OF TEMPERATE MUSSELS UNDER OCEAN WARMING AND ACIDIFICATION

Jeff C. Clements[1]*, Kirti Ramesh[2,3], Jakob Nysveen[3,4], Sam Dupont[3], Fredrik Jutfelt[5], Carla Hicks[1], Rejean Tremblay[6], and Luc A. Comeau[1]

[1]Fisheries and Oceans Canada, 343 Université Avenue, PO Box 5030 Moncton, NB E1C 9B6, Canada

[2] BeZero Carbon Ratings, Discovery House, 28-42 Banner Street, London EC1Y 8QE, England

[3]University of Gothenberg, Department of Biological and Environmental Sciences, Medicinaregatan 18, 41390 Göteborg, Sweden

[4]Vatten och Samhällsteknik AB, Oxtorgsgatan 3, 553 17 Jönköping, Sweden

[5]Norwegian University of Science and Technology, Department of Biology, Høgskoleringen 5, 7034 Trondheim, Norway

[6]Université du Québec à Rimouski, Institut des Sciences de la Mer (ISMER), 310 allée des Ursulines, C.P. 3300, Rimouski, Québec G5L 3A1, Canada

jeffery.clements@dfo-mpo.gc.ca

Global climate change is anticipated to have wide ranging effects on ecologically and economically important marine biota. Two global change stressors of contemporary interest in the marine realm are ocean acidification and warming (OAW). Herein, the potential effects of OAW on animal behaviour can act as important mediators of ecological impacts. This talk will discuss research regarding effects OAW on valve gaping behaviour of temperate Mytilid mussels. Empirical evidence from laboratory experiments suggests that warming, but not acidification, has the potential impact mussels' behavioural responses to predators (valve closures). By combining behavioural results with previous research regarding OAW effects on mussel ecophysiology, it appears that the observed effects of warming on mussel behaviour may contribute to negative effects on mussel ecophysiology. Ways in which these impacts on behaviour and ecophysiology can translate into population- and community-level impacts will be discussed, and the potential for future work in this arena will be highlighted. Furthermore, this talk will hopefully demonstrate that bivalves can serve as a model organism for the field of behavioural ecology.

AN OVERVIEW OF THE SEA GRANT HARD CLAM SELECTIVE BREEDING COLLABORATIVE (HUB)

Antoinette Clemetson[1]*, Joshua Reitsma[2], Leslie Sturmer[3], Gregg Rivara[4], Kimberly Reece[5] Jan McDowell[5], Huiping Yang[6], Ximing Guo[7], Arnaud Tanguy[8], Emmanuelle Pales Espinosa[9], Denis Grouzdev[9], and Bassem Allam[9]

[1]New York Sea Grant, 146 Suffolk Hall, Stony Brook University, Stony Brook, NY 11794-5002

[2]Cape Cod Cooperative Extension, 3195 Main Street, Barnstable, MA 02630

[3]University of Florida IFAS, P.O. Box 89, Cedar Key, FL 32625

[4]Cornell University Cooperative Extension, 3690 Cedar Beach Road, Southold, NY 11971

[5]Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, VA 23062

[6]University of Florida, 7922 NW 71st street, Gainesville, FL 32653

[7]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

[8]Sorbonne Université, Station Biologique de Roscoff, Place Georges Teissier, 29688 Roscoff, France

[9]Stony Brook University, School of Marine and Atmospheric Sciences, 149 Dana Hall, Stony Brook, NY 11794-5000

aoc5@cornell.edu; HardClamHub@gmail.com

The northern quahog (= hard clam), *Mercenaria mercenaria*, is an economical and prominent bivalve under cultivation in several Atlantic states along the eastern seaboard. Hatchery production of high-quality seed that survives adverse biological and ecological conditions would help to expand and maintain this industry. Growers along the Atlantic coast deal with infectious diseases, harmful algae, prolonged heat stress, low salinity, icing, pests, etc. Collectively, these parameters result in significant mortality. The National Sea Grant Hard Clam Selective Breeding Collaborative (HUB) was funded through the 2019 National Sea Grant Advanced Aquaculture Collaborative Programs. This project lays the groundwork for the establishment of a regional aquaculture hub to develop advanced genomic technology for selectively breeding *M. mercenaria*. This research effort includes sequencing the hard clam genome, characterization of *M. mercenaria* genetic diversity throughout the natural range of the clam, and the development of low-cost genotyping tools with the potential for multiple applications. This presentation will describe the framework being used to conduct these genomic analyses and identify major partners and collaborators.

DETERMINATION OF THE UPPER SIZE LIMIT OF MICROPLASTIC PARTICLES THAT CAN BE INGESTED BY THE QUAGGA MUSSEL, *DREISSENA BUGENSIS*

Hannah I. Collins*, Bridget A. Holohan, and J. Evan Ward

University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Rd, Groton, CT 06340

hannah.i.collins@uconn.edu

Quagga mussels (*Dreissena bugensis*) are a freshwater mussel species invasive to the United States. While their presence can cause ecosystem-wide effects in rivers and lakes, their ability to process large volumes of water (up to 8 L/hr/g-dry weight) may have applications for water clarification in freshwater systems. In particular, dreissenid mussels have been proposed to remove microplastics (MP) from wastewater treatment plants. Existing literature on particle feeding by dreissenid mussels focuses on the capture and ingestion of microalgae and bacteria. There are a lack of data on MP particle capture and whether large microfibers and microfragments are ingested or rejected. The type of biodeposit MP will be sequestered in (feces or pseudofeces) has implications for the design of removal and settling systems. To examine this issue quagga mussels were isolated in 250ml beakers and exposed to a known number of MP of the same size and shape. For each type of particle, 15-20 mussels were allowed to filter and process particles for 3.5 hours. Biodeposits were collected 1, 24, and 28 hours post exposure period, and digested using KOH to remove organics and isolate MP. Microplastics rejected in pseudofeces and egested in feces were quantified to determine the proportion of MP of each type that are rejected vs. ingested. These data will determine the approximate largest size of MP that can be ingested and therefore egested as feces by *D. bugensis* and inform future work regarding the efficiency and limits of MP removal from engineered systems by this freshwater mussel.

REVISITING ECOLOGICAL CARRYING CAPACITY INDICES FOR BIVALVE CULTURE

Luc A. Comeau[1]*, Thomas Guyondet[1], David Drolet[2], Rémi Sonier[1], Jeff C. Clements[1], Réjean Tremblay[3], and Ramón Filgueira[4]

[1]Aquaculture and Coastal Ecosystems, Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Avenue, Moncton, New Brunswick, E1C 9B6, Canada

[2]Fisheries and Oceans Canada, Maurice-Lamontagne Institute, 850, route de la Mer, P.O. Box 1000, Mont-Joli, Quebec G5H 3Z4, Canada

[3]Institut des sciences de la mer, Université du Québec à Rimouski, 310 Allée des Ursulines, Rimouski, Quebec, G5L 3A1, Canada

[4]Dalhousie University, Marine Affairs Program, 1355 Oxford Street, Rm 805, Halifax, Nova Scotia, B3H 4R2, Canada

luc.comeau@dfo-mpo.gc.ca

Ecological carrying capacity (ECC) indices for bivalve culture rely on key ecosystem turnover rates, specifically: 1) the time needed for the cultured bivalves to filter the entire bay volume (clearance time, CT); 2) the time required for the bay volume to be replaced with water from outside the system (renewal time, RT); and 3) the time needed for the phytoplankton biomass to be renewed by local primary production (production time, PT). While there is a conceptual straightforwardness to such turnover rates, there is no standard methodology on how they should be measured in the context of ECC assessments. This study compared turnover rates obtained using simple and more elaborate approaches designed to address key assumptions and augment the veracity of outcomes. Comparisons were performed across multiple bays in Prince Edward Island, Canada. Accounting for crop aggregation and bay-scale refiltration effects augmented CT by a factor of 14 to 22. In regard to RT, the level of disagreement between validated hydrodynamic models and tidal prism models was also remarkable, ranging from 7 to 86 days across the investigated bays. Conversely, PT was not influenced by contrasting phytoplankton parameterization, as pre-aquaculture (1969–1970) and contemporary (2011-2012) datasets led to similar PT outcomes; however, other metrics revealed a contemporary shift towards low phytoplankton biomass and smaller phytoplankton cells (picophytoplankton). Overall, the study rejects a common assumption that bay-scale turnover rates serving ECC indices can be easily and accurately parameterized, and therefore cautions on their usefulness for cataloguing farming activities as 'sustainable' or 'unsustainable'.

GOT THE FUZZ?: A CONVERSATION ABOUT THE EFFECT OF STALKED CILIATES ON OYSTER NURSERY CULTURE

Michael Congrove[1], Samantha Glover[1]*, Standish K. Allen Jr.[1], and Richard Snyder[2]

[1]Oyster Seed Holdings, Inc, 425 Callis Wharf Rd, Grimstead, VA 23064

[2]Virginia Institute of Marine Science Eastern Shore Laboratory, 40 Atlantic Ave, Wachapreague, VA 23480

sam@oshoyster.com

Oyster Seed Holdings, Inc (OSH) is an independent, commercial oyster hatchery located on the western shore of Chesapeake Bay in eastern Virginia. In recent years, OSH has observed periodic increased presence of stalked ciliate epibionts in nursery culture. Stalked ciliates disturb the feeding process in small oyster seed effectively by causing a steric hindrance to the feeding process and therefore slowing growth. At first, observations were limited to bottle nursery systems, but have now been seen in upwellers, not only at OSH, but at a number of locations. Through Virginia Sea Grant Fisheries Resource Grant funding, OSH led a sampling program to identify these epibiont pests during the 2022 hatchery season, in collaboration with Dr. Richard Snyder from Virginia Institute of Marine Science. Results showed that Suctorians were the dominant epibiont pest in the bottle nursery system. In upweller nursery systems, *Zoothamnium* sp. were the dominant pest. The basic biological features of these taxa will be described. Now that the enemy has been identified, OSH intends to begin experiments to explore methods for controlling infestations of these epibionts in both the bottle and upweller systems.

For discussion: To what extent are these widespread in east coast facilities? Are the infestations caused by the same stalked ciliate species along the coast? Is there seasonality to these infestations? If experiencing infestations, what seems to be the best control method?

COMMERCIAL TRIALS WITH RAS FOR OYSTER (*CRASSOSTREA VIRGINICA*) LARVAE

Michael Congrove[1], Samantha Glover[1]*, Reza Ovissipour[2], Jonathan van Senten[2], Christopher D. Bentley[3], Richard Snyder[4], and Michael Schwarz[2]

[1]Oyster Seed Holdings, Inc, 425 Callis Wharf Rd, Grimstead, VA 23064

[2]Virginia Tech VS-AREC, 102 South King St, Hampton, VA 23669

[3]31493 Curratuck Rd, Painter, VA 2342

[4]Virginia Institute of Marine Science, 1370 Greate Rd, Gloucester Pt, VA 23062

sam@oshoyster.com

Typical bivalve hatcheries rely on pumping near-shore coastal waters to support larval production. In such applications, suboptimal water quality can impair larviculture performance. The application of recirculating aquaculture systems (RAS) can potentially mitigate this risk; however, commercial use of RAS has largely been limited to fish species. To test RAS in larval culture of oysters, a team was assembled comprising the Virginia Institute of Marine Science Eastern Shore Lab, Virginia Tech – Virginia Seafood Agricultural Research and Extension Center, Virginia Sea Grant, and Oyster Seed Holdings, Inc (OSH). The project team initiated the project at OSH with a Fishery Resource Grant (FRG) from Virginia Sea Grant, which allowed construction of a pilot scale commercial system. During the 2021 production season, hatch rate, defined as survival from egg to day 2, from a total of 15 spawns was 26% in standard commercial systems and 42% in the RAS system. Overall survival from egg to eyed larvae was 4.3% in standard systems and 4.8% in RAS. For the 2022 season, the FRG project was leveraged by Virginia Tech to obtain NOAA SK funding. During the 2022 season, with 17 spawns, hatch rate was 39% in standard systems and 49% in RAS, while overall survival was 20% in standard systems and 10% in RAS. Further results from 2022 and next steps for 2023 will be discussed.

THE ROLE OF TROPODITHIETIC ACID (TDA) IN *PHAEOBACTER INHIBENS* (S4) ROLE AS PROBIONT

Jessica Coppersmith[1]*, Sydney Charette[1], Sean Ovalles[1], Kira Bernabe[2], David Nelson[2], David Rowley[3], and Marta Gomez-Chiarri[1]

[1]University of Rhode Island, Department of Fisheries, Animal, and Veterinary Science, 120 Flagg Road, Kingston, RI 02881

[2]University of Rhode Island, Department of Cell and Molecular Biology, 120 Flagg Road, Kingston, RI 02881

[3]University of Rhode Island, Department of Biomedical and Pharmaceutical Sciences, 7 Greenhouse Road, Kingston, RI 02881

jcoppersmith@uri.edu

Disease outbreaks in oyster hatcheries can decimate the stock, delay production, and cause supply chain shortages for the expanding oyster aquaculture industry. The daily addition of the probiotic bacterium *Phaeobacter inhibens* S4 (S4) to hatchery tanks protect American oyster, *Crassostrea virginica*, larvae against bacterial pathogens like *Vibrio coralliilyticus* RE22 (RE22). Mechanisms of action of S4 against RE22 pathogenicity in oysters are complex including formation of thick biofilms, inhibition of virulence factors by quorum quenching, oyster host immunomodulation, and secretion of the antimicrobial tropodithietic acid (TDA). In order to further understand pathogen-probiont interactions, transcriptomes of competition co-cultures of RE22 and S4 were sequenced. Differential gene analysis showed downregulation of several virulence factors in RE22 including genes encoding for components of secretion systems I, III, and VI, hemolysin, and motility, and upregulation of efflux pumps when RE22 is in competition with S4. In comparison, S4 had limited changes in gene expression. One gene of note in S4 was a ROK transcriptional regulator upregulated in planktonic cells, which has been linked to antibiotic production in other bacteria and may regulate TDA production in S4. Knockout of antibiotic production by S4 partially, but not totally, decreased its ability to compete with RE22. Transcriptomic analysis of the competition of antibiotic knockout of S4 with RE22 is ongoing and will yield further insights into probiotic mechanisms of action for S4.

COMPARING AVAILABLE DETERRENT METHODS TO REDUCE DOUBLE-CRESTED CORMORANT ATTEMPTS TO ROOST ON FLOATING OYSTER CAGES

Fred L. Cunningham*[1], Guiming Wang[2], Paul Burr[1], Jason Tappa[1], Madeline Redd[1], Jason Glover[1], and Brian S. Dorr[1]

[1]USDA, WS National Wildlife Research Center, Mississippi Field Station, P.O. Box 6099, Mississippi State University, Mississippi State, MS 39762

[2]Mississippi State University, Department of Wildlife, Fisheries and Aquaculture, Box 9680, Mississippi State, MS 39762

fred.l.cunningham@usda.gov

The Mississippi Field Station of the Wildlife Services-National Wildlife Research Center is working in conjunction with Mississippi State University conducted a study to test the effectiveness of several commercially available physical bird deterrents available on the open market to reduce roosting time on floating oyster cages which could reduce coliform counts in water and oysters which could lead to the closure of oyster farms due to excessive bacterial counts.

Fifteen Double-crested cormorants (DCCO) were captured in night roosts in Mississippi or Alabama. Five DCCO were released into each of three aviary enclosures containing a 0.1-acre pond stocked with catfish fingerlings. Each pond contained a floating oyster cage to which one of 6 deterrents was applied and was monitored by 3 motion activated cameras that recorded DCCO positions and movements. Deterrent methods that were tested included: Float mounted triangle, Bird B Gone Spinning Bird Deterrent®, Scarem Kite®, Zip ties around floats, Gullsweep Bird and Seagull Deterrent®, and Bird Spikes for Bird, Cat, Squirrel, Racoon Animals Repellent®. Data collected by deterrent method included 1) number of times an individual DCCO successfully landed on floats, 2) number of individual DCCO on a float, 3) amount of time individual DCCO spent on float, 4) number of times an individual DCCO unsuccessfully attempted to land on floats. Over 184,000 photos were reviewed. Data analysis from this study is underway with preliminary results indicating a variation in the effectiveness depending on the deterrent method tested.

DEVELOPING THE OYSTERBOT FOR OYSTER CAGE RETRIEVAL

Molly Curran[1] and Dale Leavitt*[2]

[1]Woods Hole Oceanographic Institution, Applied Ocean Physics and Engineering, 53 Water Street, Woods Hole, MA 02543

[2]Blue Stream Shellfish, 53 Goulart Memorial Drive, Fairhaven, MA 02719

dale@bluestreamaquaculture.com

Handling and retrieving bottom tending oyster cages in deeper water is a challenge, especially when license conditions restrict your use of vertical lines to mark cage locations due to risk for entanglement with marine megafauna. In collaboration with a marine robotics engineer, Blue Stream Shellfish is developing a remotely operated vehicle (ROV) to aid in bottom oyster cage retrieval. Following identification of cage location using sidescan sonar, the OysterBot ROV will transport a lifting line with hook to the selected cage and attach the line to a short lifting bridle. The ROV will release the lifting line and move away while the cage is retrieved by the surface vessel for servicing. A preliminary design discussion and initial trial runs information will be presented as a work in progress. This project was supported by USDA Northeast SARE Farmer's Grant – Project # FNE22-018.

TAKING AN ENERGETIC APPROACH TO PREDICTING HABITAT SUITABILITY: THE INTERACTIVE ROLES OF TEMPERATURE AND FOOD AVAILABILITY IN BIVALVE DEVELOPMENT

Raymond Czaja, Jr[1]*, Bassem Allam[1], Emmanuelle Pales Espinosa[1], Brian Beal[2,3], and Kyle Pepperman[2]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

[2]Downeast Institute, 39 Wildflower Lane, P.O. Box 83 Beals, ME 04611

[3]University of Maine at Machias, 116 O'Brien Avenue, Machias, ME 04654

raymond.czaja@stonybrook.edu

Although the impact of temperature on bivalve larvae development is well studied, less attention is placed on food availability impacts. Assessing how temperature may interact with food availability and how this interaction affects larval development at large temporal (decade) and spatial (hundreds of kilometers) scales may allow for improved management for declining bivalve fisheries including that of the Atlantic surfclam, *Spisula solidisima solidissima*. A laboratory experiment applying a unique experimental design was used to predict survival, growth and pelagic larval duration (PLD) as a function of the full temperature and food availability niches for larval surfclams. Larvae were exposed to a continuous range of temperatures (14-26°C) and food availability levels (chlorophyll concentrations of 0.2-8.0 micrograms/liter). Generalized additive models (GAM) were then used to predict the temperature and food availability levels (and the respective geographic locations within the range of surfclams) that yield ideal development. GAM showed temperature and food availability explain large variation in surfclam larvae growth and pelagic larval duration, but moderate variation in survival. Growth and survival increased with increased food availability, while PLD decreased with increased food availability. Survival decreased with increased temperature, growth peaked near 23°C and PLD was lowest near 23°C. Preliminary habitat suitability modeling suggests Georges Bank yields the highest survival, and inner shelf New York waters yield the lowest PLD and highest growth rates. Additionally, mid-shelf Middle Atlantic Bight waters yield the lowest survival, while coastal Gulf of Maine yields the highest PLD and lowest growth rates.

TRANSGENERATIONAL INHERITANCE OF OCEAN ACIDIFICATION-INDUCED FEMINIZATION IN THE PORTUGUESE OYSTER

Xin Dang* and Vengatesen Thiyagarajan

The Swire Institute of Marine Science, School of Biological Sciences, Area of Ecology and Biodiversity, The University of Hong Kong, Pokfulam, Hong Kong Special Administrative Region, China

dangxin902@outlook.com; u3006422@connect.hku.hk

Global climate change can profoundly affect the sex determination and reproductive capacity in organisms, as well as the structure and dynamics of population in ecosystem processes. Anthropogenic CO_2-induced reductions in seawater pH (known as ocean acidification, OA) have irreversible physiological and biochemical impacts on marine calcifiers, including edible oysters; however, little is known whether and how transgenerational OA changes oyster sex ratio and fecundity. In this study, the ecologically and commercially important Portuguese oyster was used (*Crassostrea angulata*) as a model to investigate the transgenerational OA impact on the sex ratio and reproductive traits of successive generations. The parental oysters were exposed to control pH (pH 8.0) and low pH (pH 7.4) conditions for one month. Their larval offspring (F1 generation) were separated into another control and OA treatments to grow until sexually matured. F1 generation from the parents exposed to OA had a significantly higher proportion of females than that of F1 from control parents. F1 larval exposure history was negligible to its sex ratio. Meanwhile, there were not significantly different between control and OA treatment in survival rate and fecundity. Finally, F2 generation was produced to validate that the female-biased sex ratio caused by OA could be passed to F2 generation. Our result presents the transgenerationally inheritable effect on sex ratio of oysters in response to OA, which helps us better understand the diversity of sex allocation and the dynamic population structure under future OA.

SATELLITE SEA SURFACE TEMPERATURE GUIDANCE FOR REDUCING *VIBRIO PARAHAEMOLYTICUS* IN SHELLFISH

Robert M. Daniels[1]*, Varis Ransibrahmanakul[2], Ava N. Ellett[2], and John M. Jacobs[2]

[1]NOAA Center for Weather and Climate Prediction (NCWCP), 5830 University Research Ct, College Park, MD 20740

[2]NOAA National Centers for Coastal Ocean Science (NCCOS), Cooperative Oxford Lab, 904 S Morris St, Oxford, MD 21654

robert.daniels@noaa.gov

Through the Ecological Forecasting Roadmap, NOAA has embarked on an effort to harness existing NOAA infrastructure (i.e., observational platforms, ecosystem models, operational framework) for application to ecological issues. Tools have been developed to predict concentrations of *Vibrio parahaemolyticus* (*Vp*) in oysters both pre- and post-harvest. Remote sensing has been helpful in guiding the handling of shellfish and adherence to State control plans for the prevention of illnesses from *Vp*. Temperature is a major driver of *Vp* growth. In general, *Vp* growth will occur once water temperatures exceed 59°F, with faster replication at higher temperatures. Sea Surface Temperature (SST) from satellites has helped locate cool surface waters for the resubmergence of oysters in Cape Cod and aided in retrospective analysis of reported illnesses. In Alaska, it is available to help shellfish growers know when to more closely monitor temperatures and to inform harvesting schedules. A web tool showing the maximum SST over the previous 7 days was developed using 750 m resolution VIIRS SST from NOAA Coastwatch and is provided along with modeled data. Examples of satellite SST in coastal waters near Alaska and Massachusetts will be demonstrated. Future opportunities for satellite SST in U.S. coastal waters will be discussed in hopes of encouraging feedback and collaboration.

USING GENOMES AND TRANSCRIPTOME DATASETS FOR FUNCTIONAL ANNOTATION OF THE IMMUNE RESPONSE OF PENAEID SHRIMP TO PATHOGENS

Marcos De Donato[1]*, Hectorina Rodulfo[1], Carlos Fajardo[1], and Acacia Alcivar-Warren[2]

[1]The Center for Aquaculture Technologies, 8445 Camino Santa Fe, Suite 104, San Diego, CA 92121

[2]Environmental Genomics, Inc., P.O. Box 196, Southborough, MA 01772

mdedonato@aquatechcenter.com

Viral and bacterial pathogens have caused worldwide disease outbreaks impacting shrimp industry production (*Penaeus vannamei* and *P. monodon*). It is imperative that knowledge on the function and immune response (IR) mechanism are deepened to design strategies to reduce the impact of diseases. Genomic resources have been developed for *P. vannamei*, *P. monodon*, *P. chinensis*, *P. japonicus*, and *P. indicus* but the high content of repetitive sequences found in shrimp genomes makes it difficult to build highly contiguous assemblies and to annotate the genes to their full length. Over 2,300 RNA-Seq data sets have been published in the National Center for Biotechnology Information Sequence Read Archive database. Even though the genome assemblies of these species are incomplete, the genomic and transcriptomic datasets represent a very valuable resource for the functional annotation of the genes in the penaeid shrimp genome.

Specific IR components have been identified in Penaeids challenged by viral and bacterial pathogens [transglutaminase and lysozyme, alpha 2-macroglobulin, caspase, RAB7, chitinase, mucin, Toll signaling pathway, anti-lipopolysaccharide factors (ALF), penaeidins, peroxinectin, hemocyanin, glutathione peroxidase, superoxide dismutase, lectins, β-glucan binding protein, scavenger receptors, Down syndrome cell adhesion molecule (DSCAM), among others]. The shrimp innate IR are activated through pattern recognition receptors, by pathogen-associated molecular patterns, and are regulated by three major types of signal transduction pathways (Toll-like, immune deficiency, JAK/STAT). The comparative analysis of the genomic and transcriptomic sequences of these genes in all shrimp species have shown that the annotation of the genes is not precise and needs further revision. Examples of improved annotation in TLR, DSCAM, ALF, crustins, Interferon alpha-inducible protein will be shown, which are conserved in *P. vannamei*, *P. chinensis*, *P. japonicus,* and *P. monodon*.

RECOVERY FROM ESTIVATION IN THE APPLE SNAIL, *POMACEA MACULATA*: NITROGEN EXCRETION

Lewis E. Deaton

Louis Condee Society, 815 Gnenvieve Dr., Lafayette LA 70503

lewis.deaton@lusfiber.net

Freshwater apple snails in the genus *Pomacea* can survive months of aerial exposure. The species *P. canaliculata* accumulates uric acid during long-term aerial exposure. Nitrogen excretion during recovery of the animals from estivation has not been studied. Individual *P. maculata* were maintained in air for 138 days. Individuals were then placed in 200 ml of de-chlorinated tap water for 24 hr and the concentrations of ammonia, urea, and uric acid in the water was measured. The rate of excretion of ammonia was 32.3 ± 15.9 nmol g live weight^{-1} hr^{-1} (n = 11). Neither urea nor uric acid was detected in the incubating water. After 72 hr the rate of ammonia excretion was 14.3 ± 7.2. The rate of ammonia excretion of control snails maintained in water was 17.0 ± 10.1. The osmotic concentration (π) of the hemolymph of the animals exposed to air for 138 days was 260.8 ± 53.6 mOsm (n = 10); after 72 hr in water, hemolymph π was 104 ± 18. The control snails had a hemolymph π of $95.1 + 9.0$ (n = 10). These results suggest that estivating snails recovering during subsequent immersion in water release ammonia, but not other nitrogenous waste products. Rates of ammonia excretion and hemolymph osmotic concentration of recovering animals return to normal values within 72 hr of exposure to water.

A COMPARISON OF SURVEY DESIGN TECHNIQUES FOR SCALLOP, *PLACOPECTEN MAGELLANICUS*, CAMERA SAMPLING

Adam J. Delargy*, Kyle S. Cassidy, and Kevin D.E. Stokesbury

University of Massachusetts Dartmouth – School for Marine Science and Technology, 836 South Rodney French Blvd, New Bedford, MA 02744

adelargy@umassd.edu

Marine invertebrate survey designs take a wide range of forms, and semi-sedentary species that lie on the seafloor can be sampled using optical techniques. A long-standing optical survey of sea scallop (*Placopecten magellanicus*) populations in the northwest Atlantic has used a systematic sampling design, where stations are evenly spaced; however, a stratified-random design may produce more accurate biomass and density estimates by using knowledge of previous scallop distributions. To address this, scallop samples from two field studies that each used a mixture of stratified-random and systematic sampling designs were compared using statistical models and density maps derived using ordinary kriging. The systematic sampling significantly overestimated scallop density compared to stratified-random sampling in one study, but no significant difference was observed in the other study. Therefore, extensive simulations were conducted to compare random, stratified-random, and systematic sampling. These simulations applied previous survey data to kriging models to generate fine scale density layers. Simulated survey sampling was then conducted from the density layers to assess which technique was most accurate compared to the 'true' density. This was conducted using over 100 different density layers, corresponding to observed survey data from different areas and years. The results from this study will either support the current sampling design or support a transition to one of the alternative sampling designs, and therefore be highly valuable to the local survey and fishery. These results will also be highly useful to other fishery-independent survey scientists or managers and could inform changes in survey design.

TESTING THE TRANSFER OF FECAL AND DIGESTIVE GLAND MICROBIOTAS BETWEEN MUSSELS (*MYTILUS EDULIS*) AND THE KING SCALLOP (*PECTEN MAXIMUS*) FOR ACCELERATED DEPURATION OF DOMOIC ACID

Margot Deléglise[1]*, Cyril Noël[2], Guillaume Barnouin[1], José Garcia-Corona[1], Clément Offret[3], Malwenn Lassudrie[4], Hélène Hegaret[1], Adeline Bidault[1], and Caroline Fabioux[1]

[1]UBO – LEMAR, UMR6539 – Institut Universitaire Européen de la Mer, Rue Dumont D'Urville 29280 Plouzané, France

[2]IFREMER-IRSI-Service de Bioinformatique (SeBiMER), Centre Bretagne, 29280 Plouzane, France

[3]Université Bretagne Sud, LBCM, EA3884, Rue Saint-Maudé 56321 Lorient, France

[4]IFREMER, LER-BO, Station marine, Place de la Croix, 29185 Concarneau, France

margot.deleglise@univ-brest.fr

Harmful algal blooms are worldwide phenomena, which can have deleterious effects on marine organisms. Their negative effects are not limited to marine organisms, as some toxins can concentrate and bioaccumulate along the trophic chain and eventually affect humans. This is the case for example of domoic acid (DA), a neurotoxin produced by microalgae of the genus *Pseudo-nitzschia*. DA levels in exploited species exceeding the sanitary threshold, lead to legislative closure of fishing sometimes for several years. The ever-increasing demand for fishery products, and the challenge of safeguarding jobs generated by this economic sector, makes DA contaminations an obstacle that needs be addressed.

Bivalves, as filter feeders, are among the most exposed organisms to *Pseudo-nitzschia* blooms. King scallops, *Pecten maximus,* are distinguished by their long retention of DA, unlike other species such as the blue mussel, *Mytilus edulis,* which depurate very quickly. It has been proposed that the high capacity to depurate could be partially linked to differences in the composition of the gut microbiota between bivalve species.

This study focused on the microbiota of mussels and scallops and its potential implication in DA depuration and in the longer term, as a way to develop probiotics as accelerant of DA depuration. King scallops contaminated with DA were exposed to either mussel digestive gland homogenate or mussel feces for two weeks. Changes in bacterial communities of their digestive gland were then analyzed by metabarcoding to investigate a possible transfer of microbiota from mussels to scallops and implication of some bacteria in DA depuration.

USING ONLY LOW-DENSITY MARKER PANELS FOR GENOMIC SELECTION CAN LEAD TO DECLINING GENOMIC ESTIMATED BREEDING VALUE ACCURACY OVER TIME

Thomas A. Delomas[1]*, Christopher M. Hollenbeck[2], Joseph L. Matt[2], and Neil F. Thompson[3]

[1]Agricultural Research Service, United States Department of Agriculture, National Cold Water Marine Aquaculture Center, 483 CBLS, 120 Flagg Road, Kingston, RI 02881, USA

[2]Texas A&M University–Corpus Christi, Marine Genomics Lab, 6300 Ocean Drive, Corpus Christi, TX 78412, USA

[3]Agricultural Research Service, United States Department of Agriculture, Hatfield Marine Science Center, Newport, OR 97365, USA

thomas.delomas@usda.gov

Aquaculture selective breeding programs often utilize family-based selection due to the high-fecundity of most aquaculture species. In these designs, siblings of the selection candidates are phenotyped but the selection candidates are not. This allows selection for lethally observed traits (e.g., meat yield, disease resistance). One of the drawbacks of family-based selection is the inability to utilize within-family genetic variation.

Genomic selection retains the advantages of family-based selection and utilizes within-family genetic variation to increase the rate of genetic gain; however, the high-density genotyping panels typically used are expensive. Many shellfish breeding programs have therefore not implemented this technique. One previously proposed solution is to use only cheaper, low-density genotyping panels. The efficacy of this method was examined by simulating multiple generations of an oyster breeding program and compared the 'genomic estimated breeding value' (GEBV) accuracy to the use of either a high-density panel for all individuals or a combined strategy relying on pedigree-informed imputation.

It was found that when phenotypes from all available generations and low-density genotyping panels were used to estimate the GEBV, accuracy declined over time. This trend was eliminated when only phenotypes from one generation (the current generation of selection candidates) were used, but the GEBV accuracy was still lower than that achieved with the two alternative strategies.

SHELLEVATOR™: AUTOMATING OYSTER PRODUCTION ON SUBMERSIBLE AND MOBILE WATERCRAFT

Angelo DePaola

Angelo DePaola Consulting LLC, 12719 Dauphin Island Parkway, Coden, AL 36523 andydepaola@gmail.com

Investment in oyster farming has lagged because it is more labor intensives, expensive and risky than other food production systems. Shellevator™ (Shellfish Elevator) is a mobile oyster farm mounted above a submersible watercraft that automates aquaculture operations and avoids harm to reduce uncertainty and improve profitability. Ascent and descent through the water column are automated by sequentially introducing and exhausting compressed air in and out of lift vessel compartments. A manifold with valves located between an air source (compressor/tank) and airlines connected to lift vessels controls ascent and descent. The lift vessels are positioned below containerized shellfish and lift oysters above sea surface when filled with compressed air. Thus, manual operations like desiccation and tumbling oysters in mass are automated. Shellevators™ can be relocated over land or sea seamlessly to enhance growth or avoid harm like floods and pollution. These capabilities have been optimized in successive prototypes deployed in coastal Alabama since 2017, which have weathered numerous severe storms. Shellevators are scalable and have been fabricated from durable materials including metals, plastics and wood with lift vessels configured into pontoons, barge compartments and air bladders. A patent issued in 2022 features lift vessels above and below a frame holding aquaculture gear. This configuration expands operational bandwidth to deeper water and allows deployment at selected depths from above sea surface to the sea floor. This presentation will show latest Shellevator™ prototypes, methods, features and capabilities as well as possible adaptations for propulsion, steering and anchoring systems to create autonomous aquaculture drones.

IN-HOUSE *VIBRIO PARAHAEMOLYTICUS* ENUMERATION IN OYSTERS BY INDUSTRY TO MANAGE RISK

Angelo DePaola[1]*, Taejo Kim[2], Andrea Tarnecki[3], and William Dewey[4]

[1]Angelo DePaola Consulting LLC, 12719 Dauphin Island Parkway, Coden, AL 36523

[2]University of Wisconsin-Stout, 415 10th Ave. E., Menomonie, WI 54751

[3]Auburn University Shellfish Laboratory, 150 Agassiz St., Dauphin Island, AL 36528

[4]Taylor Shellfish Company, 130 SE Lynch Rd., Shelton, WA 98584

andydepaola@gmail.com

Shellfish harvest restrictions triggered by *Vibrio parahaemolyticus* (*Vp*) illnesses threaten the viability of the oyster aquaculture industry. A patented multiphasic media kit in a 96-well plate, used to estimate *Vp* most probable number (MPN), shows potential for in-house testing by the oyster industry. The current study uses this kit to investigate *Vp* reductions in oysters held in a commercial refrigerated wet storage system (12°C) during summer of 2022.

The multiphasic media kit includes a bottom agar which is overlaid with alkaline peptone water immediately before inoculation. Overnight incubation at 35°C yields visual results based on fermentation of arabinose under selective conditions favoring *Vp* growth. Staff at Taylor Shellfish Company in Shelton, Washington, conducted MPN analysis on 1169 samples (12 oysters/sample) from 19 areas at harvest and daily for up to 7 days of wet storage (829 wet storage samples). Harvest lots >100 MPN/g were tested in triplicate. Totten Inlet and Samish Bay had highest *Vp* levels at harvest with some lots exceeding (>5.0) and up to 3-log variability within harvest lots. *Vp* levels declined ~95% after 3 days of wet storage and plateaued afterwards. *Vp* levels generally reached <100 MPN/g after 3-5 days of wet storage except in lots with high harvest levels (>1000 MPN/g). Purge kinetics indicate that *Vp* risk can be significantly reduced with 3-5 days of refrigerated wet storage. Simple and affordable in-house testing of oysters for *Vp* levels by industry avoided shipping costs and delays and provided capacity for intensive sampling for more informed risk management.

MECHANIZED MANILA CLAM FARMING IN NORTHERN PUGET SOUND, WASHINGTON, USA

William F. Dewey

Taylor Shellfish Farms, 130 SE Lynch Rd., Shelton, WA 98584

billd@taylorshellfish.com

Currently there are between 3,000-4,000 metric tons of Manila clams annually harvested from aquaculture facilities in Washington State. Most farm-reared Manila clams in Washington are grown semi-intensively using open or net-protected culture systems on gravel substrate beaches which are harvested by hand with short handle rakes at low tide.

Over the past 25 years, technology has emerged in northern Puget Sound to mechanize Manila clam farming. The mechanization has substantially reduced production costs, increased production efficiency, and enhanced economic stability particularly during current times while labor is in short supply. This technology uses a combination of culture methods and tools and implements more commonly associated with land-based farms. Equipment is transported to the farms typically by boat or scow and operates on the beds at low tide.

This technology is used in sandy substrate as opposed to the traditional gravel substrate. The sandy substrate is key to mechanized harvest and predator exclusion net installation. The human eye is no longer necessary to make the clam/rock determination while harvesting. The clams are simply sifted out of the sand to harvest them. Some of the early mechanical clam harvesters were adapted from the tulip bulb industry. Tractor implements designed for installing plastic sheeting in terrestrial farms have been adapted to install heavy duty plastic predator exclusion netting. Street sweeping implements on tractors are periodically used to clean clam suffocating macroalgae from predator exclusion nets. Custom built hydraulic net spoolers pull and roll predator nets for re-use prior to harvest.

ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*) POPULATION DEMOGRAPHICS THROUGH THE DECADES

Mauricio González Díaz[1]*, Eileen E. Hofmann[1], John M. Klinck[1], Daphne Munroe[2], Eric Powell[3], and Andrew Scheld[4]

[1]Old Dominion University, Center for Coastal Physical Oceanography, 4111 Monarch Way, Norfolk, VA 23508

[2]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Ave, Port Norris, NJ 08349

[3]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive Ocean Springs, MS 39564

[4]Virginia Institute of Marine Science, College of William & Mary, Andrews Hall 442, Gloucester Point, VA 23062

maugondiaz@gmail.com

The Atlantic surfclam (*Spisula solidissima*) is a long-lived benthic biomass dominant that occurs on the Middle Atlantic Bight (MAB) continental shelf between 10 m and 50 m. The Atlantic surfclam supports a lucrative commercial fishery along the U.S. east coast. Trends in Atlantic surfclam asymptotic length and population-specific growth and mortality rates were analyzed using age and length observations from NOAA Northeast Fisheries Science Center stock surveys implemented in six survey regions along the MAB from 1982 to 2019. The demographic parameters estimated for each region and for each decade showed south-north differences, with the most variability associated with mortality rates in the southern portion of the distribution. The median asymptotic length in the southern regions was small, 88 mm, relative to northern regions, 110 mm to 141 mm. The asymptotic lengths estimated for the southernmost region declined by 35% over the four decades. This region had the highest decadal-averaged specific growth rate of 0.38 yr^{-1}. The overall decadal-averaged specific mortality rate of 0.20 yr^{-1} is consistent with reported values, but considerable variability was obtained within and between survey regions. The highest specific mortality rates of 0.18 yr^{-1} to 0.58 yr^{-1} were associated with the southern regions, where the Atlantic surfclam population age is skewed to younger ages. The small asymptotic length, and high specific growth and mortality rates suggest that the southernmost populations may be trending towards local extinction in response to unfavorable environmental conditions over the past four decades.

UNDERSTANDING AND LEVERAGING THE RESPONSE OF SHELLFISH MICROBIOMES TO COASTAL POLLUTION

Rachel E. Diner[1,2]*, Kara J. Wiggin[1], and Jack A. Gilbert[1,2]

[1]University of California San Diego, Scripps Institution of Oceanography, 8622 Kennel Way, La Jolla, CA 92037

[2]University of California San Diego, Department of Pediatrics, 9500 Gilman Dr, La Jolla, CA 92093

racheldiner@gmail.com

Microbes play a critical role in coastal biology; they cycle nutrients, degrade pollutants, and can support or impair the health of important host organisms, including shellfish. Aquatic environments are rapidly changing due to development, increasing toxic pollution, and climate change, which can alter microbial processes and negatively impact both microbes and their hosts. Shellfish toxicology research typically focuses on animals of interest, but the response of associated microbes (i.e., their microbiomes) and the resulting impacts on host, ecosystem, and human health are poorly understood. Oysters were used as a model system to investigate how hosts and their microbiomes respond to pollutants as integrated systems, and to explore the potential for microbes to mitigate the negative impacts of pollution in shellfish and the environment. A conceptual framework for this research and recent results will be presented demonstrating the effects of antibiotics and phenanthrene, a model polycyclic aromatic hydrocarbon pollutant, on oysters and their associated microbiomes in an experimental laboratory system. Also, potential applications for shellfish-associated microbes in novel bioremediation efforts and to support resilient coastal systems will be discussed.

HOW PHYTOPLANKTON AND HOST MICROBIOMES INFLUENCE *VIBRIO* SPP. ACCUMULATION IN OYSTERS

Rachel E. Diner[1,2]*, Amy Zimmer-Faust[3], John Griffith[4], and Jack A. Gilbert[1,2]

[1]University of California San Diego, Scripps Institution of Oceanography, 8622 Kennel Way, La Jolla, CA 92037

[2]University of California San Diego, Department of Pediatrics, 9500 Gilman Dr, La Jolla, CA 92093

[3]Biobot Analytics, 501 Massachusetts Ave, Cambridge, MA 02139

[4]Southern California Coastal Water Research Project, 3535 Harbor Blvd Suite 110, Costa Mesa, CA 92626

racheldiner@gmail.com

Many coastal *Vibrio* spp. can infect humans, representing a growing threat linked to increasing seawater temperatures. Oysters are a globally popular seafood source, however, their filter feeding lifestyle enables pathogenic *Vibrio* species to accumulate in their tissues, potentially endangering human health. While pathogen concentrations in coastal waters are often linked to environmental conditions, these do not always correlate with concentrations in oysters. Additional factors related to oyster hosts and the microbial ecology of *Vibrio* spp. bacteria likely play a role in accumulation but are poorly understood. To address this knowledge gap, concentrations of *Vibrio parahaemolyticus* and *Vibrio vulnificus* bacteria were determined and metabarcoding used to characterize both water and Pacific oyster (*Crassostrea gigas*) microbiomes in Newport Bay, CA. Site-specific environmental conditions significantly influenced water microbial communities and *Vibrio* spp. concentrations. Oyster microbial community diversity was generally more environmentally stable; however, changes in specific microbial taxa in oyster and water samples, particularly in oyster digestive glands, were linked to elevated potential pathogens in oysters, especially *V. parahaemolyticus*. This included an increase in cyanobacteria, which could represent an environmental vector for *Vibrio* spp. transport. A decreased relative abundance of *Mycoplasma* and other key members of the oyster digestive gland microbiota was also observed, which may indicate a compromised host health state. These findings suggest that host and microbial factors, in addition to environmental variables, may influence pathogen accumulation in oysters.

REBUILDING A COLLAPSED *MERCENARIA MERCENARIA* POPULATION, RESTORING SEAGRASS MEADOWS, AND ERADICATING HARMFUL ALGAL BLOOMS IN A TEMPERATE LAGOON USING SPAWNER SANCTUARIES

Michael H. Doall*, Bradley J. Peterson, and Christopher J. Gobler

Stony Brook University, School of Marine and Atmospheric Sciences, 239 Montauk Highway, Southampton, NY 11968

michael.doall@stonybrook.edu

During the past century, bivalve populations across the globe have collapsed, resulting in negative ecosystem consequences due to their outsized impact on shallow estuaries. In response, there has been strong interest in the restoration of marine bivalve populations. A decade-long restoration effort will be presented that sought to rebuild a collapsed and recruitment-limited population of northern quahogs (= hard clams) (*Mercenaria mercenaria*) in Shinnecock Bay, New York, USA, using spawner sanctuaries: no-harvest zones where adults were planted at high densities ($\sim$27 m^{-2}). Between 2012 to 2019, more than 3.2 million clams were planted in 64 discrete sanctuary plots ($\sim$1,850 m^{2} each) located in zones with maximal larval retention and known to support high clam condition. Hydrodynamic models, quantification of hard clam larvae, and spatial recruitment patterns demonstrated larvae spawned within sanctuaries were transported to regions where clam densities increased 18-fold over seven years (2015-2021) and harvests increased more than 17-fold over nine years (2012-2021). Higher clam densities caused biological filtration times to decrease from up to three months to as low as 10 days. Concurrently, concentrations of the harmful brown tide alga, *Aureococcus anophagefferens*, and chlorophyll-*a* significantly decreased while water clarity and the extent of seagrass beds significantly increased. Increases in clam landings and improvements in water quality were not observed in adjacent lagoonal estuaries where restoration did not occur. Given these outcomes and the global need for rebuilding marine life, the implementation of spawner sanctuaries may be a promising approach for restoring hard clam and other bivalve populations in estuaries elsewhere.

MAPPING THE GROWTH AND QUALITY OF FARMED SUGAR KELP (*SACCHARINA LATISSIMI*) IN THE ESTUARIES SURROUNDING LONG ISLAND, NEW YORK

Michael H. Doall*, Timothy P. Curtin, Brooke K. Morrell, Cameron M. Provost, Margot A. Eckstein, Lucas Chen, and Christopher J. Gobler

Stony Brook University, School of Marine and Atmospheric Sciences, 239 Montauk Highway, Southampton, NY 11968

michael.doall@stonybrook.edu

Sugar kelp (*Saccharina latissima*) is an emerging mariculture crop in the United States. For Northeast U.S. oyster farmers, sugar kelp provides a compelling opportunity for crop diversification as it has an opposite growing season from oysters, can be vertically integrated to provide additive revenue streams, allows for diversification into non-food markets, and expands farm ecosystem services. New York (NY), which is near the southern edge of sugar kelp's range along the U.S. east coast, hosts a mariculture industry that is exclusively focused on oysters and seeking diversification. To evaluate the potential for kelp farming in NY waters, cultivation experiments were conducted at sixteen locations over four kelp growing seasons (2019-2022). These locations spanned all major estuarine systems surrounding Long Island, NY, covered a range of water depths (2 to 30 ft), and included 10 oyster farms within public leasing areas. Concurrently, a suite of environmental and biological variables was monitored. The experiments demonstrated the potential for high crop yields in NY waters comparable to commercial kelp farms in Northeast states, but also revealed high spatial variability in kelp growth and quality. Kelp growth was highest in areas with high nutrient loading, and was uncorrelated with water depth, with high crop yields obtained in shallow and deep waters. Kelp quality was most impacted by biofouling organisms and grazers, which varied among sites and increased as water temperatures warmed during spring. The results provide valuable information to prospective NY kelp farmers and helps identify growing regions that have maximal economic and environmental value.

EVALUATION OF TANGENTIAL FLOW FILTRATION COUPLED TO LONG-READ SEQUENCING FOR OSTREID HERPESVIRUS TYPE 1 GENOME ASSEMBLY

Aurélie Dotto-Maurel[1]*, Camille Pelletier[1], Benjamin Morga[1], Maude Jacquot[1], Nicole Faury[1], Lionel Dégremont[1], Maëlis Bereszczynki[2], Jean Delmotte[2], Jean-Michel Escoubas[2], and Germain Chevignon[1]

[1]Ifremer, ASIM, F-17390 La Tremblade, France

[2]IHPE, Univ. Montpellier, CNRS, Ifremer, UPVD, F-34095 Montpellier, France

aurelie.dotto.maurel@ifremer.fr

Since the 1990s, the Pacific oyster, *Crassostrea gigas,* has suffered significant mortality events associated with the detection of the Ostreid Herpesvirus 1 (OsHV-1). Genomes of such viruses are large and complex with long direct and inverted terminal repeats. To date, diversity of OsHV-1 has been mainly characterized via microsatellites or multi-genomic fragments analyses and more recently via high-throughput sequencing based on short-read approach (Illumina). Despite the high accuracy of this type of sequencing, it does not allow to identify and characterize structural variation and isoforms of such complex viral genome. Recently, long-read sequencing techniques like nanopore sequencing from Oxford Nanopore Technologies (ONT) have been developed and offers a solution to the short-reads sequencing limitations.

OsHV-1 being unculturable, a tangential flow filtration (TFF) method was developed to enrich for viral infective particles from infected host tissues. This virus purification allowed us to extract high molecular weight and high-quality viral DNA that was subjected to Illumina short-read and Nanopore long-read sequencing. Dedicated bioinformatic pipelines were developed to assemble complete OsHV-1 genomes with reads from both sequencing technologies. Nanopore sequencing allowed to characterize new structural variations and major viral isomers while having 99,98% of nucleotide identity with the Illumina assembled genome. Altogether, results strongly suggests that TFF-based purification method, coupled with Nanopore sequencing, is a promising approach to enable field sequencing of unculturable aquatic DNA virus.

HOW DOES RECRUITMENT CONTRIBUTE TO RECENT SHIFTS IN LONG-TERM TRAJECTORIES OF BURROWING SHRIMP POPULATIONS AND THEIR EFFECT ON SHELLFISH AQUACULTURE IN WILLAPA BAY, WASHINGTON?

Brett R. Dumbauld[1]*, Brooke McIntyre[1], Nathaniel Lewis[2], Jennifer Ruesink[3], and Wesley Hull[3]

[1]Agricultural Research Service, U.S. Dept. of Agriculture, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, OR 97365

[2]Oregon State University, Coastal Oregon Marine Experiment Station, Hatfield Marine Science Center, 2030 Se Marine Science Drive, Newport, OR 97365

[3]University of Washington, Dept. of Biology, 3737 W Stevens Way NE, Seattle, WA 98195

brett.dumbauld@usda.gov

Ghost shrimp, *Neotrypaea californiensis*, are important members of estuarine intertidal communities along the US Pacific Coast, but their burrowing behavior causes significant problems for shellfish culture. Populations of these shrimp have been monitored in Willapa Bay, Washington for three decades and in Yaquina Bay, Oregon since 2005. Ghost shrimp density increased dramatically in the 1990s in Willapa Bay, declined almost as precipitously from 2000 through 2010, and has since increased again. Similar though less dramatic population fluctuations have occurred in Yaquina Bay since 2005. These shrimp have pelagic larvae that develop in the adjacent coastal ocean and then "recruit" back to estuaries, and significant relationships between the number of recruits and the number of larger 1 year-old shrimp present have been documented for both estuaries. Recruitment events since 2010 have resulted in population increases in both estuaries, but some precipitous population declines have also recently been observed at several locations in Willapa Bay, where larger/older shrimp have either suffered mortality or moved/receded. Results from initial surveys suggest that shrimp recruit to areas where adults have disappeared, but small juveniles are subject to mortality or move from these areas as well. Population fluctuations are of significant concern to shellfish growers, especially in Willapa Bay where a program to control these shrimp on shellfish beds was recently suspended, but it is important to understand the mechanisms that influence post-recruitment shrimp survival due to their broader role and influence on other habitats at the estuarine ecosystem scale.

ASSESSING NORTHEAST FLORIDA OFFSHORE BLUE CRAB FISHING EFFORT WITHIN FLORIDA STATE WATERS

Samantha L. Ehnert-Russo*, Claire E. Crowley, and Katharine L. Becker

Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, Florida 33701

Samantha.Russo@myfwc.com

During the winter months, commercial fishery effort targeting blue crabs, *Callinectes sapidus,* increases in the offshore Atlantic waters of northeast Florida as crabbers follow the seasonal migration of female blue crabs. The present study sought to describe offshore commercial fisher behavior through a mail survey (2020) and to characterize fishing effort using landings data from 2009–2010 to 2019–2020) and an aerial survey from January to March (2021). Offshore fisher effort varied each winter, and the effort was greatest in the winters of 2011–2012 and 2018–2019. The number of participants that reported offshore landings ranged from 6 to 11. Offshore landings accounted for 2.6% of the total landings in northeast Florida and were correlated with a decrease in inshore landings. The mail and aerial surveys determined that crab traps were concentrated off two sections of the coast within 1 mi of shore: (1) from Vilano Beach to south of Ponte Vedra Beach and (2) between Neptune Beach and Atlantic Beach. Participants in the mail survey reported fishing a median of 150 traps (range = 50–400 traps), while aerial counts estimated an average ± SD of 59.5 ± 5.4 traps/crabber. Average trap counts from the aerial survey during the winter of 2020–2021 suggested that 5.8 mi of vertical line were used within the survey area. This study successfully characterized the northeast Florida offshore blue crab fishery as a small but valuable fishery for a few crabbers, with effort driven by seasonal demand and crab availability.

SENSITIVITY OF THE GROOVED CARPET SHELL CLAM, *RUDITAPES DECUSSATUS*, TO OCEAN ACIDIFICATION

Eman El-Wazzan[1]*, Nayrah A. Shaltout[2], Fedekar F. Madkour[3], Mohamed A. Abu El-Regal[3,4], Ahmed ElShazly[5], and Merna E. Awad[3,6]

[1]Invertebrates Laboratory, Aquaculture Division, National Institute of Oceanography and Fisheries, NIOF, 101 Kasr ELAiny St., Cairo, Cairo Governorate Egypt.

[2]Marine Environment Division, National Institute of Oceanography and Fisheries, NIOF, Alexandria, Egypt

[3]Marine Science Department, Faculty of Science, Port Said University, Port Said, Egypt

[4]Marine Biology Department, Faculty of Marine Science, King Abdulaziz University, Jeddah, Kingdom of Saudi Arabia

[5]Oceanography Department, Faculty of Science, Alexandria University, Alexandria, Egypt

[6]Biogeochemical Department, The Southern California Coastal Water Research Project (SCCWRP), Costa Mesa, CA, USA

emanelwazzan@yahoo.com

The current research investigated the possible impacts of ocean acidification on the grooved carpet shell clam *Ruditapes decussatus*, as a model for commercially important marine bivalve species and a promising candidate for bivalve aquaculture in Egypt. Clams were collected from Lake Timsah on the Suez Canal coast, Ismailia, Egypt. Clams (avg. shell length, SL = 22.13 ± 0.91 mm; avg. total weight, TW= 2.28 ± 0.28g) were incubated in CO_2–enriched seawater manipulated at four different CO_2 concentrations: 420 ppm (ambient control), 550, 750 and 1050 ppm. Calcification analysis was carried out using XRD and Scanning Electron Microscope (SEM), highlighting a trend towards noticeable superficial physical sensitivity to acidification. The antioxidant enzymatic activities [catalase (CAT)] were significantly different among different $p\mathrm{CO}_2$ (~20-23 µmol min^{-1} mg prot^{-1}). Lipid peroxidation [malondialdehyde (MDA)] also showed significant difference among treatments (0.21 - 0.23 nmol TBARS mg prot^{-1}). Shell microstructure analysis showed periostracum distortion in clam shells as $p\mathrm{CO}_2$ concentration increased at 1050 ppm. These results indicate that ocean acidification may exert an additional stress on bivalves through weakening their calcified shells making them more vulnerable to predators and affecting their health and survival reducing production and economic value.

DEVELOPING LARVA-SPECIFIC ENVIRONMENTAL RNA (ERNA) TOOLS FOR THE BLUE MUSSEL AQUACULTURE INDUSTRY

David A. Ernst[1]*, Brian F. Beal[2,3], Erin K. Grey[4], Kyle E. Pepperman[3], LeAnn P. Whitney[1,5], and Nichole N. Price[1]

[1]Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544

[2]University of Maine at Machias, 116 O'Brien Avenue, Machias, ME 04654

[3]Downeast Institute, 39 Wildflower Lane, P.O. Box 83, Beals, ME 04611

[4]University of Maine, School of Biology and Ecology, 5751 Murray Hall, Room 100, Orono, ME 04469

[5]Maine Maritime Academy, Corning School of Ocean Studies, 1 Pleasant Street, Castine, ME 04420

dernst@bigelow.org

In recent years, blue mussel farmers in the Gulf of Maine have experienced recurring seed recruitment failures, the effects of which can have devastating financial impacts for a farm. However, it is unclear whether the cause of these recruitment failures is linked to reproductive failure, mortality in the plankton limiting larval supply, or post-settlement survivorship. Larval supply dynamics might be elucidated through the use of highly sensitive biomonitoring tools that take advantage of environmental nucleic acids within the water column, such as environmental DNA (eDNA) and environmental RNA (eRNA). While eDNA tools have proven to be powerful for detecting and monitoring organisms in aquatic environments, current eDNA technologies only allow for species- and/or population-level resolution and cannot infer whether the source organism is metabolically active (i.e., alive). By contrast, eRNA tools have the potential to detect living organisms and dissect finer-scale organismal characteristics, such as life history stage, which is made possible through the detection of differences in gene expression throughout development. Moreover, eRNA offers greater spatiotemporal resolution due to RNA's more rapid degradation rate relative to DNA. Here, the development of tools designed to exploit the eRNA present in larvae-laden water samples to detect, quantify, and monitor blue mussel larvae in near real-time will be discussed. Using these tools, the authors aim to develop accessible, field-ready toolkits that will enable mussel farmers to quickly and accurately predict the optimal timing for spat collection, increasing their chances of successful seed recruitment and production.

AN UNDESCRIBED APICOMPLEXAN PARASITE AS A MAJOR DRIVER OF THE COLLAPSE OF THE BAY SCALLOP POPULATION IN NEW YORK: A SIDE EFFECT OF CLIMATE CHANGE?

Emmanuelle Pales Espinosa[1]*, Younes Bouallegui[1], Denis Grouzdev[1], Christopher Brianik[1], Raymond Czaja[1], Sabrina Geraci-Yee[1], Arni Kristmundsson[2], Madison Muehl[1], Caroline Schwaner[1], Stephen Tettelbach[3], Harrison Tobi[3], and Bassem Allam[1]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

[2]University of Iceland, Institute for Experimental Pathology, Keldur, Keidnavegur 3, 112 Reykjavik, Iceland

[3]Suffolk County Marine Environmental Learning Center, 3690 Cedar Beach Road, Southold, NY 11971

Emmanuelle.Palesespinosa@stonybrook.edu

The bay scallop, *Argopecten irradians*, represents a commercially, culturally, and ecologically important species naturally found along the Atlantic and Gulf coasts of the United States. The species is emblematic in New York where it represents a major fishery resource and the official state shell. Since 2019, bay scallop populations in New York have been suffering large-scale summer mortalities resulting in over 95% reduction in biomass of adult, market-size, scallops. Preliminary investigations of these mortality events showed 100% prevalence of an apicomplexan-like parasite infecting kidney tissues.

This study was designed to provide histological, ultrastructural, and molecular characteristics of the parasite, which was suggested to represent a non-described member of the newly-established Marosporida clade (Apicomplexa) and provisionally named BSM (bay scallop Marosporida). Molecular diagnostics tools were developed and used to monitor parasite presence and intensity in scallop tissues. Results showed that BSM infects and disrupts multiple scallop tissues including kidney, adductor muscle, gill, and gonad. Light and transmission electron microscopy analysis of infected scallop tissues allowed the identification of both intracellular and extracellular stages of the parasite, including early trophozoites stages that display structural characteristics of the Apicomplexa. Field surveys demonstrated a strong seasonal signature in disease prevalence and intensity, as severe cases and mortality increase as summer progresses. Overall, results strongly suggest that BSM infection plays a major role in the collapse of bay scallop populations in New York. In this framework, BSM may synergistically interact with stressful environmental conditions to impair the host and lead to mortality.

MICROPLASTIC ACCUMULATION KINETICS AND EFFECTS ON THE ENERGY CONDITION OF GIANT SCALLOP (*PLACOPECTEN MAGENALLICUS*)

Marie Faraut*[1], Youssouf Soubaneh[2], Réjean Tremblay[1], Claude Rouleau[1], and Emilien Pelletier[1]

[1]Rimouski Institute of Marine Science (ISMER), 310 All. des Ursulines, Rimouski, Quebec G5L 2Z9, Canada

[2]Université of Québec at Rimouski (UQAR), 300, allée des Ursulines, C.P. 3300, succ. A, 300 All. des Ursulines, Rimouski, Quebec G5L 3A1, Canada

marie.faraut@outlook.fr

Global plastic production is growing steadily, reaching nearly 370 million tonnes in 2019. Once plastic enters the marine environment, it will undergo various physico-chemical processes leading to its degradation. Plastic degradation leads to the creation of microplastics (0.1 µm and 5 mm) and nanoplastics (0.001 and 0.1 µm) that will be present throughout the marine environment. These plastics that are not visible to the naked eye will be characterized by different sizes and shapes. The bioaccumulation of microplastics in the various organs of living organisms such as filter-feeding bivalves poses a problem in the consumer society. The purpose of this study is to shed light on the bioaccumulation of microplastics and their effects through radioactive isotope tagging and a method of autoradiography that is unique in Canada. As a result, a period of chronic contamination and depuration lasting three months each was put in place to address the problem. Seawater samples, autoradiograms and bioenergetic samples were collected during the contamination period when the results appear to be optimistic.

INVESTIGATION OF THE *OSTREA EDULIS* LARVAL MICROBIOME THROUGHOUT A NATURAL SPAWNING EVENT

Hannah Farley*[1], Tim Regan[1], Amanda Warr[1], Frederico Batista[2], David Bass[2], and Tim Bean[1]

[1]The Roslin Institute, University of Edinburgh, Midlothian, EH25 9RG, UK

[2]Centre for Environment Fisheries and Aquaculture Science, The Nothe, Barrack Road, Weymouth, DT4 8UB, UK

h.m.farley@sms.ed.ac.uk

Oysters are an important global food source with untapped potential for increased sustainable protein production. Culturing these animals in the United Kingdom (UK) relies entirely on hatchery production which remains limited by mortality events. A key driver of these mortalities lies in the interactions between the microbiome and external environment. To elucidate the impact of shifts in the microbiome, it is crucial to understand basic information about the microbiome in natural or wild scenarios, including the variability in components of the microbiome over a season. Therefore, water and larval samples were collected throughout a natural spawning event of *Ostrea edulis* at Loch Ryan, the last remaining native oyster fishery in Scotland, UK. Samples were collected throughout June to September 2019, across eight different sampling sites on the loch and at mid, bottom and surface levels within the water column. Larval count data were obtained from these samples before bacterial ID and abundance data were obtained through long read sequencing of the 16S rRNA gene using the MinION platform from Oxford Nanopore Technologies. The microbiome between water samples collected on different dates was found to be significantly different due to the presence of *Rhodobacteraceae* which decreased in abundance as the spawning event progressed. There was no significant difference found between the microbiome from samples collected at different sampling sites or depths within the water column. The data is discussed in terms of the physicochemical parameters which may have influenced these changes to the microbiome and how these findings could be applicable to a hatchery setting.

CAN WE EAT THEM TO SAVE THEM? FARMING THE WEST COAST NATIVE OYSTER, *OSTREA LURIDA,* FOR MARKET AND RESTORATION VALUES IN TOMALES BAY, CALIFORNIA

Gary Fleener*, Maxwell Rintoul, and Austin Maguire

Hog Island Oyster Company, 20215 Shoreline Highway, Marshall, CA 94940

gary@hogislandoysters.com

Olympia oysters (*Ostrea lurida*) were once abundant as a foundation species in the bays and estuaries of the North American West Coast. Archeological remains demonstrate they were also an important wild food for Native Americans, and they were widely harvested as a food resource for waves of immigrants during and after the Gold Rush era. Commercialized harvest combined with extensive habitat degradation led to the decline of *O. lurida* in most California estuaries. This decline, in concert with the 1920s introduction of larger, faster growing Japanese oysters (*Crassostrea gigas*) also led to the virtual disappearance of native oysters from the farms and oyster bars of the West Coast.

In 2018, Hog Island Oyster Co. began experimenting with the culture of native oysters for area oyster bars and in support of local restoration efforts. In 2021, this effort received a substantial infusion of funding to generate an additional 500K animals, now all deployed on Tomales Bay farms. This presentation will give an overview of the Hog Island project, discuss commercial opportunities and challenges, and explore the potential of native oyster farming to enrich larval abundance and recruitment in nearby wild populations.

OPTIMIZING A LOW-VOLUME FLOW-THROUGH SYSTEM FOR REARING PACIFIC OYSTER (*CRASSOSTREA GIGAS*) LARVAE

Henry Fleener[1]*, Neil Thompson[2], and Chris Langdon[1]

[1]Coastal Oregon Marine Experiment Station, Oregon State University, Newport, OR 97365

[2]Pacific Shellfish Research Unit, United States Department of Agriculture, Agricultural Research Service, Newport, OR 97365

Henry.Fleener@oregonstate.edu

Shellfish breeding programs and research hatcheries often require many larval-rearing tanks to fulfill the needs of experimental designs or cohort production, requiring significant husbandry effort and floorspace. In addition, environmental variance among static larval cultures can produce highly variable results. As an alternative to static cultures, a low-volume, flow-through system was developed by modifying McDonald-style hatching jars to: 1) reduce floorspace needs, 2) decrease labor by utilizing less sieving and cleaning 3) reduce variability among replicates, and 4) produce large numbers of spat per tank. This system is named the Hatfield Ultra Density Larval System (HUDLS) and is based on the CUDLS system developed by the Cawthron Institute, New Zealand. HUDLS is wholly constructed from off-the-shelf and 3-D printed parts, using 4.3L rearing tanks with high exchange rates (24/day) and larval densities (>50/mL). Multiple microalgal densities, larval densities, and cleaning regimens were tested to determine an optimal set of parameters for the HUDLS. Once optimized, spat yields in HUDLS far exceeded those from static tanks — HUDLS produced an average of 110,159 spat (SD=22,896) per tank, while static tanks (50L) produced an average of 24,251 spat (SD=5,823) per tank. Spat yield was maximized using a residual algae concentration of 10K cells/mL and an initial larval stocking density of 160 larvae/mL. Overall, HUDLS provides an alternative to static culture that increases larval rearing and spat production efficiencies and is scalable from small research systems to large breeding programs.

NESTED SPATIAL AND TEMPORAL MODELING OF ENVIRONMENTAL CONDITIONS ASSOCIATED WITH GENETIC MARKERS OF *VIBRIO PARAHAEMOLYTICUS* IN *CRASSOSTREA GIGAS* IN WASHINGTON STATE

Brendan Fries[1,2], Benjamin J.K. Davis[1,2,3]*, Anne E. Corrigan[1,2], Angelo DePaola[4], and Frank C. Curriero[1,2]

[1]Johns Hopkins University, Spatial Science for Public Health Center, 627 N. Washington Street, Baltimore, MD, 21205

[2]Johns Hopkins University, Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, 615 N. Wolfe Street, Baltimore, MD, 21205

[3]Center for Chemical Regulation and Food Safety, Exponent, Inc. 1105 Connective Avenue #1100, Washington, DC, 20036

[4]Angelo DePaola Consulting, 12719 Dauphin Island Parkway, Coden, AL 36523

Davisb@exponent.com

The Pacific Northwest is an important commercial harvesting area for *Crassostrea gigas* in the US. The pathogen, *Vibrio parahaemolyticus,* is a major cause of seafood-borne illness and accumulates in shellfish; there are concerns about rising infections in this region.

The genetic markers of *V. parahaemolyticus* (*tlh*, *tdh*, and *trh*) and environmental conditions were estimated in Washington State oysters and the surrounding environment between May and October 2005-2019 (N = 2,836). Multilevel mixed-effects regression models were used to assess relationships between environmental measures and genetic markers. Spatial and temporal variation and statistical dependence were accounted for in the model.

Model fit improved when including environmental measures from previous weeks (1-week air temperature lag, 3-week salinity lag). Positive associations were found between *tlh* and water temperature between 15°C and 26°C, and between *trh* and water temperature up to 26°C. *tlh* and *trh* were negatively associated with 3-week lagged salinity in the most saline waters (> 27). There was a positive relationship between tissue temperature and *tdh* above 20°C. The *tdh*:*tlh* ratio displayed inverted analogous relationships to *tlh*. The non-linear associations between the genetic targets and environmental measures demonstrate the complex habitat suitability of *V. parahaemolyticus*. Additional associations with both spatial and temporal variables also suggest there are influential unmeasured environmental conditions that could further explain bacterium variability. These findings confirm previous ecological risk factors for vibriosis in Washington State, while also identifying new associations between lagged temporal measures and pathogenic markers of *V. parahaemolyticus*.

IS THE HIGH EXPLOITATION RATE RESULTING IN THE DECLINING REPRODUCTIVE OUTPUT OF BLUE CRAB (*CALLINECTES SAPIDUS*) IN THE CHESAPEAKE BAY?

Yushinta Fujaya[1], Robert Aguilar[2], Roberta Bardelli[3], Kimberly D. Richie[2], and Matthew B. Ogburn[2]*

[1]Hasanuddin University, Faculty of Marine Science and Fisheries, Makassar 90245, Indonesia

[2]Smithsonian Environmental Research Center, 647 Contees Wharf Road, Edgewater, MD 21037

[3]Department of Earth and Marine Sciences, University of Palermo, Via Archirafi, 22, 90123, Palermo, Italy

ogburnm@si.edu

The blue crab, *Callinectes sapidus*, is a key species in the Chesapeake Bay that plays an integral ecological, economic, and sociological role; however, reports suggest that there has been a significant decline in the population of these crabs as well as the recruits per spawning female. The objectives of this study were 1) to analyze the current state of blue crab reproduction in three tributaries of the upper Chesapeake Bay that vary in male crab exploitation rate, and 2) to search and find the main factors and other possible causes of the decreased reproductive output of blue crabs in the Chesapeake Bay. Mature blue crabs were collected from June to October in the Rhode, Choptank, and Patuxent rivers from fishery-independent trawls and commercial trotlines. Female crabs were brought to the Smithsonian Environmental Research Center (SERC) laboratory alive and male crabs were returned to the rivers after being recorded. The female crabs were stored in the freezer (-20°C) until further investigation. There were 180 female crabs used in this study. The parameters observed were sex ratio (including operational sex ratio in the Rhode River), maturity stages of the ovary, spermathecae index, spermathecae fullness, and sperm count. Preliminary results indicate that there is variation by tributary and month in reproductive parameters, although sample analysis is still in progress. This study also will provide important evidence that, with other information such as prey resources, environmental conditions, and water quality, will help identify factors causing the current population decline.

ONTOGENETIC SHIFTS IN SALINITY TOLERANCE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*: IMPLICATIONS FOR RESTORATION AND RECOVERY IN APALACHICOLA BAY, FLORIDA

Emily Fuqua* and Sandra Brooke

Florida State University, Coastal and Marine Laboratory, 3618 US-98 St. Teresa, FL 32358

efuqua@fsu.edu

The eastern oyster (*Crassostrea virginica*) population crash and subsequent lack of recovery in Apalachicola Bay, Florida, has been blamed on many factors, one of which being increased salinity due to lower freshwater input particularly during severe droughts. This increased salinity is believed to be an obstacle to the recovery of oyster populations, especially as salinity in estuaries is highly spatially and temporally dynamic. So, a clear understanding of how salinity affects the Apalachicola Bay oyster population is needed to formulate and implement an effective recovery plan. The main objective of this work is to address how salinity affects the growth, survival, and energetics of oysters as larvae, spat, and adults. Adults (>40 mm), spat (20-25mm), and larval oysters were experimentally exposed to ecologically relevant salinity ranges, and growth and survival were recorded. Oxygen uptake of adult and spat stages were also measured using respirometry. Reaction norms were evaluated using generalized linear models and compared among life stages. Larvae had the highest survival at a salinity of 16 and significantly decreased survival at all other salinities (10, 22, 28, 34; F_4=10.28, P < 0.01); however, adults survived at all salinities tested (4, 12, 20, 28, 36), but salinity significantly changed respiration rates (F_4=7.47, P < 0.01). These results demonstrate an ontogenetic shift in salinity tolerance in *C. virginica*, which has important implications for larval dispersal and post-settlement survival. Identification of optimal salinity regimes can influence placement of restoration efforts, and potentially enhance oyster population recovery in Apalachicola Bay.

WHITE SPOT SYNDROME VIRUS (WSSV) GENOMES FROM CHINA, ECUADOR, MEXICO AND OTHER COUNTRIES ARE NOT INTEGRATED IN THE GENOMES OF FIVE PENAEID SHRIMP SPECIES, BUT ENDOGENOUS VIRAL ELEMENTS (EVE) OF WSSV (WSSV-EVE) ARE FOUND IN THE TRANSCRIPTOME OF THE FIRST SPECIFIC PATHOGEN-FREE (SPF) *PENAEUS VANNAMEI* DOMESTICATED IN THE UNITED STATES

Mayra Galindo[1]*, Gober Asuncion[1], Victoria Alday-Sanz[1], and Acacia Alcivar-Warren[1,2]

[1]Fundacion para la Conservacion de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Environmental Genomics, Inc. P.O. Box 196, Southborough, MA 01772 USA

environmentalgenomics.warren@gmail.com

Mortalities of cultured shrimp induced by White Spot Syndrome Virus (Naldaviricetes; Nimaviridae; Whispovirus; WSSV) have occurred in Ecuador since 1996. Endogenous WSSV-like sequences (WSSV-EVE) have been reported in *Penaeus vannamei* farmed in Thailand and in expressed sequence tag (EST) libraries prepared from the first specific pathogen-free (SPF) *P. vannamei* domesticated by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP) maintained at the Oceanic Institute in Hawaii.

The WSSV genome sequence form China (AF332093.3, 305119bp), Ecuador (MH090824, 288,997bp), two isolates from Mexico, and 13 complete WSSV genome sequences in GenBank were used in this study. Twelve whole genome sequence (WGS) and 35 transcriptome shotgun assembly (TSA) databases available for Penaeoidea were used to determine if the WSSV genome, and its nimaviridae family gene *Nimav-1_LVa* (279905bp) are integrated in the shrimp genome.

Whole genome sequence searches revealed that none of the WSSV genomes are integrated in the draft genome assembly of *P. vannamei* farmed in China (ASM378908v1; ~1.8Gb) and in other draft assemblies for *P. monodon*, *P. japonicus*, *P. chinensis,* and *P. indicus*; however, large fragments of *Nimav-1_LVa* are integrated in the genome of *P. vannamei* farmed in China (*P. vannamei* breed Kehai No.1 LVANscaffold_3666 (QCYY01003664, 990704bp, 428 fragment matches). TSA analyses revealed that many cDNA and EST in the genome of SPF *P. vannamei* from USMSFP and other Penaeids are similar to portions of WSSV and *Nimav-1_LVa* sequences, representing putative WSSV-EVE sequences.

STATUS OF MANGROVE FORESTS IN ECUADOR

Mayra Galindo[1], Miriam Alcívar-Arteaga[1]*, Iris Hernández[1], César Diaz[1], Gober Asunción[1], Christian Saltos[1], Sofía Figueroa[1], Daniela Espinoza[1], Diana Villota[1], Diana Calvache[1], Oscar Jaen[1], Cesar Valarezo[1], Jorge Romero[1], Carlos Mejía[1], Freddy Aveiga[1], Marcela Mendoza[1], and Acacia Alcívar-Warren[1,2]

[1]Fundacion para la Conservacion de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Environmental Genomics, Inc. P.O. Box 196, Southborough, MA 01772 USA

fucobi@gmail.com

Multi-temporal studies on the change in mangrove forest cover and salt flats areas in the estuaries of Ecuador revealed that in 1969 there were 203 624.6 hectares of mangroves, while this figure decreased to 157,094.28 hectares in 2013. The Ministry of Environment, Water and Ecological Transition of Ecuador is currently in charge of collecting information and managing the National Mangrove Plan of Ecuador (2019-2030), through the application of Ministerial Agreement 031, April 2019, and instruments that allow an Agreement for the Sustainable Use and Custody of Mangroves, as a conservation strategy between the local population and the government.

The mangrove ecosystem is home to 52 species of birds, 15 reptiles, 19 mammals, at least 100 fish, 20 crustaceans, 70 molluscs. Regarding mangrove flora, 179 plants have been reported so far, including the iconic mangrove tree species: *Rhizophora mangle*, *Rhizophora harrisonii*, *Avicennia germinans*, *Conocarpus erectus*, *Laguncularia racemosa*, *Pelliciera rhizophorae*, and *Mora megistoperma*.

Ecuadorian mangroves are threatened by: the increase in illegal felling of mangroves; weak application of environmental regulations for the investigation and sanction in cases of affectation to the mangrove; reduction of beaches and bays; overexploitation of resources and indiscriminate use of illegal fishing gear; contamination with solid and liquid waste; sedimentation of estuaries and hydrographic basins due to deforestation and floods in winter; vulnerability to climate change; technical weakness of the Decentralized Autonomous Governments (GAD) in the Land Management of rural areas and sensitive sites for conservation; insensitivity of companies, residents and entities of local control.

EFFECTS OF ELEVATED TEMPERATURE AND TIO$_2$ NANOPARTICLES ON THE GUT MICROBIOTA AND BYSSUS PERFORMANCE OF THE THICK SHELL MUSSEL, *MYTILUS CORUSCUS*

Yiming Gao*, Li'ang Li, Saishuai Li, and Youji Wang

Shanghai Ocean University, College of Fishery and Life Science, Huchenghuan Road 999, Lingang New City, Pudong New Area, Shanghai 201306, China

1374078623@qq.com

Nano-sized titanium dioxide (nTiO$_2$) represents the highest produced nanomaterial by mass worldwide and, due to its prevalent industrial and commercial use, it inevitably reaches the marine environment that may pose potential negative impact on mussels (*Mytilus coruscus*). Meanwhile, environmental risk assessment of nTiO$_2$ exposures requires consideration of other important stressors that can take combined effect on nTiO$_2$ pollution in marine coastal habitats such as temperature. To investigate the toxicological effects of nTiO$_2$ on the intestinal health of the *M. coruscus* and byssus performance under ocean warming, firstly, the mussels were exposed to 100μg/L nTiO$_2$ with different crystal structures for 14 days at 20°C and 28°C. The 16S rRNA sequence analysis shown that the intestinal microbial community of mussel was modified and increased the mortality. Also, exposure to nTiO$_2$ changed the relative abundance of Bacteroidetes, Proteobacteria and Firmicutes. The combined stress of warming and nTiO$_2$ increased the risk of mussel being infected with potential pathogenic bacteria. Secondly, explored the effects of single and combined exposure to warming (28°C) and 100μg/L nTiO$_2$ (including food co-exposure) on shell performance of mussels over a 14-day period. The combined effect significantly decreased the mechanical strength of the byssal threads. The mRNA expression levels of mussel foot proteins (mfp-3, mfp-5) and precollagens (preCOL-D, preCOL-P, preCOL-NG) were up-regulated to varying degrees, which impaired the attachment ability and survival of *M. coruscus*. This study provided an important reference for analyzing the physiological and ecological effects of nTiO$_2$ pollution on mussels in the context of global climate change.

DIFFERENTIAL ACTIVATION OF SUBCELLULAR AND MOLECULAR MECHANISMS BY THE AMNESIC SHELLFISH POISONING TOXIN, DOMOIC ACID, BETWEEN THE SLOW-DEPURATOR *PECTEN MAXIMUS* AND THE FAST-DEPURATOR *MYTILUS EDULIS*

José Luis García-Corona[1]*, Juan Blanco[2], Hélène Hegaret[1], Elodie Fleury[1], Adeline Bidault[1], Eva Calvo[1], and Caroline Fabioux[1]

[1]Institut Universitaire Européen de la Mer, Laboratoire des Sciences de l'Environnement Marin (UMR6539 CNRS/UBO/IFREMER/IRD) Technopôle Brest-Iroise 29280, Plouzané, France

[2]Centro de Investigacións Mariñas (CIMA), Xunta de Galicia, Pedras de Coron s/n, 36620 Vilanova de Arousa, Spain

jose.corona@univ-brest.fr

Domoic acid (DA), the phycotoxin responsible for Amnesic Shellfish Poisoning, impacts economically important bivalves, such as scallops, *Pecten maximus*, and blue mussels, *Mytilus edulis*. These two species can accumulate large amounts of DA, with profound differences in their toxin decontamination kinetics; while the former takes months to years, the latter can depurate up to 90% of total DA in a few hours or days. Notwithstanding, physiological reasons for these differences are still unknown. In this work, subcellular and molecular mechanisms potentially involved in these differences were investigated by *in vitro* DA exposition of digestive gland (DG) from both bivalves for three different times (0, 40, and 120 min). The incorporation of DA in the DG of *P. maximus* was nearly 15-fold higher than in *M. edulis* (LC-MS/MS). Using immunohistochemistry, DA was visualized within autophagosome-vesicles dispersed throughout the cytoplasm of digestive cells only in exposed scallops. mRNA level analyses by digital PCR revealed a strong upregulation ($P < 0.05$) of autophagy-related genes in the DA-exposed *P. maximus,* whereas a significant overexpression of genes encoding for membrane solute-carriers (SLC) and glutamate receptors (GR) was found in DA-exposed *M. edulis*. The differential regulation of GR and SLC genes between *P. maximus* and *M. edulis* during DA-exposure could support differences in DA recognizing, as well as entry and/or exit of DA between these two species, while autophagy seems to be behind the long retention of this toxin.

THE IMPACT OF VESSEL NOISE POLLUTION ON THE EARLY RECRUITMENT OF BENTHIC INVERTEBRATES IN TWO DISTINCT SITES IN SAINT-PIERRE AND MIQUELON, FRANCE

Nathália Byrro Gauthier[1]*, Thomas Uboldi[1,3], Réjean Tremblay[1], Tarik Meziane[2], Frédéric Olivier[2], Laurent Chauvaud[3], and Gesche Winkler[1]

[1]Institut des Sciences de la Mer (ISMER), Université du Québec à Rimouski (UQAR), Rimouski, Québec, Canada

[2]Laboratoire de 'Biologie des Organismes et Écosystèmes Aquatiques' (BOREA), UMR 8067 MNHN, SU, UCBN, UA, CNRS, IRD-207 Paris, France

[3]Laboratoire des Sciences de l'Environnement Marin (LEMAR), UMR 3113, Institut Universitaire Européen de la Mer (IUEM), Université de Bretagne Occidentale, Plouzané, France

nathalia.byrrogauthier@uqar.ca

Research on the effect of vessel noise has been showing that it has a double-sided effect, either inducing biological processes such as settlement and metamorphosis of mussels or promoting stressful effects on physiological processes, behaviour, and survival of different benthic invertebrates. The effect of a gradient distance from the vessel sound on benthic invertebrates has been poorly studied.

Thus, the aim of this study was to assess if the distance from vessel sound source as well as the presence of contaminants might impact the dynamic and early-recruitment of *Hiatella arctica* and *Mytilus* spp., in the field in our two sites Saint-Pierre (SP, impacted site) and Miquelon (MI, non-impacted site). For that, a 4-month comparative monitoring was carried out using artificial collectors moored on transects at these sites. Collectors were moored at three distances from the vessel sound speakers (25-30 m, 144-175 m, and 848-890 m). Recruits (pediveligers and post-larvae) were retrieved through artificial collectors. Organisms were sorted, identified, and counted under a stereomicroscope. In addition to recruit collection, environmental parameters (i.e., characterization of trophic environment, temperature, conductivity, etc.) were monitored.

Overall, *Mytilus* spp. were significantly more abundant at 848 m than at 30 m and 144 m in SP. Conversely, recruits were highly abundant close to the sound source at MI. For *H. arctica,* lower abundances were found at 848 m, and abundances were not impacted by the presence of sound, respectively in SP and MI. The response to sound had a species-specific effect on bivalve abundances at different sites but analyses are still being carried out.

GENDER RATIOS OF OYSTERS IN STRESSED ESTUARIES IN SOUTHERN FLORIDA

Stephen P. Geiger

Florida Fish and Wildlife Conservation Commission, Fish & Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, FL 33701

Stephen.Geiger@MyFWC.com

Oyster harvest in Florida occurs in a limited number of estuaries, but oysters provide habitat and other ecosystem services wherever present. Oysters have been monitored as an indicator species for long-term restoration of the Everglades since 2005. Metrics include monthly assessment of water quality, disease, settlement and reproduction and semi-annual surveys for abundance and size.

Gender could not be determined in a high percentage of oysters during winter (December-February) but could be determined in most of the oysters in other seasons. Females represented roughly 2/3 of the oysters for which gender could be determined, beginning at sizes as small as 21 mm. Some mature female oysters were found as small as 24 mm and were common in the data set by 32 mm. The percentage of oysters classified as male declined from 42-57% of oysters less than 30mm to around 10-20% of oysters between 80 and 120 mm, with variability related to season and estuary. In most samples, a small percentage of the largest size class of oysters observed were classified as male. At one site where oysters are commonly extirpated due to low salinity events, oysters of 20-35 mm were almost exclusively classified as male. Oysters below 35 mm that were classified as female were limited to summer and fall seasons when salinities had been tolerable for several months.

OBSERVATION OF BORING CLAMS IN CALICO SCALLOPS FROM CAPE CANAVERAL, FLORIDA, USA

Stephen P. Geiger[1]*, Douglas H. Adams[1], Yasu Kiryu[1], Kyle Luba[1], and José H. Leal[2]

[1]Florida Fish and Wildlife Conservation Commission, Fish & Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, FL 33701

[2]Bailey Matthews National Shell Museum, 3075 Sanibel-Captiva Road, Sanibel, FL 33957

Stephen.Geiger@MyFWC.com

Calico scallop (*Argopecten gibbus*) abundance peaks near the 40 m depth contour, but dense nearshore aggregations can occur and scallops may wash ashore during severe weather. In April of 2022, thousands were observed on two Atlantic coast beaches. Winds were unexceptional and no evidence of cold-water masses nor harmful algal blooms were detected.

Oysters, commonly located along the auricle, were the predominant external fouling biota, suggesting this was a nearshore population. Histological samples were unexceptional with low abundance of cestodes and metacercaria. During dissection, an unusual parasite for scallops was observed in the internal face of the scallop shells, boring clams tentatively identified as juvenile members of the family Pholadidae. Clams were typically located centrally, close to the hinge. Boring clams occurred in 74% of the scallops with a range of 1 to 18 detected. Visible siphon holes on the external surface of the shell corresponded with most of the internal clam scars. Most clams were in the left valve but were also present in the right (benthic facing) valve in two severely infected scallops. Scars similar to those created by Spionid worms of the genus *Polydora* were observed in 78% of the scallops, most commonly located near the margin of either valve. The boring clams are an unusual parasite for calico scallops and a majority of the scallops observed were infected, but in over half the stranded scallops, two or fewer clams were observed, and are not likely to have been the primary cause of the stranding event.

TRIPLOID PACIFIC OYSTERS EXPERIENCE ENHANCED MORTALITY FOLLOWING MARINE HEATWAVES

Matthew N. George[1]*, Olivia Cattau[1], Mollie Middleton[2], Delaney Lawson[1], Brent Vadopalas[1], Mackenzie Gavery[2], and Steven Roberts[1]

[1]University of Washington, School of Aquatic & Fishery Sciences, 1122 NE Boat St, Seattle, WA

[2]National Oceanic and Atmospheric Administration, Environmental and Fisheries Sciences Division, Northwest Fisheries Science Center, National Marine Fisheries Service, 2725 Montlake Blvd E, Seattle, WA, 98112

mngeorge@uw.edu

Triploid oysters (3n) exhibit reduced gonad development, enhanced growth, and increased marketability with respect to diploids (2n); however, a growing body of evidence suggests that triploids can experience reduced survivorship within variable environments (‘triploid mortality’). The effect of polyploidy on environmental stress tolerance was investigated using the response of the Pacific oyster, *Crassostrea gigas,* to marine heatwaves as a model system. Adult diploid and triploid oysters were exposed to elevated seawater temperature (single stressor; 30°C), elevated temperature in combination with a desiccation stress (multiple stressor; 30°C + emersion at 44°C for 6h), or a control (17°C). No difference in mortality rate was observed across ploidy following single stress exposure; following multiple stressor exposure, triploids exhibited metabolic depression, a significant reduction in ctenidium $Na+/K+$ ATPase activity, and a 2.5-fold greater mortality rate than diploids (36.4% vs. 14.8%). An in-depth analysis of the ctenidium transcriptome identified ploidy-level differences in gene expression, including the absence of key genes associated with heat tolerance and mitochondrial function in triploids. Functional enrichment analysis of ploidy-specific gene sets identified that biological processes associated with metabolism, stress tolerance, and immune function were overrepresented within triploids. Results demonstrate that polyploidy impacts the transcriptional response of Pacific oysters to environmental stress and have important implications for food security within future climate scenarios as triploidy becomes a popular tool within marine aquaculture.

EVALUATING WHETHER A MODIFICATION TO COMMERCIAL SEA SCALLOP DREDGES CAN REDUCE BYCATCH AND INCREASE CATCH EFFICIENCY

Jennifer Gius[1]*, Jason Morson[1], Eleanor Bochenek[1], Douglas Zemeckis[2], and Joseph O'Brien[1]

[1]Haskin Shellfish Research Laboratory, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349

[2]Rutgers Cooperative Extension, 1623 Whitesville Road, Toms River, NJ 08755

jgius@hsrl.rutgers.edu

Atlantic sea scallops (*Placopecten magellanicus*) represent a valuable commercial fishery in the northeast US. Although current scallop dredge configurations allow some bycatch to escape, non-target species are still retained. In this study, a modification was made to the current legal dredge to allow changing the angle of the cutting bar relative to the seafloor. This modification was intended to create greater turbulence behind the cutting bar and lead to small sea scallops and some bycatch being ejected from the twine top before entering the chain bag. To evaluate how adjustments made to the angle of the modified cutting bar impacted bycatch and catch efficiency, paired tows (n=149) were conducted with the modified dredge and a standard commercial dredge in the US Mid-Atlantic and on Georges Bank between 2019 and 2022. Four angles were tested: 15-, 30-, 45-, and 60-degrees. With the cutting bar set at either 45- or 60-degrees, there was a statistically significant reduction (up to 87%) in bycatch of almost every commonly caught bycatch species, including economically important species like summer flounder and monkfish. There was also a significant reduction (up to 61%) in the amount of debris (shell, sponge, sand dollars) in the modified dredge compared to the standard dredge. In addition, there was a small (~10%) but statistically significant reduction in scallop catch. However, some fraction of these unretained scallops were small (<100mm) and would have been discarded anyway. While preliminary, these results suggest the modified scallop dredge could significantly reduce bycatch and catch sorting time.

HARMFUL ALGAL BLOOMS AND OYSTERS: HARM IS MULTIFACETED

Patricia M. Glibert

University of Maryland Center for Environmental Science, Horn Point Laboratory, PO Box 775, Cambridge, MD 21613

glibert@umces.edu

Harmful algae and associated harmful algal blooms (HAB) are increasing in frequency, geographic area and duration in many parts of the world, often associated with aquaculture. The term "harmful algae" is operational, rather than technical. Harmful algae include those species of microalgae that produce toxins that cause human health impacts or alter aquatic ecosystems in negative ways. The term also encompasses those that are not technically "algae," but rather are bacteria-like, the Cyanobacteria HAB (CyanoHAB), as well as those cells that may not depend on photosynthesis for their nutrition, but function as grazers of other microscopic particles. Some HAB do not produce toxins but may be harmful due to their high biomass production, which, in turn, can result in hypoxia. Thus, routes of exposure to filter feeders can be direct, via consumption of toxin, or indirect through habitat degradation or shifts in species composition. HAB may thus affect commercial products, but may also disrupt ecosystems, with ramifications for early life stages and recruitment.

This talk will introduce the major toxins that can accumulate from ingestion of harmful algae, and describe some of the more subtle negative effects of different types of HAB. Using Chesapeake Bay as an example, how improved predictive capability of several types of HAB can be applied in applications of oyster aquaculture and in oyster restoration will be described. Models are advancing and can be used not only in operational predictions but also in scenario development of effects of future climate changes.

USE OF SEAWEEDS TO PROTECT AQUACULTURED BIVALVES AGAINST CLIMATE CHANGE CO-STRESSORS AND HARMFUL ALGAL BLOOMS

Christopher J. Gobler*, Laine H. Sylvers, and Michael H. Doall

Stony Brook University, School of Marine & Atmospheric Sciences, 239 Montauk Highway, Southampton, NY 11968

christopher.gobler@stonybrook.edu

Ocean acidification (OA), hypoxia, and harmful algal blooms (HAB) are significant threats for bivalves in coastal zones. While the open ocean will acidify over the coming decades, a multitude of coastal processes including eutrophication, upwelling, and river discharge can cause ephemeral and seasonal bouts of coastal ocean acidification that can create levels of dissolved oxygen pH and $p\mathrm{CO}_2$ that are not expected in open waters until late next century. In parallel, the impacts of HAB on aquaculture have been expansive in recent decades and can range from causing slowed growth and mortality to contaminating bivalves with biotoxins and thereby restricting sale of product. While there have been decades of study regarding the mitigation of HAB and OA, many approaches have had negative consequences for bivalves and/or ecosystems, work at temporal or spatial scales irrelevant to bivalve aquaculture or have been ineffective. One exception has been the aquaculture of seaweeds. During the past decade, our group has documented the ability of temperate seaweeds including sugar kelp (*Saccharina latissima*), Irish Moss (*Chondrus crispus*), *Gracilaria tikvahiae, Porphyra* spp., and *Ulva* spp., to mitigate both ocean acidification and HAB. Highlights have included the ability of fast-growing seaweeds, *S. latissima*, and *Ulva* sp., to cause the lysis of HAB species and to transform acidified waters to supersaturated with regard to aragonite, leading to significantly increased growth rates of bivalves. Collectively, these studies demonstrate that the co-culture of bivalves with seaweeds can create a 'halo effect' around bivalves to mitigate OA and HAB.

THE COLLABORATIVE BENEFITS OF THE NEFSC SEA GRANT CONNECTION: AN EXAMPLE INVESTIGATING POOR GROWTH OF HARD CLAMS IN NEW JERSEY

Zachary Gordon[1,2]*, Meghana Parikh[1], Dale Parsons[3], Eric Robillard[1], Kira Dacanay[4], Bob Schuster[5], Bella Wasserman[6], and Gary Wikfors[1]

[1]NOAA Fisheries, Northeast Fisheries Science Center, 212 Rogers Ave, Milford, CT 06460

[2]Connecticut Sea Grant, University of Connecticut, 1080 Shennecossett Rd, Groton, CT 06340

[3]Parsons Seafood, 468 S Green St, Tuckerton, NJ 08087

[4]New Jersey Department of Environmental Protection, Fish and Wildlife Bureau of Shellfisheries PO Box 418, Port Republic, NJ 08241

[5]New Jersey Department of Environmental Protection, Bureau of Marine Water Monitoring, PO Box 405, Stoney Hill Road, Leeds Point, NJ 08220.

[6]The Hackley School, 293 Benedict Ave, Tarrytown, NY 10591

zachary.gordon@uconn.edu

The NOAA Fisheries Milford Lab has a strong history of working with industry members to solve issues related to shellfish aquaculture. Meanwhile, Sea Grant has built strong networks throughout the east coast using extension to drive advancements between research, industry, and regulators in the shellfish aquaculture industry. Through the Sea Grant Regional Aquaculture Liaison, there has been a concerted effort over the last year to create better connections between the NMFS aquaculture program and the Sea Grant aquaculture extension network to leverage new partnerships and new funding sources to promote research for sustainable shellfish aquaculture. One project that has come from this effort is an investigation into the slow growth and poor survivorship of hard clams in certain areas of New Jersey.

The Milford Lab is collaborating with growers, and state regulators in New Jersey to provide more information to understand the decreasing productivity of hard clams in Little Egg Harbor and nearby estuaries. Sampling has begun this past summer collecting water temperature and hard clam condition index. Funding secured from the Northeast SARE program will allow for an expansion of sampling to a second site, collection of additional environmental variables, and shell age analysis of aquacultured and wild clams. This data combined with existing historical data will lead to better understanding of the growth dynamics of hard clams in New Jersey, and may provide lessons for other regions in the Northeast experiencing hard clam declines.

ANALYSIS OF STRESS ASSOCIATED WITH INTER-SITE TRANSPORT OF THE EASTERN OYSTER PRODUCTION

Camille Gravel-Brunet*[1], Lisandre Gilmore-Solomon[2], and Réjean Tremblay[3]

[1]Université du Québec à Rimouski, Institut des Sciences de la Mer de Rimouski, 310 All. des Ursulines, Rimouski, QC G5L 2Z9, Canada

[2]Cégep de la Gaspésie et des Îles, 5 Chem. de la Piscine, L'Étang-du-Nord, QC G4T 3X4, Canada

[3]Université du Québec à Rimouski, Institut des Sciences de la Mer de Rimouski, 310 All. des Ursulines, Rimouski, QC G5L 2Z9, Canada

camille.gravel-brunet@uqar.ca

The eastern oyster (*Crassostrea virginica*) benefits a value-added and well-established market in Canada. In Québec, most of the production is realized in the Magdalen Islands. The northern limit distribution of eastern oysters is observed in the Gulf of St. Lawrence in New Brunswick (47°N) explaining its natural absence in the Magdalen Islands. Thus, the production is supported by importation from the Maritime provinces, as natural reproduction does not support important recruitment success and spat collection; however, since the start of this activity, episodes of mortality have been observed in the year following the transfer. This mortality seems not associated with pathogens, as no disease has been identified. That mortality may be associated to transport. The objective is to find physiological tools to quantify stress levels submitted for the development of best management practices.

The projects consisted of nine oyster groups for three origins (control and two production sites), two sizes (small and large) and two periods (before and after spawning) were compared. To characterize the oyster condition and estimate their vitality level, different physiological indicators were used: valvometry, condition index, the level of resistance to air exposure, the measures of oxygen consumption, the filtration rates, and the global accumulation of energy reserves (glycogen, lipids, and proteins). The growth and mortality rate of each group was monitored from the beginning of the transfer until the end of the first wintering. Mortality will be presented in relation to the viability and energy status of the group of oysters following interprovincial transport.

SPATIALLY-EXPLICIT OYSTER FILTRATION SERVICES IN THE HUDSON RIVER ESTUARY: RESEARCH TO HELP GUIDE RESTORATION AND PUBLIC UNDERSTANDING

Matthew Gray*[1], Damian Brady[2], Ann Fraioli[3], Matt Hare[4], Sean Kramer[5], and Kristin Schreiber[3]

[1]University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Rd., Cambridge, MD 21613, USA

[2]University of Maine, Darling Marine Center, 193 Clarks Cove Rd., Walpole, ME 04573, USA

[3]Billion Oyster Project, New York Harbor School, 550 Short Ave., New York, NY 10004, USA

[4]Cornell University, Department of Natural Resources, 226 Mann Dr., Ithaca, NY 14853, USA

[5]Norwich University, College of Science and Mathematics, Department of Mathematics, 158 Harmon Dr., Northfield, VT 05663, USA

mgray@umces.edu

After Euroamerican settlers arrived in the Hudson River Estuary (HRE), oyster populations and the valuable ecosystem services they provide declined rapidly. Environmental advocacy organizations encourage oyster restoration to revive ecosystem health but the actual ecological outcomes after such efforts remain unclear.

This project examines the filtration services of oysters in the HRE. The New York Hydrodynamic Observing and Predicting System modeling platform was used to simulate how oyster populations would interact with the overlying water. Low, moderate, and high Hudson River flows under warm conditions (August) were selected to examine how river forcing affected maximum oyster filtration services. Habitat boundaries and oyster densities across and within subregions of the HRE were estimated from historic survey maps and previously published studies.

Model results suggest oysters would filter a small fraction of the entire HRE if restored to historic densities; however, populations in some subregions (e.g., Jamaica Bay) would play a much larger role, filtering >50% of the water body within a single residence time. Restoring these subregions first may improve local water quality. An important part of this project was the development of an interactive website and curriculum for students to learn about oyster filtration and model development. This website can also be explored by the greater public to understand ecological outcomes of future restoration in the HRE.

THE EFFECTS OF PROBE AND GDNA INSERT LENGTH ON THE DE NOVO ASSEMBLY AND CAPTURE EFFICIENCY OF EXPRESSED EXOME CAPTURE SEQUENCING (EECSEQ)

Jacob M. Green* and Jonathan B. Puritz

University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd, Kingston, RI 02881

gree9242@uri.edu

Genomic sequencing of non-model organisms has transformed the way conservation ecologists and evolutionary biologists study the marine environment. Understanding the basis of local adaptation in wild populations still presents a challenge because of the cost associated with sequencing many individuals across biologically relevant regions of the genome. Additionally, high rates of genetic polymorphism within non-model populations pose challenges in accurately assembling genomic reads. Expressed Exome Capture (EecSeq) presents a unique approach to these challenges through selective enrichment of expressed genomic DNA (gDNA) using capture probes developed from mRNA. EecSeq can be applied to any organism if loci can be efficiently assembled directly from capture reads. To optimize the EecSeq molecular and bioinformatic protocols, this study quantifies the role of probe and gDNA insert length as well as tests *de novo* assembly programs. EecSeq probes and gDNA libraries were created from 50 individuals in 5 subpopulations of oysters within that State of Rhode Island. Both EecSeq probes and gDNA were fragmented to approximately 150 and 300 bp to test the effects of probe and read length on capture specificity and sensitivity. Captured reads were mapped to the eastern oyster reference genome and mapping statistics were used to calculate capture efficiency. Two assembly programs (Oases, Trans-ABySS) were utilized to build oyster *de novo* exomes. To compare these exome assemblies N50 values, annotation rates, BUSCO, and read mapping were used. This study significantly optimizes the approach to implementing EecSeq to genetically assess non-model populations.

DEVELOPING AND VALIDATING NOVEL MICROSATELLITE MARKERS IN THE RED DEEP-SEA CRAB, *CHACEON QUINQUEDENS*

Shadaesha Green[1]*, Louis Plough[2], and J. Sook Chung[1]

[1]University of Maryland Center for Environmental Science, Institute of Marine and Environmental Biology, 701 E Pratt St, Baltimore, MD 21202

[2]Horn Point Laboratory, University of Maryland Center for Environmental Science, P.O. Box 775, Cambridge, MD 21613

shadaesha.green@noaa.gov

The red deep-sea crab, *Chaceon quinquedens*, is a cold-water decapod found along the continental shelf and slope of the eastern United States. Since the early 1970s, the red deep-sea crab has supported a productive commercial fishery along the eastern US from the Gulf of Maine to Cape Hatteras, North Carolina; however, the genetic structure of red deep-sea crab populations needs to be better known, including whether distinct stocks exist and over what spatial scales. Furthermore, no nuclear genetic markers specific to *C. quinquedens* are available for examining population differentiation. To this end, the current study aimed to develop *C. quinquedens* microsatellite markers. Over 14 million paired-end reads were generated and assembled into 263,435 contigs >80bp, which were input using QDD 3.1 to identify microsatellite repeat motifs. Three of 14 scorable markers were first selected to investigate the genetic structure of *C. quinquedens* populations within three management areas (n=88). An average of 21 alleles were identified across the three loci. The mean expected (H_e) and observed heterozygosity (H_o) were 0.879 and 1, respectively, thus indicating high levels of genetic diversity for these three populations or management areas. Analysis of genetic differentiation among populations revealed a mean F_{ST} value of 0.035, indicating subtle but significant genetic structure among populations. Overall, the development of 14 novel, polymorphic microsatellite markers for the red deep-sea crab provides much-needed genetic resources for managing the species and should facilitate future, larger analyses of genetic diversity and stock structure in red deep-sea crab.

EFFECT OF BIOFOULING CONTROL AND STOCKING DENSITY ON MICROCLIMATE IN OFF-BOTTOM OYSTER CULTURE GROW-OUT BAGS: OYSTER PERFORMANCE

Julianne M. Grenn* and William C. Walton

Virginia Institute of Marine Science at the College of William & Mary, 1309 Greate Road, Gloucester Point, VA 23062

jmgrenn@vims.edu

This ongoing project investigates the degree to which farming practices may contribute to sudden spring/summer unexplained mortality events of eastern oysters, *Crassostrea virginica*. This current work addresses if biofouling control (air-dried vs. non-air-dried) and oyster stocking density (high, normal, and empty) decisions affect the microclimate (water quality parameters) inside grow-out bags, and if these differences correlate with oyster performance.

In an ongoing field experiment at a commercial oyster farm in Virginia, floating oyster bags were deployed in May 2022 in a fully-factorial 3 x 2 design (3 relative stocking densities x 2 biofouling control treatments) with 6 replicates/treatment. In a fall 2022 sampling, a significant interaction effect of stocking density and biofouling control on oyster performance was observed in whole wet weight, length, width, height, and dried shell and tissue weight ($p \leq 0.02$ for all). Oysters in highly-stocked, non-air-dried bags had a significantly lower whole wet weight, length, and dried shell weight than oysters in any other treatment. Oysters in normally stocked non-air-dried bags had the largest width and height, which significantly differed from the other groups. Dried tissue weight was highest in air-dried treatments, regardless of stocking density, followed by normally stocked non-air-dried bags, then lowest in highly stocked non-air-dried bags.

Results from this study will be combined with an assessment of the microclimates within these growing containers to determine if there is any correlation between these responses and if any of the treatments are associated with high mortalities in spring/summer 2023.

OYSTER FARMING RESILIENCE INDEX

Russell Grice[1]*, LaDon Swann[2], Steve Sempier[2], Tracie Sempier[2], and Stephen Deal[2]

[1]Mississippi Alabama Sea Grant Consortium, Auburn University Educational Complex, 21541 Coastal Gateway Boulevard, Gulf Shores, AL 36542

[2]Mississippi Alabama Sea Grant Consortium, 703 East Beach Drive, Ocean Springs, MS 39564

rtg0010@auburn.edu

Commercial oyster farming has many challenges even during the best of times. To increase the opportunity for success and recovery during extraordinary events the Oyster Farming Resilience Index (OFRI) was developed recently by a team at the Mississippi Alabama Sea Grant Consortium (MASGC). The OFRI is a self-assessment tool developed for oyster farmers to serve as a simple and inexpensive method of predicting if individual businesses are prepared to maintain operations during and after disasters. In recent years, the industry has experienced everything from hurricanes and significant environmental events to the COVID-19 pandemic, which closed restaurants for an extended period of time.

The OFRI is designed to be completed by farmers; however, Sea Grant staff are willing to meet individual farmers to assist in completing the OFRI and all conversations are confidential. When the OFRI is used, each farm should consider the farm's level of preparedness for both large- and small-scale events. Being able to withstand and adapt to events before they happen has become a focal point for businesses and industries. Recognizing the vital role that planning, reparation and collaboration play in developing and executing strategies is essential in building a resilient business. This brief presentation will cover the major sections of the tool and provide contact information for those that would like to learn more or have questions about any of the indices.

A MULTI-STUDY ANALYSIS OF GUT MICROBIOME DATA FROM THE BLUE MUSSEL (*MYTILUS EDULIS*) EMPHASIZES THE METHODOLOGICAL IMPACT OF GUT VOIDANCE ON BIOLOGICAL INTERPRETATION

Tyler W. Griffin[1]*, Mya A. Darsan[2], Hannah I. Collins[1], Bridget A. Holohan[1], and J. Evan Ward[1]

[1]University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Road, Groton, CT 06340

[2]University at Albany, Department of Biological Sciences, 1400 Washington Avenue, Albany, NY 12222

tyler.griffin@uconn.edu

The microbiomes inhabiting the stomachs and digestive glands of suspension-feeding bivalves have been a topic of interest for a decade. Although separate research efforts continue advancing the field and informing future experiments, the most appropriate way to compare data between projects is to process raw sequence files in one bioinformatic effort. Toward that end, the goal of this project was to analyze gut microbiome data from the blue mussel (*Mytilus edulis*) across several studies produced by members of one research group over eight years. In total, 167 samples of raw paired-end reads from five separate publicly available and two unpublished datasets were loaded into the analysis pipeline and processed together to look for global trends. The selected data represented a broad diversity of samples collected during an array of years and seasons by three lead authors and were generated from a breadth of experimental treatments and sampling methods. The primary trend in the results was a clear differentiation between microbial communities from mussels that had been allowed to void their gut during a no-food period prior to dissection and those from mussels that had not. This finding supports the developing paradigm about the difference between transient microbes ingested with food and then voided shortly afterward and resident microbes that reside permanently in the digestive tissues. Ultimately this effort highlights the importance of performing secondary multi-study analyses of raw microbiome sequence data, and of tailoring experimental designs and sampling schemes to match the specific experimental questions being addressed in future work.

INCORPORATING KELP AND OYSTER CO-CULTURE AT SCALE

Kimberly Grindle

Islesboro Oyster Co., PO Box 48, Islesboro, ME 04848
hello@islesborooyster.com

Islesboro Oyster Company (IOC) is a small, mother-children run business in mid-coast Maine. It currently operates a little more than four acres of leased area to co-culture eastern oysters (*Crassostrea virginica*), sugar (*Saccharina latissima*), skinny (*Saccharina angustissima*) and winged (*Alaria esculenta*) kelp, and sea urchin (*Strongylocentrotus droebachiensis*) near Islesboro Island, 3-miles from the mainland. Over the past three years, the IOC has expanded production from 30,000 oysters in year one to a currently several hundred thousand and 1800' of sugar kelp line to 10,500' of line. The oysters are grown using floating bags and cages. Kelp is grown on suspended horizontal grow lines where they have inter-cropped the kelp and oysters. There have been noticeable impacts of a cleaner, stronger shell and a meatier oyster since diversifying into seaweed.

The introduction of sugar kelp onto the oyster farm has allowed diversifications both in operations and income. The IOC believes the integration is synergistic to both crops. How small-scale oyster growers can commercially scale and incorporate kelp with minimal adaptation will be discussed. Additionally, kelp has been a major point of attraction on the farm, drawing national attention through news reports and empowering the youngest employee, Gaby (age 15), to take ownership over a portion of the business. Integrating seaweed and shellfish cultivation has opened opportunities for education and engagement with local youth and the community at large – boosting awareness of the IOC brand and resulting in a net positive business decision.

GENOMIC AND GENETIC INVESTIGATIONS OF THE BAY SCALLOP POPULATION IN THE PECONIC BAY, NEW YORK

Denis Grouzdev[1]*, Emmanuelle Pales Espinosa[1], Madison Muehl[1], Sarah Farhat[1,2], Isabelle Boutet[3], Arnaud Tanguy[3], Stephen Tettelbach[4], Harrison Tobi[4], and Bassem Allam[1]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

[2]Institut Systématique Evolution Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, 57 rue Cuvier, CP 50, 75005 Paris, France

[3]Station Biologique de Roscoff, CNRS/Sorbonne Université, Place Georges Teissier, 29680 Roscoff, France

[4]Cornell Cooperative Extension of Suffolk County, 423 Griffing Avenue, Suite 100 Riverhead, New York 11901

denis.gruzdev@stonybrook.edu

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.

Genetic and genomic analyses of bay scallop populations can provide insight into the population structure, gene flow, larval transport of this species, host-pathogen interactions, and mechanisms of resistance to infections. Such information can be used to identify core populations, devise effective management strategies, and identify areas for potential conservation and restoration efforts. Data from RNA-Seq, RAD-Seq, and mitochondrial DNA sequencing have been used to identify the population structure of New York bay scallops. The study found that the bay scallop has seen a change in population structure in New York over the past 25 years by increasing the representation of southern lineages of *Argopecten irradians*. In addition, the results indicate evidence of genetic admixture in the New York bay scallop populations. Recent hybridization between various lineages or subspecies that led to the formation of the current population cannot be ruled out. 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.

RELATIONSHIPS BETWEEN COMMUNITY STRUCTURE AND JUVENILE BLUE CRAB ABUNDANCE IN STRUCTURALLY COMPLEX NURSERY HABITATS IN THE YORK RIVER, CHESAPEAKE BAY

Nihal Guennouni*, A. Challen Hyman, Alison Smith, Michael Seebo, Gabrielle Saluta, and Romuald N. Lipcius

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

nguennouni@vims.edu

Nursery habitats are critical to the long-term stability of commercially exploited fisheries. Historically, nursery habitat quality has been connected to structural complexity and environmental variables such as water chemistry; however, less attention has been attributed to the biological components, such as community structure, which may modify the quality of a nursery habitat. The blue crab, *Callinectes sapidus,* is a commercially and ecologically important species that utilizes salt marsh nurseries in early life stages. This study evaluated the hypothesis that community structure varies with the abundance of juvenile blue crabs in salt marsh habitats along the environmental gradient associated with the axis of the York River. Between August and October of 2021, marsh habitat sites were sampled using modified flume nets. Contents of each flume net were identified to the lowest taxonomic grouping feasible and counted, while all juvenile blue crabs were counted and measured for carapace width. Principal Component Analysis was conducted on community assemblages, excluding blue crabs, to extract relevant patterns in community structure. The first two Principal Components, turbidity and river location were subsequently used as predictors for juvenile blue crab abundance in a generalized linear model. Community structure and juvenile blue crab abundance were strongly associated with the second principal component, such that crab abundance decreased with distance from the mouth of the river. Although correlative, the results suggest that blue crab abundance is linked to an aspect of community structure (e.g., prey availability) or that both phenomena are driven by the same biotic and environmental factors.

SHELLFISH AQUACULTURE IN THE GENOME ERA

Ximing Guo

Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, New Jersey 08349

xguo@rutgers.edu

Agriculture has a long history of domestication and genetic improvement. Aquaculture, as an emerging contributor to food security, is relatively new and has relied on wild seed for much of its history. Wild seed are unreliable and lack characteristics desired for aquaculture such as adaptation to high-density culture conditions, fast growth, disease resistance, and uniformity. Shellfish species are cultured in open waters and face more environmental stress than terrestrial animals. Climate changes such as warming and acidification of world oceans present new challenges to shellfish and shellfish aquaculture, making diseases and mortalities more frequent and intense. Genetic improvement is central for the sustainable development of shellfish aquaculture under these challenges.

The development of hatchery technologies in 1960s made genetic improvement of molluscan shellfish possible. Now over 30 species of molluscs are produced in hatcheries and subjected to some degrees of genetic improvement. Selective breeding has produced disease-resistant and fast-growing varieties. Triploids have become an important part of oyster farming. Shellfish biology entered the genome era with the sequencing of the oyster genome in 2012 and since then, genomes of all major cultured shellfish have been sequenced. Genomic studies yielded rich information about genes and molecular mechanisms underlie shellfish development, function, immunity, and physiology, but more efforts are needed to translate genomics to actual improvements for shellfish aquaculture. Genomic tools such as high-density SNP arrays may enable genomic selection and transform shellfish aquaculture. Such a transformation is dependent on strong partnership between academia and the shellfish aquaculture industry.

OUTCOMES AND FUTURE DIRECTIONS OF THE SUPPORTING OYSTER AQUACULTURE AND RESTORATION PROGRAM (SOAR)

Boze Hancock[1], Robert Jones[2], Aaron Kornbluth[3], Zachary Greenberg[3], Bob Rheault[4], Jordanna Barley[6]*, Rebekah Borgert[2], and Christina Popolizio[2]

[1]The Nature Conservancy, C/O URI Grad. School of Oceanography, 215 South Ferry Rd., Narragansett, RI, 02882

[2]The Nature Conservancy, Worldwide Office, 4245 N. Fairfax Dr., Arlington, VA, 22203

[3]The Pew Charitable Trusts, 901 E Street NW, Washington, DC, 20004-2008

[4]East Coast Shellfish Growers Association, 1623 Whitesville Rd., Toms River, NJ, 08755

[5]Pacific Coast Shellfish Growers Association, 120 State Ave. NE, #142 Olympia, WA, 98501

[6]University of Massachusetts Amherst, 160 Holdsworth Way, Amherst MA, 01003

[7]The Nature Conservancy, Massachusetts Chapter, 20 Ashburton Place Suite 400, Boston, MA 02108

jordanna.barley@tnc.org

In response to the Covid-19 impact on the shellfish industry, The Pew Charitable Trusts and The Nature Conservancy formed a partnership to map opportunities for linking growers with excess oysters to restoration sites on a national scale. In October 2020, the Supporting Oyster Aquaculture and Restoration (SOAR) program was launched in partnership with growers, industry associations, state regulatory agencies, universities, NGO, NOAA, and the USDA Natural Resource Conservation Service. The program features two components, oyster purchases for restoration and a Shellfish Growers Resiliency Fund. The program has generated enormous cooperation and support from all participants.

Approximately $2 million was secured for the oyster purchase program across six northeastern states plus Washington. Biosecurity risks were minimized by limiting transport distance and enacting strict pathology testing and biofouling mitigation. Because of the rapid response needed due to Covid, only existing permitted restoration sites were used by partnering with state, tribal nations, and NGO restoration managers. Monitoring parameters were provided to partners to incorporate into their existing monitoring plans. 3.5 million oysters from 125 growers, benefiting 450 jobs and supporting the creation or enhancement of nearly 40 acres of reef.

The Shellfish Growers Resiliency Fund awarded over $1.25M across 16 coastal states through 36 awards that addressed the intersection of aquaculture and conservation. Themes included: diversity, equity, and inclusion in the industry; diversifying products and marketing; encouraging grower participation in marine conservation; and enhancing farm sustainability. Program successes and challenges will be described, as well as a look ahead to SOAR 2.0.

THREE CRYPTIC SURFCLAM TAXA IN SOUTHERN NEW ENGLAND: GENETIC DIFFERENCES, BIOGEOGRAPHY, AND RELEVANCE FOR AQUACULTURE

Matthew Hare* and Hannah Hartung

Cornell University, Department of Natural Resources and the Environment, 205 Fernow Hall, Ithaca, NY 14853

mph75@cornell.edu

Morphologically cryptic taxa are common in marine systems, and when they occur in a commercially valuable species it can frustrate hatchery management or fisheries regulation. In southern New England there is an offshore fishery for *Spisula solidissima solidissima* as well as growing interest in surfclam aquaculture. The “southern surfclam,” *S.s. similis*, also supported a fishery in Long Island Sound, New York, and occurs nearshore south of Cape Cod. Crypsis between these two nominal subspecies may have confounded some published analyses of inshore/offshore life history variation. Recent genomic analyses and an absence of hybrids in sympatry confirm that *S. solidissima* and *S. similis* are full species. In addition, two evolutionarily divergent cryptic taxa were discovered within *S. solidissima*. The commercially fished taxon (B) occurs alone on the continental shelf and in Cape Cod Bay, but overlaps with and is numerically dominated by a genetically distinct taxon (A) nearshore in southern New England. Some A-B hybrids occur in the overlap zone, but their low frequency today and the substantial A-B genomic divergence suggests that these sister taxa rarely interbred for many generations. The genomic patterns supporting full species status for *S. solidissima* and *S. similis* will be presented, and the patterns of gene flow connectivity within all three taxa discussed. An update on an efficient molecular assay distinguishing all three taxa is in development will be provided.

THREE CENTURIES OF INCREASING GROWTH RATES OF A LONG-LIVED CLAM (*ARCTICA ISLANDICA*) ON THE WESTERN MID-ATLANTIC CONTINENTAL SHELF (US)

Kathleen M. Hemeon[1,2], Eric N. Powell[1], John M. Klinck[3], Roger Mann*[4], and Sara M. Pace[1]

[1]Gulf Coast Research Laboratory, University of Southern Mississippi, 703 E Beach Dr, Ocean Springs, MS 39564

[2]US Fish and Wildlife Service, Abernathy Fish Technology Center, 1440 Abernathy Creek Rd, Longview, WA 98632 (current affiliation)

[3]Old Dominion University, 5115 Hampton Blvd, Norfolk, VA 23529

[4]Virginia Institute of Marine Science, College of William and Mary, 1370 Greate Rd, Gloucester Point, VA 23062

rmann@vims.edu

The US Mid-Atlantic supports the important fishery of *Arctica islandica*. This species is extremely slow growing and long-lived, characteristics that may make this species particularly vulnerable to fishing pressure and climate change. Two populations of *A. islandica* from Georges Bank and off Long Island on the US continental shelf were evaluated for age and growth relationships. Growth rates have been increasing at Georges Bank and Long Island for the past three centuries. Growth rates at Long Island have been accelerating and have exceeded those at Georges Bank since the 1980s. Growth rates from this study support previous research that this species is sexually dimorphic, and females grow faster than males within a population post-maturation. Positive growth index periods at both sites may be synchronous with 32-y harmonics of the Atlantic Multi-Decadal Oscillation. A modification to the traditional Tanaka growth model proved the best-fit growth model to not only each population, but also to birth-year cohorts. Both the classic and modified Tanaka models used in this study are vast improvements over the von Bertalanffy models currently applied to this species in assessment and population dynamics models. Increasing growth rates over time resulted in fewer years of reproduction prior to recruiting to the fishery as *A. islandica* are reaching fishery size in an increasingly short period of time. The impact that reduced years of reproduction has on *A. islandica* stock resiliency is yet unknown.

MITIGATION STRATEGY FOR HORSESHOE CRAB IMPINGEMENT BY FLORIDA POWER PLANT

Berlynna Heres*[1], Jane Brockmann[2], Claire Crowley[1], and Ryan Gandy[1]

[1]Florida Fish and Wildlife Conservation Commission: Fish and Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, FL 33701

[2]University of Florida, Department of Biology, 220 Bartram Hall, P.O. Box 118525, Gainesville, FL 32611-8525

Berlynna.Heres@myfwc.com

Impingement of marine life is a persistent problem at energy plants throughout the world. In 2014, the Duke Energy Cape Canaveral Energy Center (Formerly Florida Power and Light; CCEC) on the Indian River Lagoon (IRL) engineered and tested a solution to reduce the impingement of American horseshoe crabs (*Limulus polyphemus*) while allowing manatees access to existing thermal refugia and the unobstructed passage of sea turtles and fuel barges. This project was approached by CCEC with active problem solving to derive a solution, not as a traditional research project. Monitoring of horseshoe crab impingement began after a prototype fence was installed in November 2014. On average 72,663 horseshoe crabs per year were entrained in this facility while the prototype fence was present. In 2017, CCEC engineered and installed a permanent submerged deterrent wall across the intake canal that achieved the goal of reducing horseshoe crab impingement and allowed the free movement of manatees, sea turtles, and fuel barges. Continued monitoring of the intake system and wall maintenance shows horseshoe crab impingement has been reduced by 98%, to an average of 757 horseshoe crabs impinged per year. This engineering accomplishment illustrates the effectiveness of well-designed barriers in reducing horseshoe crab entrainment and impingement without disrupting operations or required access for manatees to thermal refugia.

SHRIMP SCAMPI: A CITIZEN'S SCIENCE PROJECT - EDUCATING ABOUT HORMONE DISRUPTORS SUCH AS METALS AND GLYPHOSATE USING FOLDSCOPES

Iris Hernandez[1], Caroline Warren[2]*, Miriam Alcivar-Arteaga[1], Jennifer Warren[1], Cesar Diaz[1], and Acacia Alcivar-Warren[1,2,3]

[1]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada Casa 17, El Eden, Quito, Ecuador

[2]ONE HEALTH Epigenomics Educational Initative (OHEEI), Environmental Genomics Inc., P.O. Box 196, Southborough, MA 01772, USA

[3]Rotary Club of Southborough, P. O. Box 391, Southborough, MA 01772, USA

environmentalgenomics.warren@gmail.com

As part of the OHEEI international initiative, 'Shrimp Scampi' was initiated by Massachusetts (MA) students from Algonquin Regional High School in Northborough, MA to assess the adverse health effects to the environment, wildlife, pets, seafood, and people, caused by the antimicrobial and herbicide Glyphosate, glyphosate-based herbicides, and other endocrine disrupting chemicals (EDC) like metals and Bisphenol A (BPA). These EDC appear associated with obesity, diabetes, non-Hodgkin's lymphoma, non-alcoholic fatty liver disease, antimicrobial resistance, neurodevelopmental syndromes, congenital malformations, and neural tube defects.

Shrimp is the favorite seafood of Americans, most of the shrimp consumed is imported, causing a yearly ~US$4.5 billion trade deficit. Although shrimp viruses and metals have been detected in frozen shrimp sold at MA supermarkets, no official compulsory testing of contaminants in imported seafood is performed. The goal of 'Shrimp Scampi' is to educate American and Ecuadorian mothers about contaminants in the seafood they are consuming. In addition to monitoring EDC levels in muscle of frozen shrimp from US supermarkets and wild shrimp from Ecuador, another goal is to perform in-depth reviews of the scientific literature about EDC like Glyphosate, metals, and BPA and their generational epigenetic inheritance.

The Rotary Club of Southborough, MA is helping us by donating foldscopes (222 paper microscopes so far) through their 'Foldscopes: From Southborough to Ecuador' project (https://fucobi-english.weebly.com/). These paper microscopes are making microscopy available to schools in remote areas. Students and teachers have a wonderful time learning about microcosms, and teachers express their gratitude and enthusiasm for being able to have this new classroom tool since they currently do not have a science laboratory.

INVESTIGATING THE INTERSTATE MOVEMENT OF BLUE CRAB VIRUSES AND THE IMPLICATIONS FOR FISHERY BIOSECURITY

Jennifer Herrera[1]*, Mingli Zhao[1,2], Tsvetan Bachvaroff[1], Khaled Mohammed Geba[1], and Eric J. Schott[1]

[1]Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Science, P.O. Box 775, Cambridge, MD 21613

[2]Royal Veterinary College, Hawkshead Lane, Hatfield, Hertfordshire, AL9 7TA, United Kingdom

jherrera@umces.edu

The Atlantic blue crab, *Callinectes sapidus*, supports culturally and economically important fisheries on the Atlantic and Gulf coasts. In northern latitudes, the species overwinters in the benthos when water is cold; in southern latitudes, crabs are active and fished year-round. To meet the demand for blue crabs in the winter, Chesapeake region restaurants and retailers import them from southern states. Transport-related mortality is common, and dead crabs are often disposed of in estuaries. A widespread blue crab virus, CsRV1, shows regionally-specific genotypes, yet the virus strain in Maryland is similar to the variant in Louisiana. These findings raise the possibility that this virus genotype was spread by interstate transport. Metagenomic techniques are being used to document blue crab viruses entering Maryland through commercially-sourced crabs from the Gulf coast, the southeast, and the northeast. Ultimately, the goals of the project are to develop knowledge to protect the Maryland crab fishery from disease spread and increase awareness of biosecure ways to conduct interstate transport of blue crabs.

PROBIOTIC-INDUCED DISEASE RESISTANCE OF PACIFIC OYSTER LARVAE

Jennifer Hesser*, Ryan Mueller, Chris Langdon, and Carla Schubiger

Oregon State University, Carlson College of Veterinary Medicine, 700 SW 30th Street, Corvallis, OR 97331

hesserj@oregonstate.edu

Pacific oyster (*Crassostrea gigas*) hatcheries on the West coast of the U.S. are prone to mass mortalities from *Vibrio coralliilyticus* infections. Previous probiotic treatments have been evaluated for efficiency in improving the survival of oyster larvae challenged with *V. coralliilyticus*. This study aims to characterize how 1) a specific probiotic treatment and 2) *V. coralliilyticus* influence the expression of genes related to immune and inflammatory (defense) responses of one and three-day-old Pacific oysters. Treatments included a) a combination of four probiotic strains added to larvae at three time points post-fertilization, b) *V. coralliilyticus* added to two-day-old larvae, and c) larvae exposed to both the probiotics and *V. coralliilyticus*. All treatment groups were sampled at 24- and 72-hours post-fertilization along with a larvae-only control that received no bacterial additions. Differential gene expression analysis compared treatment groups to the larvae-only control. Differential expression of the total number and the number of defense-related genes increased from 24 to 72 hours post-fertilization in all treatment groups. Exposure to the probiotic combination led to increased expression of genes involved in immune signaling pathways (i.e., Myd88, IL-17, toll-like receptors). *Vibrio coralliilyticus* exposure resulted in increased expression of apoptosis genes (i.e., birc7, cas3) and suppression of inflammatory genes (i.e., mucC1, TRIM17). Addition of probiotic bacteria before *V. coralliilyticus* exposure prevented the differential gene expression associated with *V. coralliilyticus*. This study indicates that the defense response of Pacific oyster larvae undergoes important development between day one and three post-fertilization. The probiotic treatment evaluated here influences larval gene expression related to the defense response and reduces gene expression patterns associated with infection by *V. coralliilyticus*.

BRIDGING RESEARCH AND PRACTICE TO IMPROVE THE FUTURE SUSTAINABILITY AND GROWTH OF THE IRISH BIVALVE INDUSTRY (BIVALVE PROJECT)

Vivian Hlordzi[1,2], Sharon A. Lynch[1,2,3]*, and Sarah C. Culloty[1,2,3]

[1]University College Cork, School of Biological, Earth and Environmental Sciences and Aquaculture and Fisheries Development Centre, Distillery Fields, North Mall, Cork, T23 N73K, Ireland

[2]University College Cork, Environmental Research Institute, Ellen Hutchins Building, 6 Lee Rd, Sunday's Well, Cork, T23 XE10, Ireland

[3]MaREI Centre, Environmental Research Institute, Beaufort Building, University College Cork, Ringaskiddy, Co. Cork, P43 C573, Ireland

s.lynch@ucc.ie

Bivalves (mussels, oysters, and cockles) have a significant socio-economic and ecological role to play in coastal communities and environments and contribute to at least 65% of marine aquaculture volume and a circular bioeconomy in Ireland. Bivalves also play a substantial role in ecosystem function including nutrient recycling (removal of nitrogen and carbon), sediment stabilisation, and biodiversity enhancement. Pathogens and diseases represent a serious threat to the maintenance and sustainable growth of this sector. Control and mitigation strategies remain primarily reactive. Climate and environmental stressors challenge bivalve physiological limits resulting in individuals being more susceptible to infection and diverting energy from reproduction and growth. These challenges limit sustainable production output, Blue Growth, profitability, as well as ecosystem services.

The BIVALVE Project will (i) Investigate the current status of bivalve stocks and identify the key drivers of growth, reproduction, and diseases currently and into the future, (ii) Identify site influence/environmental/climate drivers or inhibitors of bivalve health, (iii) Recommend, implement and monitor best practices for smart sustainable production, and (iv) Assess and promote the socio-economic and ecosystem services provided by Irish bivalve aquaculture. BIVALVE will combine elements to address the knowledge gaps that currently exist for the Irish, as well as global, shellfish sector and also relevance and contribution to a healthy marine environment of this industry. These cross-cutting themes are integral in addressing the questions that research and industry require to support and implement the smart sustainable production/harvesting of bivalve species and the evaluation of their ecosystem services to Irish coastal environments.

CHALLENGES AND OPPORTUNITIES FOR GENOMICS-INFORMED SELECTIVE BREEDING OF HIGHLY DIVERGENT EASTERN OYSTER POPULATIONS IN TEXAS

Christopher M. Hollenbeck*[1,2], Joseph L. Matt[1], and David S. Portnoy[1]

[1]Texas A&M University - Corpus Christi, Department of Life Sciences, 6300 Ocean Dr, Corpus Christi, TX 78412

[2]Texas A&M AgriLife Research, 600 John Kimbrough Boulevard, Suite 512, College Station, TX 77843

christopher.hollenbeck@tamucc.edu

The eastern oyster (*Crassostrea virginica*) is one of the most ecologically and economically valuable species in Texas and the United States, but productive fisheries are now threatened by environmental change and intensive harvest; however, recent passing of state legislation allowing for oyster aquaculture may significantly promote economic stability and environmental resilience for the Texas coast. Central to the regulation of the fishery and the nascent aquaculture industry is the presence of two genetically divergent populations found along the Texas coast: a southern population that in U.S. waters is only present in Texas and a northern population that extends along the northern Gulf of Mexico. These populations coexist in a "transition zone" spanning several Texas bay systems that are increasingly exploited in the oyster fishery and are also well-suited for oyster aquaculture. The current understanding of the genomic and phenotypic differences between these populations will be discussed, including challenges and opportunities for genomics-informed selective breeding programs in Texas.

A FULLY-PHASED GENOME ASSEMBLY FOR *MYTILUS EDULIS* UNVEILS A HIGH DEGREE OF PRESENCE-ABSENCE VARIANCE BETWEEN MUSSEL POPULATIONS

Tiago S. Hori[1,2]

[1]PEI Marine Science Organization, PO Box 2000 Station Centre, 5th Floor Jones Building, Charlottetown, PE, C1N 7N8 Canada

[2]Atlantic Aqua Farms, 15 Queen Street, Suite 201, Charlottetown, Prince Edward Island, C1A 4A2 Canada

tiago.hori@atlanticaquafarms.com

Mussels belonging to the *Mytilus* species complex are cultivated worldwide, and Prince Edward Island produces 80% of the mussels sold in North America. Bivalve genomes are complex and contain many paralogous regions that can confound the separation of all types of variants in a genome. In addition, the mussel genome is highly repetitive and heterozygous.

To overcome the challenges imposed by these characteristics, a hybrid assembly approach was used combining PacBio CLR sequencing, Dovetail Omni-seq scaffolding, PacBio Hi-Fi sequencing and PacBio IsoSeq. We present a fully-phased chromosome level assembly of the mussel genome that enabled the genome-wide evaluation of presence-absence variance in *Mytilus edulis*.

Length and contiguity metrics were: number of scaffolds = 347; N50 = 105 Mb, NG50 = 150 Mb, Total Length = 1.58 Gb. Quality Values and completeness generated using Merqury indicated that each haplotype individually only contains ~65% of the kmers present in the raw HiFi reads, but combined both haplotypes contain ~99% of the kmers present in the raw reads. The haplotype collapsed assembly available on GenBank only contains 75% of the kmer present in the raw reads. That indicated that up to 25% of the polymorphism variation may be lost in a collapsed assembly.

In conclusion, a road map to producing high-quality chromosome-level phased assemblies for mussels was presented. It was also demonstrated the value of haplotype resolved assemblies for genomic analysis in blue mussels and showed evidence of significant PAV among different mussel individuals.

NEKTON USE OF OYSTER (*CRASSOSTREA GIGAS*) FLIP-BAG FARMS WITHIN AND ADJACENT TO NATIVE EELGRASS (*ZOSTERA MARINA*) HABITAT

Katie Houle[1]*, Kalloway Page[1], Fiona Boardman[2], and Jennifer Ruesink[2]

[1]Pacific Shellfish Institute, 1206 State Ave NE, Olympia, WA 98506

[2]University of Washington, Department of Biology, 3737 W Stevens Way NE, Seattle, WA 98195

katie@pacshell.org

Shellfish farms in Washington State have been exploring the use of flip-bags, an off-bottom growing method, to produce high-quality oysters for the singles, half-shell market. The interactions of these complex systems in native eelgrass, *Zostera marina,* have yet to be comprehensively explored. This study is the first to examine nekton use of flip-bag culture within and adjacent to *Z. marina* habitat. In 2020 and 2021, nekton communities were assessed at six farm locations in Washington State in four habitat types: flip-bags with eelgrass, flip-bags without eelgrass, eelgrass with no culture, and bare mudflat. Sampling in each habitat type occurred in both spring and summer seasons using a modified seine net to collect nekton >5 mm in size and underwater GoPro cameras set to record for 2 minutes every 10 minutes during the diel incoming tide. Nekton abundance, taxa richness, community composition and three key behaviors: transiting, resting, and foraging were quantified. Results from both seine net tows and video indicate spring nekton were more abundant and diverse with significantly more transiting behavior observed with eelgrass present. Summer nekton from the seine net tows were more abundant and diverse with eelgrass present; however, summer videos indicate more abundant and diverse nekton in flip-bags with more foraging behavior observed compared to habitats without flip-bags. Few species were exclusively in eelgrass. Most nekton appear to be generalists, utilizing the broader habitat mosaic of mudflat, eelgrass and aquaculture. These results will inform key stakeholders producing and regulating shellfish aquaculture in *Z. marina* habitat.

BIRDS ON FLOATING CULTURE, OH MY!

Bobbi Hudson

Pacific Shellfish Institute, 120 State Ave. #1056, Olympia, WA 98501

bobbi@pacshell.org

Floating culture systems are used by shellfish farms on the east and west coast of the U.S. and Canada, and the U.S. Gulf Coast. In recent years the fact that these systems provide structures for birds to perch has drawn increasing attention. Bird numbers, species, residence time, and water body dynamics and flushing rate are highly variable. The relationship of birds to fecal coliform in water and shellfish meats are undoubtedly also highly variable, compounded by seawater flow and physical water properties like temperature and salinity. The National Shellfish Sanitation Plan (NSSP) water quality monitoring program is based on measurement of indicator coliform bacteria present in all warm-blooded animal feces. The fecal coliform standard in NSSP assumes a correlation between pathogens and fecal coliform in wastewater, not birds. In fact, birds are often poor reservoir hosts of pathogens which cause illness in humans and a recent meta-analysis indicates "data are too limited and biased to make data-driven recommendations for managing wild birds to reduce enteric pathogen spillover to people". Birds have the potential to negatively impact water quality, but the potential disease risk to humans remains unknown. In the absence of an established risk threshold, shellfish farms should not be expected to attempt to manage risk. Furthermore, factors contributing to proliferation of fecal coliform varies widely and therefore risk of birds on floating culture systems in one aquatic environment cannot be assumed to be equivalent in all environments.

COLLABORATIVELY TRACKING SHELLFISH AQUACULTURE PRODUCTION DATA IN WASHINGTON STATE

Bobbi Hudson[1]*, Chris Eardley[2], Dani Toepelt[3], and Laura Butler[4]

[1]Pacific Shellfish Institute, 120 State Ave. #1056, Olympia, WA 98501

[2]Washington Dept. of Fish & Wildlife, P.O. Box 43200, Olympia, WA 98504

[3]Washington Dept. of Health, P.O. Box 47824, Olympia, WA 98504

[4]Washington Dept. of Agriculture, P.O. Box 42560, Olympia, WA 98504

bobbi@pacshell.org

Accurate and reliable harvest production reporting is critical to conduct economic analyses that support the productivity and economic sustainability of shellfish aquaculture. This information is integral to assessing changes, opportunities, and impacts on the industry. Production and economic data are also vital for consumer and market evaluations, outreach programs, extension efforts designed to support sustainable U.S. aquaculture growth, and programs to aid economic relief following catastrophic events like the COVID-19 pandemic and natural disasters. This NOAA National Sea Grant funded project (NA21OAR4170088) is utilizing a broad group of stakeholders to aid modernized data collection systems related to shellfish permitting and aquaculture reporting in Washington State. Specifically, a new data portal aims to result in complete, accurate, up-to-date statewide shellfish aquaculture production data collection, management, and reporting. The goal for the data portal is to serve as a catalyst for streamlining by updating regulations to assist sustainable shellfish aquaculture management and development, which is a "win-win" for shellfish managers and the shellfish aquaculture industry. Confidentiality concerns were also considered and seek widespread buy-in from stakeholders. This presentation is designed to inform shellfish producers and other stakeholders of project progress to date, and to invite feedback.

HABITAT-SPECIFIC ABUNDANCE AND MORTALITY OF JUVENILE BLUE CRAB, *CALLINECTES SAPIDUS*, WITH BAYESIAN INFERENCE: INFLUENCES OF POST-LARVAL ABUNDANCE, SEASONALITY, AND TURBIDITY

A. Challen Hyman*, Grace Chiu, Michael Seebo, Gabrielle Saluta, Allison Smith, Kathleen Knick, and Romuald N. Lipcius

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

achyman@vims.edu

Nursery habitats confer higher food availability, reduce predation risk, and disproportionately contribute more individuals per unit area to the population compared to other habitats. Nursery status is inferred through evaluation of four metrics: density, growth, survival, and linkage between juveniles and adults. Two nursery metrics, abundance and survival, for juvenile blue crabs in structurally complex habitats — seagrass meadows and salt marshes — and an unstructured control were evaluated in the York River, Chesapeake Bay. Effects of spatial position, seasonality, and physicochemical variables were also considered. Abundance was positively associated with both seagrass and salt marshes, turbidity, and post-larval abundance. Survival was positively associated with juvenile size and structurally complex habitats relative to unvegetated controls. Seasonally, survival peaked in April, reached a seasonal minimum in August, and increased throughout fall. Habitat-specific survival was dependent on spatial position; survival was elevated at upriver salt marsh and unstructured sand habitats than in downriver counterparts. Abundance and survival results indicate that salt marshes offer comparable per unit area nursery function as seagrass meadows. When extrapolated at the river scale to consider the area of each habitat, salt marshes contributed the majority of secondary production. Hence, salt marshes should be considered a key nursery habitat for the blue crab, even where extensive seagrass beds occur.

UNLOCKING THE POTENTIAL OF SHRIMP BREEDING THROUGH GENOMIC SELECTION

Julio Isidro y Sánchez

Centro de Biotecnologia y Genómica de Plantas, Universidad Politécnica de Madrid, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain

j.isidro@upm.es

Genomic selection (GS) is considered a powerful tool for genetic improvement of complex traits controlled by many genes, each with minor effects. It offers several advantages such as increasing the rates of genetic gain through increased accuracy of estimated breeding values significantly shorter breeding cycles, and the better utilization of available genetic resources through genome-guided mate selection. Traditional breeding approach limits the number of variety candidates to be tested, and it is the main cause of the fact that breeding programs are time and cost intensive. Genomic selection offers a more efficient alternative by using molecular markers to predict the genetic value of individuals for specific traits without phenotyping. In this presentation, an overview of GS and its implications for shrimp breeding will be provided. The current state of the field and the potential for this technology to improve the efficiency and sustainability of the shrimp industry will also be discussed.

MOBILE LAB UTILIZED IN MONITORING PHYTOPLANKTON DYNAMICS FOR SAFE SHELLFISH HARVEST IN SOUTHCENTRAL ALASKA

Annette Jarosz[1]*, Shannon Atkinson DeMaster[2], and Maile Branson[1]

[1]Chugach Regional Resources Commission, Alutiiq Pride Marine Institute, 101 Railway Ave, Seward, AK 99664

[2]University of Alaska Fairbanks, Fisheries Department and Institute of Marine Science, 17101 Pt. Lena Loop Rd., Juneau, AK 99801

annette@alutiiqprideak.org

Harmful algal blooms (HAB) are a topic of increasing concern in coastal Alaskan ecosystems, and can produce biotoxins, particularly saxitoxin and domoic acid, which accumulate primarily in shellfish. Saxitoxin and domoic acid are the causative agents for paralytic shellfish poisoning (PSP) and amnesic shellfish poisoning (ASP), respectively. The state of Alaska only tests for biotoxins in commercial shellfish and does not test recreational or subsistence harvested shellfish. Subsistence and recreationally harvested shellfish are of significant economic, food security, and cultural importance across Southcentral Alaska.

The Chugach Regional Resources Commission (CRRC) is an inter-tribal consortium serving seven tribes in the Lower Cook Inlet, Prince William Sound, and Cooper River Delta regions. The CRRC aims to advocate for the natural resource interests of these communities through policy advocacy, mariculture development, and marine research. The CRRC has established the Chugach Regional Ocean Monitoring program which includes HAB monitoring. The CRRC operates the Alutiiq Pride Marine Institute (APMI), located in Seward, Alaska. The APMI has created a HAB lab out of a 40-foot shipping Conex that has the capacity to perform enzyme-linked immunosorbent assays (ELISA), receptor binding assays (RBA), and quantitative polymerase chain reaction (QPCR). The purpose of the HAB lab is to support safer shellfish harvest practices for the CRRC tribal communities by collecting baseline environmental data, phytoplankton samples, and reporting shellfish toxin concentrations. This information will give the CRRC a better understanding of the phytoplankton dynamics in Southcentral Alaska and inform the public when toxin levels are high in shellfish close to their communities.

DEVELOPING EDNA AS A TOOL FOR MONITORING CULTURED AND WILD POPULATIONS OF SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) IN MAINE, USA

Phoebe Jekielek*[1], Heather Leslie[1], and Nichole Price[2]

[1]University of University of Maine Darling Marine Center, 193 Clarks Cove Rd, Walpole, ME 0457

[2]Bigelow Laboratory for Ocean Sciences, 60 Bigelow Dr, East Boothbay, ME 04544

phoebe.jekielek@maine.edu

The Maine eDNA program aims to use molecular tools to better understand and promote sustainable use of wild and cultured fisheries resources. Quantitative eDNA assays for sea scallops have been developed and calibrated for sperm and dockside conditions, but this assay has not been calibrated for other life stages, e.g., eggs or larvae, nor has it been tested in more dynamic field environments. Here whether eDNA from adults vs gametes and larvae can be distinguished by sampling at different depths and points in time in a wild population of sea scallops were explored. Water samples were collected at 8 different depths above a well-characterized wild scallop bed off of Hurricane Island in Penobscot Bay over a 10-week period. Results show that scallop DNA signal is more stratified outside of spawning season, with deeper depths having highest gene copy numbers per liter. Signal stratification decreases in September with spawning and scallop DNA signal increases and becomes even across all depths; however, peak gene copy numbers occur in mid-October, potentially indicating a signal from larval transport. Therefore, spatial and temporal differences in scallop DNA signals using our stratified sampling design are observed. Results from eDNA generation/degradation experiments will also be shared. Results from this work may inform the use of carefully constructed sampling designs to develop adult stock assessments or to estimate recruitment potential.

DETECTING THE MULTIPLE STATES OF OYSTER ACTIVITY AND ORIENTATION USING DEEP LEARNING IMAGE PROCESSING AND COMPUTER VISION ALGORITHMS

Yuanwei Jin[1]*, Joshua Comfort[2], and Ian Rudy[3]

[1]University of Maryland Eastern Shore, Department of Engineering and Aviation Sciences, 11868 College Backbone Rd, Princess Anne, MD 21853

[2]Salisbury University, Department of Computer Science, 1101 Camden Avenue Salisbury, MD 21801

[3]Susquehanna University, Department of Computer Science, 514 University Avenue Selinsgrove, PA 17870

yjin@umes.edu

The United Nations projects that the global human population will grow to eleven billion by 2100. As the populace increases, the demand for food will likewise grow. The global farming sector will need to help meet this increased need by boosting its efficiency and production volume. These industries will need to increase their output by improving their current practices by implementing innovative technologies that will enhance growth. One area, in particular, needs much improvement; the oyster farming industry still uses some techniques from the 19th century. Modernizing oyster farming has the potential to provide large quantities of a high-protein sustainable food source. This research aims to create an automated monitoring system that will allow oyster farmers to remotely track their oyster crops' health and activity. Creating such a monitoring system required the utilization of high-performance computing and deep learning to adapt an object detection model to recognize oysters under three different states of activity. By periodically using the object detector, farmers can use the activity to help infer the health of their oyster crops, reducing the amount of work required and thus increasing efficiency. In addition to applications in aquaculture, deploying the systems developed in this project can benefit oyster restoration efforts. For example, helping monitor the health of the restored populations, such as those in the Chesapeake Bay.

TRACKING ECOSYSTEM CONTAMINANTS TO PROTECT PUBLIC HEALTH

Steve Jones

University of New Hampshire, 105 Main St, Durham, NH 03824

Stephen.jones@unh.edu

The health of marine ecosystems, including aquaculture operations, is threatened by local to global scale changes associated with human activities. One key dimension of public health is the management of illnesses from exposure to environmental contaminants including microbial pathogens, toxic organic chemicals, and heavy metals. The regulatory framework for managing contaminants is challenging, particularly with formulating safety thresholds for emerging contaminants, and developing strategies to eliminate the difficulty in identifying contamination sources.

Combinations of research and monitoring can provide new and ongoing information to help address evolving public health issues. The use of shellfish as sentinel species to identify sources and to determine the transport, fate, and effects of localized and regional contaminants, is a proven approach for informing public health and resource management. Examples will be used to illustrate the direct benefits of this approach to inform shellfish management including the Mussel Watch and Gulfwatch programs, microbial indicators and source identification of fecal contamination, and research on pathogenic *Vibrio* species. Use of new information and tools as part of a One Health approach is important for turning the tide of current health issue trends as climate change, overdevelopment and other human-induced activities challenge Our Health.

THE PREVALENCE OF BIRDS AS SOURCES OF FECAL CONTAMINATION IN THE SHELLFISH WATERS OF THE NORTHEAST U.S.

Steve Jones[1]*, Tom Howell[2], Randi Foxall[1], and Lori Howell[2]

[1]University of New Hampshire, 105 Main St, Durham, NH 03824

[2]Spinney Creek Shellfish Inc., 27 Howell Drive, S. Eliot, ME 03903

Stephen.jones@unh.edu

Fecal contamination of coastal waters is a significant limitation of shellfish harvesting, and information on sources and abundance of different types of fecal-borne water contamination is essential for managing human health and safety risks in shellfish growing waters. Routine monitoring for bacterial indicators of fecal contamination provides little information about sources, so strategies, termed "Microbial Source Tracking" (MST), have been developed to provide this information. This study summarizes spatial and temporal patterns of measured presence and relative concentrations of different sources of bird fecal contamination that have occurred in the coastal waters of the Northeast US over the past several years, with a focus on coastal areas with chronic and unresolved fecal contamination issues. PCR/qPCR-based MST analyses were conducted on DNA extracted from water samples with assays targeting specific contamination sources to complement fecal coliform concentration results. Source-specific assays using both PCR (presence/absence) and semi-quantitative qPCR (copy number concentrations) assays were used to identify bird, gull, and Canada goose contamination. The results revealed bird fecal-borne contamination was detected at most sites, varying by season and relative significance as the source of fecal coliforms. The frequency and variable levels of detection for these sources underly our poor understanding of birds as a public health concern. As the understanding of the connection between water quality and public health evolves, shellfish managers and industry will be better able to accurately assign, locate, and manage sources of contamination.

THE RESPONSES OF TOTAL AND POTENTIALLY PATHOGENIC *VIBRIO PARAHAEMOLYTICUS* IN RESUBMERGED OYSTERS IN THE NORTHEAST U.S.

Steve Jones[1]*, Tom Howell[2], Christian M. Petitpas[3], Cheryl Whistler[1], Randi Foxall[1], Diane Regan[4], Jacob Madden[4], Lori Howell[2], Brianne Shanks[3], and Chris Nash[5]

[1]University of New Hampshire, 105 Main St, Durham, NH 03824

[2]Spinney Creek Shellfish Inc., 27 Howell Drive, S. Eliot, ME 03903

[3]Massachusetts Division of Marine Fisheries, 836 S Rodney French Blvd, New Bedford, MA 02744

[4]Massachusetts Division of Marine Fisheries, Newburyport, 84 82nd St, Newburyport, MA 01950

[5]New Hampshire Dept. of Environmental Services, Shellfish Program, 222 International Dr, Unit 175, Portsmouth, NH 03801

Stephen.jones@unh.edu

Increasing shellfish-borne illnesses from *Vibrio parahaemolyticus* (*Vp*) in the Northeast US during the past 10 years has triggered intensive management practices based on a limited understanding of risks. Current gear-based production requires extensive pre-harvest handling that, during warm months, can increase *Vp* levels in oysters and potentially increase the risk of illness. Field-testing of *Vp* control measures for pre-harvest practices was conducted in Maine, New Hampshire, and Massachusetts for 4 years where aquaculture practices, regulations, environmental conditions, and *Vp* populations all vary. Oysters were temperature-abused in Little Bay NH, Spinney Creek ME, and in Plymouth Harbor and Katama Bay MA. The abundances of total (*tlh*), potentially pathogenic (*tdh* & *trh*), and *tdh* allele-variants using assays developed to identify regionally important pathogenic strains, were measured in bottom and surface cultured oysters exposed to air for 3-48 hours from sub-tidal and inter-tidal locations. Temperature abused, un-exposed and re-submerged exposed oysters were sampled after 1-14 days. Total *Vp* concentrations significantly increased in abused oysters and remained higher than in unexposed oysters for as little as 1 day and up to 8 days. Both *tdh* and *trh* were elevated in abused oysters compared to control oysters but these pathogenic markers returned to environmental levels quicker than total *Vp*. The prevalence of specific *tdh* alleles as proxies for *Vp* strain types 36 and 631 (*tdh3*) varied and provided further resolution of this specific pathogenic population. The study provides findings for each state to use for managing pre-harvest practices to reduce *Vp*-related public health risks.

SUSCEPTIBILITY OF SHELLFISH AQUACULTURE SPECIES IN THE CHESAPEAKE BAY AND MARYLAND COASTAL BAYS TO OSTREID HERPESVIRUS-1 MICROVARIANTS

Mariah L. Kachmar*[1], Kimberly Reece[2], M. Victoria Agnew[1], Harold J. Schreier[1,3], and Colleen A. Burge[4]

[1]University of Maryland Baltimore County, Department of Marine Biotechnology, Institute for Marine and Environmental Technology, 701 E Pratt St., Baltimore, MD 21202

[2]Virginia Institute of Marine Science, William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

[3]University of Maryland Baltimore County, Department of Biological Science, 1000 Hilltop Circle, Baltimore, MD 21250

[4]California Department of Fish and Wildlife, University of California Davis, Bodega Marine Laboratory, 2099 Westshore Road/P.O. Box 247, Bodega Bay, CA 94923

mariahk1@umbc.edu

The Ostreid herpesvirus-1 (OsHV-1) and its microvariants are highly virulent pathogens that cause mass mortalities of oysters and pose a threat to the shellfish aquaculture industry globally. OsHV-1 causes economically devastating mass mortality events up to 100% in the Pacific oyster (*Crassostrea gigas*); however, OsHV-1 and its variants lack host specificity and are known to infect a range of bivalve species, such as bay scallops (*Argopecten irradians*), and be carried by the European green crab (*Carcinus maenas*). Determining the susceptibility of economically and ecologically important United States bivalve species to OsHV-1 is an essential step in improving biosecurity and disease management to protect the sustainability of the aquaculture industry. Surveys were conducted in June-August 2021 in the Maryland portion of the Chesapeake Bay to determine the prevalence and viral load of OsHV-1 at five aquaculture farms. Using qPCR, OsHV-1 was not detected at any sites. Experiments examined the susceptibility and horizontal transmission of eastern oysters (*Crassostrea virginica*) and northern quahogs (= hard clams) (*Mercenaria mercenaria*) using OsHV-1 µvar SD (San Diego, California) and OsHV-1 µvar FRA (Marennes-Olreon, France). Results of the experiments showed that OsHV-1 microvariants did not cause mortality or infection in single stocks of eastern oysters and hard clams through natural infection pathways; however, eastern oysters, when injected with OsHV-1, did transmit the virus to naïve Pacific oysters. Further experimentation using additional family lines and establishment of surveillance programs in the East and Gulf Coasts of the US is necessary to fully manage the spread and impact of OsHV-1 related disease.

PERKINSUS MARINUS INFECTION OF *CRASSOSTREA VIRGINICA* WITH A CHANGING CLIMATE IN THE CHESAPEAKE BAY: A META-ANALYSIS

Mariah L. Kachmar[1]*, Chelsea Bergman[1], Sarah Gignoux-Wolfsohn[2], Gemma Feild[1], Harold J. Schreier[1,3], Katrina M. Pagenkopp Lohan[4], Ryan Carnegie[5], and Colleen A Burge[1,6]

[1]University of Maryland Baltimore County, Department of Marine Biotechnology, Institute of Marine and Environmental Technology, 701 E Pratt St. Baltimore, MD 21202

[2]University of Massachusetts Lowell, Department of Biological Sciences, 220 Pawtucket St, Lowell, MA 01854

[3]University of Maryland Baltimore County, Department of Biological Sciences, 100 Hilltop Cir. Baltimore MD 21250

[4]Smithsonian Environmental Research Center, 647 Contees Wharf Road, Edgewater, MD 21037

[5]Virginia Institute of Marine Science, William & Mary, 1370 Greate Road, Gloucester Point, VA 23062

[6]University of California Davis, Bodega Marine Laboratory, California Department of Fish and Wildlife, 2099 Westside Road, Bodega Bay, CA 94923

mariahk1@umbc.edu

Shellfish fisheries and aquaculture within the Chesapeake Bay and its tributaries have been historically impacted by disease and climate events. Shifts in water temperature and salinity driven by climate change can alter host-pathogen-environment relationships driving or impairing disease outbreaks and spread. Specifically, an oyster disease system involving a parasite, *Perkinsus marinus*, reflects this sensitive relationship raising curiosity on how climate has and will continue to impact its life cycle. *P. marinus* has impacted the eastern oyster (*Crassostrea virginica*), both an economically and environmentally significant species. While both long-term environmental data and *P. marinus* surveys have been conducted in the Chesapeake Bay region, no recent study has compared this data. The objectives of our study are to identify i) how climate (using temperature and salinity as a proxy for climate) affects *P. marinus* prevalence and intensity within the Chesapeake Bay region over the last 30 years, ii) how seasonality and climate fluctuations influence *P. marinus* infections, iii) how environmental conditions at each latitude affects *P. marinus* infection intensity and prevalence. Using linear mixed effects models, we investigated the relationships and interactions between temperature, salinity, year, and latitude or site with prevalence and intensity of *Perkinsus marinus*.

THE TOUGH PEOPLE BEHIND THE TENDER SHELLFISH: NON-FATAL INJURIES ASSOCIATED WITH OYSTER AND CLAM AQUACULTURE IN PANACEA AND CEDAR KEY, FLORIDA

Andy Kane[1,2,3]*, Ross Brooks[1,2], Melvin Myers[1], Robert Durborow[1,3], and Kim Dunleavy[1,4]

[1]Southeastern Coastal Center for Agricultural Safety and Health, PO Box 110885, Gainesville, FL 32611

[2]University of Florida, Department of Environmental and Global Health, PO Box 110885, Gainesville, FL 32611

[3]Florida Sea Grant Program, 2306 Mowry Road, PO Box 110400, Gainesville, FL 32611

[4]Kentucky State University, School of Aquaculture and Aquatic Sciences, 400 East Main Street, Frankfort, KY 40601

[5]University of Florida, Department of Physical Therapy, PO Box 100154, Gainesville, FL 32611

kane@ufl.edu

Commercial seafood harvesting is one of the most dangerous occupations nationally. Non-fatal injuries and illnesses are largely undocumented and poorly understood across fishing sectors, including shellfish aquaculture. To support worker wellness in oyster and clam production sectors in-person surveys were used to understand the range and prevalence of occupational injuries that impacted clam and oyster farmers along the Florida Gulf Coast, 2017-2018.

Self-reported injury data from oyster (n=19, mean age=44, 3.5 yrs experience) and clam (n=17, mean age=47, 19 yrs experience) farmers translated to incidence rates of 0.89 and 0.21 injuries/FTE, respectively. Oyster farmers reported less severe injuries resulting in fewer days away from work, compared with clam farmers (0.4 vs 5.9 days/FTE); 47% of oyster farmers and 76% of clam farmers reported injuries that required medical attention, were job task limiting, and/or required days away from work. Injuries associated with heavy lifting and repetitive tasks were common for both oyster and clam farmers, leading to a follow-up participatory ergonomics training intervention study to address low back pain in clam farmers. Oyster farmers also reported cuts, lacerations, and infections from contact with grow-out gear and biofouling. Clam farmers reported puncture injuries and cuts associated with underwater hazards, i.e., contact with stingrays, bag stakes, chicken wire, and biofouling.

Injury rates were inversely proportional to # years' work experience (p=.04), indicating need for early training. Data share-back with growers included lessons-learned and interventional opportunities.

This project was supported by CDC/NIOSH through the Southeastern Coastal Center for Agricultural Safety and Health, and Florida Sea Grant.

HORSESHOE CRAB INTERACTIONS WITHIN A NEWLY-RESTORED FRINGING MARSH IN STRATFORD POINT, CONNECTICUT

Jo-Marie E. Kasinak

Sacred Heart University, Department of Biology, 5151 Park Avenue, Fairfield, CT 06825

Kasinakj@sacredheart.edu

Long Island Sound (LIS) is an urban estuary that has lost a substantial area of both low and high saltmarsh grasses. An example of loss can be seen along the western shore of the Housatonic River at Stratford Point in Stratford, Connecticut, where 24 m of sediment and marsh eroded from 2001-2012. Anthropogenic climate change has led to an increase in sea level rise and storm events, increasing erosion and degrading coastal habitats. The American horseshoe crab, *Limulus polyphemus,* is a foundational species which relies on healthy shorelines to spawn. The Atlantic Marine Fisheries Commission stock assessment report lists the population of horseshoe crabs found in LIS as “poor”. The average annual spawning counts of *L. polyphemus* in LIS have generally declined from an already low of 0.035 females/m^2 in 2010 to 0.019 females/m^2 in 2018.

Nature-based restoration efforts combining gray and green structures were used to allow habitat recovery of the Stratford Point shoreline. This hybrid living shoreline approach was successful in facilitating the establishment of a fringing saltmarsh and sediment accretion. Horseshoe crabs have been observed buried in the sand and spawning along this restored shoreline, including in the marsh grasses, from the time of the restoration. Monitoring will continue to examine the impact of this restored habitat on the spawning of *L. polyphemus* as the saltmarsh continues to mature. Restoring coastlines using intentional nature-based solutions will provide more suitable spawning habitat for adult horseshoe crabs and nursery habitat for juveniles, which may help this valuable population recover.

DEVELOPING DEFAULT DENITRIFICATION ENHANCEMENT ESTIMATES FOR RESTORED OYSTER REEFS: A CHESAPEAKE BAY EXAMPLE

M. Lisa Kellogg[1]*, Jeffrey C. Cornwell[2], and Michael S. Owens[2]

[1]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA, 23062

[2]University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Rd, Cambridge, MD 21613

lkellogg@vims.edu

Oyster reef restoration has been proposed as an approach to mitigating eutrophication in coastal waters. Prior studies have demonstrated the ability of subtidal oyster reefs to enhance denitrification; however, direct measurement of denitrification enhancement associated with oyster reef restoration is beyond the scope of most oyster reef restoration projects. In contrast, many oyster reef restoration efforts measure oyster biomass per unit area to determine whether the restoration effort was successful. If consistent relationships can be identified between oyster reef biomass per unit area and denitrification rates per unit area across multiple sites, these relationships could serve as the basis for developing default estimates of denitrification enhancement associated with oyster reef restoration.

Using data collected in Chesapeake Bay over the past decade, consistent seasonal relationships between oyster biomass per unit area and denitrification rates per unit area for subtidal oyster reefs were identified and used to estimate annual rates. In Spring, denitrification rates initially increase then decline with increasing oyster biomass. In Summer, Fall and Winter, denitrification rates increase with increasing oyster biomass. Because winter data were from a single site, they were not incorporated into annual estimates, making annual rate estimates intentionally conservative. The resulting biomass-specific annual denitrification rates were then used in combination with site-specific oyster biomass measurements to calculate annual enhanced nitrogen removal estimates for subtidal restored oyster reefs in Chesapeake Bay.

MULTI-YEAR ASSESSMENT OF THE IMPACTS OF OYSTER AQUACULTURE ON SUBMERGED AQUATIC VEGETATION

M. Lisa Kellogg*, Erin C. Shields, and Jennifer C. Dreyer

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

lkellogg@vims.edu

Faced with conflicting data, state and federal regulators justifiably take a precautionary approach and generally do not grant leases or permits for conducting oyster aquaculture in or over beds of submerged aquatic vegetation (SAV). Conversely, many in the oyster aquaculture industry argue that their practices can enhance SAV distribution and abundance, and observational data from some farms in Chesapeake Bay support the assertion that the two can co-exist. The rapid expansion of both SAV and oyster aquaculture in Chesapeake Bay has made the resolution of this issue critical for the industry and resource managers.

Working in collaboration with industry partners in the Virginia portion of Chesapeake Bay, the impacts of two commercial-scale floating oyster aquaculture farms on SAV have been assessed since 2019. As part of the project, two aquaculture companies were granted special research permits and asked to establish a new farm block over an area where SAV had been common in previous years. One site was historically dominated by eelgrass (*Zostera marina*) and the other by widgeon grass (*Ruppia martima*). Both sites were surveyed prior to farm establishment and sampling has continued following farm establishment. Data were collected on percent cover of SAV and other metrics indicative of SAV health, infauna and epifaunal community structure and biomass, underlying sediment characteristics, and local water quality. Impacts have differed significantly both between farms and between sampling periods. Results to date will be discussed in the context of farm culture methods, SAV species and local environmental conditions.

RELATING CLIMATE CHANGE TO ABUNDANCE AND REPRODUCTIVE DYNAMICS OF ATLANTIC BLUE CRAB (*CALLINECTES SAPIDUS*) IN SOUTH CAROLINA, USA

Michael R. Kendrick* and Jeff F. Brunson

Crustacean Research and Monitoring Section, Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston, SC 29412

kendrickm@dnr.sc.gov

Understanding how shifting environmental conditions affect the biology and ecology of Atlantic blue crab (*Callinectes sapidus*) is critical to developing effective management strategies. The commercial blue crab fishery in South Carolina has historically ranked among the top three fisheries in the state, with recent increases in value due to regional growth in market demand. As such, effective management is especially important when there are indications of declines in abundance since intrinsic biology and interactions with the environment affect population dynamics. The complex life history of blue crab (*e.g.*, their use of oceanic and estuarine habitats at different points in their life cycle) means this species is susceptible to the impacts of climate change across multiple environments. While the physical effects of climate warming are becoming well documented (*e.g.*, warming ocean and estuarine temperatures), the mechanisms by which they impact biological and ecological processes are less clear. To better understand how shifting environmental factors are affecting Atlantic blue crabs in South Carolina, we compiled abundance and biological data from fisheries-independent sources across a 42-year time frame (1979-2021). Analyses on a subset of data show a significant effect of drought on adult crab abundance. Furthermore, winter temperatures have important effects on the abundance of juvenile crabs as well as on the timing of spawning activity. These results highlight how crustacean populations respond to climate change in the southeastern U.S. Future efforts should include working with various stakeholder groups to develop dynamic management approaches that account for ongoing changes in environmental conditions.

DEPLETING THE IMMENSE PROTEIN FACTORY THAT WAS CHESAPEAKE BAY

Vic Kennedy

University of Maryland, Center for Environmental Science, CBL Campus - Cory Hall, P.O. Box 38, Solomons, MD 20688

kennedy@umces.edu

In 1940, Baltimore newspaper reporter H.L. Mencken referred to Chesapeake Bay as "the immense protein factory". In the late 19th century, an extensive infrastructure of boats, harvest gear, and processing facilities exploited this bounty. Fishers harvested millions of oysters, blue crabs, and shad and river herring, and thousands of sturgeons and terrapins. Processors shucked and canned oysters, salted and smoked fish, picked crab meat, nurtured soft crabs, and turned terrapins into gourmet food. Workers made millions of cans and labels for oysters and thousands of wooden barrels for salt fish. Others built sailboats for oyster dredgers, oyster tongers, and crab trotliners; made sails and ships' cordage; fabricated oyster tongs, dredges, and crab scrapes; and wove miles of fish netting. The rich fisheries supported work for thousands more people than now.

Virginia and Maryland supplied more oysters each year than any other region in North America and Europe, yielding nearly 20 million bushels in 1885 compared with about 800,000 bushels today. There were over 80 oyster processing plants in Baltimore alone, and many others in Maryland and Virginia tidewater cities. These facilities employed thousands of shuckers and canners and bought oysters from thousands of dredge boat sailors and small-boat tongers. Railroad cars carried cans of blue crab meat and trays of soft-shell crabs from some tidewater villages to cities six days a week in season. The shad and river herring industry, second only to the oyster industry in its economic value. captured millions of fish in a 2-month period in spring in the 1800s, using thousands of pound- and gill-nets and miles-long purse seines. Sturgeon and terrapins were everywhere.

As the fisheries were over-exploited, the bounty was depleted. Oyster and crab harvests are low and there are bans on harvesting shad, river herring, sturgeon, and terrapins. Eyewitness reports by early colonists as well as historical newspaper articles and federal and state management reports from the 1800s-early 1900s paint a picture of a cornucopia that one can now only imagine. The depletion of these resources raises the question of how Bay food webs might have been affected.

ENVIRONMENTAL EPIGENOMICS AND TRANSGENERATIONAL EPIGENETIC INHERITANCE IN LIVESTOCK AND SHELLFISH SPECIES

Hasan Khatib

University of Wisconsin-Madison, Department of Animal and Dairy Sciences, 1675 Observatory Drive, 266 Animal Sciences Building, Madison, WI 53706

hkhatib@wisc.edu

Environmental epigenomics is an emerging field that investigates how environmental exposures, such as diet, toxins, stress, and pollutants, can impact the epigenetic modifications of an individual's genome and phenotypes. These epigenetic modifications, such as DNA methylation or histone modification, can affect gene expression without changing the underlying DNA sequence. Environmental epigenetics provides new insights into the complex interactions between genetic and environmental factors in developing diseases such as cancer, cardiovascular disease, and neurodevelopmental disorders. Recently, the effects of paternal diet supplementation on epigenetic and phenotypic changes in the offspring was investigated using the sheep model. For the first time in any mammalian species, it was shown that supplementation of methionine to rams from weaning to puberty altered the methylation status of many cytosines and genes in the sperm. Importantly, these DNA methylation signatures were inherited by subsequent generations not exposed to the diet treatment. Fish and shrimp are particularly useful models for studying environmental epigenetics because they are exposed to various environmental factors, such as pollutants, temperature, and diet, throughout their lives. These studies could have important implications for understanding the impacts of environmental change on aquatic ecosystems and for developing interventions to protect these species from environmental stressors.

EXAMINING PHYTOPLANKTON-RELATED ECOSYSTEM SERVICES OF SESSILE SUSPENSION FEEDERS IN INNER HARBOR, BALTIMORE, MARYLAND

Allyson Kido[1]*, Makayla Stewart[2], Abdul Adaranijo[1], Khaled Geba[3], and Eric Schott[3]

[1]University of Maryland, Baltimore County, 1000 Hilltop Cir, Baltimore, MD, 21250

[2]University of South Carolina, Department of Marine Science, 701 Sumter Street, EWS 617, Columbia, SC, 29208

[3]University of Maryland Center for Environmental Science, 701 E Pratt St., Baltimore, MD, 21202

Akido1@umbc.edu

Phytoplankton filtering capabilities of sessile organisms in urban waterways around Baltimore have untapped potential for ecosystem services. Much of the current work on ecosystem services of shellfish focuses on species that are economically relevant to the seafood industry. For example, in the Inner Harbor of Baltimore, there are programs to grow oysters for restoration services. These efforts are challenged by poor water quality and microbial contamination that makes the oysters unsuitable for consumption. Recent efforts have looked at other naturally occurring suspension feeders for ecosystem services. The dark false mussel, *Mytilopsis leucophaeata*, and the bay barnacle, *Amphibalans improvisus*, readily grow on hard surfaces in the Baltimore Inner Harbor and hold promise as providers of beneficial ecosystem services; however, little is known about the filtering capabilities and natural diets of these species. Algae filtering capabilities would be beneficial as this area has frequent and intense algae blooms. Preliminary laboratory work has shown that *M. leucophaeata* and *A. improvisus* can reduce the chlorophyll levels in laboratory feeding experiments using lab cultured algae. Future studies plan to look at the natural diet of these suspension feeders and examine their filtering capacity for grazing down the natural phytoplankton community. Understanding the natural diets and filtering capabilities of these sessile suspension feeders is crucial in determining the extent of the ecosystem services these organisms can provide. This work will provide quantitative data for economic and ecological models to support the use of naturally occurring suspension feeders for best management practices to mitigate urban runoff.

IMPROVING OYSTER AQUACULTURE SITE SELECTION WITH HIGH RESOLUTION SATELLITE IMAGERY

Thomas Kiffney[1]*, Binbin Jiang[2], Gabe Hesketh[3], Romain Lavaud[4], Emmanuel Boss[5], and Damian Brady[1]

[1]University of Maine Darling Marine Center, 193 Clarks Cove Rd. Walpole, ME 04573

[2]Tongji University, State Key Laboratory of Marine Geology, 1239 Siping Road, Shanghai 200092, P.R. China

[3]University of Southern Mississippi, Department of Marine Sciences, 1020 Balch Blvd, Kiln, MS 39556

[4]Louisiana State University, School of Renewable Natural Resources, 101 Efferson Hall, Baton Rouge, LA 70803

[5]University of Maine, School of Marine Science, 178 Munson Rd, Orono, ME 04473

thomas.kiffney@maine.edu

Oyster aquaculture has seen rapid expansion in Maine with a 5-fold increase in harvest value over the last 10 years. Most Maine shellfish farms are located in narrow estuaries and bays along the convoluted coast where environmental parameters such as food and temperature vary across small spatial scales. In an effort to reduce the risk of site selection in nearshore environments high resolution (100 m and under) satellite imagery from Landsat 8 and Sentinel 2 were used to gather farm scale environmental data across the state. This work 1) highlights previous work validating high resolution products to generate suitability indexes for aquaculture and 2) demonstrates the next phase of satellite site selection with oyster growth models forced with remotely sensed products. Daily climatologies of sea surface temperature were generated from almost a decade of Landsat 8 data while food levels were derived from four years of sentinel 2 data. A satelliter dynamic energy budget model was validated with in-situ data from 4 farm sites and coupled to the satellite data to explore time to market variability along the coast of Maine. This work aims to reduce the risk of site selection for oyster industry in Maine, but the framework can be used to site other existing and emerging in the near shore environment.

ESTUARINE SHORELINE CONSERVATION AND RESTORATION IN THE URBANIZED WATERSHED OF CHARLESTON COUNTY, SOUTH CAROLINA, USA

Peter R. Kingsley-Smith[1]*, Gary W. Sundin[1], Graham A. Wagner[1], Ronald B. Dyar[2], Michael Hodges[2], Elizabeth V. Bell[3], Abigail L. Prochaska[4], and Kim C. Morganello[5]

[1]Shellfish Research Section, Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

[2]Shellfish Management Section, Office of Fisheries Management, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

[3]South Carolina Sea Grant Consortium, 287 Meeting Street, Charleston SC 29401

[4]Coastal Reserves and Outreach (CRO) Section, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

[5]Clemson University Cooperative Extension, 259 Meeting Street, Charleston SC 29401

kingsleysmithp@dnr.sc.gov

Coastal salt marshes are currently being lost at a higher rate than any other wetland habitat. The loss of estuarine habitats, including tidal salt marshes and oyster reefs, is of particular concern as these habitats represent some of the most ecologically-valuable habitats in the coastal region. Such habitat losses are in part attributable to the synergistic relationships between sea level rise, increased storminess, coastline development, and shoreline hardening. With literally dozens of people moving to the Charleston metropolitan region daily, increased coastal development and human activities are generating stressors that can affect both oyster reef and salt marsh habitats. These stressors are leading to the degradation and alteration of coastal marine and estuarine habitats, thus decreasing overall ecosystem health and resiliency within the coastal zone. This presentation will provide highlights of a current NOAA-funded restoration project focused on the urbanized watershed of Charleston County, South Carolina, USA. The presentation will feature overviews of three types of oyster reef restoration (*i.e.,* bagged oyster shell, loose oyster shell, and modified wire reefs), natural fiber-based shoreline protection using coir logs, and community-based salt marsh plantings. It will also introduce a newly developed hybrid training course intended to facilitate the adoption and implementation of living shoreline approaches by the marine contractor industry. The presentation will also briefly touch on other shellfish restoration projects being conducted by the SCDNR Shellfish Research Section involving the use of drones to map coastal habitats and address marine debris in the South Carolina coastal zone.

EFFECTS OF SHIFTS IN SALINITY AND PARASITE LOADING IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Christopher J. Kirby* and Stephen P. Geiger

Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, 100 8th Ave SE, Saint Petersburg, FL 33701

Christopher.kirby@myfwc.com

Managing water flow into Florida estuaries has been an ongoing challenge for maintaining moderately saline habitats and keeping them in a state of optimum health. The eastern oyster, *Crassostrea virginica*, is an optimal indicator species subject to monitor due to its sessile nature, providing an understanding of how extreme salinity shifts in these environments can be detrimental to estuaries. Various life aspects of the eastern oyster can be monitored to gain a better understanding of how these unnatural shifts in water quality affect estuaries.

For *C. virginica*, the density of predators and parasite loading will often increase with rising salinity. Managing water releases from Lake Okeechobee into the Caloosahatchee and Saint Lucie Estuaries can enhance or moderate rise in predator and parasite loading associated with dramatic shifts in salinity. Conditions such as heavy rain events from seasonal storms and hurricanes, or a lack of rain due to both a natural dry season and extended periods of drought can exacerbate dramatic shifts in salinity and *C. virginica* health.

Parasites can compromise the reproductive effectiveness and overall health of the oysters in this environment. Many species of nematodes and cestodes, and the protozoan parasite *Perkinsus marinus*, all play a role in negatively impacting oyster health. Maintaining proper salinity regimes may assist in lowering overall parasite loading in *C. virginica*, and as a result maintain a healthy estuary.

ESTIMATING OYSTER LARVAL DEVELOPMENT AND SUCCESS AT METAMORPHOSIS IN THE WESTERN MISSISSIPPI SOUND

James C. Klein[1]*, Eric N. Powell[1], Xiaodong Zhang[2], Danielle A. Kreeger[3], and Thomas P. Wissing[2]

[1]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39563

[2]University of Southern Mississippi, Hydrographic Science Research Center, 1020 Balch Boulevard, Kiln, MS 39556

[3]Drexel University; Partnership for the Delaware Estuary, 110 South Poplar Street, Suite 202, Wilmington, DE 19801

james.klein@usm.edu

Eastern oysters (*Crassostrea virginica*) are valuable ecologically to the estuaries that they inhabit for the various ecosystem services provided and economically as a fishery resource. Consequently, successful oyster population reestablishment is a central concern for degraded reef systems such as the western Mississippi Sound after the 2019 Bonnet Carré Spillway freshwater diversion mass mortality event and subsequent years of limited recruitment. Effective recovery requires an adequate larval stock competent of timely development and metamorphosis. Larval health and growth through metamorphosis are determined by ambient water temperature, salinity, food quantity, and food quality. Oyster larvae feed on phytoplankton and other organic seston in the water column and require a balanced protein, carbohydrate, and lipid diet to sufficiently develop, survive, and successfully metamorphose. Water samples were collected at seven historical western Mississippi Sound oyster reefs to evaluate water conditions alongside the biochemical constituents in the available food supply throughout the 2021 and 2022 spawning seasons (May through October). Data were placed into a preexisting biochemically-based larval performance model, which is unique in that it includes genetic variation among larval cohorts, tracks weight and length separately to assess condition index, and characterizes larvae and food by their biochemical composition. Synergistic effects of genetic variation, water conditions, and food conditions determine larval performance. A combination of low salinity and inadequate food supply severely constricted larval survivorship in 2021. Larval performance and survivorship are anticipated to improve with augmented 2022 food and water conditions.

EFFECTS OF HYPOXIA AND ACIDIFICATION ON EARLY-STAGE BIVALVES UNDER NATURAL AND ARTIFICIAL CYCLING CONDITIONS

Jeffrey R. Kraemer Jr.* and Christopher J. Gobler

Stony Brook University, School of Marine and Atmospheric Sciences, 39 Tuckahoe Rd. Southampton, NY 11968

Jeffrey.Kraemer@stonybrook.edu

Estuaries can experience diel fluctuations in dissolved oxygen (DO) and pH as a result of the day-night shifting balance between photosynthesis and respiration. During warmer summer months, these fluctuations are intensified, exposing estuarine bivalves to short, repeated episodes of co-occurring hypoxia and acidification. Bivalves are economically and ecologically important species; US oyster and clam aquaculture in 2019 was worth \$219M and \$122M respectively, while ecosystems services have been estimated at \$3,000-\$19,000 hectacre^{-1} year^{-1}. The impacts of diel-cycling DO and pH on bivalves is poorly understood. Here, early-stage bivalves (*M. mercenaria*, *C. virginica*, and *A. irradians*) were subjected to natural and artificial cycling conditions and impacts to larval and juvenile survival and growth were measured. Natural cycling treatments consisted of flow-through water from an adjacent embayment and the same water bubbled to mitigate DO cycling. Artificial cycling treatments consisted of a normal atmospheric equilibrium concentration (NAEC) control, 4-h, 8-h, 12-h moderate cycling (all cycling between low DO (~2 mg L^{-1}) and pH (~7.3) for the specified duration and NAEC values for the remainder of the day), and 12-h super-cycling (low DO and pH to supersaturated DO (~11 mg L^{-1}) and basified (~8.1 pH) values). Mitigation of diel DO cycling in natural water increased juvenile bivalve growth rates by 48% ($p<0.05$). Artificial cycling reduced oyster larvae survival by 74% ($p<0.01$) in super-cycling treatments compared to 4-h treatments, and clam larvae by 66% and 64% ($p<0.01$) in super-cycling treatments compared to 4-h and 8-h treatments, respectively. The consequences of these negative effects will be discussed.

INCIDENCE AND RESTORATION PRIORITIZATION OF RARE AND COMMON SPECIES OF FRESHWATER MUSSELS IN THE TIDAL DELAWARE RIVER, USA

Danielle Kreeger*, Kurt M. Cheng, Matt Gentry, and Leah Morgan

Partnership for the Delaware Estuary, 110 S Poplar St, Suite 202, Wilmington DE, 19801

dkreeger@delawareestuary.org

Freshwater mussel assemblages have been in steep decline as measured by decreasing biodiversity, range, and abundance. Most restoration attention has centered on rare species, despite the implications of losing whole mussel assemblages for critical ecosystem processes and water quality maintenance. There is emerging interest in restoring both common and rare species for their supporting and provisioning ecosystem services; however, inclusion of common species has elicited concern based on the premise that augmenting common species could undermine rare species recovery due to competition or other factors.

To inform restoration, quantitative mussel surveys were performed between 2010- 2015 in the tidal freshwater zone of the Delaware Estuary. Random 1 m^2 quadrats (n=264) were excavated in shallow subtidal areas at nine sites. Mussel percent occurrence, numerical density, and biomass were dominated by *Elliptio complanata* and *Utterbackiana implicata,* and subordinate species included *Atlanticoncha ochracea*, *Sagittunio nasutus,* and *Lampsilis cariosa*. The two dominants were found by themselves in > 38% of the quadrats, whereas *A. ochracea, S. nasutus,* and *L. cariosa* were found by themselves in 3.8%, 0% and 0% of quadrats, respectively. The greatest occurrence of subordinates was in quadrats with >10 mussels. No evidence of negative species interactions was detected, and in fact the occurrence of rarer mussel species may depend on the abundance of foundation species. Restoration programs such as the Mussels for Clean Water Initiative should adopt a phased approach to first establish mussel beds using common species, and then mimic natural assemblages at reference sites by augmenting them with rarer species.

TIME SERIES ANALYSIS OF ABALONE WITHERING SYNDROME: TRACKING RESPONSES IN MICROBIOME AND HOST HEALTH

Emily Kunselman*[1], Blythe Marshman[2], Chelsey Souza[2], James Moore[2], Kristin Aquilino[2], Sarah Allard[1], and Jack Gilbert[1]

[1]Scripps Institution of Oceanography, Center for Marine Biotechnology and Biomedicine, 8750 Biological Grade, San Diego, CA 92122

[2]University of California Davis, Marine Laboratory, 2099 Westshore Rd, Bodega Bay, CA 94923

ekunselm@ucsd.edu

Abalone Withering Syndrome is a disease characterized by presence of an intracellular parasite, *Candidatus Xenohaliotis californiensus* (CaXc), causing abnormal digestive gland morphology, muscle atrophy, and shrinking of the abalone foot tissue. Only a handful of studies have investigated the microbial and host response to this disease. To form a more holistic understanding of abalone withering syndrome, this project investigates how CaXc exposure impacts the microbiome and gene expression of endangered white abalone in captivity. Over a period of 11 months, abalone were exposed to CaXc via the feces of other infected abalone. Fecal samples were taken every 6 weeks to track changes in microbe composition over time. Tissue samples were taken prior to exposure to CaXc and again at the end of the experiment. qPCR is used to quantify pathogen loads in exposed and control animals. This data will be paired to fecal and tissue microbiome sequencing and tissue gene expression to determine the overall impact of the pathogen on the holobiome of the abalone. So far, 16S amplicon sequencing results reveal that fecal microbiome varies through time and this fecal microbiome differs from the internal tissue microbiomes. CaXc-exposure appears to impact microbiomes of the anterior region of the digestive tract more than the distal tissues and the feces.

PATTERNS AND PROCESSES UNDERLYING SPATIOTEMPORAL VARIATION IN BAY SCALLOP DENSITY AND SIZE-STRUCTURE WITHIN AND AMONG THREE SOUNDS OF NORTH CAROLINA

Melissa E. LaCroce[2]*, D. John Brooks[1,2], and David B. Eggleston[1,2]

[1]North Carolina State University, Department of Marine, Earth & Atmospheric Sciences, 2800 Faucette Drive, Raleigh, NC 27695

[2]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

mlacroc@ncsu.edu

Bay scallops (*Argopecten irradians*), once a profitable fishery species in North Carolina (NC), have declined in population size following harmful algal blooms in the late 1980s. Bay scallops are a short-lived species that exhibit variable annual recruitment abundance. Annual commercial landings of bay scallops show large fluctuations through time and are presumed to be driven by factors that affect natural mortality, such as changing climate conditions (i.e., winter freezes, high freshwater runoff), poor water quality, predation, and red tides. Field observations in seagrass beds in 2021 suggest bay scallop populations in many portions of Core Sound, NC are healthy (>0.04 per m^2), yet populations appear to decline sharply during late Fall after spawning and due to natural mortality.

The objectives of this study are to: (1) quantify spatiotemporal variation in mean bay scallop density and size-structure in seagrass beds within Core, Back, and Bogue Sounds, and (2) characterize water quality at each site to attempt to explain spatiotemporal variation in scallop density based on explanatory variables such as salinity, temperature, water depth, chlorophyll-*a* concentrations, Nitrate, and distance from the inlet.

Annual crop species such as bay scallops exhibit substantial year-to-year variability and there is little to no relationship between one year's recruits and the next. For this reason, this study will inform an annual bay scallop survey program that provides information on the status of the scallop population in a timely manner for management decisions.

THE MOLLUSCAN BROODSTOCK PROGRAM: A RETROSPECTIVE ON 25+ YEARS OF IMPROVING WEST COAST OYSTER STOCKS

Chris Langdon[1]*, Blaine Schoolfield[1], Evan Durland[2], Claudio De Melo[3], and Konstantin Divilov[2]

[1]Hatfield Marine Science Center, Oregon State University, 2030 SE Marine Science Drive, Newport, OR 97365

[2]NOFIMA AS, P.O. Box 210, NO-1431 Ås, Norway

[3]Laboratory of Marine Molluscs, Federal University of Santa Caterina, CEP 88061600-Florianópolis, SC, Brazil

chris.langdon@oregonstate.edu

The Molluscan Broodstock Program (MBP) was founded in 1996 at the Hatfield Marine Science Center, Oregon State University, to improve broodstock for the US West Coast oyster industry. The focus of the program has primarily been placed on improving farm yields of Pacific oysters, *Crassostrea gigas*, through selection for higher survival and growth rates. Over the last several years, the MBP has also responded to the twin threats of the highly pathogenic ostreid herpes virus (OsHV-1) and ocean acidification, by selecting for more resistant families. The MBP hatchery practices have also resulted in broodstock that produce larvae that metamorphose at higher rates than those from wild broodstock under both acidified and ambient seawater conditions.

In addition, the MBP has introduced new stocks of the Kumamoto (*C. sikamea*) oyster and the "Midori" strain of the Pacific oyster from the Ariake Bay in southern Japan. This was partly accomplished by the application of strict quarantine protocols and intensive disease-testing. These stocks are naturally exposed to high summer seawater temperatures and OsHV-1 in the Ariake Bay and, consequently, could be more tolerant of future elevated seawater temperatures, resulting from global warming, and OsHV-1 variants on the US West Coast.

EVALUATING ABIOTIC AND BIOTIC FACTORS INFLUENCING HARD CLAM PRODUCTION IN FLORIDA, USA

Susan Laramore[1], Bonnie Getter[1]*, Leslie Sturmer[2], Natalie Anderson[2], Angela Collins[3], Ed Philps[4], and Shirley Baker[4]

[1]Harbor Branch Oceanographic Institute at Florida Atlantic University, Center for Aquaculture and Stock Enhancement, 5600 US Hwy 1 North, Fort Pierce, FL 34946

[2]University of Florida IFAS, Shellfish Aquaculture Extension Program, 11350 SW 153rd Court, P.O. Box 89, Cedar Key, FL 32625

[3]University of Florida IFAS, Florida Sea Grant Extension, 1303 17th St W, Palmetto, FL 34221

[4]University of Florida, Fisheries and Aquatic Sciences, PO Box 110600, Gainesville, FL 32653

Bgetter2021@fau.edu

Over the last decade, *Mercenaria mercenaria* hatchery and nursery operators have experienced seed losses resulting in a negative impact on the industry. Although various factors likely account for this decline, the effects of location, water source, and food source have not been thoroughly evaluated. To address this issue a two-year monitoring program was conducted, in collaboration with industry participants. To determine relationships between water quality, bacterial load, phytoplankton and seed health, water and larval/seed samples were collected and analyzed from 8 hatcheries and 5 nurseries in three geographic locations (NW coast, Gulf of Mexico; SW coast, Tampa Bay; East coast, Indian River Lagoon) that varied in source water (well, surface) and scale of operation during production periods. Water quality parameters evaluated continuously or weekly included salinity, temperature, dissolved oxygen, pH and alkalinity. In addition, hatcheries were sampled biweekly, and water analyzed for ammonia, nitrite, nitrate, and calcium, while nurseries were sampled biweekly to determine phytoplankton abundance and species composition. Once a year, water from each facility was analyzed for ionic, heavy metal and pesticide content. Water, algae, and larvae/seed were evaluated quarterly, and during mortality events, for the presence of bacterial pathogens; larval/seed health was also evaluated histologically.

This comprehensive evaluation of a broad range of abiotic and biotic factors in seed production facilities allows hatchery and nursery operators to make informed management decisions to improve seed health and increase production. Further, a baseline is provided for future reference. Year one results will be presented.

MAINE NEARSHORE MARINE RESOURCES PROGRAM: A NEW NAME AND FOCUS

Ari E. Leach*, Meredith M. White, and J. Kohl Kanwit

State of Maine, Department of Marine Resources, 194 McKown Point Road, West Boothbay Harbor, ME 04575

ari.leach@maine.gov

The Maine Department of Marine Resources (DMR) oversees the management and conservation of marine and estuarine resources in the State through conducting and sponsoring scientific research; promoting and developing the coastal fishing industries of Maine; and cooperating with local, state, and federal officials to implement, administer, and enforce necessary laws and regulations. Recently, the Shellfish Management Program at DMR underwent an overhaul, including a name change to reflect its full management capacity, as well as a staff expansion to increase capacity for expanded monitoring and research. The newly-titled Nearshore Marine Resources Program incorporates monitoring, research, and management of seaweed, marine worms, periwinkles, whelks, and other nearshore species including all shellfish. Expanded capacity will include monitoring and research to address climate change impacts on our managed resources.

The structure of the DMR Bureau of Public Health Nearshore Marine Resources Program, identifying program personnel and responsibilities will be presented as well as an overview of how the NMRP works with municipalities to conserve and manage resources, and outline current research and future projects will be provided.

CAN A FISH FINDER FIND MORE THAN FISH?

Dale Leavitt

Blue Stream Shellfish LLC, 53 Goulart Memorial Drive, Fairhaven, MA 02719

dale@bluestreamaquaculture.com

As shellfish farms move out of the intertidal and into deeper waters, managing the placement of cages/trays and other equipment on the bottom becomes increasingly problematic. An inability to observe the distribution and orientation of structures on the bottom reduces the farm manager's capacity to optimize space use or to ensure the gear is oriented properly to allow for maximum production. A tool to aid in visualizing structures on the bottom is sidescan sonar; however, historically this technology has been expensive to own and challenging to operate properly. With the increasing availability of improved fish finding devices that employ sidescan sonar technology, shellfish farmers in deeper waters now have a tool that permits observation of farm structures on the bottom. Blue Stream Shellfish adapted a Humminbird Solix 15 fish finder to allow for portability among surface vessels and utilized software (SAR Hawk from Black Laser Learning) to develop a mosaic image of the bottom topography and gear placement on their farm(s). With the ability to visualize gear on the bottom, one can move toward better management of our farms and optimize production in our deeper water acreage. This project was supported by a USDA SARE Farmer's Grant – Project # FNE21-989.

TEMPORAL AND SPATIAL COMPARISONS OF OCEAN QUAHOG (*ARCTICA ISLANDICA*) GROWTH ON THE MID-ATLANTIC CONTINENTAL SHELF: FROM THE NEOGLACIAL THROUGH THE TWENTIETH CENTURY

Alyssa M. LeClaire[1,2], Eric N. Powell*[1], Roger Mann[3], Kathleen M. Hemeon[1], Sara M. Pace[1], Vincent Saba[4], Hubert du Pontavice[4,5], and Jillian R. Sower[1]

[1]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564

[2]CSS Inc contracted to NOAA Beaufort Laboratory, 101 Pivers Island Rd, Beaufort, NC 28516 (current affiliation)

[3]Virginia Institute of Marine Science, William and Mary, 1370 Greate Rd, Gloucester Point, VA 23062

[4]Ecosystem Dynamics and Assessment Branch, NOAA Northeast Fisheries Science Center, Geophysical Fluid Dynamics Laboratory, Princeton University Forrestal Campus, 201 Forrestal Rd, Princeton, NJ 08540

[5]Princeton University, Atmospheric and Oceanic Sciences Program, 300 Forrestal Road, Sayre Hall, Princeton, NJ 08540

Eric.n.powell@usm.edu

Ocean quahogs (*Arctica islandica*) provide long-term records of climate change, transgressing and regressing across the continental shelf numerous times during past cold and warm climatic periods. This species' availability in the death assemblage off Delmarva (DMV) over a wide geographic and temporal range permitted growth rate comparisons with living animals from New Jersey, Long Island, and Georges Bank. Growth rates of subfossils representing previous Holocene cold periods were as fast or faster than the growth rates of living individuals. Moreover, growth rates for subfossil ocean quahogs alive between 1740 and 1940 were more rapid than contemporaneous living individuals born during the same time. Higher growth rates of subfossil *A. islandica* suggest that conditions supported near maximum growth during each of the cold periods after the Holocene Climate Optimum, possibly due to increased food supply in shallow water. Considering DMV animals that lived during the past 200 years, young animals become less common after approximately 120 years before present. Following the disappearance of young animals, shifts in age distribution showed a steady loss of increasingly old animals as time progressed. Unlike many bivalves, ocean quahogs record evidence of range recessions in the temporal abundance of the juvenile animals and a shift in the trailing edge of the range is a 100+ year process. This study is the largest spatial and temporal growth comparison of *A. islandica* ever recorded and the first record of the process by which this species' inshore range regresses as temperatures rise.

BUOYS AND AUTONOMOUS SURFACE VEHICLES FOR AQUACULTURE: AN INEXPENSIVE HARMFUL ALGAL BLOOM MONITORING APPROACH

Douglas R. Levin[1]*, Steve L. Morton[2], and William Lantham[3]

[1]Watershed Innovation Laboratory, Washington College, 300 Washington Avenue, Chestertown, MD 21620

[2]NOAA/NOS/NCCOS HAB Monitoring and Reference Branch, 331 Fort Johnson Rd., Charleston, SC 29412

[3]Chief Technology Officer, Tridentis, LLC, 1199 N. Fairfax Street, Suite 410, Alexandria, VA 22314

Dlevin2@washcoll.edu

The inexpensive, rugged, compact buoy, BOB (Basic Observation Buoy), and FLO (dock-mounted), accommodates standard water quality sondes that can be "daisy chained". They record, for example, water temperature, salinity, conductivity, DO, turbidity, and chlorophyll-*a*. Available sensors include Phycocyanin/Phycoerythrin. Depth of measurement is adjustable from 22" to 45" by extending the telescoping center shaft, or cabling beneath the shaft to the bottom. The buoy is used for aquaculture, water quality monitoring and engineering applications. It is shipped globally in stackable 24"x18"x18" cartons. Ready to sample, BOB weighs less than 20lbs and can be deployed by one person from a small boat.

The buoy was designed to use In-Situ's VuLink for data telemetry. Communication occurs through cell phone or satellite transmissions. Once powered on, the sonde transmits data to a central, Internet accessible, data portal (Hydro-Vu). The Sonde and Vu-Link contain the buoy's 3 D Cell batteries which will transmit data for over 3 years.

The Advanced Coastal Monitor (ACM 3) is an autonomous surface vehicle equipped with the same water quality sensors and survey grade GPS that collects geolocated water quality data overlapping the buoy location(s). The spatial mapping across the aquaculture lease site, when coupled with the buoy data, allows for temporal changes in the data to be identified. The ACM 3 can simultaneously collect GPS tagged bathymetric, side scan, and water current data. Combined with the water quality information we can assess the best locations to grow oysters. This technology can be applied to any sessile/benthic aquaculture site and expanded to finfish grow areas.

The future objective is to access a QR code at the seafood market to see the water quality for where the seafood was grown and verify the temperatures and conditions as it was handled/shipped/trucked to the store.

GROWTH OF THE BANDED TULIP (*CINCTURA HUNTERIA*) IN TAMPA BAY, FLORIDA

Erica A. Levine* and Stephen P. Geiger

Fish & Wildlife Research Institute, Florida Fish & Wildlife Conservation Commission, 100 8th Ave. S.E., St. Petersburg, FL 33701

Erica.Levine@myfwc.com

Growth of banded tulips (*Cinctura hunteria*, G. Perry, 1811) was assessed using three methodologies: mark-recapture studies, laboratory growth, and electronic length-frequency analyses (ELEFAN). Size and age at maturity were then estimated using histological analyses. Monthly surveys occurred from October 2018 to October 2020 at two sites (three habitats at each site: 100-m^2 each of oyster reef, seagrass, and soft sediment) in Tampa Bay, Florida. The shell lengths of all banded tulips were measured, and the snails were tagged. Additional shell lengths were opportunistically collected from snails located within a 5-m radius of the survey areas. An initial group of 27 snails (with replacement as needed) were collected in February 2019 and maintained in the laboratory through February 2021 for monthly growth increments. Histological samples were collected every other month and processed for size, sex, and reproductive stage. The ages of wild and captive snails were estimated using ELEFAN size-at-age ranges to further compare growth curves between wild and captive populations.

Between the two sites, 1,286 snails were measured, 521 of which were tagged for mark-recapture analyses. The longest period between tagging and recapture was 428 days. Based on 69 recaptured snails, in situ growth rate was 0.03 mm/day. Snails in the laboratory exhibited an average growth rate of 0.02 mm/day, and ELEFAN modeled rate of wild snail growth was 0.02 mm/day. Growth rates were comparable between the three methods. Maximum age was estimated to be five years, and histology supports 50% maturity at approximately 40 mm and two years old.

DENSITY-DEPENDENT MATRIX-BASED MODELING OF BLUE CRAB, *CALLINECTES SAPIDUS,* POPULATION DYNAMICS IN THE CHESAPEAKE BAY

Jiakun Li*, A. Challen Hyman, Junping Shi, and Romuald N. Lipcius

William & Mary, 200 Stadium Dr, Williamsburg, VA 23186

jli42@wm.edu

The blue crab, *Callinectes sapidus,* is an economically and ecologically important species along western Atlantic coastal estuaries. The blue crab is heavily exploited, supporting one of the most valuable fisheries in the western Atlantic and Gulf of Mexico. Recent declines in Chesapeake Bay blue crab spawning stock necessitate understanding of the role of fishing pressure and exploitation in driving population dynamics. A density-dependent, stage-structured matrix model of the blue crab was developed to determine (1) the maximum sustainable yield (MSY) based on exploitation rate and (2) the influence of density dependence and other survival rates on the long-term stability and growth rate of the population. First, it was found that the blue crab population can withstand annual natural mortality rates as high as 1.1 without collapsing (i.e., that a non-zero stable equilibrium exists). Second, it was determined the critical values of fall survival and spring survival at which the population loses its stability at the non-zero equilibrium. Additionally, the equilibrium population abundance at various fishery exploitation levels and the corresponding maximum sustainable yield were calculated. It was determined that the blue crab population can support annual levels of exploitation up to 35% without collapsing. Furthermore, by solving for the optimized exploitation level, the MSY for the Chesapeake Bay blue crab population was calculated, and that exploitation levels needed to produce MSY were much lower than 35%.

RANKING ECOSYSTEM IMPACTS OF THE CHESAPEAKE BAY BLUE CRAB (*CALLINECTES SAPIDUS*) USING EMPIRICAL GAUSSIAN GRAPHICAL MODELS

Dong Liang*, Thomas J. Miller, Geneviève M. Nesslage, and Michael J. Wilberg

University of Maryland Center for Environmental Science, Chesapeake Biological Laboratory, P.O. Box 38, Solomons, MD 20688

dliang@umces.edu

Gaussian graphic models (GGM) are used to understand the influence of climatic, water quality, and biotic variables on the dynamics of blue crabs in the Chesapeake Bay. Estimates of blue crab recruitment and variability in the Bay for 1990-2017 were developed from the winter dredge survey. Climatic variables considered included the North Atlantic Oscillation (NAO), Susquehanna River discharge, and wind forcing at Norfolk, Virginia. Water temperature, salinity, and the hypoxic volume in the Chesapeake Bay were considered water quality variables. The relative abundance of striped bass, a potential predator of blue crab, was considered as a forcing variable in our GGM. Both direct and indirect ecosystem effects were significant elements in the most parsimonious models for both the level and variability in blue crab recruitment. The graph for the level of recruitment was less connected than the graph for the variance in recruitment. For the level of recruitment, the direct effects of age-1+ crabs and summer salinity were significant. Significant indirect effects on the recruitment level included the phase of the NAO in summer, spring, summer, and winter discharge, and the hypoxic volume. Significant direct effects of age-1+ crabs, striped bass abundance, and wind speed were detected for the variance in recruitment. Hypoxic volume was the only significant indirect effect of water quality on the variance in recruitment. These findings of significant ecosystem effects on recruitment also suggest that exploration of ecosystem-based approaches to understanding and possibly managing harvests of this species is warranted.

RESTORATION OYSTER REEFS DO NOT PROVIDE SETTLEMENT AND EARLY NURSERY HABITAT FOR THE BLUE CRAB, *CALLINECTES SAPIDUS*

Romuald N. Lipcius

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

rom@vims.edu

Restoration oyster reefs provide diverse ecosystem services, including serving as foraging grounds for large juveniles and adults of the blue crab, *Callinectes sapidus*. In a previous field experiment, azoic oyster shell was used as settlement and nursery habitat by post-larvae and young juveniles <25 mm carapace width (cw), yet other field studies have not found young juveniles in mature oyster shell reefs. This study tested the hypothesis that blue crab post-larvae and young juveniles use mature oyster reefs as nursery habitat with a manipulative field experiment. In summer 2019, shallow subtidal (<2 m depth) oyster shell reefs of 4 reef heights (7.5, 15, 22.5 and 30 cm; diam = 50 cm) were constructed in the York River, Chesapeake Bay. After 2 years, reefs had developed a natural reef community. In summer 2021, artificial seagrass plots of similar area were randomly interspersed with the reefs during blue crab settlement and recruitment. In early fall, reefs and seagrass plots were surrounded by nets to prevent crab escape and sampled with suction gear. All seagrass plots harbored newly recruited, young juvenile blue crabs (2-25 mm cw), whereas no juvenile crabs colonized the oyster reefs, which were inhabited by high densities of mud crabs. In a complementary mesocosm experiment, mud crabs excluded juvenile blue crabs from shell reef habitats. It was concluded that mud crabs inhabiting mature oyster reefs exclude young juvenile blue crabs. Consequently, restoration oyster reefs provide foraging grounds, but not settlement or nursery habitat for young juvenile blue crabs in Chesapeake Bay.

ONTOGENETIC VARIATION IN BLUE CRAB (*CALLINECTES SAPIDUS*) USE OF SEAGRASS NURSERIES: SURVIVAL AND ABUNDANCE VARY BY MICROHABITAT

Romuald N. Lipcius[1]*, Jessica Schulman Farrar[1,2], Amanda M. Bromilow[1,3], and Robert J. Orth[1]

[1]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[2]Versar, 9200 Rumsey Road, Columbia, MD 21045

[3]NOAA Chesapeake Bay Office, 200 Harry S. Truman Parkway, Suite 460, Annapolis, MD 21401

rom@vims.edu

Ontogenetic shifts in habitat use of nursery grounds occur due to tradeoffs in predation risk and growth rate between habitats. Studies focused on shifts from one habitat type to another, ontogenetic movement *between* different habitat types, such as the dispersal of larger juvenile blue crabs from seagrass to unvegetated habitats. Juvenile fish and invertebrates may also shift *within* a habitat, which has only rarely been investigated in marine species. This field study investigated the role of *within-habitat* variability on survival and abundance of juvenile blue crabs in seagrass beds. Manipulative field experiments and field sampling were conducted in seagrass beds dominated by eelgrass, *Zostera marina*, with scattered patches of widgeon grass, *Ruppia maritima,* and the exotic macroalga, *Gracilaria vermiculophylla,* in the York River, Chesapeake Bay. Tethering and suction sampling were used in artificial and natural seagrass patches varying in seagrass shoot density and percent cover. Juvenile crab size varied from 3-45 mm carapace width (cw). Survival was highest and approached 100% for the largest juveniles (17-45 mm cw) at shoot densities >1000 m^{-2} and 75-100% cover. Intermediate-size crabs (10-16 mm cw) had highest survival at shoot densities >500 m^{-2}. In contrast, small juveniles (3-7 mm cw) survived best at low shoot densities 0-350 m^{-2} and percent cover. Abundance patterns by size were similar. Differences in survival and abundance by juvenile size may result from cannibalism of small crabs by larger juveniles in dense eelgrass and indicate that population sampling in seagrass nurseries must be across the range of seagrass density.

COMPARISONS OF WILD AND FARMED SEAFOOD: NUTRITION PROFILES AND SAFETY ATTRIBUTES

Chengchu Liu

University of Maryland College Park, Maryland Sea Grant College Program, 11868 College Backbone Rd., Princess Anne, MD 21853

cathyliu@umd.edu

Aquaculture has a significant ecological advantage over wild-caught fish and husbandry animals (i.e., cattle and swine) since aquaculture fish and shellfish are far more efficient at converting feed. Therefore, aquaculture growth is critical to further increase seafood supply; however, aquaculture is often portrayed negatively (i.e., with lower nutritional quality and safety than wild seafood). This presentation will provide an overview of nutrition values and safety attributes of wild and farmed fish and shellfish. Literature including USDA FoodData Central food composition data were reviewed to compare major nutrients or proximate compositions, protein quality (amino acid profiles), lipid profiles, macro and trace mineral contents, vitamins, potential food safety concerns, and control strategies.

GENOMIC SELECTION MODELS FOR THE GROWTH AND SURVIVAL TRAITS OF THE EASTERN OYSTER IN LOW SALINITY WATER

Ming Liu*, Brittany Wolf-Bryant, and Jon Farrington

Morgan State University, Patuxent Environmental and Aquatic Research Laboratory, 10545 Mackall Road, Saint Leonard, MD 20685

ming.liu@morgan.edu

Improvement of growth and survival in low salinity waters has been one primary breeding goal of eastern oyster aquaculture in the upper and middle Chesapeake Bay. With the development of a 66K high-density single nucleotide polymorphisms (SNP) array by Eastern Oyster Breeding Consortium, it is possible to utilize genomic selection, a selective breeding based on the associations between genome-level SNP and the target traits, to expedite genetic gains for the target traits.

In this study, 768 eastern oysters (364 survived and 404 dead) were genotyped from an acute low-salinity challenging experiment. The experiment oysters were randomly collected from a two-years old oyster population that were bred from a wild population from Patuxent River, a tributary of middle Chesapeake Bay. The shell height (SH) and total weight (TW) were measured before the experiment. The survival status (SS) was recorded as 0-dead or 1-survived. The single-trait models (GBLUP, rrBLUP, Bays A, B and Cpi, etc.) and multiple-traits model are respectively employed to calculate the breeding values. Cross-validations were performed to estimate the model accuracies. The heritabilities of SH, TW and SS are 0.21, 0.11 and 0.35. The average accuracies of single trait model are very similar in SH (~0.55), but varied a lot in TW and SS. The highest accuracy for TW was found in GBLUP (0.69), and for SS was found in Bayes B (0.76). Multiple-traits analysis showed significant phenotype correlation and genetic correlation between SH and TW, the average accuracy for SH increased to 0.94 after involving TW trait.

PILOT-SCALE DEPURATION DEMONSTRATES THE SUITABILITY OF NON-PATHOGENIC *VIBRIO PARAHAEMOLYTICUS* AS A SURROGATE FOR COMMERCIAL-SCALE VALIDATION STUDIES

Spencer L. Lunda[1]*, Samantha Kilgore[2], Jennifer Hesser[1], Joy Waite-Cusic[2], and Carla B. Schubiger[1]

[1]Oregon State University, Hatfield Marine Science Center, Carlson College of Veterinary Medicine, 2030 SE Marine Science Dr., Newport, OR 97365

[2]Oregon State University, Department of Food Science and Technology, 100 Wiegand Hall, Corvallis, OR 97331

Lundas@oregonstate.edu

Oysters are often consumed raw, but are known to harbor *Vibrio parahaemolyticus*, a bacterial pathogen. Shellfish producers have proposed using depuration systems to reduce pathogen loads in oysters. Before industrial application, the efficacy of depuration must be validated using appropriate conditions. This study describes the initial experimental phase to i) compare the efficacy of depuration in various oyster species, ii) demonstrate the suitability of non-pathogenic *V. parahaemolyticus* as a surrogate, and iii) optimize depuration conditions at pilot-scale to identify variables likely to achieve >3.0-log reduction of *V. parahaemolyticus*.

Three oyster species (*Crassostrea gigas, C. sikamea, C. virginica*) were placed in containers of autoclaved seawater containing a cocktail of either non-pathogenic (NP) or pathogenic (P) strains of *V. parahaemolyticus*. Inoculated oysters were then placed in a pilot-scale depuration system. Oysters were sampled every 24 hours from days 0 through 7 and *V. parahaemolyticus* was enumerated using standard serial dilution and spread plating techniques on TCBS agar.

The inoculation procedure used in this study achieved at least a 5 log CFU/g *V. parahaemolyticus* in *C. gigas* and *C. sikamea*, with more variable results in *C. virginica.* Accumulation of NP and P cocktails was similar for all oyster species. Depuration at 11°C achieved a >3 log CFU/mL reduction of the P cocktail in *C. gigas* and *C. sikamea* tissues within five days, whereas *C. virginica* averaged a 2.8 log CFU/mL reduction. NP *V. parahaemolyticus* was reduced at a comparable rate to P *V. parahaemolyticus* indicating its suitability as a surrogate for commercial validations.

AN ECOLOGICAL THREAT AND AN ECONOMIC RESOURCE: THE ATLANTIC BLUE CRAB IN MEDITERRANEAN WATERS

Giorgio Mancinelli[1,2,3]

[1]University of Salento, Department of Biological and Environmental Sciences and Technologies - DiSTeBA, SP Lecce-Monteroni, 73100 Lecce, Italy

[2]Consorzio Nazionale Interuniversitario per le Scienze del Mare - CoNISMa, Piazzale Flaminio 9, 00196 Rome, Italy

[3]Italian National Research Council, Institute of Marine Biological Resources and Biotechnologies - CNR-IRBIM, Largo Fiera della Pesca 2, 60125 Ancona, Italy

giorgio.mancinelli@unisalento.it

Introduced to Europe at the beginning of the 20th century, *Callinectes sapidus* was, and to date has been, extensively recorded in Mediterranean waters. The species is considered invasive and ecologically and economically harmful, though there is a growing acknowledgement of its potential as a shellfish product for alimentary and non-alimentary purposes.

Here a synthesis is made of the conclusions of a risk assessment of the species funded by the European Commission and of the management measures therein proposed. In addition, a review of the projects currently under development at a national and international level is performed. An effort is made to highlight differences and commonalities in the strategies adopted to address and overcome information voids in e.g., stock abundances or on the magnitude and nature of the impacts exerted by the blue crab on artisanal fisheries.

Emphasis is put on the actions implemented in “UseIT”, a project funded in 2022 by the Italian National Research Council - CNR. The project is dedicated to the development of novel approaches in the management and economic exploitation of marine and terrestrial bioinvaders. The blue crab is taken as a key case study, where the need to control an invasive species and mitigate its ecological impact can be harmonized with the opportunity to value it as a shellfish product.

REVISITING THE NEWELL NUMBER: ESTIMATING PRE-COLONIAL OYSTER ABUNDANCE AND ECOLOGICAL SERVICES IN THE CHESAPEAKE BAY

Roger Mann[1]*, Melissa Southworth[1], Mitchell Tarnowski[2], James Wesson[3], Alexandria Marquardt[1], Juliana A. Harding[4], and Tamia Rudnicky[1]

[1]Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, VA 23062

[2]Maryland Department of Natural Resources, 580 Taylor Ave., B-2, Annapolis, MD 21401

[3]12050 Freeport Road, Gloucester, VA 23061

[4]Coastal Carolina University, Department of Marine Science, P.O. Box 261954, Conway, SC 29528

rmann@vims.edu

Estimates of rates of filtration of the volume of the Chesapeake Bay by precolonial oyster populations by Roger Newell remains as probably the most widely quoted example of benthic pelagic coupling in mid-latitude estuaries, and a rationale for restoration to provide ecological services for the entire estuarine food web. The Newell calculation builds on records of oyster harvest to “recreate” a pre-colonial estimate of population size and associated filtration capacity. Herein, the underlying estimate of oyster population extent and demographics by an alternative approach based on emerging knowledge of reef accretion rates in the recent Holocene commensurate with sea level rise is revisited. The Chesapeake Bay is approximately 10,000 years old, so sea level rise and thus bay inundation during this period is well reported. Rates of oyster recruitment, growth, mortality, and longevity are amenable to simple models that provide accretion rates adequate to maintain reef development during inundation. Estimates of reef footprints, including the option for fringing reefs, are available for both Maryland and Virginia. When demographics and spatial extent are combined, seasonal changes in filtration, and thus rates of benthic-pelagic coupling can be explored.

WESTERN BLOT STUDY OF GABA AND HISTAMINE RECEPTORS IN PERIPHERAL TISSUES OF *CRASSOSTREA VIRGINICA*

Kera Mansfield[1]*, Rosanne Wallach[1], Tia Foster[1], Christopher Pierce[2], Ruhamah Souffrant[1], Margaret A. Carroll[1], and Edward J. Catapane[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

kmansfield7885@gmail.com

Histamine and GABA are neurotransmitters in invertebrates, but rarely have been studied in bivalves. Previous research with *Crassostrea virginica* showed histamine is involved in mantle rim light reception influencing gill lateral cell cilia beating. HPLC and immunohistofluorescence detected histamine and H2 receptors in ganglia of *C. virginica*. The H1 antagonists, diphenhydramine and H2 antagonist famotidine, blocked the actions of histamine at the mantle rim. GABA was shown to have inhibitory ganglionic action on serotonin excitation of gill lateral cell cilia, that is blocked by the GABA antagonist bicuculline methchloride. Histo-immunofluorescence found GABAa receptors in cerebral and visceral ganglia. To study if histamine and GABA innervate peripheral tissues in *C. virginica* gel electrophoresis and Western Blotting was performed using 1° antibodies to histamine H1R and H2R; and GABAa and GABAb receptors followed by FITC 2° antibodies. Gill, mantle rim, palps, and heart were dissected and homogenized. Protein concentrations were determined by the Bradford method. Laemmli-treated samples were wet-loaded onto polyacrylamide gels then electrophoresed in Tris/glycine SDS buffer. Gels were transferred onto nitrocellulose membranes, incubated with 1° antibodies, then FITC 2° antibodies and viewed with an iBright Fl1500 image analyzer. Western Blots revealed H1R, H2R, GABAa and GABAb receptors in palps, heart, mantle, and gill. The study demonstrates histamine and GABA also have peripheral neurotransmitter roles in various tissues. These findings will lead to studies exploring peripheral physiological roles of histamine and GABA in *C. virginica*. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP, PSC-CUNY 62344-0050 and 62344-0051.

STRATEGIES FOR COST-EFFECTIVE GENOMIC BREEDING OF *CRASSOSTREA VIRGINICA* IN TEXAS

Joseph L. Matt[1]*, David S. Portnoy[1], and Christopher M. Hollenbeck[1,2]

[1]Texas A&M University - Corpus Christi, Department of Life Sciences, 6300 Ocean Dr, Corpus Christi, TX 78412

[2]Texas A&M AgriLife Research, 600 John Kimbrough Boulevard, Suite 512, College Station, TX 77843

joseph.matt@tamucc.edu

Genomic selection can enhance the rate of genetic improvement in selective breeding programs. For regional, small-scale breeding programs, as is common for shellfish species, genomic selection may only be economically viable if implemented at much lower cost than is typical for traditionally bred species. Broodstock sourcing regulations for *Crasssostrea virginica* in Texas necessitate a regional, low-cost breeding program to supply Texas farms with selectively bred stocks. To scale genotyping costs appropriately, high-throughput, low density genotyping is being developed with multiplexed PCR amplicon sequencing (GT-seq) to combine to higher density panels or whole genomes through imputation. Additionally, efficient logistical strategies of the breeding program are under evaluation, including early-stage combining of families, exploiting highly variable evaluation sites, and high throughput collection of DNA.

GENETIC PARAMETERS FOR HEAT AND SALINITY STRESS TOLERANCE IN NORTHERN GULF OF MEXICO EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Paul McDonald* and Eric Saillant

The University of Southern Mississippi, Gulf Coast Research Laboratory, 703 E Beach Dr, Ocean Springs, MS 39564

Paul.McDoanld@usm.edu

Summer mortalities in Gulf of Mexico eastern oyster have been linked to excessively high temperatures, and chronic exposure to low salinity. In this study, the feasibility of improving tolerance to these two stresses by selection was evaluated in common garden experiments employing a pool of 160 families. Thermal tolerance was evaluated at the seed and adult stages by applying a sustained temperature of 38-39°C to the family pool until all oysters expired. Low salinity challenges on juvenile and adult stages applied a salinity of 2.5. Survival duration of individual oysters during challenges was recorded and tissue samples were taken for genotyping and parentage assignment. The condition index was also recorded at the end of the juvenile salinity challenge.

During thermal challenges, the peak of daily mortality and 100% mortality occurred after 5 and 7 challenge days, respectively in adults versus 11 and 22 days in seed oysters. Juvenile oysters tested in the low salinity challenge experienced only 2.3% mortality over 39 days. Their response will be characterized based on the condition index. In contrast, a peak in mortalities was observed after 14 days at low salinity in the adult challenge followed by complete mortality at 25 days. During both adult challenges, oysters spawned during the acclimation period, suggesting that their reduced tolerance was related in part to spawning activity. Challenged oysters will be assigned to parents using a 192 SNP array. Heritability of tolerance traits and genetic correlations will be estimated using generalized linear models.

POPULATION GENETIC STRUCTURE AND TRANSCRIPTOMIC RESPONSE TO LOW SALINITY IN *MERCENARIA MERCENARIA*

Jan R. McDowell*, Leslie S. Youtsey, Ann J. Ropp, Richard A. Snyder, Ellen E. Biesack, and Kimberly S. Reece

Virginia Institute of Marine Science, William & Mary, P.O. Box 1346, Gloucester Point, VA 23062

mcdowell@vims.edu

The northern quahog (= hard clam), *Mercenaria mercenaria* (Linnaeus, 1758), is an economically valuable aquaculture species along the North American Atlantic and Gulf coasts, with the industry primarily limited to higher salinity habitats. To inform breeding of site appropriate aquaculture broodstocks, DArTseq™ genotyping-by-sequencing was used to characterize the genetic stock structure of wild clams collected from 15 locations from Prince Edward Island, Canada, to South Carolina, USA. A total of 4,960 single nucleotide polymorphisms from 448 individuals was used to identify five genetic breaks separating six genetically distinct populations: Canada, Maine, Massachusetts, Mid-Atlantic, Chesapeake Bay and the Carolinas (F_{ST} 0.003-0.046; $p < 0.0001$). Based on these results, population specific clam lines were created in the spring of 2019 and 2021. The low salinity stress response was assessed using RNA sequencing data from laboratory experiments with eight clam lines and crosses exposed to salinities of 35 and 15. There were 545 genes in the gills of adult hard clams and 465 genes in the whole bodies of juvenile hard clams that were significantly differentially expressed between salinities of 15 and 35. Genes showing the greatest differences included those in the categories of heat shock proteins, apoptosis, and cellular polarity. Genes differentially expressed by different clam lines included heat shock proteins, inorganic ion regulators, and free amino acid isomerase enzymes. Results from this study allow for a better understanding of how hard clams respond to low salinity stress and could inform breeding programs for enhancing low salinity tolerance in hard clams.

WILD SCALLOP POPULATION RESILIENCE: USING MULTIGENERATIONAL STUDIES TO ESTIMATE ROBUSTNESS AND ADAPTIVE POTENTIAL TO RAPIDLY CHANGING OCEAN ACIDIFICATION

Katherine McFarland*[1], Samuel Gurr[2], Genevieve Bernatchez[1], Dianna Padilla[3], Mark S. Dixon[1], Lisa Guy[1], Lisa Milke[1], Matthew E. Poach[1], Alison Novara[4], Deborah Hart[5], Louis Plough[6], Dylan Redman[1], George Sennefelder[1], Sheila Stiles[1], Gary Wikfors[1], and Shannon L. Meseck[1]

[1]NOAA Fisheries NEFSC, Milford Laboratory, 212 Rogers Ave, Milford, CT 06460

[2]National Research Council Post-Doctoral Associate at NOAA NMFS, 212 Rogers Ave, Milford, CT 06406

[3]Stony Brook University, 100 Nicolls Rd., NY 11794

[4]EPP/MSI Undergraduate Scholarship Program, NOAA, 212 Rogers Ave, Milford, CT 06460

[5]NOAA Fisheries, 166 Water St., Woods Hole, MA 02453

[6]University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Rd. Cambridge, MD 21613

katherine.m.mcafaland@noaa.gov

For calcifying organisms, such as bivalves, short term exposure to increased ocean acidification (OA; elevated ρCO_2) reduces growth, increases mortality, and disrupts shell formation; however, much of the current work has been conducted using short exposures and the effects of prolonged exposure throughout the lifespan and across generations are less understood. Current model projections assume bivalves in the future will respond to OA conditions in the same way as populations studied today, without consideration for adaptation. Therefore, to better understand the physiological effects of prolonged OA exposure, bay scallops were exposed over two generations of continuous exposure to three OA conditions (500, 800, 1200 µatm). Larvae were not tolerant of 1200 µatm ρCO_2 resulting in lethal abnormalities when exposure began during embryogenesis. When exposure to 1200 µatm ρCO_2 was initiated in post larval scallops, survival was high, but growth was slowed. During exposure to 500 and 800 µatm over the lifespan (15 months), no significant difference in shell growth was observed, but subtle physiological changes were detected between treatments, suggesting disruptions to feeding efficiency. Additionally, moderately elevated OA led to increased gonad index, but decreased adductor muscle tissue weight compared to the low OA treatment. This work suggests that OA results in physiological alterations that may affect the energy budget and supports previous work published in the literature. Ongoing work will characterize the genomic response among treatments and generations. Ultimately, this work aims to characterize the resilience of scallop populations to OA and determine their capacity for adaptation across generations.

WHAT SHELLFISH FARMERS WANT THE GOVERNMENT TO DO TO REDUCE CLIMATE IMPACTS ON THEIR BUSINESSES

Sally McGee*[1] and Bill Dewey[2]

[1]The Nature Conservancy, 4245 Fairfax Dr #100, Arlington, VA 22203

[2]Taylor Shellfish, 130 SE Lynch Rd, Shelton, WA 98584

smcgee@tnc.org

In 2022, the Shellfish Growers Climate Coalition conducted an in-person survey of shellfish farmers about the impacts of climate change on their businesses. The purpose of the survey was to understand current climate impacts on shellfish farms, what farmers are already doing to mitigate impacts, and what farmers want from the government in response to these impacts. The survey was conducted at industry association meetings in California, Washington, Louisiana, and Maine.

Respondents were asked ranked choice questions about current climate-related challenges, actions they are taking to address those challenges, and what they would like decision makers to do in the next five years to mitigate climate impacts. For each ranked choice question, respondents were also given the opportunity to provide an open-ended answer. This session will share the results and interpretation of the survey.

A COMPARATIVE STUDY OF THE BIODIVERSITY ASSOCIATED WITH FALLOW, ACTIVELY FISHED AND NON-FISHED EUROPEAN OYSTER (*OSTREA EDULIS*) BEDS

Oisín Medlar[1], Rosalind Graves[1], Sarah C. Culloty[1,2,3], and Sharon A. Lynch[1,2,3]*

[1]University College Cork, School of Biological, Earth and Environmental Sciences and Aquaculture and Fisheries Development Centre, Distillery Fields, North Mall, Cork, T23 N73K, Ireland

[2]University College Cork, Environmental Research Institute, Ellen Hutchins Building, 6 Lee Rd, Sunday's Well, Cork, T23 XE10, Ireland

[3]MaREI Centre, Environmental Research Institute, Beaufort Building, University College Cork, Ringaskiddy, Co. Cork, P43 C573, Ireland

s.lynch@ucc.ie

Bivalve aggregations are biodiversity hotspots and provide multiple ecosystem goods and services that are important ecologically and commercially. Bivalve aquaculture and fisheries are typically viewed as having a negative impact on biodiversity due to the fishing of market sized stock via dredging. Commercial bivalve beds are transitory; however, such ephemeral habitats are known to support unique biodiversity, dispersal strategies and adaptations that are distinct from or absent in species found in more stable habitats. Few studies have catalogued flora and fauna diversity at bivalve beds with varying levels of fishing disturbance.

This study recorded biodiversity present on fallow (two years post fishing), actively fished (4-year-old bed) and undisturbed (2-year-old bed) European oyster (*Ostrea edulis*) beds monthly over three months. Each bed was dredged a minimum of three times resulting in a total dredge area of 78m^2/bed. The flora community consisted of all three phyla, three classes, and twenty-two species while the fauna community consisted of eight phyla, sixteen classes and fifty-two species. Minimal differences in biodiversity were observed between all three bed types with the non-fished bed having slightly higher diversity (n=14 flora, n=34 fauna) followed by the actively fished (n=13 flora, n=32 fauna) and the fallow bed (n=12 flora, n=28 fauna). These results demonstrate how on-bottom oyster aquaculture can support a diverse ecosystem. This data supports the expansion of native oyster restoration efforts throughout Europe and may offer a means to restore localized biodiversity, as well as promoting commercial and noncommercial native bivalve species restoration globally.

JUVENILE PACIFIC OYSTER GROWTH AND FOOD RESOURCES IN EELGRASS HABITAT OF VARIABLE SHOOT DENSITY IN A US WEST COAST ESTUARY

Julianne Merrill[1]*, Brett Dumbauld[2], Brooke McIntyre[2], Fiona Thomas Nash[3], and George Waldbusser[4]

[1]Oregon State University, Marine Resource Management Program, 104 CEOAS Admin. Bldg. Corvallis, OR 97331

[2]Agricultural Research Service, U.S. Dept. of Agriculture, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, OR 97365

[3]Oregon State University, Dept of Fisheries, Wildlife and Conservation Science, 430 Strand Agriculture Hall, Corvallis, OR 97331

[4]Oregon State University, College of Earth Oceanic and Atmospheric Sciences, 2651 SW Orchard Avenue, Corvallis, OR 97331

merrilju@oregonstate.edu

Pacific oyster (*Crassostrea gigas*) aquaculture often overlaps with the federally protected native eelgrass, *Zostera marina,* in US West coast estuaries. In this study, juvenile oyster spat were deployed on tiles and shell growth evaluated within eelgrass and unvegetated habitat in Tillamook Bay, Oregon. Short-term continuous time series of water quality metrics (pH, temperature, salinity, turbidity, and chlorophyll-*a*) and bi-monthly discrete water samples collected to evaluate suspended particulate matter (SPM), particulate organic matter (POM), and chlorophyll-a concentrations within dense eelgrass and unvegetated habitats. Stable isotope values ($d^{15}N$ and $d^{13}C$) derived from oyster tissue were compared to determine whether oyster diet and food sources differed between habitats. Despite significant variation in shell growth by site (55%), results indicated that eelgrass shoot density was a significant predictor of oyster shell growth (7% of the variation). No evidence of sustained pH buffering was found within eelgrass habitat, but eelgrass consistently influenced turbidity and chlorophyll-*a*. Discrete measures of seston (SPM) and potential food concentration (POM and chlorophyll-*a*) were greatest at sites with intermediate shoot density. Oyster tissue was enriched in $d^{15}N$ and depleted in $d^{13}C$ with increased eelgrass density, indicating that oysters in eelgrass consumed different food sources than those in unvegetated habitat. Although differences in temperature, turbidity, barnacle recruitment, and water movement likely contributed to observed site differences eelgrass clearly plays an additive role in altering habitat conditions for co-located oysters. Results suggest oysters can benefit from eelgrass, but there are density-dependent and context-specific constraints that should be considered in aquaculture management.

NEW HAMPSHIRE SHELLFISH FARMERS INITIATIVE: THE IMPORTANCE OF OUTREACH IN THE AQUACULTURE INDUSTRY

Kelsey Meyer

Coordinator of New Hampshire Shellfish Farmers Initiative, University of New Hampshire, Department of Biological Sciences, 38 Academic Way, Durham, NH 03824

nhshellfishfarmersinitiative@gmail.com

The New Hampshire Shellfish Farmers Initiative (NHSFI) is a group of passionate farmers who work together to advocate for oyster growers' livelihoods, educate consumers, and plan for the future of the industry. The mission is to make the public aware of the benefits of oyster farming as a sustainable and environmentally friendly industry that benefits New Hampshire.

The NHSFI works on a variety of projects, with the overall reaching thought in mind, how will this contribute to industry and allow it to grow and improve? There are three main categories of the Initiative's work: advocacy, community building, and research/sustainability. The NHSFI wants to show that outreach and extension is vital to the growth of the industry, as well as working together as a cohesive group. Working with New Hampshire state representatives, consumers, and research teams all contributes to the industry's growth and future. The New Hampshire Farmer's Initiative is striving for this goal and is working hard to improve the aquaculture industry of New Hampshire.

TEST OF TREATMENT-SPECIFIC BIAS IN SIMULATED MARSH WITH JUVENILE BLUE CRAB, *CALLINECTES SAPIDUS*

Cole Miller[1]*, A. Challen Hyman[2], Daniel Shi[3], and Romuald N. Lipcius[2]

[1]Department of Biology, William & Mary, PO Box 8795, Williamsburg, VA 23187-8795

[2]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[3]Thomas Jefferson High School for Science and Technology, 6560 Braddock Rd, Alexandria, VA 22312

crmiller@wm.edu

The blue crab (*Callinectes sapidus*) is an ecologically and economically important species in the Chesapeake Bay. Nursery habitats, such as seagrass beds, disproportionately contribute individuals to the adult segment of populations. Salt marshes of *Spartina alterniflora* are intertidal nursery habitats which may serve as a refuge from predation for juvenile blue crabs; however, the effects of various characteristics of salt marshes on nursery metrics, such as survival, have not been quantified. Comparisons of juvenile survival between salt marshes and other habitats often employ tethering to assess survival. Although experimental bias when tethering juvenile prey is well-recognized, the potential for habitat-specific bias in salt marshes has not been experimentally tested. Using mesocosm experiments, tethering crabs in simulated salt marsh habitats produces habitat-specific bias was tested. Juvenile crabs were randomly tethered and un-tethered in mesocosms at varying simulated shoot densities. Tethering reduced survival, and its effect was not habitat specific, irrespective of shoot density, as evidenced by a non-significant interaction effect between tethering treatment and habitat. Thus, tethering juvenile blue crabs in salt marsh habitat did not produce treatment-specific bias relative to unvegetated habitat across a range of shoot densities and survival of tethered and untethered crabs was positively related to shoot density. These findings indicate that tethering is a useful method for assessing survival in multiple nursery habitats, including seagrass beds, salt marshes, and unstructured sand.

UNDERSTANDING REPRODUCTIVE DEVELOPMENT IN FEMALE WHITE SHRIMP, *PENAEUS SETIFERUS,* IN SUPPORT OF SUSTAINABLE FISHERIES MANAGEMENT

Lexi Mitchell[1,2]*, Peter R. Kingsley-Smith[1], Jeff F. Brunson[1], Graham A. Wagner[1], and Michael R. Kendrick[1]

[1]Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston, SC 29412

[2]College of Charleston, Grice Marine Laboratory, 205 Fort Johnson Road, Charleston, SC 29412

mitchella@dnr.sc.gov

Accurate assessments of female reproductive development are an important component of the sustainable management of the white shrimp, *Penaeus setiferus* fishery in South Carolina (SC) and neighboring coastal states. Reproductive development is commonly assessed macroscopically based on ovary color; however, macroscopically distinguishing females that have never spawned from those that have previously spawned can be challenging. Identifying indicators of previous spawning events is crucial for estimating reproductive output and informing decisions regarding the timing of the commercial shrimp season opening in the spring. In this study, we aim to refine reproductive assessments and strengthen our understanding of phenological patterns within the spring spawning season. Weekly samples of female white shrimp were collected from Charleston Harbor, SC in the spring of 2022. Both macroscopic and microscopic (*i.e.,* histological) assessments of ovarian development were conducted. Microscopic assessments provide high resolution information on the reproductive cycle of this batch-spawning species, thus allowing for the detection of oocyte atresia, or the degeneration of oocytes after a previous spawn. Linear models were used to explore relationships between macroscopic (*e.g.,* ovary color and turgidity) and microscopic (*e.g.*, oocyte atresia) indicators of previous spawning. Corroborating macroscopic metrics with microscopic metrics will increase confidence in the ability to distinguish repeat and first-time spawners in the field. With the timing of reproductive development expected to shift in the face of future climate variability, the results of this project provide fisheries managers with invaluable information on the reproductive phenology of white shrimp to ensure the sustainability of the commercial fishery.

MICROPLASTICS AND OYSTER AQUACULTURE

Kayla M. Mladinich*, Bridget Holohan, J. Evan Ward, and Sandra E. Shumway

University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Rd, Groton, CT 06340

Kayla.mladinich@uconn.edu

Microplastics (MP) have become a concern for the shellfish industry because the media and public have continued to raise questions regarding the perceived dangers of MP in shellfish. In particular, there are concerns regarding the amount of MP released into the environment by aquaculture activities and if farm-grown bivalves have higher MP loads than those collected from recreational beds. To explore this concept, water, aquaculture gear, and oysters (*Crassostrea virginica*) were sampled from an aquaculture site in Niantic Bay and a 2-week reciprocal transplant experiment was performed in which oysters were transferred between the aquaculture site and a plastic-free cage off the dock at the University of Connecticut-Avery Point campus. After 2 weeks, oysters were recollected, and their digestive gland-stomach complex (gut) isolated by dissected. MP were extracted from water and oyster gut samples using previously validated extraction methods. Extensive quality control and assurance measures were taken to reduce MP contamination, such as wearing cotton laboratory coats and running procedural blanks alongside collected samples. Particles in all samples were isolated, imaged under a dissecting microscope, and characterized (size, shape, polymer) using ImageJ software and micro-Fourier transform infrared spectroscopy. Water samples from both the aquaculture site and Avery Point dock contained 0-0.3 MP/L, and oysters are being processed. The polymers found up to this point are not directly associated with aquaculture gear collected at the site suggesting that aquaculture activities do not contribute largely, if at all, to MP in farmed oysters.

NANOBUBBLE OZONE TECHNOLOGY (NBOT) FOR SCALABLE EMERGING ALGAE/TOXIN MITIGATION AND REMEDIATION

Peter D. Moeller[1]*, Peter Lee[2], Mike Janech[2], Kevin Beauchesne[3], Alison Bland[2], and Nicole Schanke[2]

[1]National Ocean Service, Hollings Marine Laboratory, 331 Ft. Johnson Rd., Charleston, SC 29412

[2]College of Charleston, Dept of Biology, 331 Ft. Johnson Rd., Charleston SC 29412

[3]American marine University Research Institute, 5800 State Road 80 #295, LaBelle, FL 33935

peter.moeller@noaa.gov

Shellfish culture is a key component of global food production. It is impacted by and impacts human activity thus linking it to potential public health concerns. For example, filter-feeders such as oysters and mussels can accumulate algal biotoxins, human pathogenic bacteria and persistent chemical contaminants. Discharge of untreated waste, in turn, from shrimp farms can lead to algal blooms. Ozone has been used as a disinfectant to address many of these issues, but recent technological developments allow ozone to be infused into nanobubbles to yield a more efficient delivery system. Findings from ongoing research activities using Nanobubble Ozone Technology (NBOT) show promising results for a variety of these issues. Results from experiments using NBOT on various types of contaminated water will be presented. Elevated levels of oxygen and ozone (saturation relative to untreated samples at atmospheric equilibrium) can be observed for several days after ozone treatment has stopped. Rapid removal of dissolved organic matter is seen within minutes during the treatment phase. For contaminated brackish coastal water, enumeration of bacteria by microbial plating on marine and TCBS (*Vibrio* spp.) selective agar before and after NBOT treatment shows no bacterial growth for at least 7 days post treatment. In certain circumstances, removal of high concentrations of phosphate can be achieved.

ADVANCING ALTERNATIVES TO SHELL FOR OYSTER RESTORATION

Jennica J. Moffat*, H. Ward Slacum Jr., and Olivia Caretti

Oyster Recovery Partnership, 1805 Virginia St. Suite A, Annapolis, MD 21401

jmoffat@oysterrecovery.org

Natural oyster reefs depend on shell accretion for long-term growth and survival, and their restoration is dependent on the availability of oyster shell as substrate for successful recruitment. In most coastal environments, shell loss has been accelerated by fishing activities and increased sediment deposition. To account for this, management agencies implement shell repletion programs to restore degraded reefs. The success of these programs has increased the demand for shell, and availability is insufficient to meet demand.

To address this problem, the Maryland Aquaculture Coordinating Council created the Alternate Materials Workgroup to identify an alternative to shell for use in the remote setting process, an essential step for restoration of habitat with limited spat availability. This committee is composed of experts in aquaculture, commercial fisheries, restoration, and management, and includes representation from relevant state, federal, and non-governmental agencies, the aquaculture industry, and watermen. The Workgroup met to evaluate and discuss potential alternate materials, their biological suitability, and logistic feasibility for use in large scale restoration. In addition to reviewing the literature and other resources, the Workgroup heard from practitioners who are actively using alternate materials for oyster reef restoration. The Workgroup also discussed regulatory constraints and strategies for transitioning to the use of alternate materials. The Workgroup is composing a final report synthesizing the presentations and meeting discussions and providing recommendations for implementing the findings of this effort. These recommendations will be applicable to addressing the widespread scarcity of oyster shell across sectors in all systems grappling with limited shell availability.

BIOLOGICAL BIOFOULING CONTROL OF SALMON NET PENS USING THE GIANT RED SEA CUCUMBER, *APOSTICHOPUS CALIFORNICUS*

Emaline M. Montgomery*[1], Barb Cannon[2], and Christopher M. Pearce[1]

[1]Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Road, Nanaimo, BC, V9T 6N7 Canada

[2]Creative Salmon Co. Ltd., 612 Campbell St, Tofino, BC V0R 2Z0 Canada

Emaline.Montgomery@dfo-mpo.gc.ca

The need to regularly clean biofouling is a time consuming and often expensive process that can be a constraint to industry. Modern cleaning techniques are highly variable and range from direct infrastructure swapping to industrialized power washing that uses high-pressure water to remove the biofouling. The latter is a popular technique in the finfish industry due to its efficacy of removing biofouling, but it is time consuming, costly, and may have negative fish-gill-health consequences that are just being recognized. Development of alternative practices to prevent and control biofouling in finfish net pens is therefore warranted to help offset the time, financial, and potential fish-health costs of current cleaning technologies.

Sea cucumbers like *Apostichopus californicus* have long been recognized for their co-culture potential due to their natural ability to recycle organic-rich sediments into nutrient poor faeces, but little research has examined their ability to control biofouling. The ability of *A. californicus* to consume biofouling material on nets was tested at two organic Chinook (*Oncorhynchus tshawytscha*) farm sites using four treatments: pens with (1) fish and sea cucumbers (SC); (2) fish, but no SC; (3) no fish, but SC; and (4) no fish and no SC. Sea cucumbers were observed feeding on biofouling organisms on the nets in treatment 3 and preferentially consuming excess feed/salmon wastes in treatment 1. No negative interactions (*e.g.,* health and/or behavioural) were detected between the salmon and the sea cucumbers suggesting that this is a good partnership to explore further.

IMPLEMENTATION OF A REGIONAL "MUSSELS FOR CLEAN WATER INITIATIVE" FOR THE UPPER MID-ATLANTIC REGION

Leah Morgan*, Danielle Kreeger, Kurt M. Cheng, and Matt Gentry

Partnership for the Delaware Estuary, 110 S Poplar St, Suite 202, Wilmington DE, 19801

lmorgan@delawareestuary.org

Freshwater mussels are one of the most imperiled animal groups in North America. Interest in these bivalves has understandably been focused on conserving biodiversity rather than the ecological consequences of declines in abundance even though freshwater mussels can furnish valuable ecosystem services such as water quality improvement by removing and transforming seston and associated pollutants (e.g., nitrogen). Historic population loss coupled with modern constraints on natural recruitment therefore undermines management efforts to sustain water quality in freshwater ecosystems. The Mussels for Clean Water Initiative (MuCWI) aims to facilitate mussel restoration in streams, rivers, and lakes in the upper mid-Atlantic region. Since natural populations are depleted, the initial focus is to develop a reliable source of mussels for restoration, research, monitoring and outreach projects in the Delaware and Susquehanna River Basins. A production-scale hatchery is being designed for a site in southwest Philadelphia, Pennsylvania. This central facility will initially focus on propagating up to 500,000 juveniles per year of the more common, "foundational" species that dominate natural mussel beds. Hatchery-produced mussels will be raised to larger sizes at regional rearing centers in different states and watersheds. Pilot projects have shown that hatchery mussels can survive and grow in various stream, river, reservoir, living shoreline, and stormwater pond sites, confirming that mussel recovery projects can be viable in many areas. Programs such as MuCWI expand the toolkit of nature-based tactics that can help sustain water quality, especially because they can be implemented in freshwater areas closer to sources of impairment.

SEASONAL PATTERNS OF DISTRIBUTION AND ABUNDANCE OF WATERBIRDS IN RELATION TO OYSTER AQUACULTURE IN COASTAL RHODE ISLAND

Martina Muller, Peter Paton, and Scott McWilliams*

University of Rhode Island, Department of Natural Resources Science, 102 Coastal Institute, Kingston, RI 02881

srmcwilliams@uri.edu

The spatial distribution of waterbirds is typically seasonally dynamic, yet few detailed studies have investigated how seasonal variation in waterbird distribution and abundance relates to shellfish aquaculture operations. Weekly land-based surveys in Rhode Island were conducted from December 2020 to the present to assess seasonal variation in the distribution patterns of birds in nearshore waters and coastal ponds with and without certain types of oyster aquaculture gear (e.g., submerged vs. floating). The most abundant waterbird species in coastal Rhode Island changed seasonally: the species present in the highest densities in the winter months were waterfowl (ducks and geese) plus grebes and loons, whereas in summer, gulls, terns, and cormorants predominated. The density of gulls, terns and cormorants was highest on floating cages associated with oyster aquaculture during late-summer and early-fall, and much higher than in waters over submerged aquaculture or in surrounding waters with no active aquaculture. The peak bird use of floating gear during late summer coincides with when harmful bacteria may proliferate; thus, late-summer provides the window of opportunity for most effective use of deterrents at floating gear operations. Given that patterns of waterbird distribution and abundance will vary geographically, more regional studies are needed.

MONITORING SURFCLAMS AT OFFSHORE WIND ENERGY PROJECTS

Daphne Munroe[1]*, Jason Morson[1], and Grade Saba[2]

[1]Rutgers the State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Ave, Port Norris, NJ 08349

[2]Rutgers the State University of New Jersey, Department of Marine and Coastal Sciences, 71 Dudley Rd, New Brunswick, NJ 08901

dmunroe@hsrl.rutgers.edu

The Atlantic surfclam fishery is among the most exposed to impacts from offshore wind energy development due to potential displacement from fishing grounds that overlap with wind lease areas. These vulnerabilities underscore the need to survey surfclams in wind energy areas. A survey tool that samples over a relatively large area and consistently catches large-bodied clams is needed to accurately estimate biomass, abundance, and size structure of the surfclam stock. A scientific hydraulic sampling dredge designed to catch a breadth of sizes of surfclams was constructed and used to survey surfclams at an offshore wind lease location. Surveys of the wind lease area and control locations will continue annually through the construction of the wind farm, and a before-after-control-impact sampling design will allow changes in clam abundance due to the wind project to be evaluated. Additionally, experiments quantifying the selectivity and efficiency of the scientific dredge will be conducted on the continental shelf off New Jersey; habitats that are subject to ocean acidification and warming water conditions, environmental stressors to which surfclams are sensitive. A major gap in ocean acidification research is co-located environmental and biological response monitoring; therefore, simultaneous measurements of surfclam biological response indicators (e.g., abundance, size, growth, shell strength, condition index) will be measured in coordination with carbonate chemistry observations in the ocean. These coordinated survey programs will enhance understanding of how important fisheries resources may be impacted by construction of offshore wind projects and future environmental conditions.

GENETIC BASIS OF ABNORMAL MUSSEL MORTALITY IN FRANCE USING A FIELD AND EXPERIMENTAL INFECTION INVESTIGATIONS

Ajithkumar Munusamy[1]*, Marie Lillehammer[2], Marie-Agnès Travers[3], Elise Maurouard[1], Muhammad Luqman Aslam[2], and Lionel Dégremont[1]

[1]Ifremer ASIM, avenue Mus de Loup, 17390 La Tremblade, France

[2]Breeding and Genetics Nofima, Osloveien 1, 1430 Ås, Norway

[3]IHPE, Université de Montpellier, CNRS, IFREMER, Univ Perpignan Via Domitia, Montpellier, France

Ajithkumar.Munusamy@ifremer.fr

Abnormal mussel mortality (AMM) outbreaks started along the French Atlantic coasts in 2014 and varied among sites and years (30-100%). The etiology of AMM is still unknown. This study investigates the resistance to AMM in the two mussel species cultivated in France (*Mytilus edulis* and *M. galloprovincialis*) and mussels with genomic signatures from both species (NH). Six wild mussel populations were used to produce 100 families in January/February 2017. Mussels were deployed in two sites [La Floride (LF), and Maison Blanche (MB)] in October 2017, and their survival/growth were recorded until June 2018. AMM was only observed at MB during spring 2018, and reached 70%, 43%, and 63%, for *M. edulis*, *M. galloprovincialis*, and NH, respectively, at the endpoint. In contrast, low mortality was observed in LF, reaching 11%, 30%, and 22%, respectively. Heritability for survival was low to moderate in both sites, ranging from 0.06 to 0.34. Significant genotype-by-environment interaction for survival between sites was found with low genetic correlations (-0.05 to 0.43). In addition, experimental infection was performed in October 2018 using a pathogenic strain of *Vibrio splendidus* isolated during AMM in 2014. The mean mortality after 72 hours post-infection was 53%, 22%, and 31% for *M. edulis*, *M. galloprovincialis*, and NH, respectively. The lowest heritability was observed for NH (0.15) and highest for *M. galloprovincialis* (0.38), and more interestingly, the genetic correlation between AMM in MB and experimental infection was not significantly different from 0, suggesting that this *Vibrio* strain, is not the major cause of AMM outbreak in MB 2018.

ADDRESSING DATA GAPS IN THE CONSIDERATION OF BIRD-BASED PATHOGEN INTRODUCTION IN SHELLFISH AQUACULTURE

Rachel Noble* and Mark Ciesielski

University of North Carolina at Chapel Hill, Department of Earth, Marine and Environmental Sciences, 3431 Arendell Street, Morehead City, NC 28557

rtnoble@email.unc.edu

Widespread growth of shellfish aquaculture production in estuarine waters has coincided with concerns about aquaculture growout structures that favor the presence and, therefore, defecation of coastal and terrestrial birds. Pathogens of serious concern from bird feces include *Campylobacter* sp., *Salmonella* sp., and, more recently, avian influenza. Outbreak and causal data are unavailable and problems with illness reporting make it such that any illness associated with bird-feces contaminated shellfish would be difficult to uncover. Previous studies have been conducted on both coasts using molecular methods to demonstrate whether there is a relationship between *Campylobacter* in seagull feces and the surrounding water column. Many of these studies were hampered by the use of selective media and subsequent PCR-based methods to type isolates which has led to observed difficulties with bacterial resuscitation. More recent studies have utilized more advanced sequencing and typing techniques to quantify *Campylobacter* sp. and *Salmonella* sp. bacteria in shellfish and have demonstrated that there are strong relationships between bird fecal source markers (such as *Catellicococcus*) and *Campylobacter* and *Salmonella sp*. presence. The time is right for a comprehensive, quantitative study across the aquaculture farms to 1) understand the sources of bacterial pathogens, 2) examine easier to quantify markers for bird-fecal contamination and 3) conduct experiments to understand best grow-out practices and limit biofouling to reduce bird-based fecal pathogens. This presentation will look at the limitations and advantages of molecular tools for addressing this potential source of pathogens in the context of increased growth in the aquaculture industry.

THE EFFECTS OF STIMULATION OF MANTLE RIM SENSORY TENTACLES BY ALGAE ON GILL CILIA BEATING IN THE BIVALVE MOLLUSC, *CRASSOSTREA VIRGINICA*

Victory Obianke[1]*, Ashanti McFarlane[2], Bassem Allam[3], Emmanuelle Pales Espinosa[3], Margaret A. Carroll[1], and Edward J. Catapane[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

[3]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

v.obianke11@gmail.com

Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by serotonin and dopamine nerves from the ganglia. The motor aspects have been well studied, the sensory side has not. Limited information is available about sensory inputs. Oysters are suspension-feeders, selecting food from their environment and transporting it via the gills and labial palps to the mouth, and typically eat a few species of microalgae, including *Tisochrysis lutea* and *Thalassiosira weissflogii.* To study if mantle rim sensory tentacles detect algae and send information to the visceral ganglia (VG) to activate a motor response affecting GLC cilia beating was tested by applying *T. lutea* and *T. weissflogii* to mantle rim and measuring GLC cilia beating using stroboscopic microscopy, with and without cutting the pallial nerve that innervates the mantle rim from the VG. Whole animal preparations with shells removed were positioned in chambers so solutions could be applied to mantle rim without coming in contact with the gills. Applying *T. lutea* and *T. weissflogii* to mantle rim increased cilia beating. In experiments where the pallial nerve was cut, applying algae to mantle did not increase cilia beating. Likewise, applying algae directly to isolated, denervated gill sections did not increase cilia beating. The results demonstrate a sensory-motor integration of mantle rim sensory information and beating of GLC cilia involving the mantle rim and VG. This study shows the animals can sense edible algae and adjust GLC cilia beating appropriately to increase feeding. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP and PSC-CUNY 62344-0050 and 62344-0051.

FEMALE BLUE CRAB SPAWNING MIGRATION REVEALED BY CARAPACE BIOGEOCHEMISTRY

Matthew B. Ogburn[1]*, Cynthia C. Gilmour[1], Robert Aguilar[1], Eric G. Johnson[2], Kimberly D. Richie[1], and Anson H. Hines[1]

[1]Smithsonian Environmental Research Center, 647 Contees Wharf Road, Edgewater, MD 21037

[2]University of North Florida, Department of Biology, 1 UNF Dr., Jacksonville, FL 32224

ogburnm@si.edu

The blue crab, *Callinectes sapidus*, supports the largest fishery in Chesapeake Bay and is a key component of estuarine food webs. Management is focused on protecting female spawning stock, but the relative contribution of different nursery habitats to the spawning stock is unknown. A large-scale field experiment was conducted to determine: 1) spatial and temporal variation in carapace biogeochemical signatures, 2) whether signatures remain stable during the spawning migration, and 3) the relative contribution of nursery habitats to the spawning stock. A training dataset was generated from recently-mated female blue crabs collected from 21 locations in fall 2014. A concurrent mark-recapture experiment was conducted to obtain migrating crabs of known age and tributary of origin. Finally, spawning female crabs of unknown origin were collected in July 2015. In preliminary analyses, 6 of 19 potential biogeochemical tracers remained stable over time, varied among nursery habitats, and were informative for identifying the salinity zone of collection using discriminant function analysis (DFA, 89% reassignment accuracy). In the experiment, 92% of recaptured crabs (N=89) were correctly assigned to the release salinity zone using DFA. Of the spawning stock sample, 6.9% of crabs had signatures characteristic of low salinity habitats, 81.2% of moderate salinity, and 11.9% of high salinity. Assignment accuracy was much lower for tributary (64%) or management jurisdiction (59%). Results indicate that carapace biogeochemistry can provide novel information on blue crab spawning migrations and nursery habitat contributions to the spawning stock that could inform both fishery management and habitat conservation and restoration.

EFFECTS OF UNDERWATER NOISE ASSOCIATED WITH THE INSTALLATION OF OFFSHORE WIND TURBINES ON THE LARVAL DEVELOPMENT OF EASTERN NORTH ATLANTIC COMMERCIAL BIVALVES

Frédéric Olivier[1]*, Mathilde Gigot[2], Julien Bonnel[3], Delphine Mathias[4], Tarik Meziane[1], Réjean Tremblay[5], and Laurent Chauvaud[2]

[1]Biologie des Organismes et Écosystèmes Aquatiques (BOREA) UMR 8067 MNHN, CNRS SU, IRD 207, UCN, UA, 61 Rue Buffon CP 53, 75005 Paris, France

[2]Laboratoire des Sciences de l'Environnement Marin (LEMAR) UMR 6539 UBO/CNRS/IRD/Ifremer, rue Dumont D'Urville, 29280 Plouzané, France

[3]Woods Hole Oceanographic Institution, Applied Ocean Physics and Engineering Department, Woods Hole, MA 02543, USA

[4]Société d'Observation Multi-Modale de l'Environnement, 115 Rue Claude Chappe, 29280 Plouzané, France

[5]Institut des Sciences de la Mer, Université du Québec à Rimouski, 310 Allée des Ursulines, Rimouski, Québec G5L 2Z9, Canada

frederic.olivier@mnhn.fr

The installation phase of offshore wind turbines generates high level of underwater noise (emerging pollution = anthropophony) whose consequences on benthic marine invertebrates remain largely unknown, especially on peri-metamorphic larval stages. A synthesis of a recent French research program which aimed to assess the effects pile driving and/or drilling sounds on the larval development of commercial bivalves will be presented.

Through a set of experiments conducted in '*Larvosonic*' mesocosms (dampening of resonance and reverberation bias of sound emission in tanks), there is evidence of direct noise impacts associated to MRE installation on several variables acquired on larval and post-larval stages of the great scallop (*Pecten maximus*) (growth, survival, settlement, metamorphosis rates, lipid profiles…) but also to transgenerational processes after adults were exposed during gametogenesis.

As in ectothermic animals, temperature modifies the organism's physiology, resulting in performance variability. It was hypothesized that temperature modulation could change larval responses to noise. Thus, temperature/noise interactions were tested on larvae of the infaunal bivalve, *Venus verrucosa*. Using two rearing temperatures (15°, 20°C), physiologically different larval batches were produced with contrasting FA content and profiles (neutral and polar lipid fractions). At the pediveligers stage, a strong temperature x noise interaction indicated that response to noise was highly related to the larval physiological state. Results suggest that underwater noise reduces the compensatory mechanisms established to balance the temperature increase. Overall, the data presented underline that future research is required to assess the complex impacts of this new emerging source of pollution on coastal benthic assemblages.

THE GREENWAVE OCEAN FARMING HUB: A PLATFORM FOR SEAWEED FARMER TRAINING AND COLLABORATION

Lindsay Olsen

GreenWave, 315 Front Street, New Haven, CT 06513

lindsay@greenwave.org

In April 2022, GreenWave launched the Regenerative Ocean Farming Hub: an open-source platform designed to train, support, and connect seaweed farmers across North America and around the world. In this free-to-anyone digital space, beginning farmers can find interactive tools, how-to videos, and courses to support them throughout planning, permitting, designing, and deploying their farms; as well as the annual operations of outplanting, monitoring, harvesting, and selling their commercial crops. The Hub is designed to encourage collaboration and knowledge exchange across the seaweed industry. In an online community forum, beginning and advanced farmers alike can ask questions of one another and share innovations and updates coming off their farms. In less than a year, the Hub has attracted a global audience of over 3,000 users.

This presentation will provide a tour of the Hub and share examples of the farmer training curriculum, such as: the Farmer Forum, a monthly series of technical conversations designed to facilitate connections among active kelp farmers; the Kelp Climate Fund, a climate subsidy for kelp farmers; and Seaweed Source, a web-based application that enables interested buyers and active seaweed farmers to connect. Additionally, the co-culture of seaweed and shellfish will be highlighted and success stories from multiple geographies of how shellfish farmers have incorporated seaweed crops to diversify income and farm operations will be shared. The Hub is evidence that collaboration — more than competition — will propel the seaweed industry forward. The hope is to invite members of the broader shellfish farming community to join the movement.

TRIPLOID MUSSELS WITH BETTER ATTACHMENT MAY ACT AS IMPROVED EXTRACTIVE SPECIES

Kevin Osterheld*[1], John Davidson[2], Luc A. Comeau[3], Céline Audet[1], Tiago Hori[4], and Réjean Tremblay[1]

[1]Institut des Sciences de la Mer, Université du Québec à Rimouski, 310 allée des Ursulines, Rimouski, QC, G5L 3A1, Canada

[2]Fisheries and Oceans Canada, Gulf Region Sector Office, 165 John Yeo Drive, Charlottetown, PEI, C1E 3J3, Canada

[3]Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Avenue, Moncton, NB, E1C 9B6, Canada

[4]Atlantic Aqua Farms, 918 Brush Wharf Rd, Vernon Bridge, PEI C0A 2E0, Canada

Kevin.Osterheld01@uqar.ca

A major problem in mussel farming is the loss of mussels due to fall-off, which can result in important economic loss. The fall-off is particularly important during the reproductive season as mussel invest most of their energy in the reproduction and have less energy for byssogenesis. This leads to byssal weakening, which can ultimately result in increased fall-off.

To reduce the weakening of byssal threads due to reproduction, triploid mussels were produced. Indeed, it is known that triploid bivalves tend to have reduced fertility. Thus, they are expected to have more energy for other metabolic activities, such as growth or byssogenesis. In this study, the byssal production and mechanical properties of byssal threads of one and two years, diploid and triploid mussels, were compared. Their reproductive investment was also compared. To determine the effect of triploidy on byssal threads, diploid and triploid mussels were placed in a recirculating flume to induce production of byssal threads. The threads were then counted and collected for tensile testing. Results showed that 1- and 2-year triploid mussel produced respectively 40% and 25% more threads with improved mechanical properties. Furthermore, the gonadosomatic index and gonad volume of the mussels was compared. No significant difference was observed for 1-year mussel, but 2-year triploid had significantly reduced gonadosomatic index and gonad volume. Also, they elicited lower maturation than diploids as well as altered sex ratio. This study suggested that triploid mussels have better attachment which could reduces their fall-off and improved the production rates.

ASSESSING INTERACTIONS BETWEEN SHELLFISH AND SEAGRASS BEDS AND MACROALGAE TO PROMOTE SUSTAINABLE AQUACULTURE IN THE DELAWARE INLAND BAYS

Gulnihal Ozbay*, Tahera Attarwala, and Ali Parsaeimehr

Delaware State University, Department of Agriculture and Natural Resources, 1200 N. DuPont Hwy, Dover, DE 19901

gozbay@desu.edu

Seagrass is an important keystone species in the Delaware Inland Bays. Seagrass helps to maintain populations of fish and invertebrate species by providing permanent habitat, feeding areas for various life stages, nursery areas for successful development of juveniles, and protection from predators. Seagrass also plays a fundamental role in mitigating climate change through its potential for carbon sequestration and mitigation of ocean acidification. Due to its high importance in coastal environments, understanding the interactions between shellfish and seagrass productivity can be a determinant of aquatic environment health and can promote sustainable aquaculture. An in-depth literature review was conducted to identify the interactions between shellfish and seagrass beds and macroalgae and to determine the impact these two factors have on aquaculture practices. As a complimentary method, underwater cameras were deployed during the months of June to October for real-time monitoring of oyster reefs and aquaculture sites to get a visualization of vegetation and species diversity at oyster locations. Through these combined efforts, it was identified that seagrass has a beneficial impact on oyster productivity and can help promote sustainable aquaculture. Based on the assessment, seagrass does seem to be more present at small oyster reefs and shellfish aquaculture farms.

INCORPORATING A DECADE OF WATER QUALITY DATA AROUND WASHINGTON STATE WITHIN A REGIONAL SMART AQUACULTURE FRAMEWORK

Kalloway Page*, Steven Booth, Andrew Suhrbier, and Bobbi Hudson

Pacific Shellfish Institute, 1206 State Ave NE, Olympia, WA 98506

kalloway@pacshell.org

The Pacific Shellfish Institute (PSI) is currently partnering with researchers along the east coast to incorporate water quality data into the larger Smart Sustainable Shellfish Aquaculture Management (S3AM) project framework. The goal is to generate a variety of environmental, engineering, and economic data using smart technology to better inform management practices to maximize oyster harvest. For the past decade PSI has collaborated with local partners to collect environmental data at several stations around Washington State to further inform researchers and shellfish growers of trends in marine environmental parameters. Datasets include ocean acidification and temperature measurements which may assist in monitoring climate change driven events and ecological regime shifts experienced by growers in the west coast region. To support the S3AM project PSI is increasing accessibility of these datasets and is seeking collaborators to add to these datasets within the S3AM framework.

The Tokeland station at the north end of Willapa Bay, Washington was used as a case study to highlight the type of analysis that can be conducted with this data. Starting in 2011 YSI water quality meters were deployed, and temperature, pH, salinity, chlorophyll, and dissolved oxygen data were recorded every 15 minutes. Data was directly uploaded to the publicly available NANOOS Visual System and later synced with NOAA tidal height data to generate summary statistics on annual, seasonal, lunar, and tidal timescales. Summary statistics for parameters of interest were generated and chronological trends examined for potential implications to shellfish growers and environmental scientists.

OCEAN ACIDIFICATION, HYPOXIA, AND WARMING IMPAIR DIGESTIVE PARAMETERS AND ANTIOXIDANT RESPONSES OF MARINE MUSSELS

Yiting Pan*[1], Fahim Ullah Khan[1], Menghong Hu[1], and Youji Wang[1]

Shanghai Ocean University, College of Fisheries and Life Science, 999 Hucheng HuanRoad, Lingang New City, Pudong new District, Shanghai, 201306, P.R. China

1712905763@qq.com

Global change and anthropogenic activities have driven marine environment changes dramatically during the past century, and hypoxia, acidification and warming have received much attention recently. Yet, the interactive effects among these stressors on marine organisms are extremely complex and not accurately clarified. The combined effects of low dissolved oxygen (DO), low pH and warming on the digestive enzyme activity and antioxidant response of the mussel, *Mytilus coruscus,* were evaluated. Mussels were exposed to eight treatments, including two degrees of pH (8.1, 7.7), DO (6, 2 mg/L) and temperature (30°C and 20°C), for 30 days. Amylase (AMS), lipase (LPS), trypsin (TRY), trehalase (TREH) and lysozyme (LZM) activities were measured in the digestive glands of mussels. All the tested stress conditions showed significant effects on the enzymatic activities. Hypoxia and warming showed almost similar effects on the enzymatic activities. The effect on the antioxidant parameter levels of mussels in the gills of mussels were altered. Values for all the test parameters except glutathione (GSH) first increased and then decreased. GSH content always increased with decreased pH, decreased DO and increased temperature.

PARASITIC DINOFLAGELLATE *HEMATODINIUM PEREZI* PREVALENCE IN *CALLINECTES* SPP. IN A TROPICAL URBAN ESTUARY

Olivia Pares* and Eric Schott

University of Maryland Center for Environmental Science, 701 E Pratt St. Baltimore MD 21202

opares@umces.edu

The Atlantic blue crab, *Callinectes sapidus*, is found in the western Atlantic Ocean, the Gulf of Mexico, and the Caribbean Sea. In the tropics, *C. sapidus* and its conspecifics are also essential to the local ecosystem and economy. The protozoan parasite *Hematodinium perezi* is known to infect *C. sapidus* and other *Callinectes* spp., causing symptoms such as lethargy, and decreased feeding that lead to host morbidity and death. Outbreaks of *H. perezi* along the east coast of North America are more abundant in juvenile hosts and are associated with embayments, shallow backwaters, and higher-salinity estuaries. Prevalence of *H. perezi* is well-documented in continental temperate areas of the *C. sapidus* geographic range, where crabs overwinter and undergo seasonal migrations; however, little is known about the prevalence of *H. perezi* in *C. sapidus* populations in the tropics, where crabs are active year-round, and share habitat space with several other *Callinectes* spp. Furthermore, it is unknown how *H. perezi* prevalence may behave in an island, as opposed to continental system. This study aimed to determine the temporal prevalence of *H. perezi* among *Callinectes* spp. collected in the Torrecillas Lagoon, an urban tropical estuary in San Juan, Puerto Rico. This information is an important step for developing effective management strategies for the *Callinectes* spp. resource in Puerto Rico.

UNIVERSITY OF MARYLAND ONLINE ECONOMIC SPREADSHEET TOOL FOR OYSTER AQUACULTURE: A SHELLFISH ODYSSEY

Matt Parker

University of Maryland Extension, Prince George's County Office, 6707 Groveton Dr, Clinton MD 20735

mparke11@umd.edu

Come see the recently launched University of Maryland Online Economic Spreadsheet Tool for Oyster Aquaculture. It is not quite HAL 9000, but it is close. Come on a shellfish odyssey and watch an overview of the tool along with a live demo if WIFI capabilities are available in the session room. Use of the tool allows for more informed financial decisions about starting or expanding a shellfish aquaculture operation. Outputs from the tool may be submitted along with a business plan to support financial projections when applying for loans.

EFFECTS OF AQUACULTURE PRACTICES ON *VIBRIO* AND THE MICROBIOME OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

Salina Parveen[1]*, Esam Almuhaideb[1], Shah Manzur Rashed[2], and Nur Hassan[3]

[1]University of Maryland Eastern Shore, Department of Agriculture, Food, and Resource Sciences, 1 Backbone Road, Princess Anne, MD 21853

[2]CosmosID, 20030 Century Boulevard, Germantown, MD 20874

[3]University of Maryland, Center for Bioinformatics and Computational Biology, 8125 Paint Branch Drive, College Park, MD 20742

sparveen@umes.edu

Oyster aquaculture is a primary approach that offers a sustainable and reliable food supply. The aquaculture practices commonly used are on bottom and water floating cages; however, their effects on the oyster microbiome and *Vibrio* are not understood. This study assessed the effects of the two aquaculture practices on *Vibrio* and oyster microbiome.

Six oysters and 1L of water from each aquaculture system were collected monthly from June to November 2019, from Chesapeake Bay. Water and oyster samples were examined for the abundance of *Vibrio parahaemolyticus* and *V. vulnificus* using the three tube most probable number-real time polymerase chain reaction (MPN-rtPCR) method. Water samples were filtered through a 0.2 µm Sterivex, and an aliquot of 1.5 g of oyster homogenates and water filters were used for the DNA extraction. Resultant DNA were subject to shotgun metagenomic library preparation using Illumina-Nextera XT followed by sequencing at HiSeq-4000 platform.

Results indicated that aquaculture practices did not significantly affect the microbial richness; however, the composition of viruses, fungi, antimicrobial resistance genes and virulence factors were significantly different. *V. parahaemolyticus* and *V. vulnificus* were more abundant in the floating cages of oysters. Furthermore, results showed that *V. parahaemolyticus* and *V. vulnificus* do not thrive during the first half of the summer as environmental condition may become more favorable for other species in the first phase. The outcome of this study provides a comprehensive dataset to assess the risks associated with *Vibrio* and oyster aquaculture.

COMPARISON OF ARTIFICIAL SUBSTRATES WITH OYSTER SHELL FOR OYSTER RECRUITMENT AND BIOMASS IN THE YORK RIVER, VIRGINIA

Jainita Patel*, Kathleen Knick, Gabby Saluta, Romuald Lipcius, and Rochelle Seitz

Virginia Institute of Marine Science, William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

jpatel@vims.edu

Restoring the eastern oyster (*Crassostrea virginica*) in the Chesapeake Bay can potentially increase food security, boost the economy, and enhance ecosystem services. Oysters prefer to settle on natural oyster shell, yet sources of natural shell are limited and costly. One solution is using alternative substrates that may provide the same benefits as oyster shell substrates. The goal of this experiment was to determine how oyster recruitment and biomass vary based on natural (oyster shell) and artificial (granite, oyster castles, oyster diamonds, c-domes, or x-reefs) substrate types. Aside from the oyster castles, which were made of just concrete, the engineered structures were composed of a mix of concrete and oyster shell. In June 2021, a randomized block design was employed at three sites in the York River (6 blocks, 2 per site) with each block containing the oyster shell treatment and the five alternative reef types. One year after deployment, a quarter of each reef was physically sampled, and oysters were enumerated, measured, and weighed. Oyster density and biomass differed among substrate types. All reef types, on average, performed well above the target oyster restoration metrics for density (50 oysters per m^2) and biomass (50 g dry mass per m^2) in the Chesapeake Bay. Shell and x-reefs performed the best, and diamonds performed significantly lower than all other reefs. Results demonstrate that alternative reef types can reach some of the targets for oyster restoration, which highlights the opportunity to boost oyster restoration in shell-limited areas.

GENETIC DIVERSITY OF THE OSTREID HERPESVIRUS TYPE 1

Camille Pelletier[1]*, Germain Chevignon[1], Maude Jacquot[1], Serge Heurtebise[1], Nicole Faury[1], Lionel Degremont[1], Jean-Michel Escoubas[2], Jean Delmotte[2], Elise Maurouard[1], Tristan Renault[3], and Benjamin Morga[1]

[1]Ifremer, Unité Adaptation Santé des Invertébrés Marins, Avenue du Mus de Loup 17390 La Tremblade, France

[2]IHPE, Univ. Montpellier, CNRS, Ifremer, UPVD, 34095 Pl. Eugène Bataillon Bâtiment 24, 34090 Montpellier, France

[3]Ifremer, Département Ressources Biologiques et Environnement, 44311 Cedex 03, Rue de l'Île d'Yeu, 44980 Nantes, France

camille.pelletier@ifremer.fr

The use of next generation sequencing (NGS) is essential for studying and monitoring pathogens in bivalve molluscs in order to anticipate the emergence of new genotypes or species. The improvement of knowledge and approaches to characterize their genome allows for a better understanding of their life cycle, host interactions, and capacity for adaptation or evolution. Ostreid Herpevirus 1 (OsHV-1), a pathogen of the Pacific oyster *Crassostrea gigas*, is responsible for significant mortality of larval and juvenile oysters each year. The study of its genome is complicated by the inability to culture the virus in vitro. Currently, 52 OsHV-1 genomes are available in public databases. This emphasizes the need for the development of diversity and phylodynamic analyses, which are key elements in understanding the spatial and temporal viruses diffusion.

Through the use of "ultra-deep" short-read sequencing on individual moribund oysters, combined with a new bioinformatics pipeline, 440 de novo OsHV-1 genomes were assembled. By combining the genetic variations quantification, phylogenetic analysis, and ancestral state reconstruction of discrete traits, the connectivity of OsHV-1 viral populations between oyster farming areas was assessed. The results suggest that some oyster aquaculture areas have higher OsHV-1 diversity than others. The phylogenetic study indicates samples clustering according to host, location, and time. This work demonstrates that phylodynamic approaches can be applied to aquatic DNA viruses to determine how epidemiological, immunological, and evolutionary processes act and interact on viral diversity.

DOSE-DEPENDENT EFFECTS OF EXPOSURE TO POLYUNSATURATED ALDEHYDES ON EMBRYOS OF EARLY LARVAL STAGES OF THE BIVALVES, *CRASSOSTREA VIRGINICA* AND *MYTILUS EDULIS*

Jamie Peterson* and Paul Rawson

University of Maine, School of Marine Sciences, 5751 Murray Hall, Orono, ME 04469

jamie.peterson@maine.edu

Oxylipins are a class of compounds that are often derived from enzyme-mediated oxidation of polyunsaturated fatty acids (PUFA). These compounds are secondary metabolites in algae, plants, fungi, mosses, and animals; where dioxygenases and monooxygenases contribute to oxylipin production. Oxylipins have been shown to have teratogenic effects on a variety of marine invertebrates including copepods, tunicates, polychaetes, and urchins. While previous work with bivalves focused mostly on the effects of oxylipins on bivalve hemocytes, there has been growing concern that oxylipins produced by microalgal species are contributing to failures in shellfish hatcheries in the northeastern United States. In this study, the effects of exposure to two commercially available oxylipins on embryonic and early larval development of eastern oysters (*Crassostrea virginica*), and blue mussels (*Mytilus edulis*) were examined. Eggs and larvae from each species were exposed to different doses of the polyunsaturated aldehydes (PUA) 2,4-heptadienal and 2,4-decadienal at fertilization and the subsequent development monitored to determine LD50 for each chemical by species combination.

Preliminary analyses suggest that embryos and early larval stages of these bivalve species are more sensitive to 2,4-decadienal than 2,4-heptadienal. Significant reductions in early cleavage of embryos and the proportion of eggs “hatching” (development to D-stage) occurred at PUA concentrations similar to those affecting early development in a broad range of marine species. Exposure in early larval stages may reduce digestion and impede shell growth. Although microalgal-derived PUA are unlikely to be the only issue facing shellfish hatcheries, these results indicate they are a potential contributor.

THERMAL PRIMING JUVENILE GREEN SEA URCHINS (*STRONGYLOCENTROTUS DROEBACHIENSIS*) TO INCREASE TOLERANCE TO EXTREME FIELD HETEROGENEITY

Tara Plee* and Coleen Suckling

University of Rhode Island, Department of Fisheries, Animal and Veterinary Science, 134 Woodward Hall, 9 East Alumni Avenue, Kingston, RI 02881

tara_plee@uri.edu

The green sea urchin (*Strongylocentrotus droebachiensis*) is a commercially valuable species within the northeastern US. Production is primarily active in Maine, and the diminishing fishery has led to the expansion of the aquaculture sector. Hatchery produced seed are grown in the field to market size; however, some nearshore seed grow out sites may experience marine heatwaves (defined as periods when seawater temperature > 90th percentile ≥ 5 days in a row), which can be harmful to this cold-water species. An innovative solution to increase tolerance to marine heatwaves is thermal priming, where tolerance is enhanced under subsequent controlled stress exposures within a hatchery setting. This is an emerging adaptive strategy that has been successful in coral and seagrass restoration yet remains untested for increasing the resilience of green sea urchin seed to marine heatwaves. If successful, this could further aid the expansion of the aquaculture production sector in nearshore areas, ultimately leading to production security and expansion under progressing environmental challenges. This presentation will expand on the methodology and results from thermal priming juvenile green sea urchins.

EVALUATION OF THREE NON-LETHAL BIOPSY METHODS FOR SNP ARRAY GENOTYPING IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Louis V. Plough[1]* and Lindsey C. Schwartz[2]

[1]University of Maryland Center for Environmental Science, Horn Pt. Laboratory, 2020 Horns Pt. Rd, Cambridge, MD 21613

[2]University of Louisiana at Lafayette, Department of Biology, 410 E. St. Mary Blvd, Lafayette, LA 70503

lplough@umces.edu

With the development of cost-effective high-throughput genotyping tools in the eastern oyster *Crassostrea virginica*, the application of genomic selection in oyster breeding is becoming a reality. A critical step in this process is the non-lethal DNA biopsy of candidate broodstock for genotyping and generation of GEBV; however, non-lethal biopsy is challenging because oysters must be ‘relaxed’ with $MgSO_4$ to access tissues, and extraction of mantle or hemolymph can be time consuming and damaging to the oyster. In this study, three non-lethal biopsy methods – mantle clipping, cytology brush swabbing of viscera, and filtered culture water of individual oysters (eDNA) – were tested for their effect on DNA concentration/quality and genotype call rate using the Eastern oyster 66K HD SNP array. SNP genotype correspondence was assessed between non-lethal biopsy DNA and ‘control’ DNA extracted from the adductor muscle of the same individual. Mortality of oysters subjected to the three non-lethal sampling methods was followed for 4 weeks. Preliminary results indicated no difference in mortality between brush and mantle biopsy after 4 weeks. DNA yields were substantially higher from the brush swabs, followed by mantle clips, and eDNA extractions. Genotype call rates were >94% for all mantle and brush samples and not significantly different – call rates were lower for the eDNA extractions but still generally above 90%. DNA from brush samples had near perfect genotype correspondence with adductor-derived DNA. Overall, non-lethal cytology brush biopsy DNA provides high quality SNP array genotype data, similar to mantle or adductor-derived DNA, and is faster/easier to implement.

VISUALIZATION OF ENVIRONMENTAL *PERKINSUS MARINUS* CELL FORMS AND IMPLICATIONS FOR ITS TRANSMISSION DYNAMICS

Anna M. Poslednik* and Ryan B. Carnegie

Virginia Institute of Marine Science, 1370 Great Rd, Gloucester Point, VA 23062

amposlednik@vims.edu

The highly prevalent oyster parasite along the Atlantic coast, *Perkinsus marinus*, is and has been recognized as a major source of disease and mortality in wild and aquacultured eastern oyster populations for over half a century. While vegetative proliferation of this parasite is well described within the oyster host, the importance of zoosporulation in *P. marinus* epizootiology is far less clear, particularly in light of the life history changes associated with its intensification in the 1980s. To better understand the ecology of this parasite outside of the host, weekly surface and benthic water samples were collected over the year from January 2021 – December 2022 and filtered and preserved on 0.22 membrane filters. Parasite abundance was quantified using qPCR, and cell forms were visualized using fluorescent in situ hybridization. Environmental *P. marinus* detection closely followed established seasonal infection trends in oyster hosts, with a maximum in late summer/early fall and little detection in winter and spring, with the notable exception of a minor March peak. Preliminary visualization of cell forms revealed hypnospores and trophozoites to be the predominant stages. The consistent observation of hypnospores raises questions regarding the continued relevance for zoosporulation in *P. marinus* transmission, and a potential significance in particular in supporting the year-round transmission of *P. marinus* that has long been known to occur even during annual periods of low abundance in oyster populations.

A VIGNETTE ON THE EVOLUTION OF OYSTER MANAGEMENT: THE SEARCH FOR A TRIUMVIRATE OF REFERENCE POINTS SIMULTANEOUSLY DEFINING BIOMASS-MAXIMUM-SUSTAINABLE YIELD (B_{MSY}), FISHING MORTALITY RATE AT MSY (F_{MSY}), AND CULTCH CONTENT AT MSY

Eric N. Powell*, Laura K. Solinger, Kathleen M. Hemeon, and Sara M. Pace

University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564

eric.n.powell@usm.edu

Once upon a time, the most effective oyster management reference point was Haskin's 40% rule. The search for an improved sustainable management approach began with the constant-abundance reference point implemented in Delaware Bay in the late 1990s which stabilized the stock but did not permit goal-oriented management at msy. The recognition that oyster shell was not a sustainable resource revolutionized the challenge by requiring simultaneous management of stock and shell and led to implementation of a constant shell reference point, tested in Louisiana, but this again did not permit goal-oriented management at msy. Subsequent application of surplus production models permitted estimates of B_{MSY} and F_{MSY}, but were based on an interpretation of the relationship of broodstock and recruitment directly as a broodstock-recruitment curve, a relationship easily gainsaid by results of shell planting. The Rosetta Stone was the recognition that the broodstock-recruitment relationship was actually a relationship between effective surface area (for settlement) and recruitment. Application led to the development of an assessment model simultaneously expressing three reference points: B_{MSY}, F_{MSY}, and E_{MSY}, the last being the effective surface area for settlement at MSY; thus, simultaneously providing sustainability goals for the stock and shell bed.

TOWARD UNDERSTANDING SEX-SPECIFIC GENE EXPRESSION PATTERNS DURING THE CONDITIONING PROCESS IN EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Dina A. Proestou[1]*, Mary E. Sullivan[1], Thomas Delomas[1], Kathryn Markey Lundgren[1], Keegan Hart[1], and Seraphina Satkowski[2]

[1]USDA ARS National Cold Water Marine Aquaculture Center, 120 Flagg Road, Kingston, RI 02881

[2]University of Rhode Island, Department of Fisheries, Animal, and Veterinary Science, Kingston RI, 02881

dina.proestou@usda.gov

Methods for non-destructively assessing gender of broodstock oysters prior to spawning are extremely useful in hatcheries, particularly those involved in quantitative selective breeding. Here we describe the first step in developing such a method. Eastern oyster broodstock were obtained from a hatchery and acclimated to flow-through laboratory conditions (21-22°C, 29-33). For six-weeks they were batch fed excess Shellfish Diet 1800 and monitored for mortality daily. Three subsets (n = 30) were anesthetized and biopsied (mantle) on experiment day 2, 16, or 30. On day 44, all oysters were sacrificed, sexed, dissected, and mantle and gonad tissues processed for RNAseq. Observed mortality was low (2.2%) and all but one animal responded to anesthesia treatment. By day 44, 70% of oysters conditioned successfully (25 females and 37 males). On average, females were larger than males, but sizes overlapped greatly (62 – 83 mm). A principal component analysis suggests that sex explains > 45% of the variation in global gene expression among sequenced gonad samples, but only 14% in mantle samples collected on day 44. Similarly, 4,101 transcripts were differentially expressed between male and female gonad at a L2FC of |2| while only 66 were different between male and female mantle. Twenty-three differentially expressed transcripts overlapped between the gonad and mantle comparisons. Of the transcripts differentially expressed in gonad, one, one, and eight were differentially expressed in biopsied mantle tissues on days 2, 16 and 30 respectively. The utility of these results for developing a simple sex determination assay will be discussed.

NUCLEOTIDE AND STRUCTURAL POLYMORPHISMS OF THE EASTERN OYSTER GENOME PAINT A MOSAIC OF DIVERGENCE, SELECTION, AND HUMAN IMPACTS

Jonathan B. Puritz[1]*, Honggang Zhao[2], Ximing Guo[3], Matthew P. Hare[2], Yan He[3], Jerome LaPeyre[4], Katie E. Lotterhos[5], Kathryn Markey Lundgren[6], Tejashree Modak[7], Dina Proestou[6], Paul Rawson[8], Jose Antonio Fernandez Robledo[9], K. Bodie Weedop[5], Erin Witkop[7], and Marta Gomez-Chiarri[7]

[1]University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd., Kingston, RI 02881

[2]Cornell University, Department of Natural Resources and the Environment, 205 Fernow Hall Ithaca, NY 14853

[3]Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, NJ 08349

[4]Louisiana State University, Ag Center, 101 Efferson Hall, Baton Rouge, LA 70803

[5]Northeastern University, Department of Marine and Environmental Sciences, 430 Nahant Road, Nahant, MA 01908

[6]USDA Agricultural Research Service, National Cold Water Marine Aquaculture Center, 469 CBLS 120, Flagg Rd, Franklin, RI 02881

[7]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, 120 Flagg Road, Kingston, RI 02881

[8]University of Maine, School of Marine Sciences, 360 Aubert Hall, Orono, ME, 04469

[9]Bigelow Laboratory for Ocean Sciences, 60 Bigelow Dr, East Boothbay, ME 04544

jpuritz@uri.edu

The eastern oyster, *Crassostrea virginica,* is a valuable fishery and aquaculture species with a life-history that promotes high genetic diversity and gene flow across a wide range of coastal habitats from the southern Gulf of Mexico to the southern waters of Atlantic Canada. Whole genome re-sequencing data from 90 individuals across the eastern United States and Gulf of Mexico, plus 5 selectively bred lines was used to understand the interplay of genetic diversity, gene flow, and environmental selection. The data confirmed a phylogeographic break between oyster populations in the Gulf of Mexico and the Atlantic coast of the USA. The analysis demonstrated that domestication has artificially admixed genetic material between the two ocean basins, and selected lines with admixed ancestry have maintained heterozygosity at these sites through several generations post admixture, possibly indicating relevance to desirable aquaculture traits. Genetic and structural variation are high in both wild and selected populations, but when controlling for domestication admixture across ocean basins, wild populations have significantly higher levels of nucleotide diversity and copy number variation than selected lines. Within the Atlantic coast, subtle but distinct population structure, localized introgression of selected lines within wild individuals, an interaction between structural variation and putatively adaptive population structure, and evidence of candidate genes responding to salinity was detected. This study highlights the potential for applying whole genome sequencing to highly polymorphic species and provides a road map for future work examining the genome variation of eastern oyster populations.

FUTURE OCEAN ACIDIFICATION AND WARMING WILL INCREASE THE PHYSIOLOGICAL IMPACT AND BIOAVAILABILITY OF METALS FROM HISTORIC MINE DEPOSITS ON COMMERCIAL BIVALVE SPECIES

Helen Rastrick*, Michael Bank, Antonio Aguera Garcia, Cathinka Krogness, Tina Kutti, Terje van der Meeren, and Samuel P.S. Rastrick

Institute of Marine Research, PO Box 1870 Nordness, 5870 Bergen, Norway

Helen.Rastrick@hi.no

Historically Norway has used fjords for the disposal of waste including mine-tailing (fine grained waste material) produced whilst mining for metals, minerals, and precious stones. At present advice to regulators regarding the possible legacy effects of proposed, present, and historic mine-tailing deposits in Norwegian fjords is based on current environmental conditions; however, little is known about how metals associated with these mine tailings will interact with predicted future elevations in $p\mathrm{CO}_2$ and temperature to possibly effect costal fisheries and aquaculture. Consequently, commercial bivalve species (*Arctica islandica* and *Venerupis corrugata*) were exposed for 8 weeks to sediments collected from historic mine-tailing deposits (Repparfjorden, Norway) in combination with elevated temperature (+3°C) and/or $p\mathrm{CO}_2$ (1000 µatm) levels predicted for the end of the century.

Elevated $p\mathrm{CO}_2$ led to adjustments in coelomic acid-base balance, with increased bicarbonate concentration buffering pH in response to elevated $p\mathrm{CO}_2$; however, this bicarbonate compensation was not observed in bivalves exposed to mine tailings resulting in significant acidosis, elevated metabolic costs, reduced Scope for Growth, and increased mortality. It is suggested that the increased bioavailability of metals under more acidic conditions, in addition to, the direct effect of metal toxicity on enzymes involved in ion-regulation and bicarbonate up-take, may further exacerbated the negative effects of climate change. These results show the importance of considering future predicted environmental conditions when understanding and regulating for the possible future legacy effects of proposed, present, and historic mine-tailing deposits in Norwegian fjords.

CAN INTEGRATED MULTI-TROPHIC AQUACULTURE HELP MITIGATE THE EFFECTS OF CLIMATE CHANGE ON ECONOMICALLY IMPORTANT FILTER FEEDERS

S.P.S Rastrick*[1], Z.J. Jiang[2], X.Q. Wang[2], H.E. Graham[1], V. Collier[3], N.M. Whiteley[3], T. Strohmeier[1], J.G. Fang[2], and Ø. Strand[1]

[1]Benthic Resources and Processes Research group, Institute of Marine Research, PO Box 1870 Nordness, 5870 Bergen, Norway

[2]Key Laboratory of Sustainable Development of Marine Fisheries, Ministry of Agriculture and Rural Affairs, Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Qingdao, China

[3]School of Natural Sciences, Bangor University, Deiniol Road, Bangor, Gwynedd, LL57 2UW, UK

Samuel.Rastrick@hi.no

Elevated costs of maintaining homeostasis under elevated $p\mathrm{CO}_2$ and temperature conditions associated with climate change and ocean acidification (OA) are shown to divert energy away from growth and reproduction effecting the production of filter feeders important to aquaculture (*Crassostrea gigas, Mytilus edulis,* and *Ciona intestinalis*). It has been postulated that within an IMTA system increased energetic demand may be met by greater energy availability; however, results show that filter feeders are unable to utilise seston energy due to the effects of elevated $p\mathrm{CO}_2$ on absorption efficiency and clearance rate. Suggesting that decreased scope for growth and lower production in the future may occur independently of nutrient availability. Furthermore, when energy is available for growth smaller body size may convey an energetic, and so selective, advantage effecting production.

In some IMTA systems the fixation of inorganic carbon by macroalgae may, in part, mitigate the effects of elevated $p\mathrm{CO}_2$ on bivalves. Within field mesocosms supplied with elevated $p\mathrm{CO}_2$ water (1000 uatm) the introduction of macroalgae (*Saccharina japonica*) increased pH. This led to increased clearance rate, absorption efficiency, and growth in oysters (*M. gigas*) incubated with macroalgae compared to oysters incubated alone under predicted OA conditions. The energetic interactions between species within IMTA systems will change due to climate change. It is unlikely that the elevated costs of maintaining homeostasis can be met by increasing energy availability in the seston; however, fixation of inorganic carbon by macroalgae within some IMTA systems may, in part, mitigate the effects of OA on cultured bivalves.

PROACTIVE AND NON-INVASIVE PATHOGEN DIAGNOSTICS TO PREVENT THE SPREAD OF *BONAMIA OSTREAE*

Tim Regan, Lavanya Malini Vythalingam, and Tim P. Bean*

The Roslin Institute, The University of Edinburgh, Midlothian, EH25 9RG, United Kingdom

tim.bean@roslin.ed.ac.uk

The haplosporidian parasite *Bonamia ostreae* is one of the biggest issues facing European native oyster, *Ostrea edulis*, aquaculture and restoration. Measures to stop the spread of diseases in the United Kingdom have to date relied on the prevention of animal movement from disease positive to disease-free sites; however, these measures are not entirely successful and have seen recurrent failures in recent years, resulting in the gradual spread of *B. ostreae* across the UK. The utility of protocols for pro-active pathogen diagnostics was tested, combining a portable qPCR machine and field DNA extraction protocols with our experience detecting pathogens in disease challenge systems. A stepwise process of overnight incubation was used, sampling of substrates from the tank system, simplified DNA extraction and rapid diagnostic of the presence of *Bonamia* DNA. The concept of fully useable system that can be employed on the site of the shellfish farm will be presented. The process is now validated against a set of traditional diagnostic techniques including tissue qPCR and histopathology. This rapid, cheap and simple process allows native oyster farmers and restoration practitioners to make proactive decisions on whether to move animals, based on their up-to-date health status, and thus take full control of the risks associated with animal movement.

SMALL-SCALE INVESTIGATIONS OF BIRD DETERRENT METHODS ON AND AROUND MASSACHUSETTS SHELLFISH FARMS USING FLOATING GEAR

Joshua Reitsma[1,2]*, Abigail Archer[1,2], and Harriet Booth[1,2]

[1]Cape Cod Cooperative Extension, PO Box 367, 3675 Main St., Barnstable, MA 02630

[2]Woods Hole Sea Grant, 193 Oyster Pond Road, MS #2, Woods Hole, MA 02543

jreitsma@whoi.edu

Concern has been growing over potential public health concerns related to the interactions of birds with oysters, *Crassostrea virginica*, in floating culture gear. To help shellfish growers examine approaches to deterring birds, a funding opportunity for mini-grants was released for Massachusetts growers to explore options and report on results. While projects had several logistical challenges, limited qualitative results are summarized here though they did vary by site and species of birds. Growers reported some success with spikes or other perching deterrents on pontoons of floating cages, but zip ties were not as effective. Zip ties also had limited effectiveness on floating bags. Floating bags that were partially submerged below floats or hanging from single float were somewhat effective. Kites in the form of bird predators (falcons, eagles, or owls) had some effectiveness with terns over a limited radius but were not as effective with other species of birds. Monofilament or wire lines run over top of gear seemed effective for some farms, especially for birds that fly to the gear, though birds like cormorants that swim up to gear were still seen roosting underneath lines. Other methods that need more testing such as noise makers, impact sprinklers and lights or lasers will also be discussed in iterations attempted. Uniform concerns among the growers were the cost of implementation, how the deterrent limits gear access or functionality, and how much maintenance a particular deterrent would require.

AQUACULTURE PHYTOPLANKTON MONITORING NETWORK: A CITIZEN SCIENCE APPROACH TO MONITOR HARMFUL ALGAL BLOOMS AND CHANGES IN ENVIRONMENTAL CONDITIONS WITH THE AQUACULTURE INDUSTRY

Nia Rene*, Jennifer Maucher-Fuquay, Andrew Shuler, and Steve L. Morton

NOAA/NOS/NCCOS Hollings Marine Laboratory, HAB Monitoring and Reference Branch, 331 Fort Johnson Road, Charleston, SC 29412

nia.rene@noaa.gov

The National Phytoplankton Monitoring Network (PMN) is a community-based network of volunteers monitoring marine and freshwater phytoplankton and harmful algal blooms (HAB). Formed in 2001, the PMN enhances the ability of the Nation to respond to and manage the growing threat posed by HAB by collecting data such as phytoplankton species composition, distribution, and environmental conditions. HAB have been observed in every state resulting in over $1 billion in losses to communities that rely on recreation, tourism, and seafood harvesting. In the aquaculture industry, both shellfish and finfish, have experienced direct adverse effects of HAB, both toxin-producing species and non-toxin-producing species. For the individual aquaculture farm, blooms of certain non-toxic phytoplankton are of paramount concern because they are known to cause the mortality of shellfish and finfish worldwide.

The Aquaculture Phytoplankton Monitoring Network (AQPMN) project expands the scope of the citizen science approach of PMN to include partnership with aquaculture farms. The AQPMN will catalog existing and new phytoplankton species responsible for finfish and shellfish injury and establish a national monitoring platform operated by aquaculture farms, empowering farms to act to protect or harvest. In addition to monitoring problematic phytoplankton, AQPMN scientists will leverage scanning electron microscopy and energy-dispersive X-ray spectroscopy to analyze macroalgae grown at farm sites for the presence of heavy metals and iodine. This presentation will cover the methods used to monitor aquaculture sites and progress made by AQPMN to establish a national citizen science approach to monitor ichthyotoxic HAB, co-developed by the shellfish and finfish industries.

BIRD INTERACTIONS WITH SHELLFISH AQUACULTURE

Robert B. Rheault

East Coast Shellfish Growers Association, 1623 Whitesville Rd., Toms River, NJ 08755

Mailing: 1121 Mooresfield Rd., Wakefield, RI 02879

Bob@ecsga.org

Floating gear has become increasingly popular with oyster farmers because it typically results in faster growth, higher survival and superior product quality. Unfortunately, the gear is often also a popular roosting spot for waterfowl. In 2017 the Interstate Shellfish Sanitation Conference revised the Model Ordinance chapter on aquaculture, and the FDA insisted on new language stipulating if a farm has the potential to attract birds or mammals, the operator must propose an operational plan describing how they will deter such aggregations to prevent the contamination of shellfish crops by enteric pathogens, and to avoid the closure of harvest areas due to elevated coliform concentrations.

In the absence of regulatory guidance, state regulators have been left to interpret the new regulation in a wide variety of ways. Similarly, growers have had to develop repellents and deterrents with little guidance. Compounding these challenges is the paucity of data describing the prevalence of human enteric pathogens in bird waste. Most pathogens are highly species specific, but we cannot ignore the fact that some human pathogens have been detected in bird waste. Despite the absence of a proper Risk Analysis and a rarity of confirmed illnesses, regulators are often mandating expensive control measures. This session will review new deterrent research and examine the areas where additional research is needed to guide the development of appropriate regulations.

A COASTWIDE PERSPECTIVE ON PRODUCTION, CHALLENGES, AND STOCK IMPROVEMENT NEEDS OF *MERCENARIA MERCENARIA*

Robert Rheault*[1], Joshua Reitsma[2,3], Leslie Sturmer[4], Antoinette Clemetson[5]

[1]East Coast Shellfish Growers Association, 1623 Whitesville Rd., Toms River, NJ 08755

[2]Cape Cod Cooperative Extension, PO Box 367, 3675 Main St., Barnstable, MA 02630

[3]Woods Hole Sea Grant, 193 Oyster Pond Road, MS #2, Woods Hole, MA 02543

[4]University of Florida / IFAS Shellfish Extension, PO Box 89, Cedar Key, FL 32625

[5]New York Sea Grant, 146 Suffolk Hall, Stony Brook University, Stony Brook, NY 11794-5002

bob@ecsga.org

The northern quahog (= hard clam), *Mercenaria mercenaria*, is cultured commercially over a wide range of environmental conditions along the Atlantic and Gulf coasts of the United States. The differences in production and challenges seen by hard clam growers in different geographic regions will be discussed in relation to what traits are important in stock improvement for these regions. These industry perspectives will be discussed in the context of the Sea Grant Hard Clam Selective Breeding Collaborative and efforts to meet the needs of the hard clam aquaculture industry.

BRANT POINT SHELLFISH HATCHERY: A MUNICIPAL SHELLFISH RESTORATION INITIATIVE STRIVING TO SAVE ONE OF THE LAST COMMERCIAL BAY SCALLOP FISHERIES ON NANTUCKET ISLAND, MASSACHUSETTS

Tara A. Riley*, Leah Hill, Joseph Minella, and David Berry

Town of Nantucket, Department of Natural Resources, 131 Pleasant St. Nantucket, MA 02554

triley@nantucket-ma.gov

The waters around Nantucket, Massachusetts are home to the largest commercial bay scallop (*Argopecten irradians*) fishery in the world that historically fueled the winter economy of the island through fishery-related jobs, abundant seafood supply, recreational activities, and a continuance of history and culture dating back to the late 1800s. Since its peak in the 1980s, commercial bay scallop landings have fallen from 100,000 bushels and 350 permits to 3,500 bushels and 100 permits during the 2021 season. Implementing town initiatives to address eutrophication, habitat loss, and island growth is key to finding a balance within local marine ecosystems to facilitate the restoration of the bay scallop population.

Since the Brant Point Shellfish Hatchery began its restoration initiatives in 2010, the average seed abundance found in the long-term monitoring surveys has increased 327% and adult bay scallops 22%. While commercial landings (and monitoring surveys) indicate a high degree of mortality between juvenile and harvestable adult life stages, restoration efforts are critical to buffering the variability of natural recruitment and maintaining a baseline population. Municipal hatchery initiatives for the bay scallop fishery include a variety of stock enhancement strategies and monitoring techniques in effort to adapt to changes in the environment, island growth, and the economy of Nantucket Island.

LOW TEMPERATURE STORAGE OF BIVALVE LARVAE - A NEW MANAGEMENT TOOL FOR SHELLFISH HATCHERIES

Gregg Rivara*[1], R. Michael Patricio[1], and Thomas Allen[2]

[1]Cornell University Cooperative Extension, 3690 Cedar Beach Road, Southold, New York, 11971 USA

[2]Tolga, Ltd., P.O. Box 328, 155 Gibson Road, RR#2, Westport, Ontario K0G1X0 Canada

GJR3@cornell.edu

One of the major challenges for commercial shellfish aquaculture operations has been the seasonal fluctuation in the availability of seed stock. Unsuccessful spawns, diseases, and the seasonal nature of bivalve hatcheries present obstacles to locally-sourced fresh shellfish for the seafood industry. It would be of great advantage to shellfish hatchery operations if they are able to store larvae for an extended period of time in order to bridge between spawns (weeks to months) and seasons. In addition, since fewer spawns are needed, algal production that would normally be devoted to broodstock conditioning would become available for feeding post-set, at a time of year when hatchery demand for algae is at its highest. Traditional cryopreservation of juvenile bivalves in liquid nitrogen using proven cryoprotectants and protocols, has been attempted many times with limited results, particularly for species currently in high demand in the northeastern United States (e.g., eastern oyster and bay scallop). This project involves subzero C stasis using optimal cryoprotectants and temperature ramps without the use of liquid nitrogen. Funded in part by New York Sea Grant, NOAA, DOC project R/ATD-17.

BIRDS AND SHELLFISH SANITATION - THE NEW YORK EXPERIENCE

Gregg Rivara[1]*, Martin Byrnes[2], Wade Carden[3], and Joseph Finora[4]

[1]Cornell University Cooperative Extension, 3690 Cedar Beach Road, Southold, NY 11971

[2]Retired, Town of Islip Department of Environmental Control, 401 Main Street, Islip, NY 11751

[3]New York State Department of Environmental Conservation, 123 Kings Park Blvd., Kings Park, NY 11754

[4]Hampton Oyster Company, 1585 Hobart Road, Southold, NY 11971

GJR3@cornell.edu

In 2012, cage-based shellfish farming in New York expanded into shallower, nearshore areas of the South Shore Estuary from the Peconic Estuary where it originated. This new opportunity for access and growth of the industry coincided with advancement and availability of floating gear technologies which became the predominant choice of new oyster growers in these areas, with farms generally tended on foot. While floating gear offers many benefits to growers, it can also aggregate seabirds and concentrate their waste, thus presenting a new potential pollution source in areas otherwise meeting certified (approved) classification.

From 2015 to 2017, the New York State Department of Environmental Conservation (DEC) collected samples from floating farms that revealed elevated bacterial levels in oysters and seawater. Temporary closures were implemented with farms reopened based on satisfactory results of additional sampling after growers installed bird deterrents or submerged gear. Beginning in 2018, the DEC required growers using floating gear to submit a bird mitigation plan detailing what measures they would use to keep birds off gear and made effective bird mitigation a condition of their permits. The DEC also developed a guidance document to help growers determine what methods may work best for their situation based on the experience of other growers. Since that time, compliance has generally been good, with only a few temporary closures implemented by the DEC. Case studies of two areas on Long Island will be discussed.

OVERVIEW IN TRANSPOSABLE ELEMENT IDENTIFICATION, CLASSIFICATION, AND ANNOTATION FOR A BETTER EPIGENETIC LANDSCAPE GENERATION IN NON-MODEL EUKARYOTIC GENOMES

Fernando Rodriguez* and Irina R. Arkhipova

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, MA 02543

frodriguez@mbl.edu

Transposable elements (TE) exert an increasingly diverse spectrum of influences on eukaryotic genome structure, function, and evolution. A deluge of genomic, transcriptomic, and proteomic data provides the foundation for turning essentially any non-model eukaryotic species into an emerging model to study any and all aspects of organismal biology, ultimately shaping future directions for biomedical, environmental, and biodiversity research; however, in contrast to the progress in gene annotation achieved and standardized over the past decade, identification and annotation of the mobile genome component still lag behind the standards accepted for host gene annotation.

While culturing new species in shellfish aquaculture, it is needed to further understand the role of epigenetic change within organism-environment interactions. When trying to dissect the epigenetic landscapes in novel genomes, a comprehensive description of its mobilome component must be provided in addition to the standard genic and transcriptomic datasets. Each step of TE identification, classification, and annotation should be focused on improving TE boundary designation, reducing identification error rates, and providing accurate information on the type and integrity of TE insertions. But the detection and identification of TE in newly-sequenced species is still a challenging and time-consuming task, where different workflows have been proposed. Some of the workflows and analysis pipelines for generating TE models in *de novo* assemblies for non-model organisms, and overall, improvement of their epigenetic landscape analysis will be summarized.

ONE HEALTH APPROACH TO STUDY THE IMPACT OF ANTIMICROBIAL RESISTANCE IN SHRIMP AQUACULTURE

Hectorina Rodulfo[1]*, Marcos De Donato[2], and Acacia Alcivar-Warren[3,4]

[1]Departamento Regional de Bioingenierias, Escuela de Ingeniería y Ciencias, Tecnológico de Monterrey, Campus Querétaro, México

[2]The Center for Aquaculture Technologies, 8395 Camino Santa Fe, San Diego, CA 92121

[3]Fundación para la Conservation de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada Casa 17, El Eden, Quito, Ecuador

[4]Environmental Genomics, Inc., P.O. Box 196, Southborough, MA 01772

hrodulfo@tec.mx

One Health proposes an integrated approach to work collaboratively to study the connection between the health of people, animals, and the environment, recognizing the interconnection in the spread of pathogens and their antimicrobial resistance (AMR). Diseases in aquaculture are mainly associated with intensive cultures, poor biosecurity, and impacted environments. Antimicrobials are being used widely for the treatment of diseases, as growth promoters and to eliminate or inhibit the proliferation of pathogenic bacteria to prevent outbreaks. Metaphylaxis in aquaculture affects both pathogenic and symbiotic bacteria and it is being discussed in terms of the risk for spreading AMR, due to the emergence, persistence, and transmission of reservoirs of antimicrobial resistance genes (ARG). Shrimp producers are suffering infections by *Vibrio parahemolyticus* strains carrying a plasmid that causes acute hepatopancreatic necrosis disease (AHPND). While no concrete actions have been taken in shrimp farming worldwide from 1994 to the present, different bacteria (*Vibrio*, *Aeromona*, *Pseudomona*, *Escherichia*, *Klebsiela*, *Shigella*, and others) are reported carrying different ARG that allow them to be resistant to all generations of cephalosporins, glycopeptides, macrolides, quinolones, polymxyins, aminoglycosides, among many others. The development and implementation of systematic surveillance systems, using effective microbiological and molecular tools to characterize the shrimp product, the farm water, sediment, food ingredients and the surrounding environment, following a One Health approach will allow to apply prevention actions to cut the spread ARG to support the industry and to lessen the impact on human health.

HOW ACCURATELY CAN SEA SCALLOPS BE AGED?

Sally Roman*, David Rudders, Kaitlyn Clark, Melissa Southworth, and Roger Mann

Virginia Institute of Marine Science, William & Mary, 1375 Greate Road Gloucester Point, Virginia, 23062

saroman@vims.edu

Sea scallops, *Placopecten magellanicus*, are assessed with a ‘Catch At Size’ length-structured assessment model due to difficulties associated with accurately and precisely aging scallop shells. Development of an age-based assessment model hinges on the ability of scientists to collect scallop shells across the resource and accurately age scallop shells. The Virginia Institute of Marne Science (VIMS) has collected scallop shells since 2018 to support the development an age-based assessment. Scallop shells were aged with the traditional external ring method as well as by aging an internal structure called the resilium. To assess ageing methods for accuracy, precision, and bias, annual age-length keys (2019-2022) were generated for both ageing methods. Terminal age data for both methods was also compared to determine the relative performance of the resilium age method to the standard external ring approach. Results for age-length keys indicated a misspecification of age, especially for the smallest and oldest scallops, for both age methods. VIMS also needs to collect a larger length distribution of scallops for ageing, as scallops < 80 mm were largely absent from our collections. Despite these issues, there was general agreement between the two ageing methods in terms of age-length keys, and there was an 88 percent agreement for assigned ages between age methods for paired samples. While this work is ongoing, ageing methodologies may need to be reexamined to determine where errors are occurring to support the development of an age-based assessment in the future.

INVASIVE CRAYFISH AS POTENTIAL VECTORS OF WHITE SPOT SYNDROME VIRUS (WSSV) TO NATIVE CRUSTACEANS OF SOUTH CAROLINA, USA

Gregory Rothman[1,2]*, Jackie Allen[1], Peter Kingsley-Smith[1], Jody Beers[3], Allison Welch[3], and Michael Kendrick[1]

[1]Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston, SC 29412 USA

[2]College of Charleston, Environmental and Sustainability Studies Program, 66 George Street, Charleston, SC 29424

[3]College of Charleston, Department of Biology, 66 George Street, Charleston, SC 29424

rothmang@dnr.sc.gov

White spot syndrome virus (WSSV) is known to infect over 100 arthropod species and cause significant economic losses in both shrimp fisheries and crayfish aquaculture worldwide. While WSSV is known to exhibit rapid rates of transmission and have lethal impacts in single-species aquaculture settings, the influences of environmental factors on transmission and the pathways of interspecific transmission under natural conditions require further study. WSSV has been documented in both non-native live crayfish and frozen commodity shrimp imported into South Carolina (SC). Invasive species are an important potential vector of pathogens in terms of their transmission to native fauna. Non-native crayfish (primarily the invasive red swamp crayfish, *Procambarus clarkii*) have established wild populations throughout the coastal plain of SC, including tidal wetlands that are utilized by native commercially-important crustaceans such as penaeid shrimp (*Penaeus* spp.) and Atlantic blue crabs (*Callinectes sapidus*). The objective of this study is to investigate the transmission of WSSV from the invasive red swamp crayfish to native white shrimp (*Penaeus setiferus*). Findings indicate that interspecific transmission can occur through the ingestion of infected tissue; however, horizontal transmission through the water column has not been observed. The occurrence of WSSV in crayfish and other seafood that can potentially be introduced into the environment may pose a significant threat to native crustacean populations that support valuable commercial fisheries in SC. Understanding transmission dynamics among these crustaceans, and the impacts of environmental conditions, can inform management decisions related to minimizing impacts such as disease outbreaks caused by invasive species.

CO-CULTURE OF BAY SCALLOPS AND KELP IN CHINCOTEAGUE BAY, MARYLAND

Claire A. Rush* and Matthew R. Holloway

Baywater Seafood, 3908 Bayside Road, Snow Hill, Maryland 21863

Claire@baywaterlanding.com

Baywater Seafood is conducting a trial for the co-culture of bay scallops (*Argopecten irradians irradians*, *Argopecten irradians concentricus*) and kelp in Maryland's Chincoteague Bay. The depth at Baywater's lease is approximately seven feet and has near sea-level brine. Baywater is confident kelp planting here has the potential to thrive in these conditions. On November 29th, 2022, in conjunction with Woods Hole Oceanographic Institute, Baywater planted a variety of kelp within a one-acre aquaculture lease. WHOI compensates Baywater's time and costs in exchange for water samples. They track nutrient levels and how they affect ocean acidification. The results, along with general kelp development, will conclude a definitive answer to WHOI and Baywater's overarching question; "can bay scallops and kelp cohabitate in Maryland's Chincoteague Bay?".

Key considerations for the success of Chincoteague kelp: 1) Baywater's "southern" geographic location. Warmer water temperatures pose a hazard to survival. 2) Farm design. The proximity of aquaculture rows may hinder optimal growth and encourage tangling. The weight of mature kelp poses a threat to Baywater's system built for scallops.

Since November planting, there is notable growth of initial seed. Baywater expects a successful growing season, as harvesting takes place before high water temperatures. In 2022, the Virginia Institute of Marine Science supplied Baywater with scallop seed in exchange for monthly growth and mortality reports. Comparing monocropped Bay Scallop growth reports to reports alongside kelp may allow them to get scallops to market faster and introduce a unique kelp product to the Delmarva (Delaware-Maryland-Virginia) area.

THE USE OF NON-SANDY BEACH HABITATS BY SPAWNING HORSESHOE CRABS: A CONVERSATION ABOUT ITS IMPLICATIONS AND FUTURE RESEARCH PRIORITIES

Daniel Sasson[1]*, Jeff Brunson[2], Elizabeth Scott[1], and Michael Kendrick[1]

[1]Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

[2]Office of Fisheries Management, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

sassond@dnr.sc.gov

Evidence from multiple geographic regions along the U.S. Eastern seaboard indicate that horseshoe crabs (*Limulus polyphemus*) regularly spawn in salt marsh habitats. These habitats were previously considered unsuitable for embryonic development, but published work as well as research being presented at the 115th Annual Meeting of the National Shellfisheries Association shows that this may not be the case. The use of non-sandy beach habitats (i.e., alternative habitats) by horseshoe crabs for spawning may be common, widespread, and a potentially important source of recruitment.

By way of introduction, a brief background on what is and is not yet know about the use of alternative spawning habitats by horseshoe crabs will be presented. For the remainder of the time, there will be a facilitated, open discussion with the audience about these results. Discussion topics will address the following questions: 1) What is the diversity of alternative habitats in which horseshoe crabs regularly spawn? 2) What are the potential ecological impacts of spawning in these alternative habitats? 3) What additional data are needed to understand how the use of alternative habitats for spawning impacts management and conservation efforts?

The goals of this session will be to identify future research priorities related to improving our understanding of the use of alternative habitats for spawning and to consider how these findings might be incorporated into future management and conservation strategies.

DEVELOPING STRATEGIES FOR MANAGERS AND INDUSTRY TO ADDRESS PUBLIC HEALTH CONCERNS RELATED TO BIRD CONGREGATIONS ON FLOATING AQUACULTURE GEAR

Christopher Schillaci[1]* and Robert Rheault[2]

[1]National Marine Fisheries Service, Greater Atlantic Regional Fisheries Office, 55 Great Republic Drive, Gloucester, MA 01930

[2]East Coast Shellfish Growers Association 1623 Whitesville Rd., Toms River, NJ 08755

christopher.schillaci@noaa.gov

Floating aquaculture gear provides growers with a number of benefits over traditional bottom gear (e.g., avoiding sensitive habitats, ease of handling, improved growth rates, survival, etc.); however, floating gear may provide a roosting platform for birds. Waste associated with congregations of birds on gear can result in degradation of water quality and the introduction of enteric pathogens into growing areas; however, the risk to shellfish consumers associated with bird waste is not fully understood, and we currently do not have an estimate of the correlation of coliforms in wildlife waste and consumer risk; although, the risk is considered to be less than that from human derived sources.

With little guidance on methods to determine risks associated with floating gear and birds, and little information on the efficacy of deterrent measures, industry and state authorities have been challenged to meet new ISSC requirements associated with implementing strategies to manage risk from birds on aquaculture gear. An ISSC subcommittee has been developing guidance for state authorities that would allow for a monitoring and sampling approach to determine risk; however, many state authorities have been forced to adopt a precautionary approach or blanket policy for all floating gear due to a lack of resources, expertise, and guidance to conduct nuanced risk evaluations. Considerations related to developing management strategies that take into account a range of considerations such as bird behavior, deterrent efficacy, pathogen prevalence and purge rates, as well as discuss research needs to further refine management strategies will be discussed.

THE NOAA AQUACULTURE PROGRAM – ECOLOGICAL FORECASTING DATA NEEDS

Christopher Schillaci[1]*, Clete Otoshi[2], and Stephanie Wesyby[3]

[1]National Marine Fisheries Service, Greater Atlantic Regional Fisheries Office, 55 Great Republic Drive, Gloucester, MA 01930

[2]National Marine Fisheries Service, Office of Aquaculture 1315 East West Highway, Silver Spring, Maryland 20910

[3]National Marine Fisheries Service, Restoration Center, 200 Harry S. Truman Parkway, Annapolis, MD 21401

Christopher.schillaci@noaa.gov

A key tenant of the aquaculture mission of NOAA is to ensure U.S. marine aquaculture grows sustainably, encompassing the ‘triple bottom line’ of environmental, economic, and social sustainability. Remote sensing technologies have the potential to play a crucial role in fulfilling the needs of the regulatory, industry, human and environmental health, and research communities as aquaculture expands. NOAA Fisheries recently conducted an effort to explore the use of satellite data and other remote sensing products to support marine aquaculture. Initial ideas include improving the use and developing new applications for existing satellite and other remote sensing data and products in support of estimating aquaculture production, forecasting threats and opportunities, minimizing threats to protected resources, ensuring regulatory compliance, reducing environmental risk, maximizing biosecurity and human security.

INTEGRATING INFORMATION ON BENEFICIAL SERVICES PROVIDED BY SHELLFISH AQUACULTURE INTO THE AQUACULTURE PERMITTING AND REVIEW PROCESS

Christopher Schillaci[1]*, Julie M. Rose[2], Renee Mercaldo-Allen[2], Zachary Gordon[2], Paul Clark[2], Stephen Kirk[3], Lisa Milke[2], Daphne Munroe[4], Gillian Phillips[2], Dylan Redman[2], Kelsey Schultz[5], and Jenny P. Shinn[4]

[1]National Marine Fisheries Service, Greater Atlantic Regional Fisheries Office, 55 Great Republic Drive, Gloucester, MA 01930

[2]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Ave, Milford CT 06460

[3]The Nature Conservancy, 99 Bedford St, Suite 500, Boston, MA 02111

[4]Rutgers, The State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

[5]Northeastern University, 360 Huntington Ave, Boston, MA 02115

christopher.schillaci@noaa.gov

Shellfish aquaculture can provide a variety of beneficial services beyond food production. Cultured shellfish have been increasingly incorporated into nutrient management strategies due to their ability to assimilate nutrients into their tissue and shell. Shellfish aquaculture gear also creates complex structure used by recreationally and commercially important fish species for habitat-related activities such as foraging, shelter seeking, and reproduction around aquaculture gear. Other environmental, economic, and social benefits associated with shellfish aquaculture have also been documented to varying degrees in the literature.

Despite growing evidence that aquaculture operations can consistently provide beneficial services, the current aquaculture permitting framework largely focuses on an assessment of possible adverse effects to various environmental and socioeconomic factors. Engagement with resource managers suggests this is likely because adverse effects are often easier to quantify and document than beneficial effects, and variability in aquaculture production practices can limit manager's ability to make defensible assumptions on the types and extent of beneficial effects a proposed operation may provide. In addition, not all aspects of the current aquaculture review/permitting framework allow for, or easily lend themselves to, a synergistic evaluation of adverse and beneficial effects during the aquaculture review/permitting process.

The presentation will include results from preliminary outreach with resource managers and industry on existing regionally relevant research and literature related to ecosystem provisioning from shellfish aquaculture and data gaps, and the existing regulatory mechanisms and the types of tools/end-products for managers and growers to use to facilitate greater inclusion of beneficial effects in the aquaculture review/permitting framework.

BLUE CRAB, *CALLINECTES SAPIDUS*, REPRODUCTIVE PHENOLOGY IN CHESAPEAKE BAY

Alexandra K. Schneider*, Mary C. Fabrizio, and Romuald N. Lipcius

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

akschneider@vims.edu

Global temperatures are rising across marine ecosystems. Marine and estuarine-dependent species including the blue crab, *Callinectes sapidus*, may adapt to warming temperatures by shifting the seasonal timing of biological events, such as reproduction. Protraction of blue crab spawning duration, such as an earlier onset and later conclusion, may augment annual brood production and impact the efficacy of management strategies. In Chesapeake Bay, the spawning stock is protected by a sanctuary that is closed to fishing during the putative spawning season: mid-May to mid-September. If the time of spawning shifts, closure dates may have to shift accordingly. Moreover, shifts in spawning may impact reproductive output and recruitment success. Phenology metrics – the onset, conclusion, and duration of the blue crab spawning season – in Chesapeake Bay were estimated from 1995-2019 using fishery-independent observations of egg-bearing blue crabs from the Virginia Institute of Marine Science Juvenile Fish Trawl Survey. Although phenology metrics had no discernible trend and were variable over time, the onset and conclusion of the spawning season were earlier when spring temperatures were warmer, suggesting that continued warming may cause protraction of the spawning season and enhanced brood production. An earlier start to the spawning season during warmer springs may, however, reduce the efficacy of the spawning sanctuary and intensify spawning stock exploitation if the current closure dates remain unchanged.

ASPECTS OF THE FEEDING ECOLOGY OF *CARCINONEMERTES CARCINOPHILA* AND ITS EFFECT ON *CALLINECTES SAPIDUS* REPRODUCTIVE OUTPUT

Alexandra K. Schneider, Alexandria K. Pomroy*, and Jeffrey D. Shields

Virginia Institute of Marine Science, at the College of William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

akpomroy@wm.edu

The nemertean worm, *Carcinonemertes carcinophila*, is an egg-predator found on the gills and broods of blue crabs, *Callinectes sapidus*, in the Chesapeake Bay. Fluctuations in the blue crab population over the past 30 years have increased scientific interest in evaluating potential factors contributing to the dynamic changes in the fishery's stock. Laboratory experiments were used to provide novel data on the consumption rates of *C. carcinophila* on developing blue crab embryos (i.e., eggs). An estimate of the impact of the worm on egg mortality was quantified using worm prevalence, abundance, and intensity levels found in the blue crab spawning stock, coupled with data from the feeding experiment. During the experiment, 73% of the sampled worms fed on at least one crab egg over a 6-day period. Feeding rates ranged from 0 eggs/day to 4.5 eggs/day, with a mean of 0.52 eggs/day including worms that did not feed, and a mean of 0.73 eggs/day when excluding non-feeding worms. In the female crabs examined from May-September of 2022, worm prevalence was 65.9 ± 2.01% (SE). Of the ovigerous crabs examined, mean worm abundance was 35.9 ± 5.9 (SE) per brood, and a mean intensity of 58.8 ± 8.58 (SE) worms per brood. Considering a range of fecundities, intensities, and feeding rates, it is estimated that *C. carcinophila* can consume 0.0%-3.6% of a female's brood over the course of development of a single clutch. At current prevalence and abundance levels, egg predation by *C. carcinophila* appears to be a benign contribution to population level egg mortality.

FISH PRODUCTION AND USE OF OYSTER AQUACULTURE GEAR IN COMPARISON TO NATURAL HABITATS NORTH AND SOUTH OF CAPE COD

Kelsey Schultz*[1], Randall Hughes[1], David Kimbro[1], Stephen Kirk[2], Julie M. Rose[3], Renee Mercaldo-Allen[3], Paul Clark[3], Gillian Phillips[3], Dylan Redman[3], and Jonathan Grabowski[1]

[1]Marine Science Center, Northeastern University, 430 Nahant Rd., Nahant, MA 01908

[2]The Nature Conservancy, 99 Bedford St, Boston, MA 02111

[3]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Ave., Milford CT 06460

Schultz.k@northeastern.edu

The degradation of natural oyster reefs has led to increased restoration over the past several decades aimed at recovering lost ecosystem services. Yet, oyster restoration can be expensive; moreover, with ~85% of oyster reefs lost globally, innovative strategies are needed to recover lost services. Recent studies have indicated that bivalve and seaweed aquaculture may provide similar ecosystem services, and thus can serve as a substitute for oyster reef restoration and help facilitate ecosystem recovery. The artificial structures used in bivalve aquaculture can lead to richer ecological communities, supporting numerous trophic levels not only on the aquaculture gear, but also in the surrounding area. To investigate the ecosystem services associated with oyster aquaculture and potentially help reduce barriers to expansion, fish and crustacean use of aquaculture gear was quantified and compared to natural benthic habitats. These studies occurred at Cotuit Oyster Company, Cotuit, Massachusetts (MA) and Island Creek Oysters, Duxbury, MA from May-October of 2019-2021. Three different aquaculture gear types as well as two natural habitats were examined with the use of underwater cameras to determine if each gear type (1) augments nekton densities above unstructured habitat and (2) functions similarly to oyster reefs and rocky intertidal habitat. Commercially and recreationally important species were observed at both sites. Aquaculture gear had higher fish and crustacean visitation rates than surrounding natural habitats, including several species of juvenile fish. These results suggest that aquaculture gear may serve similar functions as essential fish habitat, which can help resource managers make more informed permitting decisions.

COMBINING PHYSIOLOGICAL ASSAYS, HIGH-THROUGHPUT SEQUENCING, AND FUNCTIONAL GENOMICS TO UNDERSTAND COSTS AND MECHANISMS ASSOCIATED WITH RESILIENCE TO ACIDIFICATION IN MARINE BIVALVES

Caroline Schwaner[1]*, Michelle Barbosa[1], Sarah Farhat[1], Isabelle Boutet[2], Arnaud Tanguy[2], John Haley[3], Emmanuelle Pales Espinosa[1], and Bassem Allam[1]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 100 Nicolls Rd, Stony Brook, NY 11794

[2]Station Biologique de Roscoff, CNRS/Sorbonne Université, Place Georges Teissier, 29680 Roscoff, France

[3]Stony Brook University Proteomics Center, Stony Brook Medicine, Basic Science Tower, T-9, Rm 167, SUNY, Stony Brook NY 11794

Caroline.Schwaner@stonybrook.edu

The acidification of the oceans (OA) through anthropogenic inputs such as combustion of fossil fuels and land use has brought about profound changes to coastal ecosystems. Acidification represents a serious and growing threat to the future of commercially and ecologically important species, such as the northern quahog (*Mercenaria mercenaria*) and eastern oyster (*Crassostrea virginica*). Some species, especially those found in heterogeneous coastal environments, have shown high levels of resilience to fluctuations in pH and a capacity to withstand acidification events; however, the accelerated pace of these changes is concerning and requires additional understanding of the capacity of populations or species to acclimate or adapt. This study combined physiological assays with 'omic' approaches (transcriptomics, genomics, proteomics) to assess the susceptibility of clams and oysters to acidification and the factors conferring resilience. Mechanisms enabling bivalves to respond to OA (from the organism level to individual genes) were investigated, taking into consideration the potential costs of OA resilience. Gene silencing experiments were used to confirm the protective role of a candidate gene (perlucin) associated with resilience to OA. While there will most likely be consequences for surviving under stressful acidification conditions, such as a reduction in immunity and shell growth and repair, *M. mercenaria* and *C. virginica*, having already been exposed to natural fluctuations in pH and carbonate chemistry for generations, appear to be capable of implementing strategies to mitigate the negative impacts of OA and persist.

IMPROVING LOW SALINITY TOLERANCE IN LOUISIANA POPULATIONS OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA,* USING GENOMIC SELECTION

L.C. Schwartz[1]*, L.V. Plough[2], R. Lavaud[3], M.K. LaPeyre[4], A.F. Pandelides[1], D. Comba[3], and B.A. Stauffer[1]

[1]University of Louisiana at Lafayette, Department of Biology, 410 E. St. Mary Blvd Lafayette, LA 70503

[2]University of Maryland Center for Environmental Science, Horn Pt. Laboratory, 2020 Horns Pt. Rd, Cambridge, MD 21613

[3]Louisiana State University Agricultural Center, School of Renewable Natural Resources, 101 Efferson Hall, Baton Rouge, LA 70803

[4]U.S. Geological Survey, Louisiana Fish and Wildlife Cooperative, Research Unit, School of Renewable Natural Resources, Louisiana, State University Agricultural Center, Baton Rouge, LA 70803

lindsey.schwartz@louisiana.edu

Louisiana contributes the majority of eastern oyster (*Crassostrea virginica*) landings in the United States, producing approximately 45% of oyster landings annually (NOAA Fisheries Landings, 2011-2021). The eastern oyster fishery has seen major declines in recent years due to changing environmental conditions. Estuarine oysters in Louisiana are subject to rapid environmental fluctuations, especially in salinity, which can decrease rapidly due to storm events and freshwater diversions. Salinity in these estuaries often drops below the optimal growth and survival range for oysters (14-28). Louisiana has seen mass mortality events potentially due to extended periods of low salinity (<5) in the last several years, resulting in reduced *C. virginica* landings.

The Leveraging Opportunities and Strategic Partnerships to Advance Tolerant Oysters for Restoration (LO-SPAT) Project was launched with the goal of selectively breeding low salinity tolerant oysters to restore Louisiana populations in protected and fished reefs. Genomic selection (GS) models for low salinity tolerance are being built based on the results of a low salinity challenge (salinity of 2) using oysters spawned from three regions across Louisiana. Following the 45-day challenge, tissue from all live and dead oysters was sent out for genotyping on a custom *C. virginica* Axiom array (~66k SNP). The results of a genome wide association study and prediction accuracies of various Bayesian and GBLUP GS models will be presented. Going forward, the best performing model will be used to select candidate broodstock for spawning and production of low salinity tolerant oysters to be planted at sites across Louisiana.

COMPARING EMBRYONIC DEVELOPMENT IN BEACH AND MARSH HABITATS FOR THE AMERICAN HORSESHOE CRAB, *LIMULUS POLYPHEMUS*, IN SOUTH CAROLINA, USA

Elizabeth Scott*, Daniel Sasson, Michael Kendrick, Jeffrey Brunson, and Peter Kingsley-Smith

Crustacean Research and Monitoring Section, Marine Resources Research Institute, South Carolina Department of Natural Resources (SCDNR), 217 Fort Johnson Road, Charleston, South Carolina 29412

scotte@dnr.sc.gov

Atlantic horseshoe crabs (*Limulus polyphemus*) typically spawn in high intertidal sediments where externally fertilized eggs develop for two to four weeks. It has long been presumed that horseshoe crabs spawn primarily in beach habitats due to their optimal conditions for embryonic development. Recent research by the SCDNR, however, shows that horseshoe crabs also spawn extensively in the marsh, but how embryonic development differs across habitats remains unclear.

To determine how development differs between spawning habitat types, nests of spawning female horseshoe crabs were marked at a paired beach and marsh site in coastal South Carolina. Each nest was excavated after either one week (n=41) or three weeks (n=41) of development. Fifty eggs from each nest were subsampled and each egg was categorized into one of seven developmental stages. Linear mixed models for each stage for week 1 and week 3 samples were conducted, with percent developmental stage as the dependent variable, habitat as the fixed effect, and number of days between nesting and excavation as a random effect.

There was no significant effect of habitat on developmental progression for week 1 or week 3 nests, indicating that marshes provide habitat comparable to beaches for developing horseshoe crabs. These results, combined with previous research by the SCDNR document, the extensive use of marshes by spawning horseshoe crabs, and suggest that marshes likely represent a large source of recruitment for horseshoe crabs. Characterizing sources of recruitment can lead to more effective management strategies for horseshoe crabs and the habitats they use.

APPLYING ENVIRONMENTAL DNA TECHNIQUES FOR EARLY DETECTION OF RUST TIDE CAUSED BY *MARGALEFIDINIUM POLYKRIKOIDES* AROUND AQUACULTURE FARMS

Abigail K. Scro[1]*, Cassidy Pilate[1], Susanna Osinski[2], Skylar Bayer[2], and Roxanna M. Smolowitz[1]

[1]Aquatic Diagnostic Laboratory, Roger Williams University, 1 Old Ferry Road, Bristol RI 02809

[2]Center for Economic and Environmental Development, Roger Williams University, 1 Old Ferry Road, Bristol RI 02809

ascro@rwu.edu

Rust tide is a harmful algal bloom caused by the rapid growth of the dinoflagellate *Cochlodinium polykrikoides* recently renamed *Margalefidinium polykrikoides*. The onset of blooms is sudden and occur in late summer and early fall months in southern New England. While the life cycle of *M. polykrikoides* has been described and the timing of blooms often follows massive rainfalls after droughts, it is still difficult to predict the bloom; leaving aquaculturists without time to prepare. The rust tide blooms pose a threat to Rhode Island's shellfish aquaculture industry as the incidence of these events increases with increasing sea surface temperatures.

Environmental DNA (eDNA) methods have been used to identify and quantify species of interest, as well as, for screening and early detection of harmful microbes. Using eDNA techniques, a new diagnostic was developed to track the spatio-temporal dynamics of rust tide events around aquaculture farms.

A species-specific TaqMan qPCR was designed to target *M. polykrikoides* from environmental samples. To validate the method, water and sediment samples were collected in triplicate during August 2022 from various locations within a Rhode Island salt pond with a history of rust tide blooms. Sampling dates corresponded with time points before, during and after a visible bloom. Preliminary results indicate the consistent presence of *M. polykrikoides* in water and sediment samples without a visible bloom. Further validation of the assay will be completed using cell cultures to relate assay results to cell counts within environmental samples, with a goal of estimating the onset of blooms.

SUCCESSFUL EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) RECRUITMENT ON TWO ALTERNATIVE SETTLEMENT SUBSTRATES IN VIRGINIA TRIBUTARIES

Rochelle Seitz[1]*, Kathleen Knick[1], Amanda Pysher[2], and Emily Suchonic[3]

[1]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[2]Old Dominion University, 1551 Hampton Blvd., Norfolk, VA 23529

[3]University of Central Florida, 4000 Central Florida Blvd., Orlando, FL 32816

seitz@vims.edu

Eastern oyster (*Crassostrea virginica*) populations have been declining, and their preferred settlement substrate, natural oyster shell, is becoming scarce. Alternative substrates are increasingly used for oyster reef restoration, and quantifying their effectiveness is warranted. Oyster Castles are commonly used as substrate, and new concrete substrates, Grow Oyster Reef Tiles, are now available. Eastern oyster recruitment and size on two substrate types, Oyster Castles (OC) and Grow Tiles (GT), were assessed over a 3-year period. Four sites in Chesapeake Bay were examined: Cherrystone Inlet, Mockhorn Bay, Lynnhaven Bay, and Elizabeth River. At each site, ten OC and ten GT were randomly interspersed parallel to shore in the intertidal. Sites were sampled in October 2019, July 2020, and June 2021. Combined data (2019-2021) were analyzed to examine influence of the factors year, site, and substrate type. Both substrate types (OC and GT) had high oyster recruitment, >50 individuals/m^2, a target density for successful oyster restoration in Chesapeake Bay. Survival was high on both substrate types, and there were differences in densities by site; highest oyster densities were in Mockhorn Bay. Two cohorts were evident for populations on both substrates, and both populations displayed an approximate 60-70 mm growth over the three years. Recruitment was greater on OC over three years, but mean oyster size was typically greater on GT. Both substrate types were successful in recruiting high densities of oysters, allowing survival of multiple cohorts, and promoting growth to adult size, suggesting both substrates could be used effectively for restoration.

BLUE CRAB AND FORAGE FISH ABUNDANCES ARE REDUCED WITH SUBESTUARY SHORELINE AND UPLAND DEVELOPMENT

Rochelle Seitz[1]*, Rom Lipcius[1], Gabrielle Saluta[1], Matt Kornis[2], Denise Breitburg[3], Tom Jordan[3], and Don Weller[3]

[1]Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

[2]US Fish and Wildlife Service, Green Bay Fish and Wildlife Conservation Office, 2661 Scott Tower Drive, New Franklin, WI 54229

[3]Smithsonian Environmental Research Center, 647 Contees Wharf Road, Edgewater, MD 21037

seitz@vims.edu

Anthropogenic stressors in nearshore habitats can impact economically and ecologically important species. Consequences of shoreline and upland development on blue crabs and forage fish throughout Chesapeake Bay were analyzed. New data on blue crab abundances from shallow-water sampling and the baywide winter dredge survey were examined, and data from fyke and seine net surveys, previously compiled for a meta-analysis, were re-examined. Upland use and shoreline development significantly affected juvenile crab abundance, which declined gradually with increasing shoreline development. For every 1% increase in shoreline development, crab abundance decreased by 0.4%. At shallow sites from the blue crab winter dredge survey, extensive upland development substantially lowered adult crab densities. Various non-linear curves were fit to the data (e.g., sigmoidal, piece-wise regression) and compared with linear fits to examine patterns in forage fish and crab abundances in comparison to shoreline development. Piecewise regression curves for crabs, spot, and croaker versus shoreline development each showed improved R^2 values (crab $R^2 = 0.34$, spot $R^2 = 0.52$, croaker $R^2 = 0.79$) compared to a linear relationship, with a breakpoint (i.e., threshold) at ~10% shoreline development. Also, sigmoidal curves for *Menidia* sp., anchovies, menhaden, and hogchoker versus shoreline development each had improved R^2 values compared to a linear relationship, with a range in the threshold of 10 to 30%. Development and upland-use decisions should consider the negative effects imposed on forage species.

ECOLOGICAL ASPECTS OF THE TRANSMISSION OF *HEMATODINIUM PEREZI* TO BLUE CRABS

Jeffrey D. Shields* and Xuqing Chen

Virginia Institute of Marine Science, The College of William & Mary, Gloucester Point, VA, 23062

jeff@vims.edu

The endoparasitic dinoflagellate, *Hematodinium perezi,* causes disease and mortality in blue crabs from the high salinity coastal bays of the eastern and Gulf coasts of the USA. Transmission is waterborne presumably through an infectious dinospore stage. Using sentinel studies with juvenile crabs, the transmission of the parasite was investigated in relation to exposure time, seasonality, and other biotic factors. Transmission was rapid in high salinity waters, with short-term exposures of 3-7 day leading to high incidence levels in these systems. Infections developed rapidly, progressing to heavy infections in 25% of newly acquired infections over a short, 7-day period. A modification of our sentinel methodology that can be used to study biotic interactions that may affect transmission of this and other pathogens to blue crabs will be presented. Using a sentinel methodology and "sandwich" experiments, filter feeding by oysters was examined as a negative biotic factor on transmission of the parasite to blue crabs. Filter feeding showed a variable effect that may be related to the intensity of transmission pressure. In hyper-endemic areas such as the coastal bays of the Delmarva Peninsula, seasonal transmission pressure can be very high, limiting the ability of filter feeders to effectively reduce prevalence of the parasite, but during periods of low transmission pressure, filter feeders may operate to reduce transmission.

HOW TO USE SOCIAL MEDIA TO COMMUNICATE YOUR SCIENCE TO THE PUBLIC AND WHY YOU SHOULD

David Shiffman

David.Shiffman@gmail.com

Public science literacy has never been more important, or more threatened. The good news is that modern communications tools make it easier than ever before in human history for experts to share their expertise with the public, media, and policymakers. This hands-on workshop will teach the basic principles and advanced tips and tricks for public science engagement, focusing on crafting your message and using some social media tools to share it with the world. Dr. David Shiffman is one of the most-followed scientists in the world on social media and is an award-winning expert in public science engagement. This workshop has been given to hundreds of scientists, managers, conservation advocates, and practitioners on five continents.

SEVEN YEARS OF MONITORING SHELLFISH ON A CONSTRUCTED, INTERTIDAL REEF IN THE DELAWARE BAY, NEW JERSEY

Jenny Shinn* and David Bushek

Rutgers, The State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349

jenny.shinn@rutgers.edu

The Gandy's Beach Nature Conservancy Preserve includes undeveloped shoreline adjacent to Nantuxent Creek and along the Delaware Bay in New Jersey. Beginning in 2014, a collaborative project constructed breakwater structures using shell bags and Oyster Castles® in an effort to slow the rate of shoreline erosion and create habitat for shellfish. Recruitment, survival, and shell height of oysters living on the artificial structures were monitored seasonally for seven years. A multi-generational population of oysters colonized the structures and demonstrated persistence through time with densities similar to wild, subtidal oyster beds in the area. Additionally, ribbed mussels were observed; sometimes at coverage densities of 95%; and likely supplied additional structural support to the reefs while diversifying the habitat and increasing filtration capacity. Oyster recruitment and survival varied annually. Although winter temperatures and ice cover on the structures were not monitored throughout this project, it was hypothesized that interannual oyster survival was impacted by winter conditions. This project provided a unique opportunity to document intertidal oyster reef development in the mid-Atlantic region via a long-term monitoring program administered by the USFWS in response to shoreline erosion caused by Hurricane Sandy.

POLYPLOID BREEDING STRATEGIES FOR *CRASSOSTREA VIRGINICA*

Jessica M. Small[1]*, Peter Kube[2], and Standish K. Allen, Jr[1]

[1]Virginia Institute of Marine Science at the College of William & Mary, 1309 Greate Road, Gloucester Point, VA 23062

[2]Center for Aquaculture Technologies, 8445 Camino Santa Fe, Suite 104, San Diego, CA 92121

jamoss@vims.edu

At VIMS, domestication of the eastern oyster has been underway for about 30 years with stepwise, significant advances in breeding strategies initially focused on diploid oysters. Today, the Aquaculture Genetics and Breeding Technology Center (ABC) is the breeding hub at VIMS for oysters and brood stock are distributed to hatcheries coast-wide. Economically important traits include survival, growth, meat yield and improved shape. The most improved lines are based on family selection, driven by quantitative genetic analysis. With the overwhelming popularity of triploids in the mid-Atlantic and southward, the ABC has expanded its focus into the genetic improvement in tetraploids. Polyploid breeding in oysters represents a new frontier. For example, there is no information to indicate which tetraploid traits would produce better triploids. Moreover, the tetraploid sire, putatively, has twice the influence over traits in triploids than the diploid dam. After more than a decade of producing tetraploid families for analysis and compiling data on traits such as DNA content, chromosome content stability, survival, and growth in different environments, the ABC now operates a parallel, family-based tetraploid breeding program, selecting for traits designed to yield chromosomally-stable, high performing tetraploids. Genetic linkages that exist between pedigreed tetraploid sires, pedigreed diploid dams, and the triploid families created with them provide a powerful approach to tetraploid breeding. Bivariate analyses of triploid and tetraploid data indicate that the genetic correlation between triploid and tetraploid survival is 0.84 while the correlation between triploid and tetraploid total weight is 0.58.

EFFECTS OF MANGANESE ON THE DOPAMINE D2R SIGNAL TRANSDUCTION PATHWAY L-TYPE CALCIUM CHANNELS AND THE CONTROL OF LATERAL CELL MEMBRANE POTENTIAL AND CILIA RESPONSE IN GILL OF *CRASSOSTREA VIRGINICA*

Shatema Small[1]*, Elizaveta Ulumbelashvili[2], Edward J. Catapane[1], and Margaret A. Carroll[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

shatemasmall@hotmail.com

Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by serotonin and dopamine. Dopamine activates D2R-like receptors hyperpolarizing GLC causing cilio-inhibition. Serotonin depolarizes GLC causing cilio-excitation. Manganese, a neurotoxin causing manganism, a Parkinson's-like disease, disrupts dopaminergic neurotransmission. The neurotoxic mechanism is not fully resolved. Lack of effective treatment for manganism is a major obstacle in its clinical management. Previous work with *C. virginica* showed manganese blocks hyperpolarization and cilio-inhibitory effects of dopamine on GLC. Activation of D2R inhibits adenylyl cyclase, activates PLC-β, opens GIRK channels and inhibits L type calcium channels (LTCC) reducing the inward flow of calcium, causing hyperpolarization and decreasing cilia beating. To determine if LTCC affects GLC membrane potential and cilia beating; and are affected by manganese, LTCC blockers verapamil and nifedipine were used to mimic the actions of dopamine. Cilia activity was measured by stroboscopic microscopy. Membrane potentials were simultaneously measured using the fluorescent dye $DiBAC_4(3)$. Verapamil slightly decreased cilia beating. Nifedipine stopped cilia beating. Both hyperpolarized the cells. In the presence of manganese, manganese did not prevent the actions of nifedipine on cilia beating or membrane potential. This physiological study shows LTCC plays a role in the D2R signal transduction pathway in GLC of *C. virginica*, but is not affected by manganese. These findings are helpful in understanding the D2R signaling pathway mechanisms as well as manganese neurotoxicity and provide evidence to guide future studies of potential therapeutic agents for manganism. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP and PSC-CUNY 62344-0050 and 62344-0051.

PREVALENCE OF *VIBRIO PARAHAEMOLYTICUS* AND *V. VULNIFICUS* IN BLUE CRABS (*CALLINECTES SAPIDUS*) AND SEAWATER COLLECTED FROM THE MARYLAND COASTAL BAYS

Jasmine Smalls[1]*, John Jacobs[2], Howard Townsend[2], Paulinus Chigbu[1], and Salina Parveen[1]

[1]University of Maryland Eastern Shore, Department of Agriculture, Food, and Resource Sciences, 1 Backbone Road, Princess Anne, MD 21853

[2]Cooperative Oxford Laboratory, 904 S Morris St, Oxford, MD 21654

jsmalls@umes.edu

Fluctuations in water quality characteristics influence the productivity of blue crabs (*Callinectes sapidus*), and the risk of human exposure to pathogenic *Vibrio* species. Thus, this study assessed the prevalence of total and pathogenic markers of *Vibrio parahaemolyticus* (*Vp*) and *Vibrio vulnificus* (*Vv*) in blue crabs and seawater from the Maryland Coastal Bays (MCB) and the correlation between *Vibrio* levels and physicochemical factors. Three to five crabs and one liter of seawater were collected monthly for three years (May 2018 to December 2020) from six sites within the MCBs. Hemolymph and crab tissue were extracted and pooled for each site. Extracted hemolymph, crab tissue, and seawater were analyzed for *Vp* and *Vv* using the Most Probable Number (MPN) and real time PCR methods. A one-way Analysis of Variance (ANOVA), correlations, and linear models were used to analyze the data. The Akaike Information Criterion (AIC) was evaluated to determine the model that provides the best fit to the data relating *Vibrio* concentrations and environmental factors. Results suggested that environmental factors could influence the growth of *Vibrio* spp. Both *Vp* and *Vv* were more prevalent during the warmer months. *Vibrio* was more prevalent in crab samples compared to seawater. A significant positive correlation was observed between *Vv* in seawater and temperature ($p=0.0143$), hemolymph and pH ($p=0.0061$), and negatively correlated in whole crab and dissolved oxygen level ($p=0.0256$). The concentration of *Vp* in seawater was significantly positively correlated with temperature ($p=0.009$) and negatively correlated with dissolved oxygen ($p=0.012$).

ROTATIONAL MANAGEMENT OF OYSTER HARVEST IN THE RAPPAHANNOCK RIVER, VIRGINIA: 15 YEARS ONWARD

Melissa Southworth[1]*, James Wesson[2], Andrew Button[3], Roger Mann[1], Alexandria Marquardt[1], and Andrew Scheld[1]

[1]Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, VA 23062

[2]12050 Freeport Road, Gloucester, VA 23061

[3]Virginia Marine Resources Commission, Conservation Replenishment Department, Building 96, 380 Fenwick Road, Fort Monroe, VA 23651

melsouth@vims.edu

The oyster fishery in the Rappahannock River, Virginia was effectively closed by epizootics until the implementation of rotational area management in 2007. Six designated areas were established with two-open and four-closed areas each year, with each area being opened every third harvest season, the latter being typically bounded between October and January. From the 2007/2008 through the 2018/2019 harvest seasons, harvest in all six areas was by an oyster scrape. Beginning during the 2019/2020 harvest season, one area was set aside as a patent tong area and has been open for harvest every year since. As part of the rotational area management, shell repletion (planting of clean substrate on the bottom) has been performed each summer following a harvest year where it was deemed necessary (i.e., shell volume was below a certain threshold determined during an annual fall stock assessment). Herein the oyster population and recruitment numbers as well as repletion efforts within the six management areas were examined and compared over a twenty-year period from 2003 to 2022 and offer advice on wider application of rotational management in exploited oyster stocks.

LEVERAGING THE SHARED RESOURCES OF OYSTER CO-OPERATIVE TO SUPPORT KELP PRODUCTION

Ken Curtis Sparta*[1], Greg Foote[2], and Leo Sparta[1]

[1]Spartan Sea Farms, 23 South Street, Freeport, ME 04032

[2]Dirigo Marine Resources, LLC. 485 Mitchell Road, Cape Elizabeth, ME 04107

SpartanDiveServices@gmail.com

The Maine Seafarmer Co-operative (MFSC) is a group of nine farmers in Yarmouth and Freeport, Maine. The Co-op was formed in 2021 to strengthen the resilience of small family farms, and to formalize the sharing of knowledge, equipment, and opportunity. In addition to farming oysters and scallops, four of the nine Co-op members cultivate two species of macroalgae: sugar kelp and skinny kelp. Sharing facilities, labor, and markets has made the addition of seaweed relatively smooth. This presentation will describe incorporating seaweed gear and operations into the farms, maximizing seaweed production even on small oyster leases, and how shared knowledge, infrastructure, and access to markets has aided in this process.

Additionally, two Co-op members launched the Freeport Oyster Bar, a community-centric restaurant dedicated to celebrating Maine's the working waterfront of Maine, housed in a restored 1830s Carriage House. The Freeport Oyster Bar sells a significant portion of oysters produced by growers across the co-operative, allowing for higher margins to farmers and direct customer interaction. It also provides opportunities to sell kelp at high margins through value-added products such as holdfast pickles and kelp infused gin. This additional sales outlet allows farmers to recoup maximum value from their seaweed harvest. In this presentation it will be shown that collaboration among shellfish farmers can derisk and accelerate the transition to co-culture of seaweeds and shellfish.

CLIMATE-INDUCED WARMING ON THE MAB SEAFLOOR: MODELING FUTURE DISTRIBUTIONS OF THE ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*)

Molly Spencer*[1], Eric Powell[1], John Klinck[2], Daphne Munroe[3], Alyssa LeClair[4], Andrew Scheld[5], Eileen Hofmann[2], Enrique Curchitser[6], and Mike Alexander[7]

[1]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Dr., Ocean Springs, MS 39564

[2]Old Dominion University, Center for Coastal Physical Oceanography, 4111 Monarch Way, Norfolk, VA 23508

[3]Rutgers the State University of New Jersey, Haskin Shellfish Research Laboratory, 6959 Miller Ave, Port Norris, NJ 08349

[4]NOAA National Ocean Service, NOAA Beaufort Lab, National Centers for Coastal Ocean Science, Coastal Resilience, Restoration, and Assessment Branch, 101 Pivers Island Rd, Beaufort, NC 28516

[5]Virginia Institute of Marine Science, College of William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

[6]Rutgers the State University of New Jersey, Department of Marine and Coastal Science, 71 Dudley Rd, New Brunswick, NJ 08901

[7]NOAA GFDL Earth System Research Laboratories, 325 Broadway, Boulder, CO 80305

Molly.spencer@usm.edu

The Atlantic surfclam, *Spisula solidissima*, a biomass dominant bivalve species off the eastern North American continental shelf, supports a lucrative commercial fishery in the mid-Atlantic that brings in roughly $30 million in revenue per year. The thermal tolerance of this economically and ecologically important species is seasonally dependent, but generally waters exceeding 20°C restrict growth and survival. The thermal regime in the north and mid-Atlantic has been rising over the past century, with climate-induced warming of bottom sea-temperatures thought to be linked to the observed distributional shift in the Atlantic surfclam population. As rapid climate change continues to influence the northern and offshore migration of species, this study hopes to predict future abundance and biomass distributions of the Atlantic surfclam from years 2020-2050, using a Spatially explicit, Ecological, agent-based Fisheries and Economics Simulator (SEFES). Results will provide communities and industries that rely on this fishery the chance to develop anticipatory management for the socio-ecological and economic impacts that may result from future range shift dynamics. Simulations show continued offshore movement of surfclams through 2050 with an expanding biomass particularly off Long Island and southern New England into deeper water. Depths reached substantially exceed the present-day offshore range boundary, but limited data suggests these are consistent with species' distribution during the Medieval Climate Anomaly. Future simulations plan to evaluate future distribution of Atlantic surfclam biomass in relation to projected offshore windfarm lease areas.

OFF-SHORE AQUACULTURE POTENTIAL FOR THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA*: FIELD OBSERVATIONS AND MULTI-STRESSOR LABORATORY EXPERIMENTS

Laura Steeves*[1], Daphne M. Munroe[1], Shannon Meseck[2], Ximing Guo[1], Sean Towers[1], Joseph Myers[3], Sam Martin[4], and Tom Dameron[5]

[1]Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, Rutgers, The State University of New Jersey, 6959 Miller Avenue, Port Norris, NJ 08349

[2]NOAA Fisheries Service, Northeast Fisheries Science Center, 212 Rogers Ave, Milford, CT, 06460

[3]Sea watch International, Ltd., 8978 Glebe Park Dr, Easton, MD, 21601

[4]Atlantic Capes Fisheries Inc. 985 Ocean Drive, Cape May, NJ, 08204

[5]Surfside Seafood Products LLC, 2838 High Street Port Norris, NJ, 08349

laura.steeves@rutgers.edu

The Atlantic surfclam (*Spisula solidissima*) supports a large commercial fishery in the United States and is consistently the most fished clam species by weight in the country. Growing surfclams in aquaculture farms presents an opportunity to support surfclam production with a unique product that would not compete with fished surfclam (i.e., a steamer sized clam ~55mm). Although surfclam aquaculture has been successfully explored in shallow protected bays, growing clams in the open ocean presents an opportunity to farm shellfish where space is less competitive, water quality is often higher, and where species naturally occur; however, farming in the open ocean requires careful consideration of physical and biological limitations. The goals of this research are 1. To explore the potential for surfclams to be cultivated at a commercial scale in the open ocean, and 2. To use laboratory experiments to examine how changing ocean conditions in potential aquaculture sites may impact surfclams. To address these goals, surfclams were successfully spawned in the fall season of 2022 and will be planted offshore New Jersey in Spring 2023 in novel cages designed to withstand offshore bottom conditions. This cohort of surfclams will also be used in laboratory experiments examining the combined effects of temperature and carbonate chemistry (reflective of ocean acidification) on surfclam survival and growth. This research is a collaborative effort with industry partners and will provide information about the potential to produce surfclams in offshore aquaculture farms, and the ability surfclam to survive and grow in changing oceanographic conditions.

MECHANISMS OF MORTALITY IN *CRASSOSTREA VIRGINICA* DURING SEVERE HYPOXIA: EFFECTS OF ENDOGENOUS AND EXOGENOUS BACTERIA, AND TEMPERATURE

Laura Steeves[1]*, Keryn Winterburn[2], Ramon Filgueira[3], Luc A. Comeau[4], Thomas Guyondet[4], Michelle Maillet[4], José M.F. Babarro[5], Jeff C. Clements[4], Martin A. Mallet[6], Rémy Haché[7], Luke A. Poirier[4], Saswati Deb[4], and Michael R.S. Coffin[4]

[1]Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, Rutgers, The State University of New Jersey, 6959 Miller Avenue, Port Norris, NJ 08349

[2]Dalhousie University, Department of Biology, 1355 Oxford Street, Halifax, NS, B3H 4R2, Canada

[3]Dalhousie University, Marine Affairs Program, 1355 Oxford Street, NS, B3H 4R2, Canada

[4]Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Ave, Moncton, NB, E1C 5K4 Canada

[5]Instituto de Investigaciones Marinas, IIM-CSIC, Rua de Eduardo Cabello 6, Pontevedra, 36208, Spain

[6]L'Etang Ruisseau Bar Ltée, Shippagan, Chem. Des Huîtres, Shippagan New Brunswick, E8S 28N, Canada

[7]Department of Agriculture, Aquaculture and Fisheries, Government of New Brunswick, 100 Aquarium Street, Shippagan, New Brunswick, E8S 1H9, Canada

Laura.steeves@rutgers.edu

Low dissolved oxygen concentrations can result in depressed bivalve defense systems while promoting anaerobic bacterial growth, ultimately increasing bivalve mortality rates. Although bivalve mortality in response to hypoxia is well studied, the specific mechanisms of mortality are not. In this study, complementary techniques (LT50, histology, 16S rRNA amplicon sequencing, and valvometry) were used in manipulative laboratory experiments and field studies to mechanistically explore how bacteria (endogenous and exogenous) and temperature influence mortality in eastern oysters (*Crassostrea virginica*) exposed to hypoxia or anoxia. Results indicated that removing both and exogenous bacterial sources increased *C. virginica* survivorship, and that the proliferation of harmful endogenous bacteria increased mortality rates. Interestingly, increased mortality rates were associated with the proliferation of primarily anaerobic endogenous bacteria in the absence antibiotic treatments. Oyster behavioural response was consistent between laboratory and field studies, demonstrating remarkable synchrony in valve closing when exposed to anoxia, with brief re-openings increasing in frequency prior to death. For exogenous bacteria, experiments at 28°C had a faster mortality rate relative to 20°C. Although oysters are well adapted to surviving low oxygen conditions, these results suggest that mortality occurring under low oxygen are facilitated by a combination of elevated temperature, the proliferation of harmful endogenous bacteria, and exposure to harmful exogenous bacterial exposure during valve openings. These findings are useful for predicting bivalve mortality rates as elevated water temperatures and hypoxic events are both predicted to become increasingly common in many coastal environments.

STUDYING *VIBRIO PARAHAEMOLYTICUS*-EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) INTERACTIONS, INCLUDING THE OYSTER-ASSOCIATED BACTERIAL COMMUNITY

Ann M. Stevens[1,2]*, Ian S. Hines[1,2], Justin Markov Madanick[1], Stephen A. Smith[2,3], and David D. Kuhn[2,4]

[1]Virginia Tech, Department of Biological Sciences, 2119 Derring Hall, 926 West Campus Dr., Blacksburg, VA 24061

[2]Center for Emerging, Zoonotic, and Arthropod-borne Pathogens, Virginia Tech Corporate Research Center, Integrated Life Science Building, 1981 Kraft Dr., Room 2036, Virginia Tech, Blacksburg, VA 24060

[3]Virginia Tech, Department of Biomedical Science and Pathobiology, 205 Duck Pond Drive, Blacksburg, VA 24061

[4]Virginia Tech, Department of Food Science and Technology, 360 Duck Pond Drive, Blacksburg, VA 24061

ams@vt.edu

Shellfish, including the eastern oyster (*Crassostrea virginica*), are important human foods, but they are also a primary source of seafood-borne gastroenteritis caused by the emerging pathogen, *Vibrio parahaemolyticus*. A laboratory-scale Biosafety Level-2 inoculation system was developed to study the interactions between *V. parahaemolyticus* and their host oysters in a controlled manner. Chesapeake Bay region oysters harvested during summer or winter months were exposed to the clinical RIMD2210633 strain carrying a chloramphenicol-selective marker (*VP* RIMDmC). Endogenous *Vibrio* spp. numbers associated with the existing microbiome were significantly reduced following chloramphenicol water-treatment. This likely contributed to higher *VP* RIMDmC oyster-associated levels after *VP* exposure in the lab, especially when winter-harvested animals were used. Summer-harvested oysters had significantly higher native *Vibrio* spp. levels and a concurrent lower level of artificial oyster-associated *VP* RIMDmC. This suggests the pre-existing microbiome appears to afford some protection from an external *V. parahaemolyticus* challenge. Additional research was conducted quarterly from winter 2020 through winter 2021 to analyze seasonal effects on the taxonomic diversity of the bacterial community in consumer-ready Eastern oysters. At each time point, 18 Chesapeake Bay watershed oysters were acquired from a local grocery store, genomic DNA was extracted from the homogenized whole oyster tissues, and the bacterial 16S rRNA gene V4 region was PCR-amplified using barcoded primers prior to sequencing via Illumina MiSeq and bioinformatic data analysis. A core group of oyster-associated bacteria was identified (*Mycoplasmataceae* and *Spirochaetaceae*), with changes in the relative abundances of other bacteria attributed to differences in seasonal water temperature.

INITIATING MUSSEL (*MYTILUS* SP.) MONITORING IN NORWAY AND BASELINE FOR 2021 AND 2022

Tore Strohmeier*, Antonio Aguera, and Øivind Strand

Institute of Marine Research, PO Box 1870 Nordnes, 5817 Bergen, Norway

tores@hi.no

The temporal and spatial distribution of mussels (*Mytilus* spp.) in the North Atlantic has changed during the last 30 years. In Norway, the Institute of Marine Research (IMR) has received an increasing number of public observations on the absence of mussels. With this as a background the IMR has started the development of a national mussel monitoring program and conducted a baseline study for four regions in the country. The aim of the monitoring program is to survey mussel population changes over time and space, and to collect metadata to enable identification of potential causes to a change in distribution. The program should also explore the potential for new technology to monitor the mussel population.

The length of the Norwegian coastline exceeds 80k km. The large distances and the aim to identify local changes in abundance required the development of a new method to determine mussel abundance. The applied methodology, the potential of the investigated new technology and a mussel baseline will be presented, along with plans modeling and assessing changes in mussel distribution.

EVALUATION OF THE DEGREE OF CO-OCCURRENCE OF SURFCLAMS AND OCEAN QUAHOGS AT FISHABLE CONCENTRATIONS

Stephanie Stromp*[1], Eric N. Powell[1], and Roger Mann[2]

[1]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Dr., Ocean Springs, MS 39564

[2]Virginia Institute of Marine Science, William & Mary, 1370 Greate Rd., Gloucester Point, VA 23062

stephanie.stromp@usm.edu

Warming of the mid-Atlantic continental shelf has resulted in a range shift of the Atlantic surfclam, *Spisula solidissima*, north and offshore into waters still occupied by ocean quahogs (*Arctica islandica*). Consequently, an ecotone now exists over much of the offshore range of the surfclam in which surfclams and ocean quahogs are both found. Regulations prohibit fishers from landing both species in the same catch, limiting fishing to locations where the target species can be sorted on deck. Fishery access to the ecotone region is vital as CPUE has declined over the core of the surfclam range. An at-sea survey sampling 50+ stations in the overlap region was conducted in September 2021 with the purpose of mapping fishable concentrations of surfclams and ocean quahogs. Size frequency and density data of both species were assessed with environmental parameters to produce trends in Atlantic surfclam and ocean quahog distribution. Species overlap between surfclams and ocean quahogs was most prominent in the 40-55 m depth range, in which mean surfclam size declined by 40mm compared to shallower waters. Density of clams shifted within this depth from surfclam dominant <40m to ocean quahog dominant >60 m. Atlantic surfclam size increased with temperature while densities remained stable, indicative of large but few animals in warmer inshore waters. This analysis emphasizes the potential for economic disruption of fisheries as climate change pushes surfclams further into the range of the ocean quahog.

EXPANDING NORTHEASTERN US GREEN SEA URCHIN AQUACULTURE PRODUCTION AND THEIR POTENTIAL TO REDUCE BIOFOULING OF SHELLFISH

Coleen Suckling[1]*, Tara Plee[1], Dana Morse[2], and Steve Eddy[3]

[1]University of Rhode Island, Department of Fisheries, Animal and Veterinary Science, 34 Woodward Hall, 9 East Alumni Avenue, Kingston, RI 02881

[2]University of Maine, Maine Sea Grant, Darling Marine Center, 193 Clarks Cove Rd, Walpole, ME 04573

[3]University of Maine, Centre for Cooperative Aquaculture Research, 33 Salmon Farm Road, Franklin, ME, 04634

coleensuckling@uri.edu

The green sea urchin (GSU), *Strongylocentrotus droebachiensis*, is an economically important species in the northeastern US, with production primarily based in Maine. The fishery has dramatically declined since the 1990s, but the demand for the GSU has increased. The GSU can be grown in open water in a wide range of gear types either alone, in polyculture with shellfish or algae or as part of integrated multi trophic aquaculture systems. They are a high value luxury seafood product and global and national demand is unmet creating an opportunity for aquaculture. This talk will overview project efforts working towards expanding the emerging aquaculture industry. These include optimizing hatchery production methods, outreach to increase the awareness of seed availability, and facilitating uptake by providing new growers with seed and technical support for experimental growth to market. Sea urchins also offer a low trophic solution towards reducing nuisance shellfish biofouling species through polyculture. Biofouling can prevent shellfish from reaching their full growth potential by >30% and sea urchins can reduce this fouling through grazing. This talk will include an overview of a new project partnering shellfish growers, hatchery producers and researchers on the use of the GSU for reducing biofouling on various shellfish species. This work is funded by the US Department of Agriculture's Northeast Sustainable Agriculture Research and Education, National Institute of Food Agriculture, and the Northeastern Regional Aquaculture Center.

OBSERVATIONS ON THE USE OF BIRD KITES AT AN OYSTER FARM IN SOUTHERN MOBILE BAY, ALABAMA

John Supan*, Charles Wilson, and Eric Bradley

Navy Cove Oyster Company, 2375 Choctaw Road, Gulf Shores, AL 36542

john.navycoveoysters@gmail.com

Guano left by shorebirds on floating oyster culture cages has become a recent topic in shellfish sanitation. A bird kite (BirdAway Hawk System, OysterGro.com) was deployed at Navy Cove Oyster Farm to observe its effectiveness as a deterrent to bird infestation. The site is a shallow (<2m depth) 4.3 ha inlet on the southern shore of Mobile Bay, Alabama (30.23290901937714, -87.97936577617104). The opening (510m wide) to the Bay is bounded by a southerly beach-shoreline of eroding pine forest. Shorebirds, including herons, gulls, and terns, commonly populate the area.

The kite was deployed in 2019 along the northern edge of the farm above 0.8 ha of sometimes 200 floating cages (OysterGro.com), particularly during the fall when Royal Terns (*Thalasseus maximus)* are most prevalent. Once airborne, the kite flew erratically as advertised and was deployed for several weeks. The withdrawal of Royal Terns from the nearby floating cages was noticed immediately without return. The following fall, the tern infestation was greater, requiring a second kite deployment to clear the entire farm effectively. Since bird infestation at the farm is not constant, the kites are deployed when needed.

Perhaps the effectiveness of bird kites is site specific rather than species specific? The authors have personally seen birds-of-prey above the farm taking flight from the trees ashore, which results in an immediate flight of any birds sitting on the cages and believe kite use simply augments the natural predator-prey response observed in the cove and are only deployed when guano may become prevalent.

PHYSIOLOGICAL AND BEHAVIOURAL RESPONSE OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) AND SOFT-SHELL CLAMS (*MYA ARENARIA*) TO HYPOXIA AND HEATWAVES

Jasmine Talevi[1]*, Shelby Clarke[1], Michael Coffin[2], Luc Comeau[2], Takashi Sakamaki[3], and Ramon Filgueira[4,5]

[1]Dalhousie University, Department of Biology, 1355 Oxford Street, Halifax, NS B3H 4R2, Canada

[2]Fisheries and Oceans Canada, Gulf Fisheries Centre, 343 Université Avenue, Moncton, NB E1C 9B6, Canada

[3]Tohoku University, Department of Civil and Environmental Engineering, Graduate School of Engineering, Aoba 6-6, Sendai, Miyagi 980-8579, Japan

[4]Dalhousie University, Marine Affairs Program, 1355 Oxford Street, Halifax, NS B3H 4R2, Canada

[5]Institute of Marine Research, P.O. Box 1870, 5817 Bergen, Norway

Jasmine.Talevi@dal.ca

Bivalves are both economically and environmentally valued species that play a vital role in coastal ecosystem functioning through water filtration and nutrient cycling. Coastal marine environments are becoming increasingly stressful habitats due anthropogenic nutrient inputs and climate change, which are leading to more frequent extreme events. Extreme events, such as heatwaves and hypoxia, cause sudden and intense changes in the environment leading to adverse effects and mass mortalities of bivalve populations globally. The purpose of this study is to understand how eastern oysters (*Crassostrea virginica*) and soft-shell calms (*Mya arenaria*) behaviourally and physiologically respond to hypoxia and heatwaves under field conditions. To investigate this, bivalves were repeatedly exposed to hypoxia during a heatwave using natural seawater. Behavioural responses related to valve gaping were monitored using a Hall element sensor valvometry system and physiological responses including oxygen consumption rate, feeding rate, assimilation efficiency, and scope for growth were measured. Despite exposure to heatwave conditions and severe hypoxia, both species were able to cope under this stress. The results suggest that in the short-term, eastern oysters and soft-shell clams can withstand these extreme conditions, though extended and cumulative effects may potentially impact the survival of these species. This information can help improve the accuracy of ecosystem models to assess the vulnerability of eastern oysters and soft-shell clams under future climate scenarios, which will be informative for aquaculture and fisheries as cultivation of more resilient bivalve species will be important to maintain revenue.

A NOVEL VIRUS OF FLAVIVIRIDAE ASSOCIATED WITH SEXUAL PRECOCITY IN *MACROBRACHIUM ROSENBERGII*

Kathy F.J. Tang*, Xuan Dong, Guohao Wang, Tao Hu, Juan Li, Chen Li, Zhi Cao, Mang Shi, Yiting Wang, Peizhuo Zou, Jipeng Song, Wen Gao, Fanzeng Meng, Guoliang Yang, Cixiu Li, Weifeng Shi, and Jie Huang

Yellow Sea Fisheries Research Institute; Chinese Academy of Fishery Sciences; Qingdao National Laboratory for Marine Science and Technology, Ministry of Agriculture and Rural Affairs; Qingdao Key Laboratory of Mariculture Epidemiology and Biosecurity, Qingdao 266071 China

ktangnelson@gmail.com

Since 2010, sexual precocity, a typical sign of the iron prawn syndrome (IPS), resulting in the reduced size of farmed giant freshwater prawns *Macrobrachium rosenbergii*, has caused substantial production losses; however, the cause of IPS was not clear. Tests for eight major shrimp pathogens were run, but none were detected from IPS-affected prawns. The histopathological examination of tissues was performed and identified eosinophilic inclusions in the perinuclear cytoplasm of cells in various tissues associated with nervous and endocrinal functions in the compound eyes. A subsequent bioassay with viral extracts of IPS-affected samples reproduced the gross signs of IPS. Metatranscriptomic sequencing identified a novel virus of *Flaviviridae* in all IPS-affected *M. rosenbergii* prawns, which was not found in samples without IPS. This virus contains a positive-sense, single-stranded RNA genome of 12,630 nucleotides (nt). Phylogenetic analysis of the conserved RdRp and NS3 domains showed that it may belong to a new genus between Jingmenvirus and Flavivirus. Under transmission electron microscopy (TEM), putative virus particles showed as spherical with a diameter of 40 to 60 nm. In situ hybridization found hybridization signals consistent with the histopathology in the compound eyes from IPS-affected *M. rosenbergii*. This virus was provisionally named infectious precocity virus (IPV) and developed a nested RT-PCR diagnostic assay and confirmed that all IPS-affected prawns tested IPV positive but normal prawns tested negative. Collectively, this study revealed a novel virus of Flaviviridae associated with sexual precocity in *M. rosenbergii*.

THE AUBURN UNIVERSITY SHELLFISH LAB: TWENTY YEARS OF INDUSTRY-DRIVEN RESEARCH

Andrea M. Tarnecki[1]*, F. Scott Rikard[1], Russell Grice[1], and William Walton[2]

[1]Auburn University Shellfish Lab, 150 Agassiz Street, Dauphin Island, AL 36528

[2]Shellfish Aquaculture Program, Virginia Institute of Marine Science, 1370 Greate Rd, Gloucester Point, VA 23062

atarnecki@auburn.edu

The Auburn University Shellfish Lab (AUSL) was established on Dauphin Island, Alabama, in 2003. The mission of the AUSL is to provide instruction, research, and outreach related to shellfish ecology and production to the citizens of Alabama, the Southeast region, and the nation. Marking the 20th anniversary of the AUSL, this presentation will summarize the accomplishments of the research and extension programs of the lab and its approach to industry-driven research.

The lab currently houses 5 graduate students and to date, 23 masters and 5 PhD students have pursued shellfish research through the AUSL. These students are now spread through the world, currently located in 4 countries and 12 states, with 11 working in the oyster industry. Members of the lab have authored an estimated 156 peer-reviewed publications. Extension agents produce an annual Alabama Oyster Farming Outlook publication each year and numerous extension publications are publicly available as resources for shellfish farmers. In-person and online farmer training programs have been established for potential oyster farmers. An oyster farming mobile app was developed in 2019 and is available for free download to aid in seed deliveries and stocking densities.

The first oyster farm in Alabama began in 2009, with at least 18 farms currently in operation, with farms now established in all five Gulf states. The AUSL has provided over 1.1 billion oysters for the commercial/private industry, research, and extension. Research collaborations have been forged with growers and institutions across the United States. Current research topics include: broodstock conditioning, genetics, breeding, physiology, restoration, health/disease, and seafood safety.

CHINESE "NATURE AND GROWER-CENTERED" OYSTER HATCHERY TECHNOLOGY: IS IT SUSTAINABLE?

Vengatesen Thiyagarajan[1]*, Ziniu Yu[2], Shu Xiao[2], Li Li[3], Weiwei You[4], Lingling Wang[5], and Clarence Chung[6]

[1]Hong Kong Oyster Hatchery and Innovation Research Unit (HKO-HIRU), The Swire Institute of Marine Science and School of Biological Sciences, The University of Hong Kong, Hong Kong SAR, China

[2]CAS Key Laboratory of Tropical Marine Bio-Resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China

[3]CAS Key Laboratory of Experimental Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, China

[4]State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen, China

[5]Liaoning Key Laboratory of Marine Animal Immunology, Dalian Ocean University, Dalian, China

[6]Lee Kum Kee Co., Ltd. Tai Po Industrial Estate, Hong Kong, China

rajan@hku.hk

China accounts for >85% of global edible oyster production, which is valued at over 6 billion USD. This massive industry is, however, facing severe challenges to simultaneously increase meat quality and quantity using indigenously developed knowledge and technologies – especially, when government and environmentalists are seriously concerned about environmental sustainability and climate change pose unprecedented threats to shellfishes. These human impacts not only directly affect the quality of oysters produced in these areas, but also seriously affect wild seed production and collection. The few collected wild seeds also experience mass mortality and their performance is often unpredictable. Thus, sustainable aquaculture in the region is now heavily dependent on hatchery-produced seeds. The nature and grower-centered oyster hatchery technology that are becoming popular in China and found to be more effective and sustainable, especially in South China and Hong Kong, will be discussed.

EFFECTS OF DESICCATION PRACTICES ON EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) CONDITION INDEX, GROWTH RATE, AND PARASITE LOAD

Skye Thomas*[1,2], Julia Buck[1,2], and Ami Wilbur[1,2]

[1]Univeristy of North Carolina Wilmington, Department of Biology and Marine Biology, 601 S. College Road, Wilmington, NC 28403

[2]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, NC 28409

sdt2007@uncw.edu

Eastern oysters (*Crassostrea virginica*) have been a staple food and aquaculture species of the east coast for centuries. A number of different culture techniques and gear have been developed to maximize growth, condition index, and minimize biofouling and parasites. Previous studies have shown exposure to air in the adjustable longline system (ALS) have resulted in oysters with significantly better condition indices than those not exposed. This study further investigates the effects of desiccation on growth, survival, condition and parasite loads (prevalence of pea crabs, *Polydora* sp., and *Bucephalus* sp.) in two lines of selectively bred oysters, one derived from an intertidal population (St. James (SJ)) and the other from a subtidal population (Herring Shoal (HS)) using an ALS. Oysters (75/basket) were stocked into 18 baskets (9 each SJ, HS) and assigned (3 each SJ, HS) to three exposure treatments: submerged, natural tidal exposure, and manual exposure for 24 hours every two weeks from March to November. Survival was evaluated every 3 months with five oysters per treatment (first and third quarterly sample) and 20 oysters per basket (halfway and final sample) haphazardly selected and frozen for later condition and parasite analysis. Condition index and growth rate data will be analyzed using a parametric two-way ANOVA separately, while mortality rates will be tested with a parametric two-way ANOVA beta-regression. The parasite presence/absence data will be tested using a binomial regression model.

OPPORTUNITY FOR GENOMIC SELECTION TO INCREASE SURVIVAL AGAINST AN OSHV-1 MICROVARIANT FROM SAN DIEGO BAY (CALIFORNIA, USA)

Neil F. Thompson[1]*, Tori Agnew[2], Bernarda Calla[1], and Colleen A. Burge[3]

[1]Pacific Shellfish Research Unit, USDA Agricultural Research Service, Hatfield Marine Science Center, 2030 SE Marine Science Dr, Newport, OR 97365

[2]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, 701 E Pratt St, Baltimore MD 21224

[3]Shellfish Health Laboratory, California Department of Fish and Wildlife, Bodega Marine Lab, P.O. Box 247, 2099 Westshore Rd., Bodega Bay, CA 94923

neil.thompson@usda.gov

Ostreid herpesvirus 1 is a pathogen of global concern that has caused severe losses in Pacific oyster aquaculture on numerous continents. Genetic selection has proven to be effective at increasing survival to OsHV-1 infection using various selection models where the pathogen is broadly distributed; however, less research has focused on increasing resistance to OsHV-1 preemptively using genomic selection methods. Using juvenile (5-10 mm shell length) Pacific oysters produced in the USDA Pacific Shellfish Breeding Center, a laboratory challenge experiment was conducted on 15 families to identify the standing genetic variation for OsHV-1 survival, quantify heritability, and determine the utility of genomic selection methods compared to pedigree methods for OsHV-1 survival/tolerance. Mean mortality was 61% for the pedigree challenge, ranging from 29 - 90 percent mortality per family. The heritability of survival is estimated to be 0.66 using pedigree methods, and a broad range of estimated breeding values indicate adequate standing genetic variation for selective breeding. Genotype data was produced with the Axiom Oyster Genotyping Array and used to compare the results from the pedigree-model experiment with a common-garden genomic selection-model experiment. There is ample potential to increase survival to OsHV-1 from San Diego Bay using genetic selection. Further development in genomic selection methodologies and refinements in laboratory challenge protocol may increase selection efficiency and be fundamental in providing the U.S. Pacific coast shellfish industry with an OsHV-1 tolerant stock to use for commercial production.

OYSTER REEF CONTROL OF CARBONATE CHEMISTRY – IMPLICATIONS FOR RESTORATION IN ESTUARIES SUBJECT TO COASTAL OCEAN ACIDIFICATION

Stephen J. Tomasetti[1]*, Michael H. Doall[2], Jeffrey R. Kraemer Jr.[2], Brendan D. Hallinan[2], and Christopher J. Gobler[2]

[1]Hamilton College, Environmental Studies Program, 198 College Hill Road, Clinton, NY 13323

[2]Stony Brook University, School of Marine and Atmospheric Sciences, 70 Tuckahoe Rd, Southampton, NY 11968

stomaset@hamilton.edu

Globally, oyster reef restoration is one of the most widely applied coastal restoration interventions. While reefs are focal points of shell formation and metabolic activity, two processes tightly linked to the carbonate system, how reef carbonate chemistry varies relative to the surrounding seawater is unclear. Moreover, coastal systems are increasingly impacted by coastal acidification which may affect reef carbonate chemistry. In this study, the variations in pH, carbonate chemistry and dissolved oxygen of reef-modified seawater (in the middle of reefs) and ambient seawater (~50 m outside of reefs) were characterized across multiple summers. High frequency monitoring across three subtidal constructed reefs revealed significant, consistent reductions of daily mean (by 0.05 - 0.07 pH units) and minimum pH (by 0.07 – 0.11) in seawater overlying reefs relative to ambient seawater (p <0.0001). The proportion of pH measurements below 7.5 (a threshold shown to negatively impact post-larval oysters) were 1.75x–5.17x higher in reef seawater relative to ambient seawater, and ~99% of severely acidified conditions (<7.25) were observed within reef habitat. Most reef seawater samples (83%) were reduced in total alkalinity relative to ambient seawater samples, suggesting community calcification was a key driver of modified carbonate chemistry. Consistent with the carbonate chemistry, juvenile oysters placed on reefs exhibited significantly slower shell growth (p<0.05) compared to oysters placed outside of the reefs. Hence, subtidal restored reef communities modified their seawater carbonate chemistry in ways that increased oyster vulnerability to acidification, and carbonate chemistry dynamics warrant consideration when determining site suitability for oyster restoration.

REMOTE SENSING FOR SHELLFISH MANAGEMENT: EFFORTS TOWARD EARLY WARNING, TOOL DEVELOPMENT, AND TRAINING FOR HARMFUL ALGAL BLOOMS IN CHESAPEAKE BAY

Michelle C. Tomlinson[1]*, Xin Yu[2], Elizabeth A. Staugler[3], Melanie Abecassis[4], Cara Wilson[5], Steve Morton[6], Jen Maucher Fuquay[6], and Richard P. Stumpf[1]

[1]National Centers for Coastal Ocean Science (NCCOS), NOAA, 1305 East-West Hwy, Silver Spring, MD 20910

[2]Oak Ridge Institute for Science and Education, 1305 East-West Hwy, Silver Spring, MD 20910

[3]Florida Sea Grant, University of Florida, 2306 Mowry Rd., Gainesville, FL 32611

[4]Cooperative Institute for Satellite Earth System Studies (CISESS), University of Maryland, College Park, MD 20740

[5]Southwest Fisheries Science Center, NOAA, 99 Pacific St, Suite 225A, Monterey, CA 93955

[6]National Centers for Coastal Ocean Science (NCCOS), NOAA, 331 Fort Johnson Road, Charleston, SC 29412

Michelle.Tomlinson@noaa.gov

Several phytoplankton species which occur in Chesapeake Bay are known to produce toxins and negatively impact important shellfisheries. High frequency monitoring through satellite remote sensing has been beneficial in protecting public and environmental health in several key US waterways. The success of these tools relies on unique optical signatures of monospecific, high biomass harmful algal blooms (HAB). In Chesapeake Bay, a variety of dense algal blooms can appear throughout the year in mixed assemblages. While high biomass dinoflagellate blooms in Chesapeake Bay can be detected from satellites, the specific species may not be determined using satellite data alone. For example, the blooms of *Alexandrium monilatum* and *Margalefidinium polykrikoides* (a.k.a., *Cochlodinium*) that occur in late summer in southern Chesapeake Bay have similar optical properties and are co-located.

Several algorithms applied to the Sentinel-3 Ocean and Land Colour Imager (OLCI) have improved our ability to detect and characterize algal blooms at higher resolution. Heuristic models constructed with information regarding the ecological niche of individual species (time of year; salinity, temperature, light, nutrients, etc) combined with satellite data can aid in species-specific identification. Combined with the NOAA Phytoplankton Monitoring Network, a Citizen Science approach to measure the relative abundance of key HAB species, hopefully the ability to respond to HAB in Chesapeake Bay will improve. Efforts are now underway to engage with important stakeholders, through the NOAA Sea Grant Program, Office of Aquaculture, and CoastWatch program to inform tool development and train those managing important shellfisheries on how to use these tools for onsite farm management.

STAGING OF CHANNELED WHELK (*BUSYCOTYPUS CANALICULATUS*) FEMALE GONADS USING GROSS AND HISTOLOGICAL ANALYSES

Benjamin C. Towne*[1], Hannah T. Cameron[1], Abigail K. Scro[1], Thomas E. Angell[2], and Roxanna M. Smolowitz[1]

[1]Aquatic Diagnostic Laboratory, Roger Williams University, 1 Old Ferry Rd, Bristol, RI, 02809

[2]Rhode Island Department of Environmental Management, 3 Fort Wetherill Rd, Jamestown, RI, 02835

btowne@rwu.edu

Stages of maturity of channeled whelk, *Busycotypus canaliculatus*, were assessed macroscopically through visual inspection, and microscopically using histological methods, in this study. Gonads of female whelks were evaluated histologically for follicle area (μm^2), then compared to macroscopic size of the gonads and shell size to produce an accurate method for determining size at reproductive maturity. The Rhode Island Division of Marine Fisheries (RIDMF) has used macroscopic evaluation of gonadal size in the past to determine maturity and would like to verify the macroscopic evaluation method.

Legal and sub-legal sized female samples were collected monthly during the spawning season from June 1, 2021 to October 31, 2022, by RIDMF and local fishers. Gonads were macroscopically evaluated for reproductive stage. Segments of the fixed gonads were processed histological and H&E-stained slides were evaluated microscopically to determine the gonad stage of development. To determine stage, follicle areas (μm^2) were measured using an elliptical function that best captured the true follicle area. Microscopic assessment of follicle area using the ellipse method found significant differences and could be correlated with macroscopic stages of maturity/size. Stages were categorized as immature, early developing, late developing, ripe/mature, and spent.

The results of this study will provide information for stock assessment and management of the regional fishery. Additionally, this data will aid in approximating the distribution and age of female whelk population in Rhode Island state waters and thus help protect the longevity of the fishery.

INTEGRATING A RAPID ASSESSMENT PROTOCOL (RAP) INTO MONITORING OF SUBTIDAL OYSTER REEFS

Allison Tracy*[1,2], Rob Aguilar[2], Carmen Ritter[2], and Matt Ogburn[2]

[1]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, University of Maryland Baltimore, 701 E. Pratt Street Baltimore, MD, 21202

[2]Smithsonian Environmental Research Center, 647 Contees Wharf Rd, Edgewater, MD 21037

amtracy@umbc.edu

Oyster reefs provide habitat, food, and other ecosystem services that support biodiversity and human livelihoods. Monitoring the status of oyster reefs is critical for informing management decisions related to restoration and fisheries; however, monitoring subtidal reefs is complicated by constant submersion and low visibility, with existing methods requiring substantial effort. The objective of this study was to integrate new technology with existing methods for an expanded monitoring toolkit. Reefs were surveyed in four tributaries across a broad salinity range in Chesapeake Bay using a Rapid Assessment Protocol (RAP) and existing metrics from diver collections. The RAP entails remotely deploying GoPro cameras and scoring the resulting images with a qualitative scoring system based on percent cover and reef height. Comparing the RAP with diver-collected metrics across 66 quadrats showed that high RAP scores successfully captured high oyster density, biomass, reef height, and rugosity, as well as multiple oyster size classes. Estimates of the time required for different methods show that the RAP is the most efficient and cost-effective across oyster densities. A series of conversations with stakeholders identified the strengths of diver collection, patent tong collection, and the RAP, as well as informing the development of use scenarios for integrating new and existing methods. The scientific findings and applications from this study contribute to a growing knowledge base on monitoring technology for restoration and fisheries management. The results will inform oyster management in Chesapeake Bay, including the innovative large-scale restoration efforts, with implications for monitoring and improving oyster reef health worldwide.

CO-OCCURRENCE PATTERNS OF OYSTER PARASITES ACROSS NATURAL AND ANTHROPOGENIC CONDITIONS IN CHESAPEAKE BAY

Allison Tracy*[1,2], Katrina Lohan[2], Ryan Carnegie[3], Carol McCollough[4], Melissa Southworth[5], and Matt Ogburn[2]

[1]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, University of Maryland Baltimore, 701 E. Pratt Street, Baltimore, MD 21202

[2]Smithsonian Environmental Research Center, 647 Contees Wharf Rd, Edgewater, MD 21037

[3]Virginia Institute of Marine Sciences, William & Mary, P.O. Box 1346, Gloucester Point, VA 23062

[4]Maryland Department of Natural Resources Cooperative Oxford Laboratory, 904 S. Morris Street, Oxford, MD 21654

[5]Virginia Marine Commission, 2600 Washington Ave, Newport News, VA 23607

amtracy@umbc.edu

The biological community associated with oysters can influence the ecological and economic services that reefs provide. In Chesapeake Bay, the impacts of protozoan pathogens, *Perkinsus marinus* and *Haplosporidium nelson,* have led to a strong knowledge base on oyster diseases and defenses; however, little is known about the interaction between these infectious parasites in tissues and the bio-eroding organisms that target shells. This study sought to address the knowledge gap by determining patterns of co-occurrence for four focal organisms (*P. marinus*, *H. nelsoni*, and bio-eroding *Cliona* sponges and *Polydora* worms) across a range of natural and anthropogenic conditions, using macro- and microscopic visual methods. More than 500 oysters were collected from 18 reefs across the Chesapeake Bay in fall 2020. Natural drivers were evaluated as predictors for each focal organism, including salinity, shell height, a habitat score based on density and reef height, and the presence or intensity of the other focal organisms. Paired harvested and non-harvested reefs at 8 sites were used to evaluate the role of harvest status. Reef, tributary, and state were also tested as predictors to evaluate broad patterns at multiple spatial scales. *P. marinus* prevalence increased with salinity and *Cliona* sponge prevalence, while *H. nelsoni* was not detected. Prevalence of *Cliona* increased with salinity and with higher oyster density and reef height. Spatial variation at the reef scale best predicted *Polydora* blister intensity. The results show that tissue parasites and bio-eroders depend on diverse environmental conditions and may influence each other with implications for oyster health.

COMMERCIAL PERFORMANCE OF BLUE MUSSEL (*MYTILUS EDULIS*) STOCKS AT A MICROGEOGRAPHIC SCALE

Réjean Tremblay[1]*, Efflam Guillou[1], Carole Cyr[2], Jean-François Laplante[2], François Bourque[3], and Nicolas Toupoint[2]

[1]Institut des Sciences de la Mer de Rimouski (ISMER), Université du Québec à Rimouski (UQAR), 310 Allée des Ursulines, CP 3300, Rimouski, Québec, G5L 3A1, Canada

[2]Merinov, Centre d'Innovation de l'aquaculture et des pêches du Québec, Secteur Aquaculture, 107-125 Chemin du Parc, Cap-aux-Meules, Québec, G4T 1B3, Canada

[3]Ministry of Agriculture, Fisheries and Food of Québec (MAPAQ - Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec), Fisheries and Commercial Aquaculture Branch, 101-125, Chemin du Parc, Cap-aux-Meules, Québec, G4T 1B3, Canada

Rejean_Tremblay@uqar.ca

Bivalve farming productivity fluctuates from one spat stock to another, even at a microgeographic scale and depends on multiple interactions between exogenous and endogenous factors. The main objective of this project was to define the modalities to obtain a blue mussel (*Mytilus edulis*) spat stock allowing high levels of productivity. The farming performance of several mussels spat stocks were assessed, according to their origins in contrasted environments (shallow lagoons and offshore environment), through a two-year production cycle and identify the mechanisms providing their performance.

According to a "stock-site" spat transfer design, it was determined that mussel originating from one small lagoon provided the best levels of performance with larger size at sleeving and best survival rate (≥ 90%) at harvest size in different studied sites. Meanwhile, the absence of summer stressful thermal condition in the offshore site, which stimulated the summer growth of mussel stocks (26%), improved the energy reserves content, doubled the condition index and favoured the final survival rates (23%). It was observed that the earlier and more intense seawater warming in the small lagoon generated a selection pressure on juvenile mussels. Application of the thermal maximum peak observed in the field (24°C for 85 hours) induced higher mortality rates (37%) on juveniles from 4.5 to 7 mm and improved the shell (22%) and tissues (51%) growth of survivors. No similar selection was observed on larvae and post-larvae (<1 mm) supporting the hypothesis that thermal selection is size dependent.

FROM BPA TO PHTHALATES TO PFAS: HOW ENVIRONMENTAL CHEMICALS ARE HARMING SHELLFISH AND HUMAN HEALTH AND WHAT WE CAN DO ABOUT IT

Laura N. Vandenberg

University of Massachusetts – Amherst, School of Public Health & Health Sciences, Department of Environmental Health Sciences, 181 Presidents Drive, Amherst, MA 01003

lvandenberg@schoolph.umass.edu

Endocrine disrupting chemicals (EDC) are chemicals that alter the actions of hormones. In recent years, experts from medical, scientific, and environmental activist groups have demanded action from regulatory agencies to protect humans and wildlife alike from the harm induced by EDC exposures. These demands are based on strong evidence from epidemiology, wildlife, and controlled laboratory studies. Some environmental chemicals have received a lot of attention in recent years including BPA, phthalates, PFAS (forever chemicals), and others. This talk will describe the conclusions drawn by experts from different scientific and medical disciplines and discuss recent findings that have changed the landscape of EDC work. There is a need to identify better "sentinel" species to characterize both exposures to EDC and their effects, and shellfish may provide valuable insights in these areas. There is also a need to expand our understanding of vulnerable periods of life, and the increasing concern that traditional methods used to evaluate toxicity of environmental chemicals are insufficient for EDC. Finally, there are reasons why current regulatory approaches have failed to protect human and wildlife health, but collaborative science could help to address these gaps.

COMPARING GENOTYPING TECHNOLOGIES FOR ESTIMATING GENETIC DIVERSITY AND GENOMIC SELECTION IN EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) BROODSTOCK

Robin L. Varney[1]* and Ami E. Wilbur[1,2]

[1]University of North Carolina Wilmington, Shellfish Research Hatchery, Center for Marine Science, CREST Research Park, 5606 Marvin K. Moss Lane, Wilmington, NC 28409

[2]University of North Carolina Wilmington, Department of Biology and Marine Biology, 601 S. College Road, Dobo Hall 1010, Wilmington, NC 28403

varneyr@uncw.edu

The eastern oyster (*Crassostrea virginica*) is an ecologically and economically important marine bivalve along the east coast of North America. Expansion of the eastern oyster aquaculture industry has produced genetically improved oyster lines through hatchery production. The UNCW Shellfish Research Hatchery is particularly interested in genetic improvement of oyster lines through selective breeding and is working to selectively breed oysters to develop lines that grow and survive well in North Carolina waters. Genotyping technologies, including microsatellites and single nucleotide polymorphisms (SNP) can provide information on genetic diversity, relatedness, and population structure, as well as for improved selection efficiency for growth traits and survival in aquacultured oysters. The recent development of a 66K SNP array for the eastern oyster by the Eastern Oyster Breeding Consortium has provided the opportunity to test genomic selection strategies for growth traits and survival. In this study, 1096 oysters from eight breeding groups were genotyped using 22 microsatellite loci and the 66K SNP array. The two genotyping technologies were utilized to estimate genetic diversity, relatedness, and genetic differentiation among the eight breeding groups. Additionally, the performance of genomic prediction approaches was compared with pedigree and microsatellite-based approaches in estimating heritability and prediction accuracy of genomic selection for growth traits (shell height, shell length, shell width, and total wet weight) and survival. The accuracy of the genomic prediction model and pedigree approach were similar at all growth traits and survival, with both consistently outperforming the microsatellite-based approach.

IMPACT OF SOUND INTENSITY RELATED TO MARITIME TRANSPORT ON THE EMBRYOGENESIS AND METAMORPHOSIS OF THE BLUE MUSSEL, *MYTILUS EDULIS*

Delphine Veillard[1]*, Stéphane Beauclercq[2], Frédéric Olivier[3], Chauvaud Laurent[4], Bertrand Genard[1], Isabelle Marcotte[2], and Réjean Tremblay[1]

[1]Institut des sciences de la mer de Rimouski, Université du Québec à Rimouski, 310 Allée des Ursulines, Rimouski, Québec, G5L 3A1, Canada

[2]Laboratoire de RMN des systèmes biologiques complexes, Département de Chimie et de Biochimie, Université du Québec à Montréal, 2005 rue Jeanne-Mance, Montréal, Québec, H2X 2J6, Canada

[3]Laboratoire de 'Biologie des Organismes et Écosystèmes Aquatiques' (BOREA), Muséum national d'Histoire naturelle, Sorbonne Université, Université de Caen Normandie, Université des Antilles, Centre National de la Recherche Scientifique, Institut de Recherche pour le Développement-207, CP53, 61 rue Buffon, 75005 Paris, France

[4]Laboratoire des Sciences de l'Environnement Marin (LEMAR), UBO, CNRS, IRD, Ifremer, LIA BeBEST, UMR 6539, rue Dumont D'Urville, 29280 Plouzané, France

delphine.veillard@uqar.ca

In recent years, maritime traffic has considerably increased with a serious concern about the effects of underwater sounds it generates, that is considered as an emerging pollutant; however, knowledge about noise impact on invertebrates, particularly on their young life stages, remains limited. The main objective of this study was to assess the impact of cargo vessel noise on larval development and settlement of the blue mussel, *Mytilus edulis*. Through an experimental approach conducted on both embryos and competent larval stages, stress levels of the mussels at tertiary (growth, survival rates) down to primary stress levels (metabolomics) were measured.

A one month-long experiment was conducted in *Larvosonic* mesocosms, where sounds can be emitted with reduced reverberation and resonance bias. The various developmental stages were exposed to contrasting sound treatments including a control and three increasing levels (from 132 to 150 dB re1µPa) of a previously *in situ* recorded sound sequence of a 120 m cargo ship. It was hypothesized that a critical window to stress could occur during larval development, and thus several ontogenetic phases including embryogenesis (embryo to larva-D) and metamorphosis (pediveliger to post-larvae) were studied. Several variables were monitored as i) prostaglandins and oxidative metabolism, ii) energy metabolism, and iii) shell larval growth to explore the stress responses to noise. Preliminary results show that larvae exposed to high sound intensity settle faster and have greater post-larval growth compared to other conditions. Pediveligers exposed to lower sound intensities delayed their metamorphosis. Such results are discussed considering energetic pathways that are stimulated by noise.

ANALYSIS OF THE EXPRESSION AND INHIBITION OF THE PIRAB^{VP} TOXIN IN *VIBRIO* AND NON-*VIBRIO* STRAINS: THE CASE OF THE PVA1 PLASMID

Marcelo Victorio-De Los Santos*, Alejandro Vázquez-Reyes, Miriam Fabiola Ayón-Pérez, Francisco Zambrano-Zaragoza, Juan Manuel Agraz-Cibrián, and Jorge Gutiérrez-Franco

Universidad Autónoma de Nayarit, Research Laboratory in Molecular Biology and Immunology, Cd. de la Cultura, CEMIC 05 building, Tepic, Nayarit, 63000, México

mvictorio@uan.edu.mx

Plasmid mediated horizontal transfer has been speculated to be one of the prime mechanism for the adaptation of bacteria to their ecological niches in marine habitat. The pVA1 plasmid encoded to binary PirAB^{vp} toxin were identified as the key factors in the AHPND pathology causing for specific strains of *Vibrio parahaemolyticus*, and other *Vibrio* species, such as *V. harveyi*, *V. campbellii*, *V. owensii*, and *V. punensis*. Similarly, a non-*Vibrio* bacterium, *Micrococcus luteus*, was also reported to carry the *pirA* and *pirB* toxin genes. These suggest that pVA1-related plasmids could be transmitted between different species. To explore the expression of strains of *Vibrio* and non-*Vibrio* was determinate the presence of the toxins PirA and PirB using western blot. The experiments revealed that *Microccocus luteus* does not express constitutively the toxin PirAB, such as AHPND-causing *Vibrio* strains. Similarly, toxin expression has been identified in some *Vibrio* strains, leading to the expression of the toxin PirB^{vp} with an apparent molecular weight of 40 kDa, suggesting that the gene encoding subunit B has significant deletions. The sequence analysis of the plasmid revealed differences in the ORF that encoding the subunit A and the subunit B. These data contribute to understanding the molecular epidemiology of the pirA and pirB genes as well as the probable ways of regulating the expression of the pirA and pirB genes contained in the pVA1 plasmid.

SPATIAL VARIATION IN NURSERY HABITAT USE BY JUVENILE BLUE CRABS IN A SHALLOW, WIND-DRIVEN ESTUARY

Erin P. Voigt[1] and David B. Eggleston*[1,2]

[1]North Carolina State University, Department of Marine Earth and Atmospheric Science, 2800 Faucette Drive, 1125 Jordan Hall, Raleigh, NC 27695

[2]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

eggleston@ncsu.edu

Nursery habitats are often targeted by conservation policies and restoration practices, yet managers must often choose where to focus limited resources, which is complicated when juveniles utilize multiple habitats. This is particularly applicable to the NC blue crab (*Callinectes sapidus*), which uses three main habitats, low salinity ephemeral *Ruppia maritima* seagrass beds, high salinity mixed species seagrass (SAV) beds, and shallow marsh detrital habitat (SDH). Spatial variation in early juvenile blue crab density and size-class was quantified within Pamlico Sound (PS) together with potential explanatory variables driving spatial variation in crab density and size. Despite being 25-40 km from inlet sources of megalopae, juvenile crab density was nearly four times greater in ephemeral *R. maritima* SAV habitats located on the western shore of PS than mixed SAV located along the eastern shore. Early juvenile crab size-frequencies were similar between mixed SAV and shallow detrital habitats located along the eastern and western shores of PS, respectively suggesting hurricane-driven transport as opposed to ontogenetic habitats shifts from east to west. Crab density in SAV decreased by approximately 7 crabs every 10km from inlet sources of megalopae, suggestive of a strong recruitment shadow. Crab density in *R. maritima* beds located along the western shore increased 10-fold with seagrass shoot density. This study highlights how dispersal patterns, in combination with locations within a region, and local-scale changes in SAV shoot densities may affect nursery habitat use by blue crabs when multiple habitats are present in a seascape.

SUPPORTING OYSTER AQUACULTURE AND RESTORATION (SOAR) IN MARYLAND: AN ADAPTIVE STRATEGY TO SUPPORT OYSTER FARMERS AND RESTORE OYSTER REEFS DURING COVID-19

Jennifer Walters[1]*, H. Ward Slacum Jr.[1], Mark Bryer[2], Boze Hancock[2], Olivia Caretti[1], Elena Wills[1], and Eric Amrhein[1]

[1]Oyster Recovery Partnership, 1805A Virginia Street, Annapolis, MD 21401

[2]The Nature Conservancy - 4245 North Fairfax Drive, Suite 100, Arlington, Virginia 22203-1606

jwalters@oysterrecovery.org

Oyster farmers primarily sell their oysters to restaurants for consumption as raw oysters on the half shell. During the Covid-19 pandemic, restaurants shut down nationwide, which eliminated the market for aquaculture oysters. In 2020, The Nature Conservancy (TNC) received funding to offset this financial strain on oyster farmers by purchasing aquaculture oysters and planting them on restoration reefs through a project called Supporting Oyster Aquaculture and Restoration (SOAR). In Maryland, the SOAR program was leveraged to purchase diploid and triploid oysters from on-bottom and cage cultured businesses. These oysters were planted on reefs in the Maryland sanctuary network. Between January and June 2021, the TNC purchased approximately 1.3 million oysters from 26 oyster farms and ORP planted these oysters on 6 sanctuary reefs in 3 different Chesapeake Bay tributaries: 1 in Eastern Bay, 2 in the St. Mary's River and 3 in the Nanticoke River. Post-restoration monitoring was conducted one year after planting to assess oyster mortality, age class distribution, and overall health of the planted SOAR oysters and reefs. Oyster mortality varied spatially and ranged from as low as 5% on a reef in the Nanticoke River to 53% on a reef in the St. Mary's River. The mechanisms driving mortality were not clear; however, efforts to assess bottom habitat prior to planting could ensure that oysters are planted in favorable conditions for survival. Collectively, oyster densities increased on all restored reefs and 26 oyster farms in Maryland were supported with approximately $500,000 in income.

FOOD WEBS SUPPORTING CRAB PRODUCTION IN ESTUARIES WITH EXPANDING COASTAL URBANISATION

Nathan J. Waltham[1]* and Rod M. Connolly[2]

[1]Centre for Tropical Water and Aquatic Ecosystem Research (TropWATER), Division of Tropical Environment and Societies, James Cook University, Queensland, 4811, Australia

[2]Coastal and Marine Research Centre, Australian Rivers Institute, School of Environment and Science, Griffith University, Queensland, 4222, Australia

Nathan.waltham@jcu.edu.au

The prospects that coastal urbanisation propagates in more fish production remains untested and thereby a fundamental question for managers challenged with approving urban expansion while also protecting and conserving habitat resources important for fish production. We tested this by collecting giant mud crabs (*Scylla serrata*) from highly urbanised waterways in Queensland, Australia, and report that this crab not only occupy urban waterways, but the range of feasible contributions (MixSIAR) for autotrophs was very broad, limiting the conclusions that could be made directly from the modelling. Patterns of contributions from pooled categories of autotrophs were clearer; at the site closest to seagrass, the pooled enriched autotroph sources contributed 69 to 87% of crab isotope signatures, while at all other sites (beyond approximately 500 m distance) it appears that crabs utilise a generalised pool of sources, either local or perhaps a mix of local transported sources. Using a spatial analysis, the crab isotope values were not significantly related to the distance from any of the vegetated habitats (mangroves, seagrass and saltmarsh). The exception was sites close to seagrass (< 500 m distance), and not saltmarsh grass, where crabs had the most enriched C value. At sites beyond approximately 500 m distance it appears crabs utilise a generalised organic producer pool, either local or perhaps a mix of transported sources. In an era of coastal urbanisation expansion and loss of natural coastal vegetated areas, results show that some fisheries have remarkable trophic plasticity to the new, engineered, habitat settings.

BUILDING A BENCHMARKING PROGRAM FOR MARKET OYSTERS

William C. Walton* and Jordan Lynch

Virginia Institute of Marine Science, PO Box 1346, 1370 Greate Road, Gloucester Point, VA 23062

walton@vims.edu

The increase in the variety of oysters in the marketplace has increased interest in product differentiation. With a greater understanding of how different culture methods can produce oysters with different attributes, some oyster growers are striving to produce oysters consistently with certain attributes (e.g., a deep cup). To assist growers with assessing how their product compares to others in the marketplace, a benchmarking program for market oysters is being built to provide a quantitative assessment of what is in the marketplace currently. This tool can also be used to measure the effects of any changes in production methods. Participating growers submit oyster samples to the program and receive reports of a variety of shell traits (e.g., dry shell weight, cup ratio, etc.) and meat characteristics (e.g., condition index, dry tissue weight, etc.) for the submitted product along with an anonymized benchmark for each attribute. As the database grows, the intent is to allow growers to conduct analyses within subsets of the data (e.g., regionally, within certain production methods, etc.). With the benchmarking program in early development, results to date will be presented and feedback on currently collected attributes as well as alternative or additional attributes that should be included will be welcome.

TESTOSTERONE AND STEROIDOGENIC GENES IN THE MALE BLUE CRAB *CALLINECTES SAPIDUS* AND THEIR RELATIONSHIP WITH INSULIN-LIKE ANDROGENIC GLAND FACTOR (IAG) AND CRUSTACEAN FEMALE SEX HORMONE (CFSH)

Tao Wang[1,2]*, Ke He[3], Lee Blaney[3], and J. Sook Chung[2]

[1]University of Maryland Baltimore County, Department of Marine Biotechnology & Institute of Marine and Environmental Technology, 1000 Hilltop Circle, Baltimore, MD 21250

[2]University of Maryland Center for Environmental Science, Institute of Marine and Environmental Biology, 701 E Pratt St, Baltimore, MD 21202

[3]University of Maryland Baltimore County, Department of Chemical, Biochemical, and Environmental Engineering, 1000 Hilltop Circle, Baltimore, MD 21250

XG90497@umbc.edu

Sexual differentiation of decapods is primarily regulated by the insulin-like androgenic gland factor (IAG) and crustacean female sex hormone (CFSH). With earlier reports of testosterone (T) presence in some decapods, this work aimed to determine if the blue crab *Callinectes sapidus* males exhibit T and if the corresponding levels are related to IAG and CFSH transcripts. To this end, *IAG* and *CFSH* transcripts are estimated in the androgenic glands (AG) and eyestalk ganglia of juvenile and adult males, respectively. *IAG* levels are significantly higher in adult AGs than in juveniles; however, this pattern contrasts with CFSH transcripts in the eyestalk ganglia with juveniles higher than adults. The T levels in adult testis, posterior vas deferens, AG, and hemolymph are significantly higher than those in juveniles. The presence of authentic T is further confirmed by liquid chromatography with tandem mass spectrometry. The expression of vertebrate steroidogenesis-related genes is determined: StAR-related lipid transfer protein 3 (*StAR3*); 3β-hydroxysteroid dehydrogenase (*3βHSD*); 17β-hydroxysteroid dehydrogenase 8 (*17βHSD8*); and, 5α-reductase (*5α-red*). Adult males contain significantly higher *StAR3* but lower *5α-red* levels in the testis, anterior vas deferens, and AG than juveniles. The *5α-red* transcripts are localized in the spermatocytes and spermatids in the testis and AG cells in the AG using *in situ* hybridization. These results indicate that CFSH may suppress IAG expression; T levels may be related to the male reproductive activity; and a putative regulatory interaction among IAG, CFSH, and steroidogenic genes in T synthesis may present in decapod crustaceans.

SEGREGATION DISTORTION AND NULL ALLELES IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

Zhenwei Wang* and Ximing Guo

Haskin Shellfish Research Laboratory, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349

zw233@hsrl.rutgers.edu

Organisms with high fecundity often exhibit high polymorphism and harbor high levels of deleterious mutations that affect fitness. Understanding how genetic variation is maintained in the genome is central to evolutionary biology. The segregation of single-nucleotide polymorphisms (SNP) in families of the eastern oyster (*Crassostrea virginica*) with a high-density SNP array was studied. Four full-sib families were produced using parents from an inbred line, a selected line and Delaware Bay wild population including a hybrid family between the inbred and selected lines. High mortality was observed during the larval stage with the complete loss of the inbred family. Two parents and 96 progenies sampled at 6 months from three surviving families were genotyped with a 66K SNP array. Segregation analysis revealed high proportion of loci (11.4%) showing unexpected progeny genotypes indicative of null alleles or indels, providing an explanation for heterozygosity deficiency and a mechanism for dominance or heterosis. Segregation distortion (SD) was observed at 7.9-14.2% of loci with higher values observed for loci segregating in males, suggesting that selection is stronger against deleterious alleles from the male. Segregation distortion was not randomly distributed on chromosomes, pointing to the existence of major chromosome regions with mutations affecting larval fitness. Results show that the eastern oyster genome contains high levels of null alleles (or indels) and deleterious mutations that can both contribute to heterosis, providing guidance for further research and oyster breeding.

PREDICTING LARVAL DISPERSAL AND POPULATION CONNECTIVITY OF SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) IN COASTAL MAINE THROUGH COMPUTER MODELING AND POPULATION GENOMICS

Kelsey M. Ward*, Paul Rawson, and Huijie Xue
University of Maine, 168 College Ave, Orono, ME 04469
kelsey.ward@maine.edu

This research combines computer modeling and population genomics approaches to estimate sea scallop (*Placopecten magellanicus*) larval dispersal along the eastern Maine coast. A hydrodynamic model of the coastal currents from the Bay of Fundy westward through the Gulf of Maine has been adapted to include an individual-based scallop larval development and behaviors module. Larvae are released along the coastline during the months of August through October, and dispersal is driven using the hydrodynamical model result for the region from 2014 through 2018. The origins of particles that "settle" in focal areas, such as Blue Hill Bay, Jericho Bay, and Hurricane Island, are determined from model runs, and the frequency with which recruits settling at focal sites originate from various source populations is analyzed.

Larval dispersal in the region is dominated by the Eastern Maine Coastal Current (EMCC) suggesting high connectivity between source populations in the eastern Gulf of Maine and populations to the west; however, preliminary model results suggest that complex structure inshore of the EMCC can lead to larval retention in several bays, resulting in lower levels of connectivity with other populations. Model predictions will be tested using population genomic analyses and assignment tests to compare the degree of genetic similarity among predicted source sites and settlement sites. Project results will provide insight into the population connectivity and genetic diversity of the wild scallops in Maine and allow for the identification of source populations that could be important in sustaining both the wild fishery and seed sources for scallop aquaculture.

ARE METALS ENDOCRINE-DISRUPTING CHEMICALS (EDC) IN SHELLFISH?

Caroline Warren[1]*, Iris Hernandez[2], Miriam Alcivar-Arteaga[2], and Acacia Alcivar-Warren[1,2]
[1]Environmental Genomics Inc. (EGI), P. O. Box, Southborough, MA 01772, USA
[2]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada Casa 17, El Eden, Quito, Ecuador
fucobi@gmail.com

The US Environmental Protection Agency defines endocrine-disrupting chemicals (EDC), also called 'endocrine disruptors', as 'an exogenous agent that interferes with synthesis, secretion, transport, metabolism, binding action, or elimination of natural blood-borne hormones that are present in the body and are responsible for homeostasis, reproduction, and developmental process'. EDC are ubiquitous in the environment, including several natural and synthetic compounds that may interfere with the major functions of the endocrine system (bisphenol, dioxins, perfluoroalkyl and polyfluoroalkyl substances, PCB, others). EDC are found in everyday products, including some plastic bottles and containers, liners of metal food cans, food, and also in pesticides like glyphosate. Metals chelated by glyphosate may cause adverse health effects on shrimp. Their agonist or antagonist endocrine effects may be achieved by interferences with the biosynthesis or activity of several endogenous hormones, and epigenetics. Zn atom from the Zn fingers of the estrogen receptor can be replaced by several heavy metals. Low-level exposure to Cd interferes with the biological effects of steroid hormones in reproductive organs. Arsenic (As) binds to the glucocorticoid receptor thus disturbing glucocorticoids biological effects. Hg may induce alterations in male and female fertility, affect function of the hypothalamo-pituitary-thyroid axis or the hypothalamo-pituitary-adrenal axis, and disrupt biosynthesis of steroid hormones.

As part of the 'Shrimp Scampi: A Citizens Science Project', 30 (15 toxic and 15 nutrient) elements in shrimp sold in MA supermarkets and shrimp from Ecuador have been tested. The same metals were tested in hair of mothers of children with congenital malformations from Santa Elena, Ecuador. A literature review was performed using NCBI databases and the words 'metals' AND 'edc' AND 'endocrine system', and replacing the term 'metals' with name of each of the 30 metals tested in shrimp. In fish, Al, Cd, Cu, and Pb can act as EDC. No information was found about disruption of the shrimp endocrine system by metals.

IS GLYPHOSATE AND ENDOCRINE DISRUPTING CHEMICAL (EDC) IN PEOPLE AND SHRIMP? - A LITERATURE REVIEW

Caroline Warren[1]*, Iris Hernandez[2], Miriam Alcivar-Arteaga[2], and Acacia Alcivar-Warren[1,2]

[1]Environmental Genomics Inc. (EGI), P.O. Box, Southborough, MA 01772, USA

[2]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada Casa 17, El Eden, Quito, Ecuador

fucobi@gmail.com

Glyphosate is a broad-spectrum herbicide (common trade name “Roundup™”) first sold to farmers in 1974. The volume of glyphosate-based herbicides (GBH) applied has increased approximately 100-fold and usage continues to rise, scientists expressing concerns over the use of GBH, and risks associated with exposures. The half-life of glyphosate in water and soil is longer than previously recognized, often contaminating drinking water sources, precipitation, and air, especially in agricultural regions. Glyphosate and its metabolites are widely present in the global soybean supply. In Ecuador, the major shrimp producer in the Western Hemisphere, genetically engineered soybeans are used for production of shrimp feeds. Human exposures to GBH are also rising, particularly near banana plantations close to shrimp farms where GBH are sprayed to control banana pests. Glyphosate is considered “probably carcinogenic to humans” by the World Health Organization’s International Agency for Research on Cancer.

As part of the ‘Shrimp Scampi’ project, glyphosate and metabolite AMPA in shrimp sold at MA supermarkets and on Ecuadorian shrimp and people is being tested. A literature review of NCBI databases was performed using the keywords ‘glyphosate’ AND ‘edc’ AND ‘shrimp’ and ‘glyphosate AND ‘edc’ AND ‘human’. Only three review papers were related to humans. One review paper published in 2021 used 10 key characteristics (KC) of EDC and concluded that glyphosate satisfies at least 8 KC of an EDC, but prospective cohort studies are still needed to elucidate the real effects in the human endocrine system. No information was found on disruption of the shrimp endocrine system by glyphosate. Toxic effects of glyphosate on histopathology and intestinal microflora of juvenile *Penaeus vannamei* shrimp after 48 hours of exposure were reported. Shrimp epidemiology research is urgently needed, that draws on the principles of endocrinology to determine whether the effects of GBH are due to endocrine disrupting activities.

ECOTOXICOLOGICAL EFFECTS OF MICROPLASTICS ON MUSSELS: INSIGHTS FROM IMMUNE DEFENSE, OXIDATIVE STRESS, AND ENERGY METABOLISM

Shuaishuai Wei*, Huaxin Gu, and Youji Wang

Shanghai Ocean University, College of Fishery and Life Science, Huchenghuan road 999, Lingang New City, Pudong New Area, Shanghai 201306, China

1781283052@qq.com

Microplastics (MP) pollution is an emerging environmental problem that poses ecological risks for marine ecosystems; however, there is still insufficient information on the toxicity mechanism of MPs to marine shellfish. The highly hydrophobic surfaces make microplastics a potential carrier of organic pollutants. To explore the toxic effects of polybrominated diphenyl ethers (BDE-47) combined with microplastics on marine organisms, the marine mussel, *Mytilus coruscus,* was exposed to MP combined with BDE-47 for 21 days to determine the immune defense, oxidative stress, and energy metabolism of the mussels. The results showed that the clearance rate (CR) of mussels exposed to single micro-PS, single BDE-47 or both was lower than control group. In general, compared to single BDE-47 exposure, the combination of MPs and BDE-47 significantly increased respiration rate (RR), activities of acid phosphatase (ACP) and alkaline phosphatase (ALP), reactive oxygen species (ROS) production and malondialdehyde (MDA) concentrations, but significantly decreased lactate dehydrogenase (LDH) activity and the relative expression of heat shock protein (Hsp70 and 90). Overall, combined stress has more adverse effects on defense performance and energy metabolism in mussels and MP seem to exacerbate the toxicological effects of BDE-47. As microplastics pollution may deteriorate in the future, the health of mussels may be threatened in organically polluted environment, which eventually changes the stability of the structure and function of intertidal ecosystem.

ENHANCING MARINE AQUACULTURE IN THE TROPICAL U.S.: METHODS FOR SUSTAINABLE COMMERCIAL CO-CULTIVATION OF SHELLFISH AND SEAWEED IN FLORIDA

Aaron Welch*[1] and Loretta M. Roberson[2]

[1]Two Docks Shellfish, PO Box 9493, Bradenton, FL, 34206

[2]Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543

twodocksshellfish@gmail.com

The principal goal is to develop a system that will enhance ocean alkalinity, provide nutrient remediation benefits, and enhance the productivity and resilience of farmed shellfish. This goal will be accomplished through three main objectives: (1) Develop grow-out systems for the integrated cultivation of local macroalgae and shellfish species; (2) Quantify the ocean alkalinity enhancement of integrated shellfish/macroalgae culture in hatchery and field conditions; and (3) Quantify the impact of co-cultivation on shellfish and macroalgae growth and survivorship. The focus is on the production of hard clams (*Mercenaria mercenaria*) and the economically valuable macroalgae, *Gracilaria,* although production of other species of bivalves is being considered, especially sunray venus clams (*Macrocallista nimbosa*). Development of reliable IMTA systems for the production of shellfish and macroalgae will encourage the growth and increase the resilience of the U.S. shellfish industry as well as generate valuable ecosystem services that will benefit a wide range of stakeholders. This will be done through a network of academic, industry, and extension partnerships that bring knowledge and expertise from sustainable shore-based hatchery and nursery systems to nearshore and open water grow-out systems, to support both aquaculture operations and the ecosystem services that in-water farm systems can provide. This project will directly address the sustainability of seafood production and harvesting in a region that is underdeveloped and underutilized through the first commercial multi-trophic seafood operation in the tropical U.S. and the state of Florida.

VIBRIO PARAHAEMOLYTICUS POPULATION IN NATIVE AND CULTURED OYSTERS IN NEW HAMPSHIRE

Cheryl A. Whistler*, Randi Foxall, Benjamin Wasson, and Stephen Jones

Northeast Center for Vibrio Disease and Ecology, University of New Hampshire, 46 College Rd, Durham NH 03824

cheryl.whistler@unh.edu

The Great Bay Estuary (GBE) of New Hampshire lies just to the north of aquaculture areas where human illnesses caused by virulent strains of *Vibrio parahaemolyticus* have repeatedly occurred in recent years, primarily from the invasive ST36 lineage. Increased disease incidence and establishment of the hypervirulent ST36 in several aquaculture areas to the south of NH necessitated intensive post-harvest management to curtail human illnesses and led to restrictions on movement of oysters from regions associated with disease into NH aquaculture areas. Even though ST36 has not been detected in GBE and no local-source infections have yet been linked to this lineage, temporal analysis of archived strains and ongoing analyses from the GBE was conducted and revealed populations are changing towards increased prevalence of non-native strains with genetic markers including *Vibrio* pathogenicity islands (VPaI) harboring hemolysin encoding genes (*tdh* and *trh*) associated with pathogens. This also revealed that pathogenic strains first detected in commercial oysters later increased in wild oysters. Though this suggests imported seed could be a source for introduction of non-native strains it also highlights an important opportunity for reduction of risk of introduction of pathogens. The geographic location of the GBE at the margin of pathogen expansion in the Northeast and documentation of these changes highlights that further study of this population could provide valuable insight into the ecology of pathogen invasion.

MICROPLASTICS AS VECTORS OF *VIBRIO PARAHAEMOLYTICUS* TO THE PACIFIC OYSTER

Kara Wiggin*, Sarah Allard, and Jack Gilbert

Scripps Institution of Oceanography, University of California San Diego, 9500 Gilman Drive, La Jolla, CA 92093

kwiggin@ucsd.edu

Microplastics in the marine environment harbor a rich assemblage of microorganisms in their surface biofilms. Recent research suggests the enrichment of potentially pathogenic species, including *Vibrio*, on the surface of microplastics. To determine the potential for *Vibrio parahaemolyticus*, the leading cause of shellfish-related illness in the US, to grow biofilms on plastic, polypropylene surfaces were incubated with *Vibrio parahaemolyticus* for 24h at varying temperatures, and biofilm growth was evaluated using a standardized crystal violet and optical density protocol. Eight strains were tested, all demonstrating significant biofilm growth on the plastic surface. All strains had higher cell growth at higher temperatures yet only 7 of 8 strains showed increased biofilm growth at higher temperatures, demonstrating varying implications for future climate change scenarios. To evaluate the vector capabilities of microplastics, the uptake of *V. parahaemolyticus* in the tissue of *Crassostrea gigas* was quantified after exposure to microplastics with a *V. parahaemolyticus* biofilm or free-floating *V. parahaemolyticus*. Preliminary results revealed a significant increase of *V. parahaemolyticus* in the digestive gland when exposed to microplastics with a *V. parahaemolyticus* biofilm ($p=0.01$), indicating that microplastics have the potential to magnify the uptake of pathogenic microbes into shellfish bound for human consumption. The Pacific oyster (*C. gigas*) is a species of immense economic importance around the world as it encompasses the majority of global oyster aquaculture. The role of microplastics in the transport and uptake of human pathogens of concern into seafood bound for human consumption is a sorely understudied topic and must be explored with further research.

DETERMINING FEEDING RATES IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) USING NATURAL SESTON FLOW-THROUGH SYSTEM

Laura E. Wiltsee* and Matthew W. Gray

University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Road, Cambridge, MD 21613

lwiltsee@umces.edu

Eastern oysters (*Crassostrea virginica*) are highly valued for the ecosystem services they provide, largely due to their filter feeding activity. Previous studies on the filtration services of oysters have examined physiological responses under laboratory conditions with monoculture diets and single parameter variation on day to hour-long *in situ*; however, little is known about how filtration rates vary over weeks to months in relation to variations in natural seston and environmental conditions. Studies that closely track direct effects of environmental changes are labor intensive and time consuming, leading to large data gaps. This study leverages recent advances in aquatic observing, such as real-time flow-through oyster feeding monitoring and fine temporal scale water quality measurements, to track long-term feeding responses of the eastern oyster in response to subtle variation in environmental conditions.

Oyster clearance rate was measured under *ex situ*, flow-through conditions and logged in real-time using fluorometers among replicate oysters over week-long experiments. Oyster filtration response to prevailing conditions is estimated from signal differences among sensors during post processing. These data were used to create an oyster clearance rate model that is able to estimate clearance rate from water quality predictors, as well as estimate the impact of these predictors on oyster feeding. This monitoring system and resulting model enables a deeper understanding of how natural seston conditions and environmental variability directly influence oyster physiology.

SEABED CLASSIFICATION OF OYSTER FARMS USING A SINGLE BEAM SCANNING SONAR WITH MACHINE LEARNING

Michael Xu[1]*, Keshav Rajasekaran[1], Alan William[2], Allen Pattillo[3], Matt Gray[2], and Miao Yu[1]

[1]University of Maryland, Department of Mechanical Engineering, 2181 Glenn L. Martin Hall, Building 088, College Park, MD 20742

[2]Horn Point Laboratory, University of Maryland Center for Environmental Science, 2020 Horns Point Rd, Cambridge, MD 21613

[3]Wye Research & Education Center, 124 Wye Narrows Dr, Queenstown, MD 21658

mixu1235@umd.edu

On-bottom oyster aquaculture enables large-scale production with lower input cost while providing many of the ecosystem services (e.g., water filtration, nutrient removal, and habitat). As a result, oyster aquaculture is considered one of the most sustainable forms of seafood production; however, on-bottom oyster production is currently bottlenecked by outdated tools and technologies. The industry would significantly benefit from imaging tools that can help identify suitable substrates for planting and provide oyster inventory information for harvest planning.

Traditional optical imaging methods face great challenges in the estuary ecosystems where oysters are grown, due to the high-water turbidity levels in these systems. This work proposes the use of sonar imaging with Machine Learning (ML) to overcome the limitations of optical imaging. In a lab experiment, a low-cost single beam sonar device was used to obtain sonar images. An ML model was trained to perform classification of different substrates (e.g., shell, sand) and oyster size ranges and to determine the ratio of living and dead oysters. The results demonstrated that with the ML model, over 85% accuracy can be achieved in all the classification scenarios. The ML enhanced sonar technology offers great potential for accurate bottom substrate characterization, enabling better farm lease site selection. Furthermore, it has the potential to provide farmers with accurate crop inventory information that is critical for business planning and production optimization.

MAKING SENSE OF THE TAXONOMY OF THE MOST COMMERCIALLY IMPORTANT SHRIMP *PENAEUS FABRICIUS*, 1798 S.L. (CRUSTACEA: DECAPODA: PENAEIDAE): A WAY FORWARD

Chien-Hui Yang[1], Ka Yan Ma[2,3], Ka Hou Chu[3,4], and Tin-Yam Chan[1]*

[1]Institute of Marine Biology and Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung 202301, Taiwan

[2]School of Ecology, Sun Yat-Sen University, No.66 Gongchang Road, Guangming District, Shenzhen, Guangdong 518107, China

[3]Simon F.S. Li Marine Science Laboratory, School of Life Sciences, The Chinese University of Hong Kong, Shatin, N.T., Hong Kong, China

[4]Southern Marine Science and Engineering Guangdong Laboratory (Guangzhou), No. 1119, Haibin Road, Information Technology Park, Nansha Street, Nansha District, Guangzhou 510301, China

tychan@ntou.edu.tw

Members of *Penaeus* s.l. are the most economically important shrimp, but there has been substantial confusion about their classification over the last few decades. In this study, a robust molecular phylogeny for these shrimps was reconstructed based on the most extensive dataset to date in terms of the number of molecular markers (four nuclear and three mitochondrial) and taxon coverage (31 of 32 known species in *Penaeus* s.l.). Two of the six genera proposed for *Penaeus* s.l. were revealed to be paraphyletic. Moreover, none of the morphological characters generally used for separating the species groups are synapomorphic or evolutionarily informative. As synapomorphic characters have yet to be discovered for all the main clades within *Penaeus* s.l., it is appropriate to retain these shrimps in a single genus to reflect their evolutionary relationships in terms of integrated taxonomy. A single genus classification scheme is also the least disruptive to the taxonomic names of these very important commercial shrimps.

CHALLENGE OF HEAT SHOCK ON NORTHERN QUAHOGS FOR GENOME-WIDE ASSOCIATION STUDY

Huiping Yang*, Jayme C Yee, Yangqing Zeng, Elise Bently, and Alex Bell

University of Florida, School of Forest, Fisheries, and Geomatics Sciences, 7922 NW 71st St., Gainesville, FL 32653

huipingyang@ufl.edu

Genomic selection is to breed candidates based on the genomic estimated breeding value (GEBV) predicted from genome-wide high-density markers. Accuracy of estimation of GEBV and design of training populations are important for effective breeding. This study aimed to develop the GEBV prediction in correlation with the heat tolerance of northern quahogs, *Mercenaria mercenaria.* Three aquaculture stocks from local farms (n = 1034) were formed into the training population. After acclimating to seawater with a salinity of 25 and a temperature of 24°C for three weeks, quahogs were challenged with heat shock in a recirculating system with temperature controlled using a heat pump and a temperature controller (Model No. DC24S, Aqualogic). The temperature was increased at 1°C per day from 24°C to 35°C and maintained for three days, and then returned to 24°C within three days and maintained at 24°C for 10 days. During the challenge process, quahogs were examined every 3-4 hr and moribund ones were removed with tissue sampled. During the temperature increase, a total of 483 quahogs died, while during the temperature decrease, a total of 328 quahogs died. After the challenge, hemocytes from the individual survivors (n = 223) were sampled. By April 2022, a total of 47 quahogs survived and were conditioned as broodstock for F1 production which is now in the field growth period for survival and growth estimation. Samples from the first 328 and last 328 moribund quahogs during the challenge are in process of SNP genotyping. Further analysis will be performed and reported.

CRYOPRESERVATION OF *TETRASELMIS STRIATA* THROUGH SYSTEMATIC EVALUATION OF MULTIPLE PARAMETERS

Jayme Yee* and Huiping Yang

University of Florida, Fisheries and Aquatic Sciences, 7922 NW 71st St. Gainesville, FL 32653

jayme.yee@ufl.edu

Microalgae are essential food for fish and shellfish. Pure strains have been isolated and need to be maintained. Cryopreservation is a useful technology in preserving and maintaining isolated pure strains of microalgae. The goal of this study was to develop an effective cryopreservation protocol for *Tetraselmis striata.* The objectives were to 1) determine the staining concentration and time of neutral red (NR) for accurate determination of cell survival; 2) evaluate acute toxicity of cryoprotectants on fresh algal cells up to 2 hr at room temperature, using dimethyl sulfoxide (DMSO), glycerol, methanol, and propylene glycol (PG) at concentrations up to 25%; 3) evaluate effects of cooling rates between 1-20°C/min and vitrification, and thawing temperatures (30-50°C) on post-thaw survival, and 4) evaluate effects of a 5% sugar addition (fructose, glucose, raffinose sucrose, and trehalose,) on post-thaw survival and continued growth. Cell viability was confirmed using a 0.01% concentration of NR for 5+ minutes. Acute toxicity revealed cryoprotectant concentrations ≤15% did not show a significant difference in cell viability up to 60 min. Cooling rates of 1°C/min yielded the highest post-thaw survival using glycerol or DMSO at final concentrations of 5-10%. Thawing temperatures did not show significant differences. The addition of sugars (5%) yielded the highest post-thaw viability (87-90%) in groups of DMSO + trehalose, glycerol + sucrose, and glycerol + raffinose. Post-thaw growth was confirmed in glycerol + sugar addition regardless of sugar type. Overall, cryopreservation protocols were generated for *T. striata* and could potentially be applied to other *Tetraselmis* species.

A NOVEL AND RAPID qPCR PROBE ASSAY FOR THE DETECTION OF THE ROSEOVARIUS OYSTER DISEASE (ROD) BACTERIUM, *ALIIROSEOVARIUS CRASSOSTREAE,* IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

Lengxob 'Lenny' Yong[1]*, Ryan Carnegie[2], Peter Kingsley-Smith[1], and Tanya Darden[1]

[1]Marine Resources Research Institute, South Carolina Department of Natural Resources, 217 Fort Johnson Road, Charleston SC 29412

[2]Virginia Institute of Marine Science, College of William & Mary, Department of Aquatic Health Sciences, Post Office Box 1346, 1370 Greate Road, Gloucester Point, VA 23062

yongl@dnr.sc.gov

Roseovarius Oyster Disease (ROD) has been a significant cause of eastern oyster (*C. virginica*) mortalities in parts of the northeastern United States since the late 1980s and is an epizootic threat in both wild and aquaculture settings. The pathology and morbidity arising from ROD are attributed to the presence of *Aliiroseovarius crassostreae*, a marine alpha-*Proteobacteria* bacterium, in the tissues of infected individuals. Due to high rates of intraspecific transmission and a predominance of mortality occurring in young oysters, seed importation is of high concern in the shellfish industry as a potential pathway of the introduction for *A. crassostreae*. This concern has prompted the development of several diagnostic tools based on gross observations and histology, but these can be limiting for both pathogen detection in low abundance, *i.e.*, cell and copy numbers, and quantitative purposes. Here, this study reports the development of a new probe-based qPCR assay for rapid, sensitive, and quantitative detection of *A. crassostreae.* The probe targets a unique and small genetic region (139bp) of the interspacer region of the 16S-23S genes. Tested on *A. crassostreae* synthetic and bacterial DNA, the assay has an estimated detection limit of 1-3 copies per µL of DNA. The qPCR assay was also successfully implemented for rapid diagnosis on live oyster tissue and bacterial quantitation. Moreover, this new sensitive and diagnostic tool can help to illuminate basic aspects of ROD pathogenesis and dynamics, particularly infection level in asymptomatic oysters and disease spatial distribution, which together will help to reduce the spread of ROD.

REVERSE TRANSCRIPTASE-RELATED GENES AND THEIR POSSIBLE ROLE IN THE HOST CELL RESPONSE TO TRANSITION METAL POLLUTION

Irina Yushenova*, Fernando Rodriguez, and Irina Arkhipova

Marine Biological Laboratory, Josephine Bay Paul Center, 7 MBL street, Woods Hole, MA 02543 USA

iyushenova@mbl.edu

Reverse transcriptase-related (*rvt*) genes are a distinct class of domesticated reverse transcriptases (RT) with unusual properties. Most notably, this is the only RT type found in bacteria, fungi, protists, plants and invertebrates from aquatic and soil-dwelling environments. These are cellular single-copy genes preserved by natural selection, potentially performing biological function that is applicable to both prokaryotes and eukaryotes.

Reverse transcriptase-related (*rvt*) genes represent the first known case of protein-primed RT encoded by a chromosomal non-selfish gene. Moreover, the N-terminal coiled-coil domain allows RVT proteins to form multimers and could potentially interact with metal ions. Since most free-living organisms can be frequently exposed to hazardous pollutants including transition metals, they therefore need potent mechanisms to cope with such stresses.

Three free-living organisms dwelling in activated sludge with active *rvt* genes in their genome (filamentous gliding bacterium *Herpetosiphon aurantiacus*, ascomycete fungus *Neurospora crassa,* and the bdelloid rotifer *Adineta vaga*), display signs of altered growth and behavior after exposure to increased concentrations of several metal ions (Ni^{2+}, Co^{2+}, Fe^{2+}, Zn^{2+}) in growth media and strongly induced expression of *rvt* genes. All examined organisms demonstrate specificity of *rvt* response to a specific metal ion. Moreover, when recombinant RVT from *H. aurantiacus* is expressed in *E. coli,* bacterial clones survived better on iron-rich medium. Participation of domesticated RT in metal stress response could reveal an ancient function of these genes in early evolution. Most importantly, it can also unmask novel pathways to environmental adaptation with the potential to employ corresponding proteins in biotechnological applications.

AQUACULTURE REGULATIONS: WHY THE COMPLEXITY?

Paul Zajicek

National Aquaculture Association, PO Box 12759, Tallahassee, FL 32317-2759

paul@thenaa.net

The Clean Water Act and Endangered Species Act have reached their 50th anniversary. All citizens should celebrate this iconic legislation; however, for US aquaculture regulatory costs continue to increase and the time, effort, and cost to acquire permits grows and lengthens. Why this has occurred is explored through the lenses of the additional little-known legislation, Commerce Clause of the US Constitution, state sovereignty, federal delegation, agency silos and the unique nature of the United States. Practical advice as to how to be an effective and knowledgeable farmer in the age of "The Next Regulation is the Best Regulation" will also be presented.

EVALUATION OF IMMUNOLOGICAL RESPONSES TO ENVIRONMENTAL SALINITY CHANGE IN NORTHERN QUAHOGS, *MERCENARIA MERCENARIA,* USING FLOW CYTOMETRY

Yangqing Zeng* and Huiping Yang

University of Florida, School of Forest, Fisheries, and Geomatics Sciences, Institute of Food and Agricultural Sciences, 7922 NW 71st Street, Gainesville, FL 32653

zengyangqing@ufl.edu

The northern quahog, *Mercenaria mercenaria,* is an important aquaculture and fishery species along the Atlantic west coast. As an estuarine species, they are frequently exposed to fluctuating salinity levels. To tolerate salinity pressure, the organisms could have integrated physiological, immunological, and molecular mechanisms. The goal of this study was to evaluate the impacts of long-term salinity pressure on the immunological response using flow cytometry. Based on our pilot study, the long-term challenge was made at salinities of 15, 25, and 35 for three months. The objectives were to evaluate 1) the osmotic pressure changes of hemolymph; 2) the viability, phagocytosis, reactive oxygen species (ROS), and lysosome of hemocytes using flow cytometry, and 3) the morphology changes of hemocytes using transmission electron microscopy (TEM). Market-sized quahogs from local farms were used in this study. Before the challenge, quahogs were acclimated in a recirculating system at a salinity of 25 for one month (T = 22°C). After a 3-month challenge, the osmotic pressure of hemolymph in quahogs became the same as that of environmental salinities (425 mOsmol/kg for salinity of 15; 752 mOsmol/kg for salinity of 25; 1014 mOsmol/kg for salinity of 35). The survivals of quahogs were over 95% and no differences ($P = 0.630$) were found among the three salinities. The immunological data and TEM samples are in the process of analysis. Further detailed data will be presented at the meeting. The study intends to reveal the physiological and immunological response of quahogs to salinity change and understand the mechanism at the cellular level.

THE GENOME OF *PENAEUS VANNAMEI* SOLINVIVIRUS (PVSV; OP265432) IDENTIFIED IN DISEASED SHRIMP FROM BRAZIL IS IDENTICAL TO WENZHOU SHRIMP VIRUS 8 AND *P. VANNAMEI* PICORNAVIRUS IN WILD SHRIMP FROM CHINA - PORTIONS OF THESE VIRUSES ARE PRESENT IN ONE (ASM373033V1) OF THE TWO GENOME ASSEMBLIES AVAILABLE FOR *P. VANNAMEI*

Gladys Zuniga[1]* and Acacia Alcivar-Warren[1,2]*

[1]Fundación para la Conservación de la Biodiversidad (FUCOBI), San Miguel de Anagaes E17-300, Conjunto Nueva Granizada, Casa 17, El Eden, Quito, Ecuador

[2]Environmental Genomics Inc., P.O. Box 196, Southborough, MA 01772 USA

fucobi@gmail.com

A novel Homology searches using BLASTN (nt) revealed 93% identity to Wenzhou shrimp virus 8 strain shrimp14543 (KX883984.1, 10,445bp) and 91% identity to *P. vannamei* picornavirus (OK662577.1, 10,550bp).TSA results showed various transcripts of *P. vannamei* including hepatopancreas RNA from Shrimp Improvement Systems, FL collected in 2011 (GETD01041508.1 10492bp) and hepatopancreas RNA from wild shrimp from Sonora, Mexico, collected in 2013 (GETZ01046206.1 10791bp). They showed similarity to hypothetical protein [Wenzhou shrimp virus 8, YP_009336733.1], polyprotein [*P. vannamei* solinvivirus, UWY63979.1], and hypothetical protein [*P. vannamei* picornavirus, UIU06302.1].

UWY63979.1 protein, BLASTP searches RNA-dependent RNA polymerase (RdRp) (5648-6742), and putative G-patch (9725-9814). Cruz-Flores et al. 2022 included an additional domain, calicivirus coat protein (nucleotides 7880-8353), but we couldn't confirm this domain in .

WGS searches identified portions of the 3'-end of OP265432.1 identical (92-93%) to three sequences [QWLK01003484.1 (7431bp), QWLK01003486.1 (1501bp), QWLK01003485.1 (5151bp)] in the contig-level genome assembly ASM373033v1 of *P. vannamei* F1 breed (GenBank: GCA_003730335.1, genome size 96.78Mb). But OP265432.1 is not present in the large scaffold-based genome assembly ASM378908v1 of *P. vannamei* breed Kehai No.1 farmed in China (GenBank: GCA_003789085.1; 1,663.57Mb). Similar results were found in the 3'end of KX883984 and OK662577, suggesting endogenous viral elements (EVE) of PvSV in *P. vannamei* genome. PvSV-EVE-like were present in cDNAs from *P. vannamei* hepatopancreas. Considering that the expected genome size for SPF *P. vannamei* domesticated in the United States is ~2.83Gb, a new, continuous whole reference genome for *P. vannamei* is needed to confirm presence of the three viruses in the shrimp genome.

INVESTIGATING THE EFFECTS OF COASTAL STRESSORS ON THE GENOMIC VARIATION OF OYSTER POPULATIONS IN NARRAGANSETT BAY, RHODE ISLAND

Amy Zyck[1]*, Rebecca Stevick[2], Marta Gomez-Chiarri[3], and Jonathan B. Puritz[1]

[1]University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd., Kingston, RI 02881

[2]Institut Pasteur, Department of Microbiology, R+2 28 Rue du Docteur Roux 75724 Paris Cedex 15 France

[3]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, 120 Flagg Rd., Kingston, RI 02881

amaelia_zyck@uri.edu

Coastal environments are characterized by multiple stressors that may be occurring simultaneously and linked through biological processes. These stressors can have negative effects on the survival and development of important coastal species like the eastern oyster, *Crassostrea virginica*. Oysters have a complete sessile adult stage making them dependent on their pelagic larval stage for long-distance dispersal to facilitate gene flow across populations. Larvae are more sensitive than adults to a variety of natural and anthropogenic stressors making them a natural conduit for adaptation to environmental stressors. Multiple co-occurring coastal stressors may act as barriers to gene flow, limiting larval exchange by selective mortality (only letting resistant larvae pass), structuring populations through reduced connectivity. To investigate the effects of coastal stressors on the genomic variation of oyster populations, adult oysters were collected from eight sites in Narragansett Bay varying in environmental conditions, including dissolved oxygen, pH, and sewage effluent. Environmental profiles spanning multiple summers were compiled from long-term fixed-site monitoring data and Onset HOBO logger data. Sequence capture probes were generated from mRNA extracted from larval oysters exposed to coastal stressor treatments. These probes were used to capture regions of the adult genome highly expressed in response to these stressors. Preliminary population and seascape genomic analyses revealed high genetic differentiation of oysters from a site characterized by low salinity and higher temperatures compared to the other populations. Understanding the effects of coastal stressors on population connectivity can help inform decisions for active oyster restoration in Narragansett Bay.

INVESTIGATING CAGE DEPTH, WATER QUALITY PARAMETERS, AND OYSTER CONDITION IN REHOBOTH BAY, DELAWARE

Emily Andrade*, Lukesh Sundar, Tahera Attarwala, Juan Ramos, Zack Riggi, Kevin Knight, Jackie Maina, Ali Parsaeimehr, and Gulnihal Ozbay

Delaware State University, Department of Agriculture and Natural Resources, College of Agriculture, Science, and Technology, 1200 N Dupont Hwy, Dover, DE 19901

Eandrade21@students.desu.edu

Oyster aquaculture returned to the Delaware Inland Bays with the issuing of shellfish leasing areas in 2018, bolstering local economies, improving water quality, and providing structured habitat for fish and invertebrates. Successful management of oyster farming and restoration efforts depends on continuous monitoring of oyster growing conditions. The project goal is to monitor and identify relationships between cage depth, oyster condition, and water quality parameters including temperature, dissolved oxygen, pH, and total suspended solids (TSS) in Rehoboth Bay, DE.

This project will analyze how each of the different parameters impact oyster aquaculture and water quality in Sally's Cove—an aquaculture farm in Rehoboth Bay, Delaware. In-situ water quality data is measured using a YSI 556 Multiprobe and water samples are collected from surface and bottom depths. Oysters from deep and shallow depths are collected and weighed before and after drying to determine the total weight of the oyster shell, meat, and liquor. To quantify oyster condition, the Oyster Conditioning Index (CI) was calculated using various measurements taken from the oysters. A low CI indicates the oyster and its offspring are more vulnerable to disease and impacts from environmental stressors. This project is currently ongoing and is expected to be completed in Winter 2023.

MICROBIAL COMPOSITION OF *CRASSOSTREA VIRGINICA* TANK SEAWATER ASSOCIATED WITH EXPOSURE TO MICROPLASTICS

Jamal Andrews[1]*, Hannah Haskell[1], Evelyn Takyi[1], Andrew J. Davies[2], Coleen C. Suckling[3], and Marta Gomez-Chiarri[3]

[1]University of Rhode Island, Biological and Environmental Sciences Graduate Program, 120 Flagg Rd., Kingston, RI 02881

[2]University of Rhode Island, Graduate School of Oceanography, 215 S Ferry Rd, Narragansett, RI 02882

[3]University of Rhode Island, Department of Fisheries, Animal and Veterinary Science, 134 Woodward Hall, Kingston, RI 02881

js_andrews@uri.edu

Marine microplastics are known to harbor distinctive biofilm communities that differ from those of seawater and are enriched in particular species, such as vibrios. Microplastics can act as a transport vector into different ecosystems and potentially change the microbiome composition of marine species that ingest them, serving as potential disease vectors. Eastern oysters, *Crassostrea virginica,* were incubated with varying levels of microplastics (polyester fibers) to evaluate the effects of microplastics on oyster physiology and bacterial community composition. Microplastic treatments were environmentally relevant (2 and 95 microplastics L^{-1}), to more accurately represent concentrations seen in natural populations, as well as a higher concentration (950 microplastics L^{-1}) to make this study more comparable to previous studies. Water samples were collected on day 37 after the start of the experiment from the top and bottom of tanks containing the oysters. Bacterial community structure (diversity and taxonomic composition) was analyzed through 16S rRNA gene amplicon sequencing. The bacterial community structure of seawater collected from the top of the tanks (all treatments) significantly differed from the community of seawater collected from the bottom of the tanks, possibly due to organic buildup at the bottom of the tanks. Treatment of oysters with plastics had a small effect on the bacterial community structure of seawater from the oyster tanks. Relationships between the effect of plastics on oyster physiology and bacterial composition is currently being investigated.

THE EFFECTS OF DIFFERENT WATER QUALITY CONDITION ON EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, DEMOGRAPHICS AND DISEASE DYNAMICS ON SAPELO ISLAND, GEORGIA

Wil E. Atencio* and John M. Carroll

Georgia Southern University, Department of Biological Sciences, 4324 Old Register Road, Statesboro, GA 30460

wa03052@georgiasouthern.edu

Reef building eastern oysters, *Crassostrea virginica*, are both economically and ecologically important by providing valuable commercial products, forming complex habitats, improving water quality, and protecting shorelines. Despite this, oyster populations have experienced drastic declines worldwide, driving incentives for management and restoration. For these practices to be successful, it is important to investigate factors that currently influence oyster demographics and disease to understand how those factors might change in the future. Water quality parameters such as temperature, salinity, dissolved oxygen, and pH are all important environmental factors that influence oysters and will be affected by changing climate. To explore impacts of multiple water quality parameters on oysters, long-term data from the four System-wide Monitoring Program (SWMP) stations at the Sapelo Island National Estuarine Research Reserve (SINERR) was leveraged to examine seasonal and long-term trends in water quality conditions. Additionally, preliminary surveys of oyster populations at the SWMP stations were conducted to pair with long-term water quality data. Specifically, high-resolution drone imagery was used to examine variation in reef size and extent among the four SWMP sites, benthic surveys for oyster abundance, size, and condition, as well as disease prevalence and intensity, and monthly recruitment monitoring. Generally, sites exhibited the greatest variation in salinity and temperature, both important drivers of oyster populations. Larger oysters and high recruitment were found at the site with the lowest temperature and greatest salinity.

ASSESSING EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) PREDATION UTILIZING REAL TIME MONITORING AND EDNA ANALYSIS IN DELAWARE INLAND BAYS

Tahera Attarwala*, Juan Ramos, Emily Andrade, Marcus Teat, Zachary Riggi, Kevin Knight, Jackie Maina, Cassandra Miller, Ali Parsaeimehr, and Gulnihal Ozbay

Delaware State University, Department of Agriculture and Natural Resources, 1200 N. DuPont Hwy, Dover, DE 19901

tattarwala17@students.desu.edu

Eastern oyster (*Crassostrea virginica*) aquaculture is an important industry in Delaware that generates tens of thousands of dollars in sales every year. In addition to the economic value of oysters, they are known as keystone species that offer vital ecosystem services including water filtration, nutrient removal, and providing habitation and food for many aquatic species. Eastern oysters are preyed upon by different species of fish, crustaceans, and gastropods. In this study, cameras were deployed for real time monitoring and molecular biology approaches were used to monitor oyster predation and species diversity at five different oyster sites around Rehoboth Bay. The sites include artificial reefs, aquaculture farms, and control sites. Cameras are secured into recreational crab traps equipped with battery extenders. They are deployed for approximately two to three hours before retrieval. All documented aquatic species are identified and recorded for comparisons between sampling locations. Isolation of Environmental DNA (eDNA) is also performed as a compilatory tool for species identification. This study will provide up-to-date information on oyster restoration efforts in Rehoboth Bay, Delaware.

THE LOW TROPHIC SPECIES LABORATORY AT THE INSTITUTE OF MARINE RESEARCH IN NORWAY

Antonio Aguera*, Tore Strohmeier, Cathinka Krogness, Helen Rastrick, and Øivind Strand

Institute of Marine Research, Nordnesgaten 50, N-5020 Bergen, Norway

antonio.aguera@hi.no

The low trophic initiative at the Institute of Marine Research (IMR) focus on research on advancing knowledge on production biology and modelling production- and ecological carrying capacity of low trophic species that are proposed as a route to obtain more food, feed, and biomass from the oceans.

With this aim the group has built and equipped the Low Trophic Laboratory, at the IMR research station in Austevoll, southwest Norway. These facilities provide access to natural conditions and seston with a modular space to work on different candidate species (currently suspension feeders and deposit feeders) and with different life stages (larva, juveniles or adults). Laboratories are equipped with instrumentation to monitor and control environmental conditions: temperature, salinity, pH, flow rates, and seston. The labs include state-of-the-art technology to provide high temporal resolution measurements in metabolism and feeding activity. The research station offers access to technical expertise and equipment for diverse techniques including phytoplankton culture, bomb calorimetry, and a chemistry lab.

TUSK SHELLS (SCAPHOPODA) IN A RIDGE-SWALE BENTHIC ECOSYSTEM AT CAPE CANAVERAL, FLORIDA, USA

Patrick Baker

University of Florida, Program in Fisheries and Aquatic Sciences, School of Forestry, Fisheries, and Geomatics Sciences, 7922 NW 71st Street, Gainesville, FL 32653

pkbaker@ufl.edu

Tusk shells are small, infaunal marine molluscs that comprise their own class, Scaphopoda. They have no modern fishery value outside the shell trade but are common in most oceans, and feed mainly on Foraminifera, shelled protozoans. Tusk shells were sampled during a six-year survey of a sandy ridge-swale system near Cape Canaveral, Florida. The most common tusk shell was *Paradentalium americanum*, at densities of up to $129\cdot m^{-2}$, but *Graptacme calamus*, *G. eborea*, and *Fustiaria liodon* were also present. Tusk shells occurred almost entirely in swale (deeper) habitats, which exhibited significantly finer sediments, higher organic content, and higher numbers of Foraminifera. The cone-worm, *Pectinaria gouldii* (Polychaeta: Pectinariidae), occurred with tusk shells and superficially resembles them, but is a deposit feeder. Other invertebrate groups in swales included other polychaete worms, bivalve mollusks, and heart urchins (Echinoidea: Spatangoida). The shallower ridge habitats, which lacked tusk shells, had coarser sediments and were dominated by amphipod species, lancelets (*Branchistoma virginiae*), free-living bryozoan colonies (*Reussirella doma*), and sand dollars (Echinoidea; Clypeasteroida). Ridges and swales differed by only a few meters of relief, but these modest differences defined distinct benthic communities.

WATER TEMPERATURE AND SEASON LENGTH INTERACT TO EXPLAIN A RARE NON-LINEAR ECOGEOGRAPHIC CLINE IN BODY SIZE OF THE AMERICAN HORSESHOE CRAB

Savanna C. Barry[1], Matthew D. Smith[2], Berlynna Heres[3], Travis M. Thomas[1], Brittany J. Scharf[4], and H. Jane Brockmann[2]*

[1]Nature Coast Biological Station, University of Florida, 552 1st Street, Cedar Key, FL 32625

[2]University of Florida, Department of Biology, 876 Newell Dr., Gainesville, FL 32611

[3]Crustacean Research Section, Florida Fish and Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, FL 33701

[4]Florida Sea Grant, University of Florida, 16110 Aviation Loop Dr., Brooksville, FL 34604

hjb@ufl.edu

The American horseshoe crab (*Limulus polyphemus*) is a widely-distributed marine arthropod previously reported to exhibit larger body sizes in the center of its population range. Adult body size often changes systematically across large-scale environmental gradients (e.g., latitude, temperature) creating ecogeographic clines; however, the form of body size clines varies across taxonomic groups, with linear (increasing, decreasing) and nonlinear (bowl-shaped, dome-shaped, and sawtooth) patterns in body size observed in nature. Non-linear body size clines have received less study and questions remain about how environmental gradients interact to produce non-linear clines. The body size distribution of *L. polyphemus* was examined and body size measurements from more than 49,000 individuals from 14 US states and 3 Mexican states were complied, representing the entire geographic range of the species. For each location, the mean male prosoma width and the mean female prosoma width were extracted from either the literature or calculated from raw data, resulting in 153 observations of adult horseshoe crab body size. A general additive modelling approach test of the hypothesis that the effects of temperature and season length can interact multiplicatively to create a non-linear, dome-shaped distribution in horseshoe crab body size was applied. Results confirm previous reports of a strong dome-shaped body size cline across latitude for horseshoe crabs. Model results indicate temperature and season length could indeed act multiplicatively to produce dome-shaped clines. Considering climate change projections, these results predict drift in the mean population body sizes could occur over time in horseshoe crabs.

EXAMINING THE SUSTAINABILITY OF THE FLORIDA STONE CRAB (*MENIPPE MERCENARIA*) FISHERY: TESTING INTRASPECIFIC INTERACTIONS BETWEEN SINGLE- AND TWO-CLAWED INDIVIDUALS

Talia Barry* and Kristian Taylor

University of Tampa, Department of Biology, 401 W Kennedy Blvd, Tampa, FL 33606

Talia.barry@spartans.ut.edu

The Florida stone crab (*Menippe mercenaria*) is an economically important species native to the southeast coast of the US and Mexico. The fishery is unique in that only a single claw is harvested and then the crab is released. Due to such regulations the fishery is considered sustainable. This project sought to examine the interactions between single-clawed and two-clawed individuals. It was hypothesized that smaller, two-clawed individuals would outcompete larger, single-clawed individuals that were impacted by the fishery. Large (carapace > 80 mm), single-clawed individuals were paired with smaller (< 80 mm), two-clawed individuals and placed simultaneously in a tank with a single artificial burrow. A 'winner' was recorded as the crab remaining in the burrow at the end of one hour. A total of 27 trials were run using 54 specimens and all behaviors were recorded and coded. Smaller, two-clawed individuals outcompeted larger, single-clawed individuals 41% of the time, compared to larger individuals securing the burrow only 29% of the time, with no set winner for 30% of interactions. The significance with which smaller, two-clawed individuals outcompeted larger, single-clawed conspecifics brings into question the impact of this fishery on population dynamics and whether it is truly sustainable. Although smaller individuals might be juveniles, this research demonstrates that genetically smaller individuals can outcompete larger individuals impacted by the stone crab fishery. This work should be continued to examine how the stone crab fishery might be directly impacting the population genetics of this economically important species.

POTENTIAL PITFALLS OF TEXAS COM (CULTIVATED OYSTER MARICULTURE) LEGISLATION TO THE FUTURE LOWER LAGUNA MADRE OYSTER FARMERS

David Bazan* and Joanne Rampersad-Ammons

University of Texas Rio Grande Valley, School of Earth Environmental and Marine Sciences, 1201 West University Dr., Edinburg, TX 78539

dbazan6722@hotmail.com

In 2019, Texas became the last US coastal state to allow cultivated oyster mariculture (COM) when Texas governor Greg Abbot signed into law Texas House Bill 1300 officially allowing for COM on the Texas coast for the first time; however, this newly established legislation does not come without its hardships such as. The State's long permitting processes, requirement of 100,000 seeded oysters per acre, its 500 ft buffer zone between farming areas, and seagrass to name a few. When comparing processes in Texas to another state like Maine, the difference is substantial. For example, it could be as quick as three weeks to acquire the necessary permits in Maine, whereas the same process in Texas could take upwards of a year. Consequently, currently only three fully permitted oyster grow out operations, and only two fully permitted oyster hatcheries now exist in Texas. Although there have been improvements to the permitting process (guides to help new applicants, a webpage that allows electronic submission and tracking of permits) there is still room for improvement. The problems with this legislation and its potential effects on the farmers of the Lower Laguna Madre which has over 60% of the State seagrass beds will be discussed along with potential solutions.

THE EASTERNMOST MARINE SCIENCE FIELD STATION IN THE U.S.: A PARTNERSHIP BETWEEN THE UNIVERSITY OF MAINE AT MACHIAS AND THE DOWNEAST INSTITUTE

Brian F. Beal[1,2]*, Dianne Tilton[2], Jeff Robinson[2], Kyle Peppermen[2], Robert J. Holmberg[2], and Sara Randall[2]

[1]University of Maine at Machias, 116 O'Brien Avenue, Machias, ME 04654

[2]Downeast Institute, 39 Wildflower Lane, P.O. Box 83, Beals, ME 04611

bbeal@maine.edu

Marine science research and education are stronger and more active than ever in the easternmost coastal U.S. After 19 years of planning and development, the University of Maine at Machias and its nonprofit partner, the Downeast Institute (DEI), have announced that the newest marine science field station in the U.S. is open for business. Located on a 16-acre campus and adjacent to a 1,200-acre preserve owned by The Nature Conservancy, this pristine setting is located 40 coastal miles east of Acadia National Park in a traditional fishing community in Washington County, Maine. The marine research laboratory and adjacent shellfish production and development center are only 100-ft from deep water that covers nearly 3,000 ft rocky intertidal shoreline where tides vary 12- to 14-ft every six hours. Visiting scientists and their students have access to a 30-seat classroom equipped with running seawater, moveable tables/benches, microscopes, seawater holding tanks, and Polycom communication capabilities. Six offices look out upon the Western Bay where spectacular sunsets are the norm, and where lobster fishermen ply their trade so close to shore during early mornings that you can almost reach out and touch their boats. A 1,000 ft^2 ecology wet lab can be used for experimental work, or to hold organisms prior to field trials. Adjacent to the wet lab is a business incubator, quarantine lab, and climate control chamber. In addition, a state-of-the-art ocean acidification lab was constructed to examine the effects of current and future levels of CO_2 on calcifying organisms.

EVALUATING THE RESPONSE OF *MYTILUS TROSSULUS* TO CHRONIC AND VARIABLE HEAT CONDITIONS USING GENE EXPRESSION BIOMARKERS

Zachary Bengtsson*, Olivia Cattau, Christine Mantegna, Aidan Coyle, Sarah Tanja, Matthew George, and Steven Roberts

University of Washington-Seattle, School of Aquatic and Fishery Sciences, 1122 NE Boat Street, Room 116, Seattle, WA 98105

zbengt@uw.edu

Planning for future climate challenges is limited by current understanding of how organisms cope with changing environmental conditions at the molecular level. For marine bivalves like the foolish mussel (*Mytilus trossulus*), transcriptional mechanisms which convey resilience to rising coastal temperatures and increasingly frequent heatwave events are especially important. This study investigated heat stress response in foolish mussels using quantitative PCR methods to examine the expression of heat stress-related genes under chronic and variable heat conditions. Mussels were exposed to one of three conditions: chronic heat (18°C), variable heat (cycling between 15°C and 21°C), and control (12°C). After seven days of exposure, gill tissue samples were dissected and run through RNA extraction and reverse transcription. qPCR runs were completed for each sample in duplicate using primers for heat shock protein cognate 70 (HSC70), heat shock protein 90 (HSP90), and small heat shock protein 24.1 (small HSP24.1)–protein coding genes known for their involvement in heat stress response. Preliminary results show differential expression of heat shock protein coding genes across the three treatment groups, particularly between heat exposure and control conditions. Further examination of how stress related gene expression changes under possible climate futures informs how mussels cope with environmental stress and allows managers to prioritize the mitigation of multiple stressors.

VIBRIO PARAHAEMOLYTICUS AND *VIBRIO VULNIFICUS* LEVELS IN TRIPLOID OYSTERS HARVESTED DURING THE SUMMER IN GEORGIA

Thomas H. Bliss[1]*, Erin Arneson[1], John Pelli[1], Justin Manley[1], and Erin Lipp[2]

[1]University of Georgia, Shellfish Research Laboratory, Marine Extension and Georgia Sea Grant, 20 Ocean Science Circle, Savannah, GA 31411

[2]University of Georgia, College of Public Health, Health Sciences Campus, 105 Spear Road, Athens, GA 30602

tbliss@uga.edu

The bacteria, *Vibrio parahaemolyticus* and *Vibrio vulnificus,* are found in brackish and saltwater environments where oysters are cultured. Currently, the *Vibrio* plan in the State of Georgia closes oyster harvest when water temperatures are above 81°F (June-September). In 2020, regulations were adopted that allows the state to lease sub-tidal areas to utilize floating gear. With the migration to floating gear, there is interest from regulators and the industry to evaluate the potential for summer harvest. The goal of this study was to establish *V.p.* and *V.v.* levels in triploid oysters held in floating bags and cages. Gear was placed in Mud River in May 2020 and 90 oysters from each gear type were harvested every two weeks. Half the oysters were placed immediately on ice while the other half were held on the deck of the boat for 2-hours prior to refrigeration. Composite samples of 15 oysters were examined for *Vibrio* spp. levels following NSSP guidelines. Mean levels of *V.p.* in oysters for iced and 2-hour treatments were 3.50 log CFU/g and 3.73 log CFU/g, respectively and were significantly different ($p=0.04$). Mean *V.v.* levels in oysters for iced and 2-hour treatments were almost identical with 1.89 log CFU/g and 1.85 log CFU/g, respectively and did not differ ($p=0.79$). Our data found that mean Vibrio spp. concentrations did not exceed safety thresholds established by FDA and indicate that summer harvest of oysters either by placing on ice or in refrigeration within 2-hours could be adopted for Georgia.

ANALYSIS OF GENETIC DIVERSITY OF A NEWLY DISCOVERED TREMATODE PARASITE OF THE BAY SCALLOP, *ARGOPECTEN IRRADIANS,* IN NORTH CAROLINA

Connor Brainard[1,2]*, Julia Buck[1,2], Robin Varney[1], Tal Ben-Horin[3], and Ami Wilbur[1,2]

[1]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K Moss Ln, Wilmington, NC 28409

[2]University of North Carolina Wilmington, Department of Biology and Marine Biology, 601 S. College Road, Wilmington, NC 28403

[3]Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC, 28557

cb1216@uncw.edu

Parasite infections have the potential to impact the sustainability of aquaculture by causing mortality and reducing product quality. A novel parasite was observed in 2012 infecting the afferent vessel in the gill of the bay scallop, *Argopecten irradians*. Subsequently, infections have been seen in scallops from North Carolina (NC) and Florida (FL). Preliminary condition analysis of infected scallops shows reduced proportional weight of muscle and gonad tissue compared to uninfected specimens, meaning lowered marketability and fecundity of cultured organisms. DNA sequence data from a nuclear 28S rDNA fragment indicates that samples from NC and FL are the same species of trematode belonging to the family Didymozoidae (Superfamily Hemiurodea) and that it forms a well-supported clade with a recently described Australian species (*Saccularina magnacetabula*). This study investigates the genetic diversity of trematodes infecting scallops collected from five NC locations (Back Sound, Core Sound, Chadwick Bay, Becky's Creek, and Masonboro Sound). A 913bp fragment of the cox1 mitochondrial gene was sequenced for each parasite sample and analyzed for genetic diversity. Results of this analysis will be discussed.

SMALLER MICROPLASTICS ACCUMULATE WITH AGE IN THE PHILIPPINE COCKLE, *ANADARA ANTIQUATA*

Lilibeth Bucol*[1], Bernadette Vasig[2], Hiroko Watanabe[3], and Tomoya Kataoka[3]

[1]School of Environmental Science & Management, 568R+PMH University of the Philippines-Los Banos, 4031 Laguna, Philippines

[2]Negros Oriental State University, Kagawasan Avenue, 6200 Dumaguete City, Negros Oriental, Philippines

[3]Ehime University, 3 Bunkyo-cho, Matsuyama, Ehime 790-8577, Japan

lilibethabs2013@gmail.com

Bivalves are potential bioindicators for microplastic (MP) pollution owing to their biology (i.e., sedentary and filter feeders) and importance to the seafood industry. This paper describes the characteristics (size, diameter, polymer type) of microplastics isolated from the cockle (*Anadara antiquata*), a locally consumed bivalve, from Bais Bay in central Philippines. Of the 134 MP identified using µFTIR, PEPP (polyethylene-polypropylene) comprised 19%, PE (polyethylene) 16%, PA (polyamide) with 9%, while the remaining half (50%) were unclassified. All identified MP particles were smaller than 1000µm (maximum sizes ranged 19-894 µm; diameter 47-527 µm), coinciding the size range of diatoms (2-1000 µm). This suggests that bivalves selectively ingest certain particle size range and could sort particles depending on their physical and chemical characteristics. Mean MP size and diameter gradually decreased with age (based on external growth rings), suggesting that as the bivalve ages, smaller MP remain in the individual, while larger ones are easily excreted. This study also observed a gradual increase in MP mass (mg) with age in *A. antiquata*. MP mass also increased positively with shell size and weight, though not statistically significant. As smaller MP have higher probability to adsorb hydrophobic organic pollutants due to larger specific surface area, *A. antiquata* may be more exposed to these toxic chemicals over time but this aspect needs further investigation.

DEVELOPING A COLLABORATIVE FRAMEWORK TO MAXIMIZE OYSTER PRODUCTION AND ECOSYSTEM BENEFITS

Olivia N. Caretti* and H. Ward Slacum, Jr.

Oyster Recovery Partnership, 1805A Virginia Street, Annapolis, MD 21401

OCaretti@oysterrecovery.org

Optimizing oyster production to maximize and maintain restoration benefits requires a collaborative approach. Historically, oyster practices co-occur in space, require overlapping resources, and have conflicting user interests, which creates challenges for sustaining oyster production in areas requiring multiple management strategies. In Eastern Bay, a tributary to the Chesapeake Bay, there is a collective interest in improving oyster resources; however, oyster stakeholders involved in restoration, wild harvest, and aquaculture compete for resources and disagree on where and how oyster activities should occur. Oyster Recovery Partnership is leading a collaborative effort to develop a strategic plan for optimizing oyster production by using a consensus-driven process to establish oyster production goals that consider all stakeholder interests. This approach requires stakeholders to set objectives and develop metrics to track progress both collectively and for each stakeholder's interest. Existing oyster management zones will be re-delineated to identify areas suitable for oyster production strategies developed through the stakeholder process. The expected outcome will be a unified plan that connects the major oyster stakeholders and identifies clear and transparent goals for all three stakeholder groups, as well as resources required for the long-term maintenance of oyster production in Eastern Bay. The approach developed here can be applied to other estuaries hosting oyster multi-use areas to foster a collaborative approach to maximize oyster production, restore oyster ecosystem services, and sustain benefits over the long term.

COASTAL STRESSORS AFFECT THE SURVIVORSHIP OF OYSTER LARVAE (*CRASSOSTREA VIRGINICA*)

Hailee Carlson*, Ben Peopsel, Alexandra Hooks, and Jonathan Puritz

University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd, Kingston, RI 02881

hailee_carlson@uri.edu

The eastern oyster, *Crassostrea virginica*, encounters coastal stressors that decrease their survivorship by affecting the marine ecosystems they inhabit. This includes a decrease in salinity and pH levels which are influenced by climate change events such as an increase in precipitation. Locating a change in survivorship due to coastal stressors can indicate the current state of eastern oyster populations as climate change arises. To identify changes in eastern oyster survivorship with exposure to coastal stressors, approximately 100,000 larval oysters were inserted into nine, 1-L jars. Three of each of the nine jars represented a treatment group either of ambient water from the Narragansett Bay which was the control group (salinity of 30 and 7.7 pH), a low salinity of 5, or a low pH of 7.0. An initial density sample before exposure to stressors of each jar was recorded followed by a post-24-hour exposure density sample. Using a Sedgwick Rafter, 3 mL of the 1-L sample was counted and used to estimate the total number of larvae in the treatment groups before and after exposure to coastal stressors. The results showed that low salinity decreased oyster larvae survivorship while low pH did not significantly impact survivorship. This means that an influx in storms will likely increase larval oyster mortality, and spawnings during these storms will fail to produce future adult oysters. These results signify an importance in decreasing activities that promote climate change as they are decreasing the survivorship of eastern oyster populations.

PERFORMANCE OF WILD AND SELECTIVELY BRED EASTERN OYSTERS IN THE NORTHEASTERN UNITED STATES

Angel Carrasquillo*[1], Rob Hudson[1,2], Dina Proestou[3], Tal Ben Horin[4], Alexandra Moura[1], and Marta Gomez-Chiarri[1]

[1]University of Rhode Island, Fisheries, Animal and Veterinary Sciences, 9 East Alumni Avenue, Kingston, RI 02881

[2]Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol, RI 02809

[3]United States Department of Agriculture, Agricultural Research Services, 120 Flagg Road, Kingston, RI 02881

[4]North Carolina State University, Center for Marine Sciences and Technology, 303 College Circle, Morehead City, NC 28557

alcarr@uri.edu

Selective breeding programs have been developed in the Mid-Atlantic region of the United States (US) to produce commercial lines of eastern oysters (*Crassostrea virginica*) with fast growth and increased survival in areas affected by infectious diseases. Some of these commercial lines show a decrease in performance when grown in the Northeast due to genotype by environment interactions. The goal of this research is to inform the development of a selective breeding program for the Northeast US by evaluating performance of regional wild stocks that may be better adapted to local environmental conditions. In 2020, broodstock oysters from four wild stocks from Southern New England sites and two hatchery commercial lines commonly used in the Northeast US were spawned and deployed at a Rhode Island farm to compare performance. Growth and survival were periodically measured in tagged oysters (55 oysters x 3 bags per stock) from July 2021 to October 2022. Tagged oysters were also sacrificed at 18 months of age for disease diagnosis and genotyping. Oysters from the wild stocks showed varying degrees of mortality for the 2022 breeding season, ranging from 9% (SD=4.11) for oysters from the Thames River (CT) stock to 80% (SD=0) for oysters from the Narrow River (RI) stock. Commercial lines showed 20% (SD=18) to 25% (SD=4) mortality, and significantly faster growth than the wild stocks. Information from this research will be used to establish a founder population for the Northeast Eastern Oyster Breeding Program.

THE POTENTIAL FOR RIBBED MUSSELS TO ENHANCE LIVING SHORELINES PROJECTS IN COASTAL GEORGIA

John M. Carroll[1]*, William K. Annis[1,2], and Risa Cohen[1]

[1]Georgia Southern University, Department of Biology, 1332 Southern Drive, Statesboro, GA 30458

[2]Clemson University, Department of Forestry and Environmental Conservation, 261 Lehotsky Hall Box 3403317 Clemson, SC 29634

jcarroll@georgiasouthern.edu

Ribbed mussels, *Geukensia demissa*, are ecologically important bivalves that act as a secondary foundation species in salt marshes along the Atlantic coast. Within marshes, mussels filter water, cycle nutrients, and stabilize sediments which enhances marsh grass productivity and resilience. Due to these ecosystem benefits, ribbed mussels have received attention in restoration efforts throughout the northeast, however, they are overlooked in marsh management practices, like living shorelines (LS), in Georgia. Incorporating mussels into LS designs in Georgia could facilitate grass survival and reestablishment, however, Georgia marshes experience large tidal range and high energetics, coupled with mussel abundances typically concentrated on the marsh platform, thus innovative techniques for building LS must rely on location-specific data.

This project sought to determine whether the presence of ribbed mussels placed in marsh grasses immediately adjacent to a living shoreline project would increase plant productivity in Georgia. A control, low- and high-density mussel plots were established and monitored the change in plant productivity over the course of 15 months. Results demonstrate mussel-driven enhanced plant productivity from a combination of higher plant density and taller plant heights; however, mussel mortality was high throughout the study period, potentially limiting their local use as a restoration tool. Mussels in Georgia marshes are located on the platform, far from creekbanks, likely due to high predation. Therefore, if effective strategies for mussel transplantation are developed (i.e., higher numbers, protective devices), using ribbed mussels on LS projects can help marsh grass to grow back faster and healthier in Georgia.

CULTURE TECHNIQUES OF THE ICHTHYOTOXIC DINOFLAGELLATE, *MARGALEFIDINIUM POLYKRIKOIDES,* FOR LABORATORY EXPOSURE EXPERIMENTS

Shawna Chamberlin[1]*, Hannah Mitchell[1], Allex Gourlay[1], Evelyn Takyi[1], Annabelle Jones[1], Lisa Guy[3], Gary H. Wikfors[3], Roxanna M. Smolowitz[1,2], Timothy Scott[1], and Skylar Bayer[1]

[1]Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol RI 02809

[2]Roger Williams University, Aquatic Diagnostic Laboratory, 1 Old Ferry Road, Bristol RI 02809

[3]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford CT 06460

schamberlin@rwu.edu

The ichthyotoxic, chain-forming dinoflagellate. *Margalefidinium* (formerly *Cochlodinium*) *polykrikoides* (*Mp*), is responsible for rust tide blooms in coastal waters throughout the world, including the East Coast of the United States. Although *Mp* is not toxic to humans, it can have devastating effects on fish, crustacean, and bivalve populations that are exposed to a bloom, through mortality and/or reduced growth rates. *Mp* exposure trials with affected organisms, varying quantities of *Mp* cells as well as other environmental variables can improve understanding of environmental bloom consequences. Very little publicly-available information exists on effective culture methodology for *Mp* for laboratory-based exposure trials. The goal of this presentation is to describe the culturing methodology developed by the Center for Economic and Environmental Development of Roger Williams University to produce bloom-simulated cell densities of *Mp*. Through experimentation, it was determined that factors such as temperature, inoculation density and age, media type, sampling, and inoculation protocols, as well as cell preservation techniques, are imperative to maintaining and scaling-up a long-term *Mp* culture. These culture methods and observations can serve as a baseline for future work with *Mp*, so that further exposure trials can be completed efficiently.

GABA INHIBITS THE SEROTONERGIC INNERVATION OF THE GILL FROM THE VISCERAL GANGLIA IN THE BIVALVE MOLLUSC, *CRASSOSTREA VIRGINICA*

Patricia Chery*, Jennipher Chery, Edward J. Catapane, and Margaret A. Carroll

Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

Patricia.chery@student.mec.cuny.edu

Gill lateral cells (GLC) in *Crassostrea virginica* and *Mytilus edulis* are innervated by excitation serotonin and inhibitory dopamine nerves from visceral ganglia (VG). GABA, an inhibitory neurotransmitter in molluscs and other animals, has not been well studied in bivalves. To test if GABA is an inhibitory neurotransmitter to serotonin neurons in VG of *C. virginica* the effects of applying GABA and a GABA agonist to VG on GLC cilia beating were studied. Cilia beating was measured by stroboscopic microscopy in preparations with VG innervation via the branchial nerve to gills intact. Preparations were positioned in observation chambers separating VG from gill so drugs could be applied to VG or gill without leakage to other tissues. Applying serotonin to VG caused a dose-dependent increase in cilia beating. Applying GABA to VG prior to serotonin reduced the increase. Cutting the branchial nerve that innervates the gill prevented the response of serotonin, with or without GABA. Applying the GABAb agonist SKF 97541 (3-Aminopropylmethyl phosphinic acid) to VG also blocked serotonin, demonstrating GABA is working as an inhibitory neurotransmitter to serotonin nerves in VG. The study provides evidence that the GABA receptor may be a GABAb type G protein-coupled receptor that mediates slow and prolonged inhibitory action, via activation of Gai/o-type proteins. More experiments with other agonists/antagonists need to be done to verify this. Bivalve gill is a useful model to study cilia activity as well as pharmacology of drugs affecting biogenic amines. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP, and PSC-CUNY 62344-0050 and 62344-0051.

SUSTAINABLE AQUACULTURE: ADVANCING IRISH BIVALVE BIOMASS PRODUCTION BY PROMOTING SEED ABUNDANCE AND MORE DISEASE RESILIENT STOCKS (SUSAQUA PROJECT)

Catherine Collins[1,2], Sharon A. Lynch[1,2,3]*, and Sarah C. Culloty[1,2,3]

[1]University College Cork, School of Biological, Earth and Environmental Sciences and Aquaculture and Fisheries Development Centre, Distillery Fields, North Mall, Cork, T23 N73K, Ireland

[2]University College Cork, Environmental Research Institute, Ellen Hutchins Building, 6 Lee Rd, Sunday's Well, Cork, T23 XE10, Ireland

[3]MaREI Centre, Environmental Research Institute, Beaufort Building, University College Cork, Ringaskiddy, Co. Cork, P43 C573, Ireland

s.lynch@ucc.ie

Bivalves play a substantial role in economic decoupling by achieving economic growth while preserving a healthy environment by recycling nutrients (removal of nitrogen and carbon), stabilising sediments, and enhancing biodiversity. Pathogens and diseases and inconsistent seed supply represent a serious limitation to the sustainable growth of the Irish and global bivalve sector. A changing climate and environmental stressors challenge bivalve physiological limits resulting in individuals being more susceptible to infection and diverting energy from reproduction and growth. These challenges limit sustainable biomass production, Blue Growth, profitability, as well as socioeconomic benefits that bivalve culture provides to near shore coastal communities.

The overarching goal of the SusAqua Project is to advance biomass production of Irish mussel and oyster stocks by (a) promoting reproductive output in mussels, *Mytilus* spp., and native oysters, *Ostrea edulis,* by better understanding the impact that pathogens and disease have in all life stages of production and the environmental triggers that promote fecundity, (b) assessing the stimulatory role of seaweed species, their biocompounds and the essential trace mineral selenium have on gonad development and their antimicrobial properties, (c) supporting the capture and grow out of seed using Biodegradable Ecosystem Engineering Elements (BESE) that are more resilient to pathogens and disease, which will contribute to offspring that will be less susceptible to infectious agents, and (d) investigating the role of antimicrobial photodynamic therapies (aPDT) in promoting the survival of all bivalve life stages (larvae, seed/spat, broodstock) and the reduction of pathogenic bacteria and protozoa in a hatchery setting.

LIVING IN A FRAGMENTED, PATCHY WORLD: THE ROLE OF SEAGRASS BED EDGES AND SEMI-INFAUNAL BIVALVES IN SEA URCHIN HABITAT SELECTION

Raymond Czaja Jr[1]* and Christopher Pomory[2]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

[2]University of West Florida, Department of Biology, Building 58C, Suite 104, 11000 University Parkway, Pensacola, FL 32514

raymond.czaja@stonybrook.edu

Anthropogenic disturbances (habitat fragmentation) disrupt seagrass beds and increase the availability of seagrass bed edges. Microhabitat selection and substrate use were examined for edge effects of the seagrass-associated sea urchin *Lytechinus variegatus* in St. Joseph Bay, Florida. Additionally, the roles of semi-infaunal bivalves (mussels and pen shells) and seagrass characteristics (shoot density, blade length, and epiphytes) in habitat selection were investigated. Monthly field surveys were conducted in *Thalassia testudinum* beds from June 2017 to May 2018. Microhabitat use was quantified by measuring faunal abundances in interior seagrass, sandflat, and edge (the seagrass-sandflat interface) habitats. Substrate use by *L. variegatus* was quantified relative to semi-infaunal bivalves and seagrass substrate. Density of *L. variegatus* was highest in interior seagrass habitat. Seagrass shoot and semi-infaunal bivalve densities were higher in interior seagrass habitat. Sea urchins displayed a preference for mussel substrate, suggesting that mussels may be affecting the spatial distribution of *L. variegatus*. The results have implications for seagrass overgrazing events and seagrass-associated faunal responses to habitat destruction and fragmentation.

EFFECTS OF CHANGING HABITAT ON CONDITION INDEX AND GROWTH OF BLUE MUSSELS (*MYTILUS EDULIS*) AND RIBBED MUSSELS (*GEUKENSIA DEMISSA*): A RECIPROCAL TRANSPLANT EXPERIMENT

Mya A. Darsan[1], Tyler W. Griffin*[2], and J. Evan Ward[2]

[1]University at Albany, Department of Biological Sciences, 1400 Washington Avenue, Albany, NY 12222

[2]University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Road, Groton, CT 06340

tyler.griffin@uconn.edu

Marine bivalves are prevalent suspension-feeders in near-shore environments that act as ecosystem engineers. Blue mussels (*Mytilus edulis*) inhabit intertidal zones of open coasts and attach to hard substrates; ribbed mussels (*Geukensia demissa*) inhabit intertidal salt marshes and attach to plant roots. While physiological and ecological aspects of both species are well-studied, their response to a sudden change in habitat is not. The project goal was to perform a 4-week reciprocal transplant with *M. edulis* from UConn Avery Point docks and *G. demissa* from Barn Island salt marsh in Connecticut to evaluate the impact on the gut microbiome, percent shell growth and condition index. Environmental parameters were recorded throughout the experiment. Barn Island displayed variable conditions and higher temperature, total suspended solids, and chlorophyll-*a*. The transplant resulted in no significant change to condition index for either species. A significant reduction in shell growth for *M. edulis*, but not for *G. demissa* was observed. *G. demissa* displayed resilience to the change in environment which indicates they acted as habitat generalists. High seawater temperatures observed at Barn Island can explain the reduction in shell growth for translocated *M. edulis*. Notably, the condition index of *M. edulis* did not change in response to the transplant, which may imply that mussels were successfully meeting their basal nutritional needs, but allocated energy towards physiological activities other than shell growth. These results serve to better inform how mussels may respond to climate change and how their ecological roles may be impacted.

BALANCING HEALTH RISKS AND BENEFITS OF RED MANGROVE CRAB CONSUMPTION

Andrée De Cock*, Marie Anne Eurie Forio, Siska Croubels, Luis Dominguez-Granda, Liesbeth Jacxsens, Carl Lachat, Heydi Roa-López, Jenny Ruales, Victoria Scheyvaerts, Michelle Carolina Solis Hidalgo, Pieter Spanoghe, Filip M.G Tack, and Peter L.M. Goethals

Ghent University, Department of Animal Sciences and Aquatic Ecology, Faculty of Bioscience Engineering, Coupure Links 653, 9000, Ghent, Belgium

andree.decock@ugent.be

Mangrove forests provide vital food resources and are an endangered ecosystem worldwide due to pollution and habitat destruction. A risk-benefit assessment (RBA) on the red mangrove crab (*Ucides occidentalis*) from the Guayas mangroves in Ecuador was performed. The objective was to evaluate the combined potential adverse and beneficial health impact related to crab consumption and defined a recommended safe intake (SI) to ensure safe food intake. Target hazard quotients (THQ), benefit quotients (BQ), and benefit-risk quotients (BRQ) were determined based on the concentrations of the analyzed contaminants (121 pesticide residues, 11 metal(loid)s, and 3 classes of antimicrobial drugs) and nutrients (fatty acids, amino acids, and essential nutrients).

Except for inorganic arsenic (iA), the THQ was below 100 for all contaminants, suggesting that the average crab consumer is exposed to levels that do not introduce negative non-carcinogenic or carcinogenic health effects in the long and/or short term. Concentrations of inorganic arsenic were of concern due to its potential to induce negative health effects on long-term consumption. Based on different risk reference values, related to different safety levels, four SI values (0.002, 0.04, 4, and 18 crabs/day) were obtained. The highest safety level advice against consumption and indicates a concern for current consumption habits.

In conclusion, the red mangrove crab consists of various essential nutrients and can be part of a balanced diet for the Ecuadorian population when consumed in limited portions. This study highlights the importance of protecting the quality of the environment as a prerequisite for acquiring nutritious and safe food.

TESTING THE SURVIVABILITY OF THE NEOPLASTIC CELLS OF *MERCENARIA MERCENARIA* UNDER VARIOUS SALINITIES

Casey M. Dunbar*[1], Abigail K. Scro[2], and Roxanna M. Smolowitz[3]

Aquatic Diagnostic Laboratory, Roger Williams University, 1 Old Ferry Road, Bristol RI 02809

cdunbar941@g.rwu.edu

Hemic Neoplasia (HN) is a contagious, leukemic-like disease that affects bivalves primarily along the East Coast of the United States. As the disease progresses within the organisms, neoplastic cells proliferate in the hemolymph (blood) and fill the vascular system causing significant mortality of cultured northern quahogs (=hard clams) (*Mercenaria mercenaria*). Laboratory research has shown HN is contagious to naïve clams and that it spreads between animals most likely by neoplastic cells within the water column that were expelled from infected individuals.

The study focused on testing the survivability of cells exposed to various salinities in the water column. Exposure treatments, conducted in cell culture plates, were prepared with hemolymph from neoplastic clams (>70% HN) and seawater adjusted to salinities of 0, 10, 20, 25, 30, 35 and 40 ppt. Temperature and pH were recorded and kept constant. An Erythrosin B stain was added to the plate and left to sit for 15 minutes, before counting the live hemocytes using a hemocytometer. The results from an ANOVA test displayed that the differences between the means of each salinity were statistically significant ($p = 0.006$). The information collected from this study will help to further describe the neoplastic cells and, more importantly, will aid in understanding the epidemiology concerning environmental conditions under which the neoplastic cell spreads from one animal to another at a bivalve culture site.

STUDY OF ANTIMICROBIAL PEPTIDES IN THE SALINITY STRESSED HONG KONG OYSTERS, *CRASSOSTREA HONGKONGENSIS*

Mohamed Madhar Fazil*, Kanmani Chandra Rajan, and Vengatesen Thiyagarajan

The University of Hong Kong, School of Biological Sciences, Kadoorie Biological Sciences Building, Pok Fu Lam Road, Hong Kong SAR, China

fazilsmm@connect.hku.hk

Oysters are considered a highly esteemed seafood delicacy worldwide and are well-known for their rich protein content. Oyster aquaculture in Hong Kong is known for its cultural heritage of 700 years. Hong Kong oyster, *Crassostrea hongkongensis,* contributes one-fourth of the global oyster production; however, the effect of high salinity stress, along with other stressors, causes these filter-feeding bivalves to strive hard in the fluctuating coastal environment. Recent research concludes that immune response and antioxidant peptides influence adaptability from low to high salinity gradient. Short bioactive peptides (<10 kD) are being actively studied for their role in host innate defences and antioxidant properties in both invertebrates and vertebrates. The role of bioactive peptides in the perception of high salinity stress has yet to be fully understood. This work focuses on unveiling novel peptides responsible for salinity tolerance in *C. hongkongensis* that are involved in immune response and antioxidant properties.

MULTIPLE COASTAL STRESSORS INDUCE DIFFERENTIAL RNA EXPRESSION IN LARVAL OYSTERS

Megan E. Guidry[1]*, Kathleen E. Lotterhos[2], Johanna A. Harvey[3], Margaret E. Schedl[4], and Jonathan B. Puritz[4]

[1]University of Rhode Island, Biological and Environmental Sciences, 120 Flagg Road, Kingston, RI 02881

[2]Northeastern University, Department of Marine and Environmental Sciences, 430 Nahant Road, Nahant, MA 01908

[3]University of Maryland, Department of Environmental Science and Technology, 1443 Animal Sciences Bldg, College Park, MD 20742

[4]University of Rhode Island, Department of Biological Sciences, 120 Flagg Road, Kingston, RI 02881

mguidry@uri.edu

The high concentration of human populations and development in coastal areas has dramatically impacted ecosystem quality for shellfish, particularly at the vulnerable larval stage. While many studies have investigated the effects of stressors (i.e., acidification, temperature, nutrient loading, salinity changes) these stressors do not occur in isolation. There is still not a comprehensive, mechanistic understanding of how multiple stressor environments impact shellfish populations. Urbanized estuaries are particularly susceptible to complex changes in water chemistry. Nutrient input (from sewage effluent (SE)) increases CO_2 (from increased respiration) leading to coastal acidification (CA). There is a need to understand how populations in heavily influenced estuaries are impacted by these co-occurring multiple stressors (CA and SE) particularly at the larval stage where populations can experience major bottlenecks. This study examined the impact of CA and SE (independently and coupled) on the mRNA expression of larval eastern oysters. In the summer of 2017, replicate mesocosms of ~125,000 trochophore larvae were exposed to one of 4 different treatments for 24 hours. The four treatments were Control (CON), CA, SE, and CASE (combined CA & SE). Pre- and post-exposure larval samples were flash-frozen preserving DNA/RNA. Treatments were analyzed using differential gene expression analysis and WGCNA. These findings will help describe mechanistic underpinnings of multi-stress response in the larval stage of a valuable shellfish species.

THE MANGROVE ACTION PROJECT EDUCATION OUTREACH AIMS TO CONSERVE AND RESTORE VITAL MARINE SHELLFISH HABITAT

Monica Gutierrez-Quarto* and Alfredo Quarto

Mangrove Action Project, PO Box 1854, Port Angeles, WA 98362-0279

monicagquarto@olympus.net

Since its inception in 1992, the Mangrove Action Project (MAP, www.mangroveactionproject.org) has aimed to raise awareness about the need to conserve and restore mangrove forest wetlands - vital habitat for a wide array of marine life, including shellfish. The MAP Community-based Ecological Mangrove Restoration (CBEMR) training courses, the Marvelous Mangrove Curriculum, and the MAP annual Children's Mangrove Art Contest, along with the biweekly MAP News, all combine to raise awareness through education and training in order to conserve and restore coastal wetlands where shellfish and other marine life thrive.

The MAP annual Children's Mangrove Art Contest connects children from all corners of the Earth to mangrove forests, through an educational and creative competition. It is an opportunity for the younger generation to feel a connection with the natural world and to learn about the vital role mangroves play to both communities and our environment. The 2022 competition had over 350 entries from 34 countries and included some brilliant artwork of mangrove trees and associated wildlife, underwater scenes, and community life unique to the countries and cultures they depict. Many of the artworks include images of shellfish which play an important dietary role for local communities. Many participants, their schools and representative NGO offered feedback on how important the children's art competition is. A past participant stated, 'I find this competition a wonderful way of encouraging children all over the world to know more about the mangroves!' The incredible artwork has resulted in our 2023 Children's Mangrove Art Calendar-one of our most beautiful calendars to date (https://mangroveactionproject.org/shop/2023-map-mangrove-art-calendar/).

A STUDY OF “WINTER MORTALITY SYNDROME” IN HONG KONG OYSTER, *CRASSOSTREA HONGKONGENSIS,* IN THE DEEP BAY

Lee Tin Hang*, Xin Dang, and Vengatesen Thiyagarajan

The Swire Institute of Marine Science and School of Biological Sciences, Area of Ecology and Biodiversity, and State Key Laboratory of Marine Pollution, The University of Hong Kong, Hong Kong Special Administrative Region, China

davidlth@connect.hku.hk

There are many challenges in the rapidly growing aquaculture industry around the globe. Repeatedly occurring mass mortality events are one of the main obstacles found in modern aquaculture. The study of such events is extremely crucial for the development of both long-term and short-term mitigation strategies. The Hong Kong oyster, *Crassostrea hongkongensis,* is an important commercial edible oyster that is widely cultured in Hong Kong and southern China. One main challenge and perhaps the most threatening one to this oyster aquaculture industry in Hong Kong is the “Winter Mortality Syndrome” (WMS). WMS in Hong Kong is something that has never been scientifically studied before and its cause and result are only speculated by oyster growers. The common believe amongst oyster growers is that high salinity environment during the winter season will lead to a mass mortality in oysters. Field observation confirmed that a 90% mortality occurred between January to April. Histopathology examination did not show bacterial infection or microscopically identifiable parasites in the mantle and gill area. 18s metagenomics revealed a few potential pathogens and further confirmation via PCR is still undergoing. After reviewing other oyster mass mortality events across the world in combination with the Hong Kong winter mortality observations and molecular analysis, it is suspected that an unknown pathogen in combination with the change in environmental condition is the main cause of the WMS happening in Hong Kong.

EFFECT OF PROBIOTIC ADDITION TO *ARGOPECTEN IRRADIANS* LARVICULTURE ON OVERALL SURVIVAL AND GROWTH WITH DEAD OR LIVE ALGAL INTERACTION

Morgan Hawkins*, Bailey Kilroy, and Sandra Brooke

Florida State University Coastal and Marine Laboratory, 3618 US-98, St Teresa, FL 32358

Mhawkins@bio.FSU.edu

Harmful marine bacteria can cause an infection called vibriosis in larval shellfish. These diseases normally remain undetectable until much of the culture is lost. Shrimp hatcheries commonly use probiotics to combat this issue, but they have not been widely adopted by other shellfish hatcheries. Probiotics present viable spores or live micro-organisms that can maintain balanced ‘healthy’ microbial communities. Probiotics will not remove harmful bacteria, but instead introduce dormant bacteria spores to grow in the culture and out-compete them. Florida State University Coastal and Marine Laboratory (FSUCML) research hatchery has completed a pilot study on the effect of probiotic addiction to larval bay scallop (*Argopecten irradians*) culture with an interaction of food type. The probiotic tested contained strains of *Bucellis* sp. which help combat larval disease. They inundate larval cultures with beneficial bacteria that colonize the gut of at-risk shellfish to help aid digestion, as well as increase immune response to pathogens. Results of the pilot study were promising and suggested an increase in survival and growth, but further experimentation is necessary. Preliminary results, discussion of the feasibility to implement probiotics into commercial hatcheries, and future directions and further experimentation at FSUCML research hatchery will be presented.

TONG DEPLETION SAMPLING FOR OYSTER HABITAT ASSESSMENT AND MONITORING: A QUANTITATIVE AND COST-EFFECTIVE ALTERNATIVE TO QUADRAT DEPLETION SAMPLING

Lauren L. Hintenlang*, Ross Brooks, and Andrew S. Kane

University of Florida, Department of Environmental and Global Health, 2173 Mowry Road, Gainesville, FL 32611

llhinten@ufl.edu

Oyster habitat assessment and monitoring have become increasingly important and in greater demand with the notable decline of oyster populations, increased funding, and the resultant heavy focus on restoration. Coastal resource managers tasked with monitoring oyster habitat to assess population size and structure are, however, resource limited, precluding appropriate monitoring schedules and limiting knowledge of restoration outcomes.

This study validated tong depletion sampling as a cost-effective, quantitative alternative to “gold-standard” quadrat depletion sampling using SCUBA diving. Replicate depletion samples were collected from six managed oyster reef habitats in Apalachicola Bay, Florida. Oyster population dynamics discerned using tong and quadrat depletions at four of the six study sites were statistically indistinguishable. Further workup of the two study sites (East Hole and Hotel Bar) where the Kolmogorov-Smirnov test output ($p<0.05$) suggested rejection of the null hypothesis (that both tong and quadrat sampling approaches yield the same population size and density data) indicated that one site (East Hole) could be interpreted as a Type I error, while the other (Hotel Bar) only had significant differences between the depletion sampling approaches (Wilcoxon signed-rank test $p<0.05$) in two size bins, 51-75 mm and >75 mm.

It can be concluded that standardized tong depletion and quadrat depletion sampling approaches produce equivalent monitoring data for all size bins in the majority of study sites. Hand tong depletion sampling makes oyster habitat assessment and monitoring more accessible and less costly for resource managers, supporting monitoring compliance and facilitating restoration.

EVALUATION OF FOUR SELECTIVELY BRED TETRAPLOID LINES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Jillian Jamieson*, Samuel Ratcliff, and Ximing Guo

Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6959 Miller Ave, Port Norris, NJ 08349

jillian.jamieson@rutgers.edu

Tetraploids are organisms with four sets of chromosomes. They can mate with normal diploids and produce 100% triploids that have three sets of chromosomes. Tetraploids were first produced in the Pacific oyster and subsequently proven to be highly effective in triploid production. In this study, four tetraploid lines (WX1-WX4) were produced and evaluated along with one selected (22N7) and one wild (22DW) diploid controls. The four tetraploid and two diploid groups were spawned at the Rutgers Cape Shore Facility in June 2022 and were deployed in three replicate bags on Cape Shore flat once the individuals reached 4 mm in length. All groups were sampled (50 per group) and measured in November 2022 to compare the relative growth. No difference in mortality was observed, which was low in all groups.

The four tetraploid crosses showed significantly higher whole weights compared to the wild control, with a mean of 3.25 g. The wild control had significantly lower whole weights, with means of 2.44 g. The same patterns can be seen in the mean heights, with the tetraploid groups having a mean of 32.3 mm, and the wild control having a mean of 26.5 mm. These results indicate tetraploid oysters grow faster than the wild oysters at juvenile stage, which is an improvement over early generations of tetraploids. The tetraploids did not grow as fast as the selected line and may be improved further through continued selective breeding.

EVALUATION OF PARALYTIC SHELLFISH TOXIN CONGENERS IN BIVALVES FROM RESURRECTION BAY, ALASKA 2021-2022

Annette Jarosz[1]*, Maile Branson[1], and Shannon Atkinson DeMaster[2]

[1]Chugach Regional Resources Commission, Alutiiq Pride Marine Institute, 101 Railway Ave, Seward, AK 99664

[2]University of Alaska Fairbanks, Fisheries Department and Institute of Marine Science, 17101 Pt. Lena Loop Rd., Juneau, AK 99801

annette@alutiiqprideak.org

The presence of algal biotoxins in Alaska marine waters threatens food security and public health by reducing the safety of shellfish resources. Paralytic shellfish poisoning (PSP), caused by a suite of neurotoxins collectively known as paralytic shellfish toxins (PST), is the most severe biotoxin problem in Alaska. The PST produced by the marine dinoflagellate, *Alexandrium,* are regularly detected in Alaska shellfish at levels unsafe for human consumption. Illness and death have been attributed to PSP in Alaska for centuries, yet there is still limited capacity for PST testing for culturally important shellfish species.

Toxicity and retention of PST vary across shellfish species. Due to this variation, having species-specific information is critical for determining risk levels of harvesting wild shellfish. Alutiiq Pride Marine Institute (APMI), a major subsidiary of the Chugach Regional Resources Commission, is working to monitor PST in subsistence and recreational harvest of shellfish for the Southcentral region of Alaska. From April to September of 2021 and 2022, APMI staff collected bi-weekly samples of three different bivalve species: blue mussels (*Mytilus edulis*), soft-shell clams (*Mya arenaria*), and cockles (*Clinocardium nuttallii*) (n = 83) from a local beach in Resurrection Bay. These samples were analyzed by the Department of Environmental Conservation using high-pressure liquid chromatography. This method identifies 12 PST congeners allowing us to understand which congeners are most abundant in our local ecosystem and identify the risk level to harvesters in Resurrection Bay. Additionally, the two-year time series will help us identify toxin retention time in each bivalve species.

IMPACT OF FLUCTUATING PH ON PRODUCTION OF *MERCENARIA MERCENARIA* POST-SET IN AN IMTA SYSTEM

Meghan Keough*[1], Jade Salis[2], David Bradshaw[1], Richard Baptiste[1], and Susan Laramore[1]

[1]Harbor Branch Oceanographic Institute at Florida Atlantic University, Center for Aquaculture and Stock Enhancement, 5600 US 1 North, Fort Pierce, FL 34946

[2]Coastal Carolina University, Gupta College of Science, Conway, SC 29528

mkeough2021@fau.edu

The land-based IMTA system at Harbor Branch (HBOI-LB-IMTA) utilizes various fed, assimilative and extractive components. Bivalves are good extractive candidates for this system due to their filtering capabilities. The importance of the northern quahog (=hard clam), *Mercenaria mercenaria,* to aquaculture industry in Florida makes it a natural choice for this system. Maintaining a stable environment is important for consistent production, yet this system is subject to large pH swings. These fluctuations may lead to stress and decreased production. To better understand the impact of pH on post-set clam production, a short-term eight-week study examined the effects of stable (low, high) and fluctuating pH levels.

Three-week-old clam post-set (1,200±75, 537±85 µm) were added to one of three treatments, 8.0, 7.4 or fluctuating pH (N=5 replicates) and fed *Tisochrysis lutea* and *Chaetoceros neogracile* twice daily. Dissolved oxygen, temperature, and salinity were monitored daily and pH continuously. Ammonia, nitrite, and alkalinity were measured weekly. Growth was evaluated bi-weekly, and survival, condition index, bacterial analysis, and shell composition at experimental termination. Growth was significantly lower at pH 7.4 ($P \leq 0.05$). No difference was seen in survival or condition index. Total bacterial ($P \leq 0.05$) and *Vibrio* ($P \leq 0.012$) counts were higher at pH 7.4. Clams subjected to fluctuating pH levels had higher calcium and strontium levels. These results indicate that post-set clams are not affected by fluctuating pH levels inherent in the LB-IMTA system. These results have implications for wild or cultured clams in estuarine ecosystems subjected to pH fluctuations and confirm the negative impacts of low pH.

DIEL-CYCLING HYPOXIA AND ACIDIFICATION INCREASES SUSCEPTIBILITY TO ROSEOVARIUS OYSTER DISEASE IN *CRASSOSTREA VIRGINICA*

Katrina Kulesh[1]*, Amaelia Zyck[1], Jonathan Puritz[1], and Marta Gómez-Chiarri[2]

[1]University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd., Kingston, RI 02881

[2]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, 120 Flagg Rd., Kingston, RI 02881

katrina_kulesh@uri.edu

Roseovarius oyster disease (ROD) impacts eastern oyster, *Crassostrea virginica,* nurseries along the Northeast Coast of the United States of America. Its presence typically results in notable juvenile (<25mm shell size) oyster mortality, especially in nursery upwellers in shallow water bodies with little circulation, e.g., marinas and inlets. It is hypothesized that exposure of juvenile oysters to diel cycling hypoxia and acidification increases susceptibility to ROD. Larval oysters were exposed to either control or diel-cycling hypoxia and acidification conditions from 2 to 10 weeks of age. After this period, all oysters were acclimated to control seawater conditions, and each replicate was split into two groups. Upon acclimation, *Aliiroseovarius crassostreae* CV919-312, the causative bacterial agent of ROD, was inoculated into the ROD-challenge group and mortality was recorded over three weeks. Pre and post ROD-challenge samples were taken for protein and genotype analysis. With 95% confidence, mortality ranged from 8.4% +/- 1.8% in the control no-ROD group to 61.3% +/- 11.9% in the diel-cycling-exposure ROD-exposed group. The diel-cycling no-ROD and the control ROD-exposed groups showed 21.4% +/- 8.5% and 24.2% +/- 7.0% mortality respectively. These results indicate that exposure to diel cycling hypoxia and acidification during larval and juvenile stages increases susceptibility to ROD. The factorial design of this experiment will provide insight into *C. virginica* genotypes associated with tolerance to the stand-alone and combined factors of ROD and diel-cycling hypoxia and acidification. This research will inform selective breeding programs for eastern oysters in the Northeast US.

SCEMFIS 2022: A YEAR IN REVIEW

Kelsey M. Kuykendall[1]*, Eric N. Powell[1], Roger Mann[2], and Karen Reay[2]

[1]University of Southern Mississippi, Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, MS 39564

[2]Virginia Institute of Marine Science, William and Mary, 1375 Greate Road, Gloucester Point, VA 23062

Kelsey.kuykendall@usm.edu

The Science Center for Marine Fisheries (SCEMFIS) is a National Science Foundation (NSF)-funded industry/university cooperative research center (I/UCRC) established in June 2013. SCEMFIS has two sites: The University of Southern Mississippi (USM) and Virginia Institute of Marine Science (VIMS). Since 2013, SCEMFIS has grown to include researchers from USM, VIMS, Cornell University, Rutgers University, University of Rhode Island, University of Maryland Center for Environmental Science, The University of Massachusetts-Dartmouth, University of Texas-Austin, and Old Dominion University, along with other U.S. and Canadian academics and consultants and 14 industrial partners. SCEMFIS provides NSF sanctioned research to meet the needs of industry partners with the goal being sustainability of both the shellfish and fish stocks and their associated fisheries. Achievements for SCEMFIS graduate students in 2022 include four non-academic graduate student research internships placed in member companies and the NMFS. Additionally, SCEMFIS was awarded 9 REU and Veterans supplements. SCEMFIS awarded over $400,000 in research grants in 2022, with projects including research on surfclam and ocean quahog growth and age-frequency distributions, the influence of wind energy development and climate change on mid-Atlantic shellfish fisheries, several forage fish projects emphasizing menhaden, economic studies of the menhaden and summer flounder fisheries, and development of improved gear for commercial and survey applications for the surfclam and ocean quahog resource. SCEMFIS is looking back at a successful year and forward to more progress in 2023 as more academics and industries become involved with the Center and its ongoing projects.

HIGH-SENSITIVITY ELISA TEST FOR DETECTION OF DOMOIC ACID IN SHELLFISH AND FISH AQUACULTURE

John Lance, Fernando Rubio, and Boris Polyak*

Gold Standard Diagnostics Horsham, Inc. 124 Railroad Drive, Warminster, PA 18974

Boris.Polyak@us.goldstandarddiagnostics.com

Domoic acid is a naturally occurring toxin produced by certain types of algae. Shellfish and fish can accumulate domoic acid without apparent ill effects leading to harmful or fatal consequences for humans consuming contaminated seafood. Because there is no antidote for domoic acid, which causes Amnesic Shellfish Poisoning (ASP) manifested by vomiting, nausea, diarrhea, and abdominal cramps followed by neurological symptoms, there is a critical need to monitor levels of domoic acid in shellfish aquacultures and fisheries for the safe seafood consumption quality. The regulatory level in shellfish is 20 mg/kg tissue.

This study evaluated a sensitive enzyme-linked immunosorbent assay (ELISA) for quantitatively detecting domoic acid in shellfish meat and water samples, including drinking water, freshwater, and seawater. The domoic acid ELISA allows the determination of 41 samples in duplicates, while only a few milliliters of samples are required for testing in less than two hours. No false positive or negative results were observed on numerous shellfish samples, including clams and mussels. After extraction and dilution, the domoic acid ELISA test sensitivity for shellfish is 150 ppb (parts per billion, i.e., 15-µg domoic acid per 100g sample). The domoic acid ELISA test sensitivity for freshwater and drinking water was determined to be 6.50 ppt (parts per trillion) and 3.75 ppb for seawater samples after necessary dilution.

This study demonstrates that sensitive domoic acid ELISA is suitable for analyzing seafood, freshwater, and seawater samples, alerting the presence of the algal toxin and preventing ASP in humans.

CLASSIFICATION OF OYSTER SANCTUARIES AND HARVEST AREAS IN THE CHESAPEAKE BAY, MARYLAND, USA

Amy B. Larimer*, Frank Marenghi, and Laurinda Serafin

Maryland Department of Natural Resources, Shellfish Division, 580 Taylor Ave., Annapolis, MD 21401

amy.larimer@maryland.gov

The relative oyster productivity of 51 sanctuaries and 39 harvest areas were examined using data from the Maryland Department of Natural Resources Annual Fall Oyster Dredge Survey (Fall Survey). The goal was to develop criteria to evaluate the performance of sanctuaries and harvest areas and develop a classification system based on those criteria. Data collected within a ten-year period (2011 to 2020) was used to classify oyster sanctuaries and harvest areas according to several metrics: density of market (≥76 mm), small (1+ yr. and <76 mm), and spat (<1 yr.) oysters, volume of cultch, and observed mortality from box counts (empty but articulated valves). Values of the metrics were sorted into ranks and the ranks combined to give a final score. Based on that score, each sanctuary and harvest area were classified into levels A-E, with 'A' being the best performing area, 'D' being the worst performing area, and 'E' was reserved for areas with insufficient data. Based on this method, the top performing sanctuaries were St. Marys River, Nanticoke River, Manokin River, Harris Creek, and Little Choptank River sanctuaries. The top harvest areas were Broad Creek, Fishing Bay, Pocomoke Sound, Tred Avon River, and the northern portion of Tangier Sound.

SEASONAL VARIATIONS OF HEMOCYTE ACTIVITIES IN DIPLOID AND TRIPLOID EASTERN OYSTERS

Joshua M. Lee*, Christopher J. Brianik, and Bassem Allam

Stony Brook University, School of Marine and Atmospheric Sciences, 100 Nicolls Rd, Stony Brook, NY 11794

Joshua.m.lee@stonybrook.edu

Triploid oysters are becoming an increasingly popular aquaculture product as their associated sterility leads to enhanced available energy and improved growth rates. Although triploids represent the largest fraction of oyster production in many regions, very little is known about how basic aspects of their biology (sterility, larger cells, increased energy reserves) may influence immune parameters and activity. In this study, half-sibling triploid and diploid oysters were collected every six weeks throughout the reproductive period and hemolymph was harvested and used for the assessment of hemocyte activities. Flow cytometry was used to analyze hemocytes for the production of reactive oxygen species (ROS), phagocytosis, cell viability, mitochondrial counts, and mitochondrial potential. ROS production and mitochondrial potential were significantly higher in triploid granulocytes as compared to diploids during the pre-spawn spring period. Hemocyte phagocytic activity was also significantly greater (~20%) in triploids when compared to diploids during the pre-spawn period. While the phagocytic activity of triploid hemocytes remained consistent throughout the reproductive season, diploid hemocytes became phagocytically more active as time progressed. Despite the typically larger size of triploid cells, no significant difference was observed in the number of mitochondria per cell when compared to diploids. Taken together, results show that differences in immune parameters and activities seem to be the most pronounced between triploids and diploids during the pre-spawning period, with convergence of immune parameters occurring during spawning, post-spawning, and recovery periods. Further understanding the nuances of triploid immunological responses throughout the seasons may help improve triploid oyster production.

REGRESSION ANALYSIS OF SHELLFISH YIELD WITH PHYSICOCHEMICAL PARAMETERS AND ELEMENTS IN THE VEMBANAD LAKE ECOSYSTEM, INDIA

Joe Prasad Mathew and Sobha Merina George*

St. Berchman's College, Department of Zoology, Changanacherry, Kottayam, Kerala 686101, India

georgesobhamerina@gmail.com

Vembanad Lake is an estuarine lake in Kerala, India (9.5968° N, 76.3985^0E). Five freshwater rivers flow into Vembanad lake and the lake opens into the Arabian sea. This study was conducted for three years. The objective of the study is to predict the future shellfish availability based on the independent variables in the future. The shellfish species in Vembanad Lake comprises of six species: *Fenneropenaeus indics, Metapenaeus indicus, Penaeus monodon, Macrobrachium rosenbergii,* and *Cardina naderjoni*. There was a statistically significant relation or in predicting the independent variables such as Mn, Cu, Fe, Na, K, Mg, Ca, and dissolved oxygen, biochemical oxygen demand, pH, salinity, and temperature.

The shellfish yield of *F. indicus* was statistically predicted from the independent variables temperature and dissolved oxygen at $F_{(2,34)} = 10.269$, $p<0.05$, $R^2 = 0.384$, where all other independent variables were showed insignificant relationship. *M. indicus* yield is statistically significantly predicted, FY, $F_{(2,34)} = 7.640$, $p<0.05$, $R^2 = 0.316$ from the variables such as temperature and Na. All other species were predicted from the temperature level. In conclusion, the future shellfish availability in the Vembanad Lake ecosystem is dependent on available temperature, dissolved oxygen, and sodium.

STIMULATION OF MANTLE RIM SENSORY TENTACLES BY ALGAE AFFECTS GILL CILIA BEATING IN THE BIVALVE MOLLUSC, *CRASSOSTREA VIRGINICA*

Ashanti McFarlane[1]*, Victory Obianke[2], Bassem Allam[3], Emmanuelle Pales Espinosa[3], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

[3]Stony Brook University, School of Marine and Atmospheric Sciences, 145 Endeavour Hall, Stony Brook, NY 11794

ashantimcfarlane18@gmail.com

Gill lateral cell (GLC) of Crassostrea virginica are innervated by serotonin and dopamine nerves from the ganglia. The motor aspects have been well studied, the sensory side has not. Limited information is available about sensory inputs. Oysters are suspension-feeders, selecting food from their environment and transporting it via the gills and labial palps to the mouth, and typically eat a few species of microalgae, including *Tisochrysis lutea* and *Thalassiosira weissflogii*. To study if mantle rim sensory tentacles detect algae and send information to the visceral ganglia (VG) to activate a motor response affecting GLC cilia beating was tested by applying *T. lutea* and *T. weissflogii* to the mantle rim and measuring GLC cilia beating using stroboscopic microscopy, with and without cutting the pallial nerve that innervates the mantle rim from the VG. Whole animal preparations with shells removed were positioned in chambers so solutions could be applied to the mantle rim without coming in contact with the gills. Applying *T. lutea* and *T. weissflogii* to the mantle rim increased cilial beating. In experiments where the pallial nerve was cut, applying algae to the mantle did not increase cilial beating. Likewise, applying algae directly to isolated, denervated gill sections did not increase cilial beating. The results demonstrate a sensory-motor integration of mantle rim sensory information and beating of GLC cilia involving the mantle rim and VG. This study shows the animals can sense edible algae and adjust GLC cilia beating appropriately to increase feeding. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP and PSC-CUNY 62344-0050 and 62344-0051.

GENOMIC VARIABILITY IN MARINE MUSSELS FROM THE GENUS *MYTILUS*

Manuel Mendoza[1,2]*, Carlos A. Canchaya[1], and Ximing Guo[2]

[1]Marine Research Centre, Comparative Genomics Laboratory, School of Marine Sciences, Universidade de Vigo, Rua Fonte das Abelleiras S/N, Vigo 36310, Spain

[2]Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, NJ 08349, USA

manuel.sanchez.mendoza@gmail.com

Marine mussels from the genus *Mytilus* have the highest levels of genomic variability described in eumetazoans. These astonishing amounts of variants could provide an evolutionary profit to adapt to the environmental changes that are happening in the oceans induced by anthropogenic activities. Although the genomic variability of mussels has been quantified using multiple techniques, the new high-throughput sequencing data and the availability of reference genomes have unveiled the cryptic variants, making heterozygosity and nucleotide diversity estimates more accurate. The three European species, *M. edulis*, *M. galloprovincialis* and *M. trossulus*, all showed similar heterozygosity levels from 10% to 15%. Conversely, *M. trossulus* has a higher nucleotide diversity than the other species. Classifying the single nucleotide variants obtained by their genomic position, most of them (more than 90%) came from the intergenic regions. For protein-coding genes, untranslated regions and splice sites were most conserved, suggesting that mRNA processing performance and post-transcriptional regulation may play an essential role in the potential response of mussels to external stimuli. Finally, the analysis of the genes under selective pressure ($piN/piS \gg 1$) yield more information about the impact of ocean change on marine mussels, including pressure on the gills (response to external stimuli, multi-xenobiotic resistance, and the maintenance of ciliary structures).

INSIGHT INTO A GENETIC ANALYSIS OF RESISTANCE IN MUSSELS TO ABNORMAL MUSSEL MORTALITY (AMM) IN FRANCE: FIELD AND LAB EXPERIMENTS

Ajithkumar Munusamy[1]*, Marie Lillehammer[2], Marie-Agnès Travers[3], Elise Maurouard[1], Muhammad Luqman Aslam[2], and Lionel Dégremont[1]

[1]Ifremer ASIM, Avenue Mus de Loup, 17390 La Tremblade, France

[2]Breeding and Genetics Nofima, Osloveien 1, 1430 Ås, Norway

[3]IHPE, Université de Montpellier, CNRS, IFREMER, Univ Perpignan Via Domitia, Montpellier, France

Ajithkumar.Munusamy@ifremer.fr

Since 2014, abnormal mussel mortality (AMM) outbreaks started along the French Atlantic coasts and mortality rates differed among years and sites (30-100%). Still, the etiology of the AMM is undefined. This research explores the resistance of two mussel species (*Mytilus edulis* and *M. galloprovincialis*) and natural hybrids (NH) cultivated in France to AMM. 100 mussel families produced by using six wild mussel populations in January/February 2017. Mussels were tested in two sites [La Floride (LF) and Maison Blanche (MB)] in October 2017, and their survival/growth was documented until June 2018. AMM was only observed at MB during spring 2018, and reached 70%, 43%, and 63%, for *M. edulis*, *M. galloprovincialis*, and NH, respectively, at the endpoint. In contrast, low mortality was observed in LF, reaching 11%, 30%, and 22%, respectively. Heritability for survival was low to moderate in both sites and it ranged from 0.06 to 0.34. Significant genotype-by-environment interaction for survival between sites was found with low and not significant genetic correlations (-0.05 to 0.43). In October 2018, experimental infection was performed for 100 families using a pathogenic strain of *Vibrio splendidus* isolated during AMM in 2014. The mean mortality after 72 hours post-infection was 53%, 22%, and 31% for *M. edulis*, *M. galloprovincialis*, and NH, respectively. The lowest heritability was noticed for NH (0.15) and highest for *M. galloprovincialis* (0.38), and the genetic correlation between AMM in MB and experimental infection was not significantly different from 0, suggesting that this *Vibrio* strain, is not the major cause of AMM outbreak in MB 2018.

A LABORATORY AT LAND'S END: COMMUNITY-BASED SHELLFISHERIES RESEARCH AT THE CENTER FOR COASTAL STUDIES

Owen C. Nichols* and Sarah D. Oktay

Center for Coastal Studies, 5 Holway Avenue, Provincetown, MA 02657

nichols@coastalstudies.org

Founded in 1976, the Center for Coastal Studies (CCS) is a 501(c)(3) non-profit organization based in Provincetown on Cape Cod, Massachusetts. Through its Marine Fisheries Research Program and interdisciplinary studies, the CCS works among local communities to conduct applied research on wild and cultured shellfisheries in partnership with federal, state, and local agencies. Collaborative projects with the fishing and shellfish farming communities include bycatch reduction in the sea scallop fishery, derelict gear recovery and research, hydraulic clam dredge impact studies, and analyses of environmental effects on squid distribution and early life history. The Center worked with two towns to designate a 50-acre subtidal aquaculture development area in Cape Cod Bay, granting shellfish farmers and researchers a place to experiment with novel techniques. Scientists at the CCS study shellfish at an ecosystem scale, conducting field research on species distributions relative to habitat type and measuring the effects of restoration and climate change. The CCS fleet of research vessels includes several platforms uniquely suited for shallow-water sampling and habitat mapping. Samples collected in the field are analyzed at the CCS marine laboratory, which includes instruments for microscopy, spectrometry, particle size, pollutant and nutrient analysis, and an expanding capacity for eDNA and genetics research. University partnerships create undergraduate and graduate student opportunities for field and laboratory research. The geographic location of the CCS, field station and laboratory facilities, and diverse interdisciplinary research capacity support a community-based approach to, "Science that Matters," for shellfisheries.

CORRELATION BETWEEN ENVIRONMENTAL VARIABLES AND *MARGALEFIDINIUM POLYKRIKOIDES* CONCENTRATIONS ON A RHODE ISLAND SHELLFISH FARM

Susanna Osinski[1]*, Evelyn Takyi[1], Abigail K. Scro[1,2], Cassidy Pilate[1], Chamberlin Shawna[1], Roxanna M. Smolowitz[1,2], Timothy Scott[1], Gary H. Wikfors[3], and Skylar Bayer[1]

[1]Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol RI 02809

[2]Roger Williams University, Aquatic Diagnostic Laboratory, 1 Old Ferry Road, Bristol RI 02809

[3]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford CT 06460

sosinski@rwu.edu

Shellfish aquaculture on the East Coast is a $170M industry supporting many jobs in rural coastal communities. There is, however, great concern about the occurrence of dinoflagellate blooms. *Margalefidinium polykrikoides*, previously named *Cochlodinium polykrikoides*, is an ichthyotoxic dinoflagellate that causes intense, localized rust tides. Not toxic to humans, *M. polykrikoides* can cause shellfish mortality, including oysters, resulting in economic losses. The spatial and temporal dynamics of when and where rust tides appear are not well understood; therefore, this research aims to explore the dynamics of rust tides using environmental DNA monitoring.

To this purpose, environmental DNA was extracted from sediment and water samples in August 2022 from various locations throughout one of the salt ponds in Rhode Island. This pond had a history of rust tide blooms surrounding aquaculture farms. Concentrations of *M. polykrikoides* were quantified using qPCR techniques. Environmental variables such as temperature, wind, precipitation, dissolved oxygen, and salinity, were recorded during each sampling period. Additional water samples were collected for nutrient and chlorophyll-*a* analysis.

Resulting correlations between *M. polykrikoides* concentrations and environmental variables will provide the baseline data to predict blooms before they happen and develop mitigation methods for Rhode Island aquaculturists. Further sampling through multiple periods and different locations will provide more data to support preliminary results.

FRIDAY HARBOR LABORATORIES: MARINE SCIENCE IN THE PACIFIC NORTHWEST

Dianna Padilla[1,2]*, Bernadette Holthuis[1], Mason Wiley[1], and Megan Dethier[1]

[1]Friday Harbor Laboratories, University of Washington, 620 University Road, Friday Harbor, WA 98250

[2]Stony Brook University, Department of Ecology and Evolution, Stony Brook, NY 11794

dianna.padilla@stonybrook.edu

The Friday Harbor Laboratory (FHL) is a marine station located on San Juan Island, about 70 miles NW of Seattle in the inland marine waters of Washington State. For almost 120 years, the station has supported research and education in the marine sciences in an egalitarian, collaborative culture. Part of the University of Washington College of the Environment, the FHL is the home of active research programs in ocean acidification, vertebrate functional morphology and biomechanics, and restoration of declining sea star populations, eelgrass meadows, and kelp beds. One building is currently being renovated as a Marine Genomics Center. The FHL is open year-round to visiting researchers from around the globe, working in fields from physical oceanography to conservation and from genetics and development to anatomy and ecology. In spring, summer, and fall, the FHL offers graduate and undergraduate courses on similarly diverse topics. To help defray costs for students, the Labs offers financial assistance from generous private donations.

Campus facilities include 13 lab buildings, most of which have running seawater for maintaining marine organisms; a variety of modern equipment for shared use; several classrooms; a full-service Dining Hall; and roughly 200 beds in housing units ranging from student dormitories to private apartments, all on a forested, ca. 500-acre biological preserve. Also, on the FHL campus, the Helen Riaboff Whiteley Center provides a refuge (seven cottages and a study center) for established scholars and artists to create and interact in a peaceful environment. As space allows, the FHL also rents its facilities for workshops and conferences.

DETECTION OF *VIBRIO* SPECIES IN *CRASSOSTREA VIRGINICA* AND *CALLINECTES SAPIDUS* USING MULTIPLEX SYBER GREEN REAL-TIME PCR

Ali Parsaeimehr* and Gulnihal Ozbay

Delaware State University, Department of Agriculture and Natural Resources, College of Agriculture, Science, and Technology, Dover, DE 19901

aparsaeimehr@desu.edu

A multiplex real-time PCR assay was used for rapid detection of *Vibrio parahaemolyticus*, *Vibrio vulnificus*, *Vibrio coralliilyticus*, and *Vibrio tubiashii* in *Crassostrea virginica* and *Callinectes sapidus*. In this regard, a set of primers were searched against the NCBI database platform for specificity confirmation of the selected primers, and the specificity of the primers was confirmed using a conventional PCR. At the next step, a SYBER Green based real-time PCR has been optimized to detect the pathogenicity genes of the studied *Vibrio* species at low level of bacterial population (10^2 CFU). The assay was examined based on linearity and limitation in bacterial detection using a series of bacterial dilution. Finally, the validation of the test was examined using samples from the *Crassostrea virginica* tissues and *Callinectes sapidus* hemolymph. The high sensitivity of this multiplex real-time PCR assay makes it suitable for detection of low copies of *tlh*, *vvh*, and dnaJ in *Vibrio* spp.

SEWAGE EFFLUENT AFFECTS OYSTER LARVAL SIZE

Benjamin Poepsel*, Alexandra Hooks, Amy Zyck, Hailee Carlson, and Jonathan B. Puritz

University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd., Kingston, RI 02881

bpoepsel@uri.edu

The matter of what to do with human waste is an issue that is growing in importance as coastal populations continue to increase. In the United States, many water treatment centers are specialized to remove certain types of waste (nitrogen, pathogens, etc.) before releasing it back into coastal waters. Marine organisms, such as shellfish, are particularly vulnerable to changes in their local environment. Many shelled organisms, such as the eastern oyster, have been affected by sewage effluent (SE). They often display altered physiology such as growth rates and shell sizes. To study the effects of sewage effluent, oyster larvae were subjected to a sewage effluent treatment (5% solution mixed with seawater) as well as a control treatment for 24 hours. Larval shell growth and mortality were estimated from subsamples taken pre- and post-exposure. The results of these tests suggest that oyster larvae exposed to sewage effluent grew larger compared to control larvae. This possibly is due to some larvae being able to resist the negative effects of SE and benefit from reduced competition. Genomic samples collected during the experiment will help determine potential genetic differences between the larvae that survived the SE treatment and those in the control.

IMPACT OF A MARENNINE-LIKE PIGMENT PRODUCED BY THE DIATOM *HASLEA* SP. ON THE GROWTH AND PHYSIOLOGY OF BAY SCALLOPS (*ARGOPECTEN IRRADIANS*)

Caroline Polder[1]*, Catharina Alves-de-Souza[1], Robert Whitehead[1], and Ami Wilbur[1,2]

[1]University of North Carolina Wilmington, Center for Marine Science, 5600 Marvin K Moss Ln, Wilmington, NC 28409

[2]University of North Carolina Wilmington, Department of Biology and Marine Biology, 5600 Marvin K Moss Ln, Wilmington, NC 28409

cep8750@uncw.edu

The pennate diatom, *Haslea* sp., produces a unique blue-green pigment known as marennine. This pigment is water-soluble and is usually expelled into the seawater by the diatom during growth in the winter season. It has been shown to have antibiotic properties and may function as an immunostimulant for bivalves. Other research suggests that there may be negative impacts on physiology, particularly at higher concentrations. This project evaluates the physiological impacts of exposure to different concentrations of this blue water (BW) obtained from *Haslea* sp. cultures on bay scallops. *Haslea* sp. was collected from North Carolina (Cedar Island and Stump Sound), isolated and cultured in the UNCW Algal Resources Collection. After collection from cultures, BW was diluted to establish different concentrations and a relative percentage of marennine-like pigment by spectrophotometry. Bay scallops (shell height = 43.87±0.29 mm) were exposed to three concentrations (zero, low = 20%, high = 40%) of BW over 48 hours. Post-exposure, scallops (12 per treatment) were maintained in a flow-through aquarium system for 8 weeks. Growth, survival, oxygen consumption, and clearance rates were assessed at the beginning, at 4 and 8 weeks. The results of this experiment will be discussed.

SHELL RECYCLING ALLIANCE

Thomas C. Price

Oyster Recovery Partnership, 1805 Virginia St, Annapolis, MD 20401 Tprice@oysterrecovery.org

In 2010, the Shell Recycling Alliance was created in response to the critical need for oyster shell in Chesapeake Bay oyster restoration. Since its formation, the program has run under the banner of “No Shell Left Behind” and has focused on recovering used oyster and clam shells from restaurants, caterers, wholesalers, and the public across the Mid-Atlantic region. The Shell Recycling Alliance works in cooperation with the University of Maryland Horns Point Laboratory where oyster shells are used as oyster substrate to form “spat-on-shell.” Spat-on-shell created using recycled shell is deployed on restoration reefs within the oyster sanctuary network in Maryland.

The replenishment of reserved shell stockpiles in Maryland has stalled as seafood processors have shifted their shell sales towards the more profitable growing aquaculture market. With the reserved stockpiles no longer replenished by the seafood processing industry, reliance on the recycling of distributed shellfish has sharply increased. The Shell Recycling Alliance (SRA) is in its 12th year and at over 200 members, is the largest network of oyster and clam shell recycling-establishments in the nation. It has grown from a few restaurants donating only 3,800 bushels in its first full year, to as many as 36,00 bushels annually. To date, the program has recycled a total of nearly 290,000 bushels.

OYSTER CULTIVATION AND BREEDING AT THE RUTGERS CAPE SHORE LABORATORY

Sam Ratcliff*, Jillian Jamieson, and Ximing Guo

Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6959 Miller Ave, Port Norris, NJ 08349

samratcl@hsrl.rutgers.edu

The Rutgers Cape Shore Laboratory is a New Jersey Agricultural Experiment Station and a field station located on the shore of Delaware Bay in Cape May, New Jersey (NJ). Laboratory facilities at the site include two hatcheries with quarantine space, an office, dry lab, classroom space, and an on-site dormitory providing housing for laboratory technicians, students, and visiting researchers. Culture systems include a land-based nursery and a quarantine holding system for non-native oyster species. The site also includes 7 acres of intertidal flats located in front of the laboratory which is used for field grow out of oyster lines generated by the Rutgers long-standing shellfish breeding program.

Current work at the lab includes the production and evaluation of Rutgers disease-resistant oyster lines, the production of tetraploid lines and other experimental crosses in support of genomic research and genomic selection. The Cape Shore site, which is where most oyster farms in NJ based, is ideal for breeding disease and stress tolerance because of its harsh environmental conditions and reliable exposure to MSX and Dermo. Each year, over 20 selected lines and genetic groups were produced and after field evaluation, broodstock from the top performing lines are selected and distributed to hatcheries for commercial production. In addition to supporting university research and teaching, the lab serves the shellfish aquaculture community by providing guidance on hatchery production, nursery and grow-out, and service for tetraploid broodstock certification.

EFFECTS OF INBREEDING ON EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) LARVAL SURVIVAL AND SUBSTRATE PREFERENCE

Lauren Renna[1,2]*, Zhenwei Wang[2], and Ximing Guo[2]

[1]Washington University in St. Louis, Department of Biology, 1 Brookings Drive, St. Louis, MO 63130

[2]Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6959 Miller Ave, Port Norris, NJ 08349

Laurenrenna@wustl.edu

Rutgers University has been breeding eastern oysters for disease resistance since 1960. Long-term selective breeding may lead to inbreeding that depresses larval fitness. This experiment looked at the effects of inbreeding on eastern oyster larval survival and substrate preference. Three genetic lines of oysters were produced in the hatchery, two inbred pure lines, and the third, a hybrid produced by crossing the two inbred lines. The larvae were cultured until they set and metamorphosed into spat. The hypothesis was that due to inbreeding depression (decrease in fitness with increased genome-wide homozygosity that occurs in the offspring of related parents), inbred larvae would have lower survival and growth rates in comparison to the hybrid line, and that the larvae would exhibit no shell preference. Results showed that the hybrid line and one inbred line survived equally well, while the other inbred line had very low survival. There were also significantly more larvae setting on oyster shells than clam or scallop shells. The implications of the results highlight that not all inbreeding leads to inbreeding depression and that inbreeding could potentially be used to purge recessive deleterious alleles from selected lines.

COMPLETE MITOGENOME SEQUENCE ANALYSIS OF *CRASSOSTREA HONGKONGENSIS* AND ITS PHYLOGENETIC CONSEQUENCES

Basanta Pravas Sahu* and Vengatesen Thiyagarajan

The Swire Institute of Marine Science, School of Biological Sciences, Area of Ecology and Biodiversity, The University of Hong Kong, Pokfulam, Hong Kong Special Administrative Region, China

basanta@hku.hk

The genus *Crassostrea* contains several commercially important oyster species. Among those, five species are primarily cultured along the coastal region of China. In comparison with its related species, *C. hongkongensis* is considered as the best oyster due to its high market value and bigger size; however, in the past few years, the wild *C. hongkongensis* populations have been reduced rapidly due to overexploitation, habitat destruction, seasonal mortality, and climate change. To address this issue, the aquaculture industry is anticipating continuously developing a specific breed that can withstand harsh environments like high salinity. Mitochondrial DNA (mtDNA) is considered a marker of choice due to its high polymorphism, maternal inheritance, lack of recombination and thus used for population genetic analysis of various animals. The newly-assembled complete mitogenome through transcriptome mapping resulted in 18,617 bp. It included 12 protein-coding genes, 23 tRNAs, and two rRNA. The A/T content of the mitogenome was higher than its G/C content. Similar values and features were previously found for six other specimens of *C. hongkongensis*. A phylogenetic analysis based on the 12 protein-coding genes and complete mitochondrial sequence indicated that the six specimens of *C. hongkongensis* formed a monophyletic group and shared a sister group relationship with *C. ariakensis*, *C. nippona*, *C. sikamea, C. angulata, C. gigas*, and *C. iredalei*. The newly-sequenced mitogenome had more singleton sites than previously published *C. hongkongensis* mitogenomes.

GROWTH AND SURVIVAL OF TRANSPLANTED SOFT-SHELL CLAMS (*MYA ARENARIA*) DURING A WINTER-TO-SUMMER GROW-OUT PERIOD IN THE YORK RIVER, VIRGINIA

Natalia J. Schoenberg*, Kathleen E. Knick, Michael S. Seebo, and Rochelle Seitz

Virginia Institute of Marine Science, William & Mary, PO Box 1346, Gloucester Point, VA 23062

njschoenberg@vims.edu

The soft-shell clam (*Mya arenaria*) is an infaunal, filter-feeding bivalve commonly found in coastal and estuarine habitats throughout its native range on the US East Coast. In recent decades, commercial aquaculture and harvest of the species has mainly been concentrated in the northern portion of its range, yet there are benefits to growing the clams in the warmer climates of the Chesapeake Bay. This project investigated the feasibility of establishing *Mya arenaria* aquaculture in Virginia waters and whether soft-shell clams planted in the fall could grow to market size of 50 mm before elevated summer temperatures threatened their survival. In October 2021, six experimental plots each with six predator-exclusion clam cages were deployed across two York River locations. Marked and measured soft-shell clams (n = 324, mean initial shell length = 30.1 mm) were planted within the cages at a density of 150 clams per m^2 (nine clams per cage). Cages were harvested monthly from April to September to assess survival and growth. Preliminary results indicate that clams grew to >50 mm shell length over the winter and spring before experiencing a large-scale mortality event when temperatures reached the upper end of their temperature limits in July 2022. This suggests that soft-shell clams in VA can grow to market size before temperatures rise, and winter soft-shell clam aquaculture could be viable in Virginia.

CLIMATE ADAPTATION IN FISHERY MANAGEMENT AND NATURAL RESOURCES-BASED ECONOMIES IN MARYLAND

Amanda Small[1,2]

[1]Maryland Department of Natural Resources, 580 Taylor Avenue, E-2, Annapolis, MD 21401

[2]NOAA Office for Coastal Management, 2234 South Hobson Avenue, Charleston, SC 29405

amanda.small@maryland.gov

Climate change encompasses a variety of environmental parameters including water temperature, precipitation, sea level, and pH. Predictions of future environmental conditions are variable, and the resulting impacts on fish stocks are still uncertain. These complications pose challenges to monitoring and fisheries management structure in Maryland. The purpose of this project is to develop recommendations for climate adaptation strategies that support resilient and sustainable fisheries. Phase 1 identified areas of climate vulnerability. The Maryland fishing economy relies heavily on blue crab (*Callinectes sapidus*) and eastern oyster (*Crassostrea virginica*), which both have "very high" climate vulnerability scores. While blue crabs may benefit from milder winters and range expansion, oysters may suffer from hypoxia, salinity, and acidification. Additionally, high-tide flooding and sea level rise threaten commercial and recreational access to dockside facilities. Phase 2 will identify options for adaptive management that grant flexibility as environmental conditions and stock productivity change. Focus will be directed on drafting language for state fishery management plans and updating licensing structures to allow harvest of new northern-migrating stocks like shrimp. In coordination with the Maryland Coastal Management Program, fisheries representatives will also assist in developing and implementing statewide priorities for natural resource management in the Maryland NextGen climate adaptation plan. With climate change being a multi-faceted issue, fisheries managers must adapt a holistic approach to both understanding the potential impacts and planning adaptation and resilience strategies.

EFFECTS OF MANGANESE ON THE DOPAMINE D2R SIGNAL TRANSDUCTION PATHWAY L-TYPE CALCIUM CHANNELS AND THE CONTROL OF LATERAL CELL MEMBRANE POTENTIAL AND CILIA RESPONSE IN GILL OF *CRASSOSTREA VIRGINICA*

Shatema Small[1]*, Elizaveta Ulumbelashvili[2], Edward J. Catapane[1], and Margaret A. Carroll[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

shatemasmall@hotmail.com

Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by serotonin and dopamine. Dopamine activates D2R-like receptors hyperpolarizing GLC causing cilio-inhibition. Serotonin depolarizes GLC causing cilio-excitation. Manganese, a neurotoxin causing manganism, a Parkinson's-like disease, disrupts dopaminergic neurotransmission. The neurotoxic mechanism is not fully resolved. Lack of effective treatment for manganism is a major obstacle in its clinical management. Previous work with *C. virginica* showed manganese blocks hyperpolarization and cilio-inhibitory effects of dopamine on GLC. Activation of D2R inhibits adenylyl cyclase, activates PLC-β, opens GIRK channels and inhibits L type calcium channels (LTCC) reducing the inward flow of calcium, causing hyperpolarization and decreasing cilia beating. To determine if LTCC affects GLC membrane potential and cilia beating; and are affected by manganese, LTCC blockers verapamil and nifedipine were used to mimic the actions of dopamine. Cilia activity was measured by stroboscopic microscopy. Membrane potentials were simultaneously measured using the fluorescent dye $\text{DiBAC}_4(3)$. Verapamil slightly decreased cilia beating. Nifedipine stopped cilia beating. Both hyperpolarized the cells. In the presence of manganese, manganese did not prevent the actions of nifedipine on cilia beating or membrane potential. This physiological study shows LTCC plays a role in the D2R signal transduction pathway in GLC of *C. virginica,* but is not affected by manganese. These findings are helpful in understanding the D2R signaling pathway mechanisms as well as manganese neurotoxicity and provide evidence to guide future studies of potential therapeutic agents for manganism. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP and PSC-CUNY 62344-0050 and 62344-0051.

ARE THERE ENOUGH OYSTER LARVAE? A POPULATION VIABILITY ANALYSIS EXAMINING OYSTER LARVAL ABUNDANCE IN GREAT BAY ESTUARY, NEW HAMPSHIRE, USA

Alyssa Stasse*, Kelsey Meyer, Bo-Young Lee, and Bonnie L. Brown

University of New Hampshire Department of Biological Sciences, 38 Academic Way, Durham NH 03824

alyssa.stasse@unh.edu

Along with being the most economically important bivalve in aquaculture, eastern oysters, *Crassostrea virginica*, also provide ecosystem services such as physical habitat for other estuarine species, coastal protection through a decrease in wave energy, biofiltration of the water column, nutrient biosequestration and removal, and nutrient processing. As a result of overharvesting, habitat modification, disease, and invasive species, oyster populations are declining drastically throughout their historical range. In Great Bay Estuary (GBE) in New Hampshire, oyster reef restoration is being conducted by stocking dying reefs with large cultivated oysters, called "uglies," in hopes of enhancing numbers of larvae and recruits to the wild population. Over a 5-year period, oyster larval abundance and recruitment were recorded in the Bay throughout the period when it was thought that oysters were most reproductively active (March through November). These data, in combination with physicochemical data, predator effects on larvae and adults, pathogen occurrence and intensity, acreage of suitable area, and adult population demographics, were used in hierarchical multi-population viability analysis simulations using RAMAS MetaPop 6.0 to determine the likelihood of Great Bay Estuary eastern oyster population success. This model is a critical component of evaluating the current restoration effect and can be used to inform future restoration practices to ensure that oysters chosen to deploy for supplementation are capable of producing adequate numbers of larvae to survive predation, disease, climate change, and other stressors to the natural oyster population of GBE.

THE VALUE OF PRE-RESTORATION HABITAT SURVEYS FOR SITING OYSTER RESTORATION

Patrick Temple[1]*, Olivia N. Caretti[1], Jennica Moffat[1], Jennifer Walters[1], H. Ward Slacum Jr.[1], Jodi Baxter[2], and Laurinda Serafin[2]

[1]Oyster Recovery Partnership, 1805A Virginia St. Annapolis, MD 21401

[2]Fishing and Boating Services, Maryland Department of Natural Resources, 580 Taylor Ave., B-2, Annapolis, Maryland 21401

ptemple@oysterrecovery.org

Optimizing oyster restoration location and design is necessary to maximize restoration success. Pre-restoration habitat surveys can ensure efforts are sited in areas that support oyster growth and survival. Comprehensive pre-restoration habitat surveys are conducted as part of the Chesapeake Bay large-scale oyster restoration program in tributaries selected by the Maryland Oyster Restoration Interagency Workgroup. Pre-restoration surveys determine whether areas can support oyster restoration and guide the selection of the most appropriate restoration treatment. Oyster Recovery Partnership conducts systematic pre-restoration habitat surveys using patent tongs, which are commercial oyster gear efficient at sampling benthic conditions, particularly oyster reefs. Data gathered from the patent tong survey includes bottom type, habitat quality, and pre-existing oyster density, which are used to generate habitat score maps that inform restoration decisions and provide a baseline to assess restoration progress. From 2019-2022, pre-restoration surveys were conducted in the Manokin River Sanctuary on 616 acres of habitat. Habitat suitability scores revealed that 300 acres were suitable for restoration using spat-on-shell (SOS) only and 196 acres required the construction of substrate prior to treatment with SOS. An additional 120 acres are currently being assessed. This information will guide restoration efforts on 441 acres in the Manokin River over the next three years to meet the Chesapeake Bay Program oyster restoration goals. A similar framework should be applied in other restoration programs to properly site oyster restoration and ensure effective and efficient use of resources. Understanding the pre-existing habitat conditions is fundamental for improving restoration processes and outcomes.

SHALLOW-WATER OYSTER FARMS WITH PVC POST AND LINE SYSTEMS

Alan Urteaga*[1], Joshua Banda[1], Allan Vazquez[1], Cesar Villanueva[1], Lawrence Cano[1], Noe Vargas Hernandez[1], and Joanne Rampersad-Ammons[2]

[1]University of Texas Rio Grande Valley, Department of Mechanical Engineering, 1201 West University Drive, Edinburg, Texas, 78539

[2]University of Texas Rio Grande Valley, School of Earth, Environmental and Marine Sciences, 1201 West University Drive, Edinburg, Texas, 78539

alan.urteaga01@gmail.com

Shallow-water oyster farming using short, horizontal-line PVC post systems tackle the issue of farming oysters in shallow bays such as South Texas' Laguna Madre. PVC posts form the main supports of this short line underwater oyster farm and anchors provide the primary source for tension on the oyster lines. This proposed system was designed to be efficient, cost effective, uses readily available materials and is simple to implement with minimal effort in order introduce newcomers to oyster farming. A team of mechanical Engineering senior design students advised by faculty at the University of Texas Rio Grande Valley (UTRGV) (1) examined forces associated with seafloor embedded PVC posts to determine minimal embed depth, (2) developed a simple excel calculator that the farmer could use to deploy posts, (3) looked at line to post attachment methods, (4) evaluated anchoring designs for line ends. Drawings, calculations, and final system hardware prototypes are presented.

WESTERN BLOT STUDY OF HISTAMINE AND GABA RECEPTORS IN PERIPHERAL TISSUES OF *CRASSOSTREA VIRGINICA*

Rosanne Wallach[1]*, Kera Mansfield[1], Tia Foster[1], Christopher Pierce[2], Ruhamah Souffrant[1], Margaret A. Carroll[1], and Edward J. Catapane[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, NY 11225

[2]Kingsborough Community College, 2001 Oriental Blvd, Brooklyn, NY 11235

rosewallach@hotmail.com

Histamine and GABA are neurotransmitters in invertebrates, but rarely have been studied in bivalves. Previous research with *Crassostrea virginica* showed histamine is involved in mantle rim light reception influencing gill lateral cell cilia beating. HPLC and immunohistofluorescence detected histamine and H2 receptors in ganglia of *C. virginica*. The H1 antagonists, diphenhydramine and H2 antagonist famotidine, blocked the actions of histamine at the mantle rim. GABA was shown to have inhibitory ganglionic action on serotonin excitation of gill lateral cell cilia, that is blocked by the GABA antagonist bicuculline methchloride. Histo-immunofluorescence found GABAa receptors in cerebral and visceral ganglia. To study if histamine and GABA innervate peripheral tissues in *C. virginica* gel electrophoresis and Western Blotting was performed using 1° antibodies to histamine H1R and H2R; and GABAa and GABAb receptors followed by FITC 2° antibodies. Gill, mantle rim, palps and heart were dissected and homogenized. Protein concentrations were determined by the Bradford method. Laemmli-treated samples were wet-loaded onto polyacrylamide gels then electrophoresed in Tris/glycine SDS buffer. Gels were transferred onto nitrocellulose membranes, incubated with 1° antibodies, then FITC 2° antibodies and viewed with an iBright Fl1500 image analyzer. Western Blots revealed H1R, H2R, GABAa and GABAb receptors in palps, heart, mantle and gill. The study demonstrates histamine and GABA also have peripheral neurotransmitter roles in various tissues. These findings will lead to studies exploring peripheral physiological roles of histamine and GABA in *C. virginica*. Supported by grants NIGMS-2R25GM06003, NIH-K12GM093854, DoEd-P120A210054, NYS-CSTEP, PSC-CUNY 62344-0050 and 62344-0051.

DERELICT FISHING GEAR RETRIEVAL IN THE CHESAPEAKE BAY: A COLLABORATIVE APPROACH WITH THE BLUE CRAB INDUSTRY

Jennifer Walters[1]*, H. Ward Slacum, Jr.[1], Eric Amrhein[1], David Wong[2], Marc Mole[2], and Olivia Caretti[1]

[1]Oyster Recovery Partnership, 1805A Virginia Street, Annapolis, MD 21401

[2]Versar, Inc., 9200 Rumsey Rd #100, Columbia, MD 21045

jwalters@oysterrecovery.org

The Chesapeake Bay supports the largest commercial blue crab fishery in the United States as well as extensive recreational and commercial shipping activities. Derelict crab traps accumulate in significant densities where these activities overlap. Derelict fishing gear becomes marine debris, competes with active fishing gear, and increases blue crab and bycatch mortality through ghost fishing. In 2022, the Oyster Recovery Partnership (ORP) received funding from the Baltimore County Department of Environmental Protection and Sustainability to hire commercial crabbers to retrieve derelict crab pots and other debris near the mouth of the Patapsco River in Maryland. Side-scan sonar was used to map approximately 2,000 acres of Bay bottom and identified around 3,000 pots or pieces of debris. The team set a goal of retrieving 50% of the detected derelict gear. ORP hired 14 local commercial crabbing vessels to remove the detected derelict gear. Utilizing towed grappling hooks, more than 2,000 pieces (~70%) of derelict gear or debris were collected over 6 days. Removed gear included crab traps, eel traps, and various types of wire or cable. While a large portion of the detected gear was removed during this project, fishing gear continues to be lost and accumulate on an annual basis in heavily fished areas. This project was only focused on a small portion of the Chesapeake Bay but provided a framework that can be translated to other regions to indirectly enhance the blue crab fishery and provide direct economic support for industry members.

INCORPORATING ADVANCED PHOTOBIOREACTORS AS THE PRIMARY SOURCE OF MICROALGAL PRODUCTION IN A TECHNOLOGY DRIVEN BIVALVE HATCHERY

Steven Weschler*, Matthew Martin, and Stephan Abel

Ferry Cove Shellfish LLC., Ferry Cove Oyster Hatchery, Sherwood, MD 21665

sweschler@ferrycove.org

For decades, bivalve hatcheries regularly encounter production issues which directly impact and limit the amount of available larvae and seed for sale to aquaculturists. Most of these limiting factors are normally environmental and not always controllable by hatchery systems, however there are other problems that can be controlled or mitigated, such as biosecurity protection and algal production. High volumes of multiple species of dense microalgae are required to feed bivalve broodstock, larvae, and seed. Algae production is often a bottleneck which forces hatchery managers to make tough husbandry decisions. With the development of photobioreactors that include automation and advanced features, the problem of under-producing microalgae is alleviated. The photobioreactors are extremely efficient and simple to use and allows hatcheries to maximize biomass output and increase the longevity of cultures with minimal labor and overhead. Ferry Cove Oyster Hatchery, located in the Chesapeake Bay, has implemented various automated technology solutions throughout the facility to manage water quality and its overall hatchery production systems. In addition, the hatchery has installed seven compact bioreactors as its exclusive and sole method of culturing microalgae for its production operations. After operating the photobioreactors for a season, staff have developed a set of best management practices in their general operation and methodologies in maximizing biomass output. They have proven to be highly reliable and fully capable of producing multiple species of microalgae in a high production and algae-demanding environment.

CONTEXTUALIZING RECENT MID-ATLANTIC BIGHT COLD POOL DEGRADATION USING OCEAN QUAHOG (*ARCTICA ISLANDICA*) SHELL GROWTH AND CHEMISTRY PAIRED WITH HIGH-RESOLUTION OCEAN MODELS

Nina Whitney[1,2], Caroline Ummenhofer[2], Konrad Hughen[3], Roger Mann[4], Eric Powell[5]*, Torge Martin[6], Alan Wanamaker[7], Madelyn Mette[8], Eileen Hofmann[9], John Klinck[9], Soenke Dagendorf[10], Maya Feldberg-Bannatyne[11], and Gabriel Mcinnis-Hernandez[1]

[1]Western Washington University, Marine and Coastal Science, 516 High Street, Bellingham, Washington, 98225

[2]Woods Hole Oceanographic Institution, Department of Physical Oceanography, 266 Woods Hole Road, Woods Hole, MA, 02543

[3]Woods Hole Oceanographic Institution, Department of Marine Chemistry and Geochemistry, 266 Woods Hole Road, Woods Hole, MA, 02543

[4]Virginia Institute of Marine Science, Fisheries Science, 1370 Greate Road, Gloucester Point, VA, 23062

[5]University of Southern Mississippi, School of Ocean Science and Engineering, 730 East Beach Boulevard, Long Beach, MI 39560

[6]Ocean Circulation and Climate Dynamics, GEOMAR Helmholtz Centre for Ocean Research Kiel, Düsternbrooker Weg 20, 24105 Kiel, Germany

[7]Iowa State University, Department of Geological and Atmospheric Sciences, 2237 Osborn Drive, Ames, IA, 50011

[8]U.S. Geological Survey, St. Petersburg Coastal and Marine Science Center, 600 4th Street South, St. Petersburg, FL, 33701, United States of America

[9]Old Dominion University, Center for Coastal Physical Oceanography, 4111 Monarch Way, Norfolk, VA, 23529

[10]Tulane University, River-Coastal Science and Engineering, 6823 St. Charles Avenue, New Orleans, LA, 70118

[11]Carleton College, Department of Geology, 1 North College Street, Northfield, MN, 55057

Eric.N.Powell@usm.edu

The Mid-Atlantic Bight Cold Pool is a seasonal, cold bottom water feature that establishes the community structure, including the benthic dominants surfclams (*Spisula solidissima*) and ocean quahogs (*Arctica islandica*), over a large area of the western North Atlantic Shelf. Recently, the Cold Pool has been shown to be warming and shrinking, leading to shifts in *S. solidissima* range and concern for the future of the fisheries in this region. The chemistry (specifically oxygen isotope measurements) and shell growth of *A. islandica* collected off of Long Island was used along with a high-resolution ocean-sea-ice model (VIKING20X, an Atlantic Ocean 1/20° nest in a global 1/4° ORCA025 model) to reconstruct past oceanographic variability in the Cold Pool region in order to put recent observed bottom water temperature changes into context. The oxygen isotope and modeling results agree well ($r=-0.592$, and 0.63 respectively, $p<0.001$) with the instrumental record from expendable bathythermographs deployed from the *CMV Oleander* since the 1970s, showing that bottom water temperatures in the region have been increasing since then. Prior to the late 1970s, oxygen isotopes and model simulations suggest multi-decadal temperature variability and no long-term trends. Preliminary results will be presented and future work will extend the temperature reconstruction over multiple centuries.

ADVANCING EUROPEAN BIVALVE PRODUCTION SYSTEMS (BIVALVI PROJECT)

Dulani Wickramanayaka[1,2], Sarah C. Culloty[1,2,3], and Sharon A. Lynch[1,2,3]*

[1]University College Cork, School of Biological, Earth and Environmental Sciences and Aquaculture and Fisheries Development Centre, Distillery Fields, North Mall, Cork, T23 N73K, Ireland

[2]University College Cork, Environmental Research Institute, Ellen Hutchins Building, 6 Lee Rd, Sunday's Well, Cork, T23 XE10, Ireland

[3]MaREI Centre, Environmental Research Institute, Beaufort Building, University College Cork, Ringaskiddy, Co. Cork, P43 C573, Ireland

s.lynch@ucc.ie

Bivalves provide consumers with high value essential nutrients such as omega-3 fatty acids and iodine. The environmental footprint of bivalve production is low. However, the technological development of the European bivalve production sectors lie far behind other aquaculture sectors. BIVALVI aims to advance bivalve production in Europe in a sustainable way by combining genetics and reproductive technologies with improved health and production management.

BIVALVI will focus on mussels *Mytilus* spp., Manilla clams, and Pacific oysters, the bivalve species with the highest production in Europe. BIVALVI combines technology and social sciences to enhance the impact and acceptability of bivalve production. Work-packages will characterise the health and reproduction status and immune functions of diploid and triploid bivalve stocks (WP1); survey and optimise farming management systems (WP2); advance breeding programmes and map disease resistance genes (WP3); and support sustainable quality stocks through stakeholder and ecosystems services studies, a study on organoleptic properties of triploids and developing non-invasive and high-throughput recording systems (WP4).

BIVALVI will increase the sustainability of these sectors by adapting and integrating technological developments in large parts of their value chains (seed quality, reproductive health and control, production management, immunity and pathogen and disease control, and product quality). An important added value of BIVALVI is the close co-operation between R&D and the bivalve industries in Ireland, Italy and Norway. The technology transfer between species and countries and the extensive dissemination program will ensure the impact of BIVALVI will occur beyond the time frame of the project.

GENETICS, AGE DEMOGRAPHICS, AND SHELL SIZE OF ATLANTIC SURFCLAMS FROM THE SOUTHERN EDGE OF THEIR RANGE

Brynne Wisner[1]*, Zhenwei Wang[2], Ailey Sheehan[2], Ximing Guo[2], and Daphne Munroe[2]

[1]Michigan State University, Department of Natural Resources, 480 Wilson Road, East Lansing, MI 48824

[2]Rutgers University, Haskin Shellfish Research Laboratory, Department of Marine and Coastal Sciences, 6059 Miller Avenue, Port Norris, NJ 08349

wisnerbr@msu.edu

The Atlantic surfclam (*Spisula solidissima solidissima*) is a cold-water clam species that supports one of the largest bivalve fisheries in the United States. Until recently, the federal fishery had not fished for surfclams on the southern edge of the surfclam range due to low population numbers resulting from mortalities in the 1990s. Recent large catches have raised the question of whether the surfclam population has returned to the region or if a single cohort survived. *Spisula solidissima similis* is a shallow water cryptic subspecies of the Atlantic surfclam. The two subspecies are morphologically indistinguishable; however, *S. s. similis* grows to a smaller overall size and is genetically distinct. Questions have also been raised about the possibility of *S. s. similis* being part of the population fished off the coast of Virginia, and whether the clams being fished there are from a population that derives from regular recruitment. To address these questions, a sample of surfclams was taken off the coast of Virginia. Genetic samples were taken and compared to both Atlantic and cryptic subspecies in DNA sequences. Surfclams were aged, and length and weight were recorded for each clam. Size and weight were then compared to clams of the same age from the center of the population. Sequence analysis suggest there is a cyptic subspecies surfclam or a hybrid within the sampled population, surfclams of multiple ages were found within the sample, and the southernmost surfclams were smaller than clams of the same age from the population center.

THE ROLE OF CSDE1 IN REGULATING VARIOUS CELLULAR PROCESSES IN RESPONSE TO STRESS IN HEMOCYTES OF *CRASSOSTREA VIRGINICA*

Nadeen H. Yassin[1]*, Rachel A. Breidbart,[2] Rowan M. Hanna[3], and Maureen K. Krause[1]

Hofstra University, Department of Biology, 1000 Hempstead Turnpike, Hempstead, NY, 11549

nyassin1@pride.hofstra.edu

Hemocytes that are exposed to an environmental or immune stress alter their gene expression to mediate cell survival. Studies attempting to determine the mechanistic basis of the stress response and resistance to stressors focus on transcriptional control rather than translational regulation of gene expression. Hemocytes are key mediators of the stress response and respond to stresses with a global suppression of translation. RNA binding proteins (RBP) facilitate the upregulation of translation of select genes essential for cell survival. The cold shock domain-containing protein E1 (CSDE1) is a translational regulator that binds mRNA transcripts to alter their stability and abundance to mediate gene expression. CSDE1 is highly expressed in hemocytes, and our previous work shows that its localization changes in response to hypoxia and following immune challenge. It is hypothesized that CSDE1 regulates translation of proteins involved in a variety of cellular stress responses. In order to establish the key functional roles of CSDE1, silencing RNA (siRNA) is being used to knockdown CSDE1 expression in primary hemocyte cultures from the eastern oyster, *Crassostrea virginica*. Based on its known multifaceted roles in other species, we are testing the hypothesis that CSDE1 plays a role in regulation of phagocytosis, reactive oxygen species (ROS) production, morphology, and motility of hemocytes. Analysis of the role CSDE1 has on these cellular processes provides insight to the hemocytic response to stress and more broadly to the role of translation control in regulating stress responses.

THE EFFECTS OF DIEL-CYCLING ACIDIFICATION AND HYPOXIA ACROSS MULTIPLE DEVELOPMENTAL STAGES OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

Amy Zyck* and Jonathan B. Puritz

University of Rhode Island, Department of Biological Sciences, 120 Flagg Rd., Kingston, RI 02881

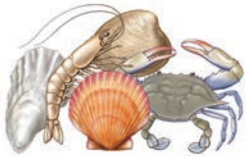
amaelia_zyck@uri.edu

In coastal waters, daily fluctuations in pH and dissolved oxygen occur due to diurnal cycling of photosynthesis and respiration. These fluctuations can be extreme, especially in summer months, resulting in multiple events of acidification and hypoxia. In species that spawn in the summer, like the eastern oyster, their early life-history stages will likely encounter several months of extreme cycling which can span the full larval developmental stage and early juvenile stage. Encountering stress at the larval stage can affect how an organism responds to the same stressor later in life. At the physiological level, stress exposure at one life-history stage can carry over to the next stage resulting in either an improved or reduced response under the same stressor. In terms of evolution, selective mortality at the larval stage can create a population of juveniles and adults better adapted to a more stressful environment. To link stressor response across multiple life-history stages, oysters were exposed to either a control treatment or diel-cycling acidification and hypoxia treatment from the pediveliger larval stage, through settlement, and into 8 weeks of the juvenile stage. Mortality, size, and respiration data were collected pre- and post-larval exposure as well as pre- and post-juvenile exposure. Genomic samples collected pre- and post-larval and juvenile exposures will help elucidate differences in selection across life history stages and identify shared and unique genes related to stress response across developmental stages.

The National Shellfisheries Association
would like to recognize and thank

BioOne

For supporting sustainable scholarly
communications, and enhancing and
expanding the visibility of the
Journal of Shellfish Research.



Thank You to Our Sponsors!

UNITED STATES ENVIRONMENTAL PROTECTION AGENCY

Northeastern Regional Aquaculture · CENTER ·

Sea Grant Maryland

FERRY COVE SHELLFISH

BioOne

Sheridan CJK GROUP

BLUE OYSTER ENVIRONMENTAL EST. 2019

KGL KnowledgeWorks Global Ltd. CJK GROUP

MatuNuck Oyster Farm

Fundación para la Conservación de Biodiversidad FUCOBI

REED MARICULTURE USA

The Nature Conservancy

HARD CLAM SELECTIVE BREEDING COLLABORATIVE Sea Grant www.HardClamHub.org

Oyster Recovery Partnership® ORP

VIMS William & Mary Virginia Institute of Marine Science

GOLD STANDARD DIAGNOSTICS

UMBC

unesco Intergovernmental Oceanographic Commission

FlowCam® FLUID IMAGING TECHNOLOGIES, INC.

IMET Institute of Marine and Environmental Technology

HATCHERY INTERNATIONAL

xylem Let's Solve Water

GloFouling PARTNERSHIPS

AQUACULTURE INFORMATION EXCHANGE

BREICON GENOMICS

NON SOLUS ELSEVIER

NOVAMONT

5m Books