National Shellfisheries Association

Program and Abstracts of the 116th Annual Meeting

March 17–21, 2024
Charlotte, North Carolina

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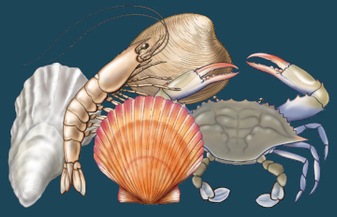

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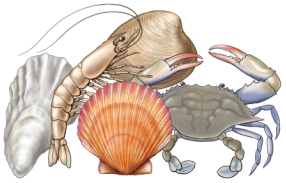

NSA 116th ANNUAL MEETING
National Shellfisheries Association
Sheraton - Le Meridien Hotel Complex - Charlotte, North Carolina
March 17–21, 2024

SUNDAY, MARCH 17, 2024

6:30 PM	STUDENT ORIENTATION Symphony Foyer
7:00 PM	PRESIDENT'S RECEPTION Symphony Foyer

MONDAY, MARCH 18, 2024

6:30-7:45 AM	STUDENT MENTOR-MENTEE BREAKFAST (NSA student members only – advanced sign-up required) Symphony Foyer				
8:00-9:10 AM	PLENARY LECTURE: Dianna Padilla (Stony Brook University) Symphony V-VI-VII				
ALL DAY	NSA AT THE MOVIES –FILM FESTIVAL –CONTINUOUS SHOWINGS Symphony I				
	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
9:15-10:30 AM	UNDERGRADUATE RESEARCH COLLOQUIUM	GENETICS, GENOMICS & BREEDING	OYSTERS	SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM	SHRIMP ENCODE
10:30-11:00 AM	MORNING BREAK				
11:00-11:30 AM	SHELLFISH & CARBON SEQUESTRATION WORKSHOP	GENETICS, GENOMICS & BREEDING	OYSTERS	SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM	SHRIMP ENCODE
11:30 AM-12:30 PM	SHELLFISH & CARBON SEQUESTRATION WORKSHOP	GENETICS, GENOMICS & BREEDING	OYSTERS	SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM	MANGROVE SHELLFISH
12:30-1:30 PM	LUNCH BREAK				
1:30-3:00 PM	SHELLFISH MICROBIOMES	GENETICS, GENOMICS & BREEDING	OYSTERS	SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM	MANGROVE SHELLFISH
3:00-3:30 PM	AFTERNOON BREAK				
3:30-5:00 PM	NORTHEAST BIVALVE HATCHERY HEALTH CONSORTIUM	GENETICS, GENOMICS & BREEDING		DIVERSITY, EQUITY & INCLUSION	MANGROVE SHELLFISH

TUESDAY, MARCH 19, 2024

8:00-8:50 AM	PLENARY LECTURE: Jeanne Serb (Iowa State University) Symphony V-VI-VII				
ALL DAY	NSA AT THE MOVIES –FILM FESTIVAL –CONTINUOUS SHOWINGS Symphony I				
	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
9:15-10:30 AM	DISEASE	ROBOTICS & EMERGING TECHNOLOGY	CLIMATE CHANGE, OCEAN ACIDIFICATION & MODELLING	SHELLFISH REPRODUCTION	GENERAL CONTRIBUTED I
10:30-11:00 AM	MORNING BREAK				
11:00-11:45 AM	DISEASE	ROBOTICS & EMERGING TECHNOLOGY	CLIMATE CHANGE, OCEAN ACIDIFICATION & MODELLING	GENERAL CONTRIBUTED II	GENERAL CONTRIBUTED III
11:45AM-12:30 PM	DISEASE	GENERAL CONTRIBUTED IV	AQUACULTURE AS A TOOL FOR RESTORATION	GENERAL CONTRIBUTED II	GENERAL CONTRIBUTED III
12:30-1:30 PM	LUNCH BREAK				
1:30-2:30 PM	DISEASE	SOCIAL DIMENSIONS OF SHELLFISHERIES	AQUACULTURE AS A TOOL FOR RESTORATION	eDNA APPLICATIONS FOR SHELLFISH	SCIENCE & PUBLIC ENGAGEMENT WORKSHOP
2:30-4:00 PM	OsHV-1 NOROVIRUS	SOCIAL DIMENSIONS OF SHELLFISHERIES	AQUACULTURE AS A TOOL FOR RESTORATION	eDNA APPLICATIONS FOR SHELLFISH	SCIENCE & PUBLIC ENGAGEMENT WORKSHOP
4:00-6:00 PM	POSTER SESSION AND HAPPY HOUR Symphony IV				
7:00-10:00 PM	STUDENT ENDOWMENT FUND AUCTION Symphony Foyer				

WEDNESDAY, MARCH 20, 2024

8:00-8:50 AM	PLENARY LECTURE: Eileen Hofmann (Old Dominion University) Symphony V-VI-VII				
ALL DAY	NSA AT THE MOVIES –FILM FESTIVAL –CONTINUOUS SHOWINGS Symphony I				
	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
9:15-10:30 AM	HATCHING A PLAN FOR AQUACULTURE COMMUNICATIONS	BIRDS & SHELLFISH SANITATION	MACROALGAE-SHELLFISH CO-CULTURE	ANTHROPOGENIC POLLUTANTS AND THEIR IMPACTS ON SHELLFISH BIOLOGY AND ECOLOGY	ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS WORKSHOP
10:30-11:00 AM	MORNING BREAK				
11:00-12:30 PM	THE FUTURE OF AQUACULTURE AT THE NOAA FISHERIES SERVICE	BIRDS & SHELLFISH SANITATION	MACROALGAE-SHELLFISH CO-CULTURE	ANTHROPOGENIC POLLUTANTS AND THEIR IMPACTS ON SHELLFISH BIOLOGY AND ECOLOGY	ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS WORKSHOP
12:30-2:00 PM	NSA BUSINESS LUNCHEON Symphony Foyer				
2:00-4:30 PM	SCALLOP GALLOP EXPLORE CHARLOTTE!!				
4:30-6:00 PM	POSTER SESSION AND HAPPY HOUR Symphony IV				

THURSDAY, MARCH 21, 2024

8:00-8:50 AM	**PLENARY LECTURE: Gregory Dietl (Cornell University) Symphony V-VI-VII**			
ALL DAY	**NSA AT THE MOVIES –FILM FESTIVAL –CONTINUOUS SHOWINGS Symphony I**			
	Symphony II	**Symphony III**	**Symphony V**	**Symphony VI**
9:15-10:15 AM	**DOWN ON THE FARM**	**COMMERICAL SHELLFISHERIES**	**HARMFUL ALGAL BLOOMS**	***VIBRIO***
10:15-10:45 AM	**MORNING BREAK**			
10:45-11:30 AM	**DOWN ON THE FARM**	**COMMERICAL SHELLFISHERIES**	**HARMFUL ALGAL BLOOMS**	***VIBRIO***
11:30 AM-12:00 PM	**DOWN ON THE FARM**	**SHELLFISH RESTORATION & CONSERVATION**		***VIBRIO***
12:00-1:00 PM	**LUNCH BREAK**			
1:00-3:30 PM	**HATCHERIES**	**SHELLFISH RESTORATION & CONSERVATION**	**ADVANCING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM**	***VIBRIO***
3:30-6:30 PM	**CLOSING HAPPY HOUR Symphony Foyer**			

POSTERS and All BREAKS are in Symphony IV.

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

PLEASE REMOVE YOUR POSTERS BY NOON ON THURSDAY

MONDAY
March 18, 2024

6:30-7:45AM	**STUDENT MENTOR-MENTEE BREAKFAST (NSA STUDENT MEMBERS ONLY – *Advanced sign up will be required*)** **Symphony Foyer**				
8:00-9:10AM	**PLENARY: Dianna Padilla (Stony Brook University) - *Gastropods - the other shellfish*** **Symphony V-VI-VII**				
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Symphony I**				
ROOM	**Symphony II**	**Symphony III**	**Symphony V**	**Symphony VI**	**Symphony VII**
SESSION TITLE	**UNDERGRADUATE RESEARCH COLLOQUIUM** **Ed Catapane & Margaret Carroll**	**GENETICS, GENOMICS & BREEDING** **Louis Plough**	**OYSTERS** **Bill Fisher**	**SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM** **Nicole Kirchhoff & Angela Collins**	**SHRIMP ENCODE** **Acacia Alcivar-Warren & Kathy Tang-Nelson**
9:15AM	Presence of glutamate neurons and glutamate receptors in ganglia of the eastern oyster, *Crassostrea virginica* **Pierre*, Wallach, Foster, Catapane, Carroll**	Site-specific differences in upper thermal tolerance and transcriptomic responses of Atlantic Canadian blue mussels (*Mytilus edulis*) **Ignatz, Clarke, Hori, Comeau, Filgueira**	Eastern oyster, *Crassostrea virginica*, population genomics in a well-mixed estuarine system (Great Bay Estuary, New Hampshire, USA) **Stasse*, Brown**	This workshop will introduce the concept of enterprise budgets, evaluate risks the industry faces when doing business, and discuss ways the industry may be supported to ensure their financial success in the future.	Shrimp genomics and epigenomes (ShrimpENCODE): recognition to students and "2024 Young Outstanding ONE HEALTH Researchers in Aquaculture and Fisheries" Awards **Alcivar-Warren, Tang-Nelson**
9:30AM	A neurophysiological role of glutamate in ganglia of the bivalve *Crassostrea virginica* **Obianke*, Myrbel, Carroll, Catapane**	Transgressive gene expression and expression plasticity under thermal stress in hybrid *Mytilus* mussels **Schwartz, González, Strong, Truebano, Hilbish**	Ontogenetic stage influences on survivorship disparity between diploid and triploid eastern oysters **Brianik*, Rivara, Patricio, Proestou, Liu, Topping, Jamieson, Ratcliff, Guo, Pales Espinosa, Allam**		Putative Endogenous Viral Elements (EVE) identified in three whole reference genome assemblies available for the Pacific whiteleg shrimp, *Penaeus vannamei* **Yuan, Alcivar-Warren**
9:45AM	6-Hydroxydopamine treatment causes supersensitivity of dopamine D2R receptors in gill lateral cells of *Crassostrea virginica* **Cayemitte*, Saqib, Carroll, Catapane**	Signatures of positive selection to ocean acidification resilience in larval Mediterranean mussels *Mytilus galloprovincialis* **Chancellor*, Churches, Kim, Jacobson, Nuzhdin**	Growth and survival of tetraploid eastern oysters, *Crassostrea virginica*, in different salinity environments in the Gulf of Mexico **Capps, Rikard, Spellman, Chaplin**		FIC domain-containing enzyme genes in invertebrates: a tale of transposons, pathogenic, and integrated viruses **Kawato, De Felice, Frizzo, Wegner, Rosani**
10:00AM	Comparison of the neurotoxic actions of 6-hydroxydopamine and manganese on gill lateral cell dopamine D2R receptors of *Crassostrea virginica* **Small*, Wilson, Joseph, Carroll, Catapane**	The hologenome of the Chilean blue mussel, *Mytilus chilensis*, exposed to hypoxia **Gallardo-Escárate, Valenzuela-Muñoz, Roberts**	The effects of water chemistry on the survival and growth of eastern oyster, *Crassostrea virginica*, larvae in culture **Hall*, Gima, Hu, Blaylock**		Issues related to the delisting of Infectious Hypodermal and Hematopoietic Necrosis (IHHN) as a notifiable disease by the World Health Organization for Animal Health (WHOA) **Tang, Alcivar-Warren**
10:15AM	Western blot study of the neurotoxic effects of Manganism and Parkinson's Diseases **Mansfield*, Acheampong, Foster, Carroll, Catapane**	Genome sequencing reveals genomic basis for domestication and environmental adaptation in Kumamoto oysters, *Crassostrea sikamea* **Liu, Liu, Guo, Itoh, Chang, Lin, Xue**	Ecological assessment of environmental health and oyster aquaculture grow-out conditions in Rehoboth Bay, Delaware **Andrade*, Attarwala, Ramos, Parsaeimehr, Ozbay**		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*, Alday-Sanz, Tang, Galindo, Alcivar-Warren**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**SHELLFISH & CARBON SEQUESTRATION WORKSHOP** **Max Zavell & Ramon Filgueria**	**GENETICS, GENOMICS & BREEDING** **Louis Plough**	**OYSTERS** **Bill Fisher**	**SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM** **Nicole Kirchhoff & Angela Collins**	**SHRIMP ENCODE** **Acacia Alcivar-Warren & Kathy Tang-Nelson**
11:00 AM		Assessing the evolutionary response of the eastern oyster to exposure to coastal acidification and sewage effluent: a case study **Puritz, Zyck, Harvey, Lotterhos**	Acute and long-term responses of juvenile oysters to dynamic multiple coastal stressors **Guidry*, Randall, Puritz**		Repetitive elements from the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, produced in the United States **Alcivar-Warren, Bao, Yuan, Guo, Karoonuthaisiri, Uengwetwanit, Sittikankaew, Asunción, Alcivar-Arteaga**
11:15 AM		Comprehensive genomic analysis of *Argopecten irradians* across the United States: Revealing population diversity and evolutionary history **Grouzdev, Pales Espinosa, Tettelbach, Tobi, Goodheart, Hollenbeck, Wilbur, Allam**	Interacting climate change stressors and carryover effects in oysters **McDonough*, Donelan, Miller, Gignoux-Wolfsohn**		DNA transposons from the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, produced in the United States **Bao, Alcivar-Warren, Yuan, Guo**
SESSION TITLE	**SHELLFISH & CARBON SEQUESTRATION WORKSHOP** **Max Zavell & Ramon Filgueria**	**GENETICS, GENOMICS & BREEDING** **Louis Plough**	**OYSTERS** **Bill Fisher**		**MANGROVE SHELLFISH** **Acacia Alcivar-Warren & Karin Tome**
11:30 AM		Eastern oyster (*Crassostrea virginica*) cis-defensin antimicrobial peptides: gene structure, expression, and diversity **Hanna*, Flora, Kuldell, Drawec, Krause**	The pros and cons of long-term datasets: a case study of eastern oyster (*Crassostrea virginica*) reproduction in south Florida estuaries **Levine, Geiger, Kirby**		Mangrove shellfish: from carbon storage to epigenetics: recognition to students and "2024 Outstanding ONE HEALTH Researchers in Aquaculture and Fisheries" Awards **Alcivar-Warren, Tome**
11:45 AM		Immortalized marine invertebrate cell lines for biomedicine and biotechnology **Davis**	A controlled flow-through system for studying the effects of ocean acidification on bivalve larvae **Hainey*, Zinck, Jennings, Fleener, Langdon**		What is Rotary and how does Rotary work for shellfish? **Puttock**
12:00 NOON		Direct measurement and genetic parameter estimation of Dermo resistance traits in an eastern oyster breeding population **Proestou, Delomas, Small**	*In situ* valve opening response of eastern oysters to estuarine conditions **Lavaud, Archer, La Peyre, Campanino, Casas, La Peyre**		
12:15 PM		Selection response of Gulf of Mexico eastern oyster (*Crassostrea virginica*) bred for performance in low salinity environments **King*, Yang, Sturmer, Hollenbeck, Stoeckel, Rikard, Gima, Stannard, Lucas, Buckmaster, Akter, Tarnecki, Saillant**	Machine learning and computer vision techniques to identify and monitor Ostreidae nondisruptively **Mekovsky*, Emmert, Rudy**		
12:30-1:30 PM	**LUNCH BREAK**				

* denotes student presenter ᵖ denotes non first-author presenter

MONDAY
March 18, 2024

NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Symphony I

ROOM	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
SESSION TITLE	**SHELLFISH MICROBOMES** **Rachel Diner & Tyler Griffin**	**GENETICS, GENOMICS & BREEDING** **Louis Plough**	**OYSTERS** **Bill Fisher**	**SHELLFISH AQUACULTURE ECONOMICS, RISKS & INSURANCE REFORM** **Nicole Kirchhoff & Angela Collins**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren & Karin Tome**
1:30 PM	Shellfish microbiomes: Challenges and Opportunities for Aquaculture and Ecology **Diner, Griffin**	Summer mortality in 2N and 3N Virginia- and North Carolina-derived oyster lines **Small, Audemard, Ciesielski, Noble, Reece, Wilbur, Ben-Horin**	A comparison of settlement plate material for monitoring oyster spat recruitment **Capps, Rikard**	This workshop will introduce the concept of enterprise budgets, evaluate risks the industry faces when doing business, and discuss ways the industry may be supported to ensure their financial success in the future.	The Mangrove Epigenome (MangroveENCODE) Project: a ONE HEALTH approach to conserving mangrove biodiversity **Alcivar-Arteaga, Lopez, Galindo, Asunción, Hernandez, Espinoza, Figueroa, Alcivar-Marcillo, Alcivar-Marcillo, Alemán, Alcivar-Parrales, Alcivar-Parrales, Alcivar-Loor, Alarcon-Mieles, Alcivar-Herrera, Calvo, Alcivar-Loor, Ortega, Alcivar-Arteaga, Nicolalde, Echevarria, Mishra, Chinnaiah, Ikeogu, Aveiga, Henry, McClennen, Mejia, Aveiga, Hall, Alejandro-Tigrero, Alejandro-Rosales, Alcivar-Warren**
1:45 PM	A bioinformatic search for viruses in the blue crab, *Callinectes sapidus*, across the U.S. geographical range of the species **Herrera*, Bachvaroff, Geba, Schott**	Comparative performance of triploid oysters, produced by chemical induction and mated triploid techniques, to their diploid counterparts **Vignier, Reardon, Exton, Rolton, Delisle, Malpot, Scholtens, Welford, Zamora, Ragg, Dunphy, Adams**	Advances in oyster primary cell and organ cultures **Sullivan*, Morrison, Steketee, Regan, Bean**		An estimate of carbon storage capabilities of wild and cultured shellfish in the northwest Atlantic and their potential inclusion in a carbon economy **Zavell*, Lindahl, Filgueira, Shumway**
2:00 PM	Selective capture of prokaryotes by mussels and ascidians as determined though microbiome sequencing in inhalant and exhalant waters **Griffin*, Capriotti, Dadon-Pilosof, Holohan, Yahel, Shumway, Ward**	Evaluation of the 2022-year class eastern oysters selected for disease resistance and fast growth **Ratcliff, Jamieson, Wang, Chriss, Tyburski, Abrams, Luu, Martindale, Huntzinger, Sabol, Gabris, O'Hala, Stucki, Coyne, Guo**	The Oyster Conservationist Program: a community science effort in Great Bay, New Hampshire **Arlen**		Identification of new *Vibrio campbellii* strains harboring the pVA1 plasmid isolated from *Penaeus vannamei* post-larvae affected by outbreaks of Acute Hepatopancreatic Necrosis Disease (AHPND) in Mexico **Soto-Rodriguez, Gomez-Gil, Lozano-Olvera, Aguilar-Rendón, González-Gómez*[P]**
2:15 PM	Characterizing the tissue-specific resident and transient microbial communities of the quagga mussel, *Dreissena bugensis* **Collins*, Griffin, Ward**	Genomic selection for growth traits of the eastern oyster in east Maine **Beal, Liu[P], Pepperman, Wolfe-Bryant**	Using the Driver-Pressure-State-Impact-Response (DPSIR) framework to support sustainable and healthy oyster production in Mississippi **Pruett, Fisher, Bernard, Darnell**		Protecting Freshwater Ecosystems: A Rotary International Partnership with the United Nations Environment Programme **Rico**
2:30 PM	Variable to their core: bivalve microbiomes have core bacteria but are altered by environment **Gignoux-Wolfsohn, Ruiz, Barron, Ruiz, Lohan**	Genomic selection for Dermo resistance in the eastern oyster, *Crassostrea virginica* **Wang*, Casas, La Peyre, Williams, Tarnecki, Rikard, Bushek, Guo**	Using an objectives hierarchy to support sustainable and healthy oyster production in Mississippi **Fisher, Pruett, Bernard, Darnell**		Time to integrate the "ONE HEALTH Approach" into Endrocrine Disrupting Chemicals (EDC) Research **Alcivar-Marcillo*, Alcivar-Parrales, Figueroa-Alemán, Alcivar-Marcillo, Galindo, Hernandez, Asunción, Ortega, Lopez-Zavala, Alcivar-Arteaga, Nicolalde, Alcivar-Loor, Alcivar-Warren**
2:45 PM	Can microbiome data be used to improve predictive models of critical estuarine habitats? A case study in Chesapeake Bay **Gnanadesikan, Arora-Williams, Holder, Jin, Yisrael, Zhang, Preheim**	Oyster survival in response to a laboratory challenge with *Perkinsus marinus* is a polygenic trait **Delomas, Proestou, Small**	Oyster insurance options from USDA Risk Management Agency **Sereno, Olive, Wilkin, Place, White**		
3:00 – 3:30 PM	**AFTERNOON BREAK**				
SESSION TITLE	**NORTHEAST BIVALVE HATCHERY HEALTH CONSORTIUM** **Marta Gomez-Chiarri & Rob Hudson**	**GENETICS, GENOMICS & BREEDING** **Louis Plough**		**DIVERSITY, EQUITY & INCLUSION** **Aswani Volety & Angela Caporelli**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren & Karin Tome**
3:30 PM	The objectives for this consortium are: (1) identify the causes of bivalve hatchery larval mortalities and crashes along the East Coast of the U.S. through an integrated, collaborative, and proactive approach to sample collection and analysis; and (2) develop strategies and protocols to manage and minimize larval crashes in hatcheries.	Genetic improvement of the eastern oyster and prospects of genomic selection **Guo, Ratcliff, Wang, Jamieson, Liu, Chriss, McGurk, Burt, Bushek**		Priming the pump and creating pipelines: example of increasing under-represented students to STEM areas at a State university **Volety, Roseboro, Loh**	Trace metal concentrations in *Penaeus vannamei* from Ecuador and El Salvador, and a review of metals and pesticides contaminating mangrove sediment and red mangrove crabs (*Ucides occidentalis*) at the Guayas Estuary of Ecuador **Aveiga*, De Cock, Alcivar-Arteaga, Henry, Astrofsky, Alcivar, McClennen, Figueroa, Espinosa, Alcivar-Warren**
3:45 PM		Single nucleotide polymorphisms (SNP) genotyping tools and their application in shellfish breeding programs: pedigree management to genomic selection **Allen, Verbyla, Stannard, Plouffe, Cerezo[P]**		Aquaculture in the midst of social change **Caporelli**	
4:00 PM		Time for a check-up: comparing levels of genetic diversity and inbreeding among hatchery lines with offspring from wild populations of eastern oysters (*Crassostrea virginica*) **Varney, Katsuki, Lotterhos, Small**			The role of probiotics in shrimp aquaculture: a comprehensive review in the Ecuadorian context **López-Zavala*, Asuncion, Galindo, Alcivar-Arteaga, Alcivar-Warren**
4:15 PM		Development of a microhaplotype-based genotyping panel for aquaculture, restoration, and fisheries management for *Crassostrea virginica* **Weber*, Matt, Delomas, Portnoy, Hollenbeck**		Diversity, equity, and inclusion in the Oyster Aquaculture and Restoration Space **Foster, Altagracia, Waters, Greenberg**	Shrimp Scampi: A citizen science project - educating about microbes and hormone disruptors like metals and glyphosate in shrimp using foldscopes **Hernandez*, Warren, Alcivar-Arteaga, Warren, Diaz, Figueroa-Zambrano, Reyes, Alcivar-Warren**
4:30 PM		Microhaplotypes boost power for relatedness analysis from SNP-based amplicon sequence panels in the Pacific oyster **Thompson, Sutherland, Green, Delomas**		Discussion	Citizen science approach to mitigate the effects of harmful algal blooms in Costa Rica **Morton, Vanopdenbosch, Shumway**
4:45 PM		Optimization of low-density SNP panels for genotype imputation in oysters **Hollenbeck**			
5:00 PM		Methods and results of applying low-cost genomic tools for selective breeding of *Crassostrea virginica* in Texas **Matt, Weber, Portnoy, Hollenbeck**			Workshop: How to write effective global grants for funding by Rotary International **Puttock, Tome**
5:15 PM					
5:30 PM					

* denotes student presenter [P] denotes non first-author presenter

TUESDAY
March 19, 2024

8:00-8:50AM — **PLENARY: – Jeanne Serb (Iowa State University) - *Seeing the light, tasting the ocean: how bivalves sense their environment***
Symphony V-VI-VII

NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Symphony I

ROOM	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
SESSION TITLE	**DISEASE** **David Bushek, Ryan Carnegie & Tal Ben-horin**	**ROBOTICS & EMERGING TECHNOLOGY** **Allen Pattillo & Yang Tao**	**CLIMATE CHANGE, OCEAN ACIDIFICATION & MODELLING** **Eric Powell & Roger Mann**	**SHELLFISH REPRODUCTION** **Kaitlyn Kowaleski**	**GENERAL CONTRIBUTED I** **Paul Rawson**
9:15AM	New insights into the life history of *Hematodinium perezi* (Dinoflagellata: Syndiniales) in juvenile blue crabs (*Callinectes sapidus*) **Chen*, Reece, Shields**	STREAM – A satellite-based water-quality monitoring system for effective assessment of aquaculture operations **Pahlevan, Wainwright, Ashapure, Golpayegani, Ashapure, Smith, O'Shea, Kabir, Saranathan**	Projected range shift of the Atlantic surfclam, *Spisula solidissima*, from climate-induced benthic warming: forecasting fishery influence in the Mid-Atlantic Bight throughout the 21st century **Spencer*, Powell, Klinck, Munroe, LeClair, Scheld, Hofmann, Borsetti, Curchitser**	Gonads and gourmet: Unveiling farmed scallop's plump treasures and aquaculture's bounty potential **Jekielek*, Williams, Maier, Martin, Leslie, Price, Hopple**	Razor clam growth rates in relation to sediment type **Harris*, Morse, St. Gelais, Rawson**
9:30AM	Dynamics of Bay Scallop Marosporida (BSM) in the host and environmental samples from the Peconic Bays, New York **Cacot, Pales Espinosa, Mannino, Trainer, Snyder, Tettelbach, Tobi, Allam**	Assessing the feasibility of renting Smart Sustainable Shellfish Aquaculture Management (S^3AM) as a service for small oyster farms **Ojha*, van Senten**	The future of fisheries and renewable energy: modeling potential impacts of U.S. offshore wind energy development on the Atlantic surfclam, *Spisula solidissmia*, fishery in the Mid-Atlantic Bight **Moya*, Powell, Munroe, Scheld, Klinck, Hofmann, Borsetti, Curchitser, Spencer**	Extreme population densities impact oocyte production in Atlantic sea scallops, *Placopecten magellanicus* **Kowaleski*, Roman, Mann, Rudders**	Growth and survival of transplanted softshell clams (*Mya arenaria*) during a winter grow-out period in the York River, Virginia **Schoenberg*, Knick, Seebo, Seitz**
9:45AM	Effect of chronic temperature alterations on disease development and mortality in the northern bay scallop, *Argopecten irradians irradians* **Trainer*, Tobi, Dominguez, Cacot, Pales Espinosa, Tettelbach, Allam**	High-pressure processing (HPP) as an emerging technology: microbial and physicochemical effects on precooked blue crab meat **Liu, Bhetwal, Min, Nindo**	Cross-generational effects of ocean acidification on a third generation of bay scallops **McFarland, Gurr, Padilla, Bernatchez, Dixon, Guy, Milke, Poach, Hart, Plough, Redman, Sennefelder, Stiles, Veilleux, Wikfors, Meseck**	Understanding reproductive development in female white shrimp, *Penaeus setiferus*, in support of sustainable fisheries management in South Carolina, USA **Mitchell*, Wagner, Brunson, Kingsley-Smith, Kendrick**	Thermal tolerance of Mercenaria spp. during a simulated marine heatwave in southwest Florida, USA **Hutchins, Sea, Hesterberg**
10:00AM	Comparison of *Perkinsus marinus* and *Haplosporidium nelsoni* prevalence and intensity in oysters across four sites on Sapelo Island, Georgia **Atencio*, Ziegler, Carroll**	Effects of high-pressure processing (HPP) on the sensory quality and consumer acceptability of precooked ready-to-eat (RTE) Atlantic blue crab meat **Liu, Nash, Watts, Takacs, Feng, Nindo**	Multistressor laboratory experiments with the Atlantic surfclam (*Spisula solidissima*): ocean warming and acidification **Steeves, Honecker, Meseck, Guo, Towers, Munroe**	Salinity and food supply influence oyster larval performance and recruitment limitation in the western Mississippi Sound: a modeling study **Klein*, Powell, Kreeger, Zhang, Pace, Kuykendall, Thomas, Wissing**	
10:15AM	Phenology of *Perkinsus marinus* and climate change **Scott*, Bushek**	A panel discussion on high-pressure processing (HPP) technology: challenges and opportunities for better quality and clean label seafood products **Liu, Phan, Feng, Pattillo**	Ocean acidification and ocean dumping: comparing past and present carbonate chemistry and dissolved oxygen conditions of sea scallop and surfclam habitat along a coastal shelf **Tomasetti, Kraemer, Jr., Gobler**	Investigating the influence of phytoplankton size distribution on the success of eastern oyster (*Crassostrea virginica*) larvae in the Mississippi Sound: a modeling study **Coltman*, Powell, Zhang, Mojica, Kreeger, Klein**	
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**DISEASE** **David Bushek, Ryan Carnegie & Tal Ben-horin**	**ROBOTICS & EMERGING TECHNOLOGY** **Allen Pattillo & Yang Tao**	**CLIMATE CHANGE, OCEAN ACIDIFICATION & MODELLING** **Eric Powell & Roger Mann**	**GENERAL CONTRIBUTED II** **Gulnihal Ozbay**	**GENERAL CONTRIBUTED III** **Shirley Baker**
11:00 AM	Non-zoonotic tissue parasites in the eastern oyster **Gaona-Hernandez, Jurgens, Quigg**	Leveraging the r-strategy and unmanned aerial vehicles to overcome predation in shellfish restoration projects **Hale, Osborne**	Improving resilience of hatchery-reared blue mussels (*Mytilus edulis*) to ocean acidification with diet and seawater buffering **Holmberg, Tripler, Young, Moretti, John, Root, Smith, Sun, Pepperman, Beal**	Monitoring temporal trends in the distribution of the range expanding blue crab (*Callinectes sapidus*) in southern Maine estuaries **Crane, Gutzler, Burke, Goldstein**	Growth and physiological responses of freshwater mussels (*Utterbackiana implicata* and *Sagittunio nasutus*) reciprocally transplanted between a pond and stream site **Gentry*, Kreeger**
11:15 AM	Expanding the phylogeography and connectivity of *Perkinsus* species across North and Central America **Yisrael, DiMaria, Ciminera, Aguirre-Macedo, Martinez, Ruiz, Torchin, Hill-Spanik, Gnanadesikan, Lohan**	Discussion	Predicting restoration and aquaculture potential of eastern oysters through an eco-physiological mechanistic model **Lavaud, La Peyre, Couvillion, Pollack, Brown, Palmer, Keim**	A multifaceted approach to study the northern range expansion of Atlantic blue crabs, *Callinectes sapidus*, in the Gulf of Maine **Batchelder, McMahan, Bradt**	Creating a histological atlas for Maryland freshwater mussels **Preziosi, McCollough**
11:30 AM	Update on the Connecticut oyster disease monitoring program **Bienlien, Carey**		Predicting larval dispersal and population connectivity of sea scallops, *Placopecten magellanicus*, along the coast of Downeast Maine **Ward, Xue, Kingston, Rawson[p]**	Blue crab (*Callinectes sapidus*) population characteristics and Callinectes sapidus Reovirus 1 (CsRV1) identification **Ramos*, Attarwala, Andrade, Parsaeimehr, Ozbay**	Comparing ribbed mussel settlement in natural fringing marshes versus living shorelines in the Chesapeake Bay **Rose*, Bilkovic, Isdell**
SESSION TITLE	**DISEASE** **David Bushek, Ryan Carnegie & Tal Ben-horin**	**GENERAL CONTRIBUTED IV** **Allen Pattillo**	**AQUACULTURE AS A TOOL FOR RESTORATION** **Angela Collins, Charles Weirich & Mark Rath**	**GENERAL CONTRIBUTED II** **Gulnihal Ozbay**	**GENERAL CONTRIBUTED III** **Shirley Baker**
11:45 AM	Development of novel molecular technique to diagnose presence and severity of hemocytic neoplasia in northern quahogs (= hard clam) (*Mercenaria mercenaria*) **Torselli, Scro, Gast, Sharon, Smolowitz**	Tides Out: Washington shellfish crew and manager training program **Epps, Naar, Poe**	Restoring native shellfish communities for improved water quality and economic resiliency in the Indian River Lagoon, Florida **Osborne, Ibarra-Castro, Sturmer**	Science to support management of invasive green crab: a Washington State case study **McDonald, Grason, Tepolt, Litle, Rubinoff, Stote**	Settlement and metamorphosis of the ribbed mussel, *Geukensia demissa*, in response to environmental cues **Anderson*, Padilla**
12:00 NOON	Applying novel molecular workflows to monitor potential agents of disease **Ciesielski*, Smith, Ben-Horin, Noble**	A year in review: the Commercial Oyster Aquaculture Sector Training (COAST) Program **Tarnecki, Grice**	Assisted seagrass recovery using co-plantings of the native southern hard clam (*Mercenaria campechiensis*) in southwest Florida, USA **Hesterberg, Hutchins, Sea, Furman, Patranella, Congdon, Smyth, Laws**	Assessing short-term effects of marine heat waves and hypoxia on Jonah crab (*Cancer borealis*) feeding behavior and survival **Mabaka*, Kraemer, Tracy, Tomasetti, Doall, Gobler**	Why mussels can survive without oxygen, but are sensitive to anoxia **Foekema, Keur, Peterson, Peck, Murk**
12:15 PM	Analysis of genetic diversity of a newly discovered trematode parasite of the bay scallop (*Argopecten irradians*) in North Carolina **Brainard*, Buck, Varney, Ben-Horin, Wilbur**	Removal of nocturnal hypoxia increases juvenile bivalve growth **Kraemer, Jr.*, Gobler**	Calling all clams: coordinating partners to maximize project impact and prioritize research objectives for clam restoration initiatives in Florida **Collins, Ryan, Chiles, Hurt, Osborne, Smyth, Williams**	Aerobic scope and thermal tolerance: contrasting responses in shrimp, crayfish, and mussels **Abdelrahman, Hussain, Fogelman, Roy, Stoeckel**	Cytochrome P450-dependent mixed function oxidases (MFO) system dynamics during the Poly aromatic hydrocarbon (PAH) metabolism in green mussel *Perna viridis* (Linnaeus, 1758) **Chinnaiah**
12:30-1:30 PM	**LUNCH BREAK**				

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TUESDAY
March 19, 2024

NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Symphony I

ROOM	Symphony II	Symphony III	Symphony V	Symphony VI	Symphony VII
SESSION TITLE	**DISEASE** **David Bushek, Ryan Carnegie & Tal Ben-horin**	**SOCIAL DIMENSIONS OF SHELLFISHERIES** **Adriane Michaelis & Don Webster**	**AQUACULTURE AS A TOOL FOR RESTORATION** **Chuck Weirich, Mark Rath & Angela Collins**	**eDNA APPLICATIONS FOR SHELLFISH** **Phoebe Jekielek**	**SCIENCE & PUBLIC ENGAGEMENT WORKSHOP** **David Shiffman**
1:30 PM	Infection with *Sacculina* sp. reduces egg quantity but not egg quality of the bay scallop, *Argopecten irradians* **Buck, Boggess, Andrade, Ben-Horin, Wilbur**	How representative is your sample? Demographic data in the US shellfish aquaculture industry **Michaelis, Walton**	Streamlining regulation to facilitate seagrass and native clam restoration aquaculture **Williams*, Ankersen, DePaolis, Collins**	Multifaceted study of an ongoing range expansion of blue crabs (*Callinectes sapidus*) **Henry*, Grey, Goldstein, Crane, Miller, McMahan, Batchelder**	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.
1:45 PM	Potential impacts of the parasitic trematode, *Bucephalus cuculus*, in a collapsed oyster fishery **Kirby, Geiger, Levine, Davis**	Adopting principles of food justice for equitable oyster aquaculture industry development **Sandolo, St. Gelais, Costa-Pierce, Miller-Hope, Hood, Hale, Black, Young**	The effects of bivalve shellfish aquaculture on sediment denitrification in Florida **Foursa, Collins, Sturmer, Gassen, Anderson, Smyth**	Using DNA metabarcoding to understand the feeding ecology of the Atlantic sea scallop, *Placopecten magellanicus* **Munoz*, McDowell, Rudders**	
2:00 PM	Improved resistance to *Vibrio coralliilyticus* and ostreid herpesvirus 1 mortality in juvenile Pacific oysters (*Crassostrea gigas*) selected for a single nucleotide polymorphism on chromosome 8 **Lunda*, Divilov, Green, Sutherland, Jennings, Mandour, Mueller, Wang, Jin, Langdon**	Impacts of gentrification, loss of access, and a changing coastal environment on the softshell clam fishery in Maine **Farr, McMahan, Batchelder**	Oyster enhancement for New Hampshire oyster growers and estuaries **Jones, Grizzle, Ward, Gross**	eDNA metabarcoding to survey shellfish in the Gulf of Maine **Bolton Jr.*, Grey-Avis, Peters**	
2:15 PM	Maximizing oyster aquaculture yield across diverse disease defense traits **Bulmer*, Gomez-Chiarri, Proestou, Ben-Horin**	Exploring resilience in the oyster farming industry of North Carolina **Eimers*, Murray, Noble**	Three-dimensional reefs: moving oyster restoration out of the Stone Age **DePaola**	eDNA: Casting a new net for monitoring sea scallop (*Placopecten magellanicus*) fisheries **Jekielek*, Leslie, Price**	
SESSION TITLE	**OsHV1 NOROVIRUS** **Kimberly Reece**	**SOCIAL DIMENSIONS OF SHELLFISHERIES** **Adriane Michaelis & Don Webster**	**AQUACULTURE AS A TOOL FOR RESTORATION** **Chuck Weirich, Mark Rath & Angela Collins**	**eDNA APPLICATIONS FOR SHELLFISH** **Phoebe Jekielek**	**SCIENCE & PUBLIC ENGAGEMENT WORKSHOP** **David Shiffman**
2:30 PM	Multiple omics to disentangle new facets of the enigmatic family of mollusc herpesviruses **Rosani, Bortoletto, Bai, Krupovic**	Increasing shellfish aquaculture intersections with oyster restoration: implications for shellfish health management **Carnegie**	Adapting aquaculture techniques to enhance oyster populations, *Crassostrea virginica*, in reef restoration **LoBuglio, Capps, Golightly, Rikard**	Environmental DNA early-warning systems for biofouling: promises and pitfalls **Grey, Moline, Havener, Noren, Pierce, Brady**	
2:45 PM	Knowledge is power: resolving the geographic distribution and host range of OsHV-1 on the East and Gulf coasts to mitigate impediments on shellfish aquaculture commerce **Burge, Prado-Zapata, MacIntyre, Hudson, Webster, Carnegie, Reece**	Survey of shellfish aquaculture management priorities in Maine, North Carolina, and Florida **Arthur*, Murray**	Quantifying habitat provision services of oyster (*Crassostrea virginica*) aquaculture and performance among two farmed strains grown along a tidal gradient **Campbell, Hudock, Motz, Carlisle, Hale**	Enhancing blue mussel seed collection through larval-specific environmental RNA (eRNA) tools **Ernst, Beal, Grey, Salter, Whitney, Price**	
3:00 PM	Update on laboratory challenges to *Crassostrea virginica* families and lines with OsHV-1 microvariants **Reece, Small, Agnew, MacIntyre, Scott, Burge**	Values, problem definitions, and policy preferences in Maine aquaculture **Fail*, Murray**	Concerned oystermen restoring estuaries **Grice, Swann**	Environmental deoxyribonucleic acid (eDNA): Does the science make sense? **Zajicek, Stone**	
3:15PM	Impact of bacterial community and acclimation on mortality of juvenile Pacific oysters (*Crassostrea gigas*) caused by OsHV-1 infection **Day, Sarowar, Lunda, Zanuzzo[p], Langdon**	A roadmap for advancing social license to operate for aquaculture: East and West Coast USA **Whitmore, Noll, Davis, Avena**	Leveraging aquaculture for restoration: An overview of the Supporting Oyster Aquaculture and Restoration Program **Foster, Hancock, Jones, Greenberg, Borgert**	Assessing eastern oyster *Crassostrea virginica* predation utilizing real-time monitoring and eDNA analysis in Delaware Inland Bays **Attarwala*, Ramos, Andrade, Riggi, Boukari, Venello, Parsaeimehr, Ozbay**	
3:30 PM	Discussion	Best Practices help growers improve social license **Rheault**	Feasibility of using shellfish aquaculture for water quality improvement initiatives in Florida **Smyth, Ankersen, Baker, Collins, Foursa, Grogan, Lovestrand, Patterson, Sturmer**		
3:45 PM		Empowering seafood servers to tell the stories of aquacultured oysters: 2024 update on the Oyster Essentials Training Program **Walton, Bliss, Marquez, Michaelis, Petrolia, Rider, Sturmer, Walton**	The New Jersey Shellfish Aquaculture Exchange — a cross-cutting approach to habitat restoration and resiliency **Rowe, Calvo, DeLuca, Munroe, Babb, Normant, Steuber, Evert, Thompson**		
4:00 – 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Symphony IV**				
7:00 - 10:00 PM	**STUDENT ENDOWMENT FUND AUCTION** **Symphony Foyer**				

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WEDNESDAY
March 20, 2024

8:00-8:50AM	**PLENARY: Eileen Hofmann (Old Dominion University) – *Models in shellfish biology - what can they tell us?*** **Symphony V-VI-VII**				
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Symphony I**				
ROOM	**Symphony II**	**Symphony III**	**Symphony V**	**Symphony VI**	**Symphony VII**
SESSION TITLE	**HATCHING A PLAN FOR AQUACULTURE COMMUNICATIONS: STRATEGIES, RESOURCES & PARTNERSHIPS** **Brianna Shaughnessy**	**BIRDS & SHELLFISH SANITATION** **Bob Rheault**	**MACROALGAE-SHELLFISH CO-CULTURE** **Michael Doall**	**ANTHROPOGENIC POLLUTANTS AND THEIR IMPACTS ON SHELLFISH BIOLOGY AND ECOLOGY** **Evan Ward & Kayla Mladinich**	**ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS** **Eric Heupel**
9:15AM	A snapshot of NOAA resources for seafood communications and engagement **Shaughnessy**	Management of bird-related pathogen risk in shellfish aquaculture **Rheault**	Shellfish and seaweed aquaculture ecosystem services horizon scan: project update **Michaelis, Bricker[p], Hollarsmith, Rose, Theuerkauf**	Investigating the interactions between microplastics and freshwater bivalves **Olatunji*, Collins, Holohan, Ward**	This workshop will discuss a number of core ideas and techniques that can help scientists and researchers create more engaging power point slides and posters resulting in a more effective way to communicate science to all audiences.
9:30AM	Fishermen or scientists? How ideology shapes who the public trusts for information on aquaculture **Whitmore, Noll, Davis, Safford, Hamilton**	High-resolution monitoring of avian communities at mariculture operations yields insights into community dynamics, biogeochemistry, and sanitation risks **O'Keefe*, Fodrie**	Strategies for co-culturing seaweed and bivalves: scientific and industry perspectives **Bailey, Olsen, Barbery**	Investigating suspension-feeding invertebrates as bioindicators of microplastics **Mladinich*, Holohan, Shumway, Ward**	
9:45AM	Window to an underwater world: sharing the habitat value of shellfish farms with a broad audience **Jabanoski, Rose, Phillips, Clark, Dixon, Redman, Smith, Mercaldo-Allen**	Seabirds, *Campylobacter*, and off-bottom oyster aquaculture **Matvey*, Tarnecki, Rikard**	Expanding the ecosystem services of oyster farms with the co-cultivation of sugar kelp, *Saccharina latissima*: maximizing nitrogen bioextraction **Doall, Curtin, Morrell, Eckstein, Chen, Meichenbaum, Gobler**	Extreme heat event influences the toxic impacts of TiO_2 nanoparticles with different crystal structures on the mussel, *Mytilus coruscus* **Li*, Li, Wei, Mao, Hu, Wang**	
10:00AM	Aquaculture communications resources and initiatives provided by NOAA National Sea Grant **Rath, Weirich, Shaughnessy, Davis, Meltzer, Dupree, Garber**	Assessing the risk of pathogen contamination from roosting birds on aquaculture gear **Richard, Muller, Paton, Lavoie, Gomez-Chiarri, McWilliams**	Nutrient remediation capacity of three New Zealand kelp species: considerations for IMTA applications with *Perna canaliculus* **McCarthy*, Wing**	Effects of perfluorooctanoate and nano titanium dioxide on male gonads of the thick-shell mussel, *Mytilus coruscus* **Pan*, Sun, Hu, Wang**	
10:15AM	Discussion	Establishing a framework for understanding risks associated with birds on shellfish and co-culture operations **Noble, Blackwood, Bennett, Clerkin, Smith, Eimers, O' Keefe, Ciesielski**	Achieving carbon neutral bivalve aquaculture via the cultivation of seaweeds **Gobler, Tomasetti, Doall**	Ocean acidification may increase the biological impact of metal pollution on commercial bivalves, a case study from mine waste deposits in Arctic Norway **Rastrick, Jiang, Brown, Aguera, Bank, van der Meeren, Jiang, Rastrick[p]**	
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**THE FUTURE OF AQUACULTURE AT THE NOAA FISHERIES SERVICE** **Danielle Blacklock**	**BIRDS & SHELLFISH SANITATION** **Bob Rheault**	**MACROALGAE-SHELLFISH CO-CULTURE** **Michael Doall**	**ANTHROPOGENIC POLLUTANTS AND THEIR IMPACTS ON SHELLFISH BIOLOGY AND ECOLOGY** **Evan Ward & Kayla Mladinich**	**ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS** **Eric Heupel**
11:00 AM	In this workshop, participants will use instant response technology to take part in prioritization discussions of existing aquaculture related services the NOAA Fisheries Service provides	Risk of pathogen transfer from birds is unknown **Hudson**	The impacts of two macroalgal species, *Ulva* sp. and *Gracilaria* sp. on the growth and survivorship of eastern oyster, *Crassostrea virginica* **Eckstein, Doall, Gobler, McGuire, Chen, Sylvers**	Mapping impact risks assessment of navigation noise on giant scallop beds in the Gulf of St. Lawrence, Canada **Poitevin, Aulanier, Olivier, Jezequel, Archambault, Chauvaud, Tremblay**	
11:15 AM		Discussion	Greening aquaculture: cultivation of native sea lettuce (*Ulva* spp.) for polyculture research **Mundy*, Carroll**	Exposure to plastic debris alters expression of biomineralization, immune, and stress-related genes in the eastern oyster (*Crassostrea virginica*) **Eierman, Landis**	
11:30 AM			The mitigation of harmful algal blooms (*Alexandrium catenella*, *Pseudo-nitzschia* spp., *Dinophysis acuminata*, *Margalefidinium polykrikoides*) by cultivable seaweeds **Sylvers*, Gobler**	Identification of molecular biomarkers against xenobiotics in the marine green mussel, *Perna viridis* **Chinnaiah**	
11:45 AM					
12:00 NOON					
12:15 PM					
12:30-2:00 PM	**NSA BUSINESS LUNCHEON** **Symphony Foyer**				
2:00 - 4:30 PM	**SCALLOP GALLOP** **EXPLORE CHARLOTTE!!**				
4:30 - 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Symphony IV**				

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THURSDAY March 21, 2024				
8:00-8:50AM	**PLENARY: Gregory Dietl (Cornell University) – *Conservation paleobiology: putting the dead to work*** **Symphony V-VI-VII**			
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Symphony I**			
ROOM	**Symphony II**	**Symphony III**	**Symphony V**	**Symphony VI**
SESSION TITLE	**DOWN ON THE FARM** **Leslie Sturmer & Bill Walton**	**COMMERCIAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**	**HARMFUL ALGAL BLOOMS** **Steve Morton**	***VIBRIO*** **Steve Jones**
9:15AM	Comparing performance of various triploid oyster (*Crassostrea virginica*) seed lines and stocking densities in novel subtidal aquaculture gear **Klein*, Powell, Harman**	Using the intertidal zone as a nursery for juvenile cultured softshell clam: a comparative experiment from three Maine communities **Beal, Coffin, Randall, Houston**	Uptake, distribution, and depuration of PSP-inducing phycotoxins in Arctic surfclams *Mactromeris polynyma* (Stimpson 1860) **Sanders*, Beal, Leighfield, Morton, Shumway**	Host specificity of predatory bacteria against human pathogenic strains of *Vibrio parahaemolyticus*: potential intervention strategies for *Vibrios* in market oysters **Richards, Williams, Watson, Jones**
9:30AM	Differences in tolerance and responses to thermal stress between diploid and triploid eastern oysters (*Crassostrea virginica*) from the northern Gulf of Mexico **Boyd*, Abdelrahman, Rikard, Tarnecki, Stoeckel**	Decadal population variability in subtidal bay clams in Tillamook Bay, Oregon, USA: implications for management of commercial bay clam dive fishery **D'Andrea, Gellhaus, Swanson, Hansen**	Annual spatial and temporal dynamics of *Margalefidinium polykrikoides* in Rhode Island **Whitney*, Scro, Osinski, Savastano, Sharon, Scott, Smolowitz**	Use of direct-fed microbes to enhance shrimp resistance to a *Vibrio parahaemolyticus* strain causing Early Morality Syndrome (EMS) **Kuhn, Smith, Williams, Galagarza, Thompson, Drahos, Stevens[p]**
9:45AM	A FARMS approach to address oyster mortality in the off-bottom oyster aquaculture industry in Florida **Sturmer, Anderson, Roberts**	Interactive effects of size and intraspecific density on growth and survival of cultured juvenile Arctic surfclam, *Mactromeris polynyma*, in two eastern Maine intertidal flats **Beal, Pepperman, Salter, Houston**	Investigating the relationship between seawater nutrients and harmful algal blooms at Rhode Island shellfish farms **Osinski, Savastano, Whitney, Scro, Scott, Sharon, Smolowitz**	Expanding industry applications of biphasic assays for *Vibrio* enumeration in oysters **DePaola, Kim, Tarnecki, Dewey**
10:00AM	Assessing the effects of husbandry decisions on mortality, growth, and time-to-market in off-bottom oyster aquaculture **LaGanke*, Walton**	A numerical investigation of size selectivity in a modified scallop dredge **Boisvert*, Cowles**	Algal toxins in cultured oysters across diverse coastal sites **Simpson*, Schnetzer, Ben-Horin**	Development of identification and detection methods for emerging causes of vibriosis **Jones, Pruente, McGough, Hyde-Leard, Neil**
10:15-10:45AM	**MORNING BREAK**			
SESSION TITLE	**DOWN ON THE FARM** **Leslie Sturmer & Bill Walton**	**COMMERCIAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**	**HARMFUL ALGAL BLOOMS** **Steve Morton**	***VIBRIO*** **Steve Jones**
10:45AM	Antifouling surface texturing of equipment and biofouling monitoring benefits for shellfish aquaculture **Dürr, Shaw, Conlan, Sharp**	Modifications to a scallop dredge twine top to reduce flatfish catch **Roman, Rudders, Watson, Rossiter**	The synergistic effects of harmful algae and ocean acidification on larval bivalve survival **Tracy*, Farrell, Tang, Callahan, Gobler**	Climate change and infectious diseases: The *Vibrio* model **Brumfield, Usmani, Jutla, Huq, Colwell**
11:00 AM		The United States sea scallop resource: its historic success and present decline **Stokesbury**	Assessing behavioral changes in the eastern oyster, *Crassostrea virginica*, when exposed to *Margalefidinium polykrikoides* **Brothers, Scro, Whitney, Brosnahan, Chamberlin, Sharon, Scott, Smolowitz**	Long-term seasonal ecology of *Vibrio parahaemolyticus* in the northeast US **Jones, White, Foxall, Whistler**
11:15 AM	Recovery mechanisms of eelgrass (*Zostera marina*) following mechanical harvest of Pacific oysters (*Crassostrea gigas*) **Boardman*, Ruesink**	NOAA-supported resources for commercial shellfisheries researchers, managers, and operators **Wright-Fairbanks, Perotti[p]**	Participatory science approach to monitor harmful algal blooms, and changes in environmental conditions with the aquaculture industry **Morton, Rene, Maucher-Fuquay, Shuler**	Efficacy of refrigerated wet storage to reduce *Vibrio parahaemolyticus* as demonstrated by a novel test kit **Dewey, Louma, Wood, DePaola, Kim**
11:30 AM	Oyster farming resilience index **Grice, Swann, Sempier, Sempier, Deal**			Relationship between gaping behavior of the eastern oyster, *Crassostrea virginica*, and *Vibrio* spp. load **Kleist*, Stoeckel, Tarnecki, Rikard**
SESSION TITLE	**DOWN ON THE FARM** **Leslie Sturmer & Bill Walton**	**SHELLFISH RESTORATION & CONSERVATION** **Dave Eggleston, Martin Posey & Peter Kingsley-Smith**		***VIBRIO*** **Steve Jones**
11:45 AM	Development of the softshell clam aquaculture in Maryland waters **Liu, Wolfe-Bryant, Farrington, Wolfe-Bryant, Bhandari, Knoche**	Impacts of oyster aquaculture on adjacent natural reefs **Posey, Alphin, Lytle, Darrow**		Influence of polycyclic aromatic hydrocarbons (PAH) on concentrations of human-pathogenic *Vibrio* spp. in oysters and sediments under *in situ* conditions **Audemard, Brown, MacIntyre, Prossner, Vogelbein, Mainor, Wargo, Reece, Unger**
12:00-1:00 PM	**LUNCH BREAK**			

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THURSDAY March 21, 2024				
NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY Symphony I				
ROOM	**Symphony II**	**Symphony III**	**Symphony V**	**Symphony VI**
SESSION TITLE	**HATCHERIES** **Don Webster**	**SHELLFISH RESTORATION & CONSERVATION** **Dave Eggleston, Martin Posey & Peter Kingsley-Smith**	**ADVANCING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM** **David Bushek, Ryan Carnegie, Karen Hudson & Tal Ben-horin**	***VIBRIO*** **Steve Jones**
1:00 PM	Evaluating abiotic and biotic factors influencing northern quahog (= hard clam) production in Florida, USA **Anderson, Sturmer, Laramore, Getter, Collins, Philps, Baker**	Distribution of oyster settlement on novel Reefense modules and implications for artificial reef colonization **Shinn, Coli, Bushek, Holland, Ruszala, Nassif**	Advancing the Regional Shellfish Seed Biosecurity Program (RSSBP) **Bushek, Carnegie, Hudson, Ben-Horin, Safi, Rheault, Gustafson, Walton, Pollack, Sturmer, Rowe**	Assessing the abundance of *Vibrio parahaemolyticus* and *V. vulnificus* in cultured oysters associated with macroalgae from Rhode Island **Scro, Geisser, Smolowitz, Fulweiler**
1:15 PM	Developing a pilot scale shellfish hatchery in Delaware – first year progress update **Campbell, McIntosh, Campbell, Hale**	Exploring whether carbonate chemistry should be considered for site selection for eastern oysters (*Crassostrea virginica*) **Lemaire*, Carroll, Hoskins-Brown, Hintz**	Infection prevalence and intensity of *Perkinsus marinus* in hatchery oyster seed from the US East Coast **Safi, Bushek, McGurk, Carnegie, Crockett**	Phylogeography of north Atlantic populations of sequence type 36 *Vibrio parahaemolyticus* **Whistler, Foxall, Means, Marcinkiewicz, Xu, Hall, Schillaci, DeRosia-Banick, Cooper, Jones**
1:30 PM	Probiotic-induced protection of Pacific oyster (*Crassostrea gigas*) larvae from vibriosis in hatchery settings **Thorstenson, Schubiger, Lunda, Mueller, Langdon**	Tracking sources and sinks of eastern oyster (*Crassostrea virginica*) metapopulations in Shinnecock Bay, New York, USA **Woodard*, Doall, Dana, Eckstein, Curtin, Morrell, Gobler**	Status, participation, and progress of the Hatchery Compliance Program of the Regional Shellfish Seed Biosecurity Program (RSSBP) **Hudson, Bushek, Carnegie, Ben-Horin, Safi, Rheault, Gustafson, Marxen, Walton, Pollack, Sturmer, Rowe**	
1:45 PM	Improving spawning success of the sunray venus clam, *Macrocallista nimbosa* **Laramore, Baptiste, Perri, Sturmer**	Analysis and variability of metapopulation connectivity in oyster restoration **Lipcius, Shen, Schulte**	A comparison of shellfish importation regulations across East and Gulf Coast States **Safi, Hudson, Sturmer, Bushek, Carnegie, Ben-Horin, Rheault, Gustafson, Marxen, Walton, Pollack, Rowe**	
2:00 PM	Pangenome analysis of *Phaeobacter inhibens*, a marine probiont for oysters **Coppersmith*, Nelson, Rowley, Gomez-Chiarri**	Oysters as an ecological indicator for everglades restoration **Geiger, Levine, Kirby**	An overview and discussion on the Regional Shellfish Seed Biosecurity Program (RSSBP) database and mapping tool **Marxen, Safi, McGurk, Bushek, Carnegie, Hudson, Ben-Horin, Rheault, Gustafson, Walton, Pollack, Sturmer, Rowe**	
2:15 PM		Increased macrofaunal secondary production with oyster artificial substrates in the York River, Virginia **Seitz, Patel, Knick, Saluta, Lipcius**	Expanding the Regional Shellfish Seed Biosecurity Program (RSSBP) in the southeast US and across the Gulf of Mexico **Ben-Horin, Walton, Pollack, Sturmer, Bushek, Carnegie, Hudson, Safi, Rheault, Gustafson, Marxen, Rowe**	
2:30 PM		Using uncrewed aerial systems to map intertidal eastern oyster (*Crassostrea virginica*) reefs to inform management and restoration practices in the southeastern United States **Sánchez, Sundin, Faulk, Mitchell, Simpson, Kingsley-Smith**	Advancing the Regional Shellfish Seed Biosecurity Program (RSSBP) **Carnegie, Ben-Horin, Bushek, Hudson, Safi, Rheault, Gustafson, Marxen, Walton, Pollack, Sturmer, Rowe**	
2:45PM		The evolution of customizable, wire-based reef-building substrate for oyster (*Crassostrea virginica*) habitat restoration in coastal South Carolina, USA **Kingsley-Smith, Sundin, Faulk, Mitchell, Hodges, Swain, Lambert**	DISCUSSION	
3:00 PM		A long and winding road: 20 years into hard clam restoration in central Great South Bay, New York **Starke, LoBue**		
3:15 PM		Exploring the recovery and spatial distribution of Pismo clams (*Tivela stultorum*) on Pismo Beach, California **Bills*, Gianni, Ross, Bean, Ruttenberg**		
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* denotes student presenter ᵖ denotes non first-author presenter

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AEROBIC SCOPE AND THERMAL TOLERANCE: CONTRASTING RESPONSES IN SHRIMP, CRAYFISH, AND MUSSELS

Hisham A. Abdelrahman[1]*, Aya S. Hussain[2], Kaelyn J. Fogelman[3], Luke A. Roy[4], and James A. Stoeckel[5]

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Mortality events driven by thermal stress pose a critical challenge to the cultivation and conservation of crustaceans and mollusks in many parts of the world. To investigate the physiological mechanisms behind upper lethal limits in decapods and bivalves, the connection between empirically measured thermal limits and absolute aerobic scope (AAS), representing the ability to generate energetic capacity above basic maintenance needs was explored. Because traditional methodology to calculate maximum metabolic rate via respirometry (MMR_{resp}) is problematic for bivalves, this project investigated whether AAS as calculated using MMR derived from an enzymatic assay (MMR_{ets}) is a useful concept for understanding the physiological basis of thermal tolerance. This approach was first tested using Pacific white shrimp (*Litopenaeus vannamei*). Resting metabolic rate (RMR), MMR_{ets}, and critical thermal maximum (CT_{max}) were assessed in two shrimp size classes exposed to rising temperatures. Small shrimp exhibited a higher CT_{max} than larger counterparts, with upper lethal limits of 40.6°C and 39.0°C, respectively. Notably, AAS reached its minimum near peak RMR and within 2°C of CT_{max}, indicating a reduction in AAS as a key driver of thermal tolerance in *L. vannamei*; however, extending this methodology to freshwater mussels and crayfish revealed limitations in using MMR_{ets} to estimate AAS. In these species, RMR and MMR_{ets} varied by orders of magnitude, only minor AAS decreases toward upper thermal limits. This suggests MMR_{ets} is not a useful approach for calculating AAS in crayfish or freshwater mussels. The reasons for the wide divergence are unknown at this time and deserves further investigation.

WESTERN BLOT STUDY OF THE NEUROTOXIC EFFECTS OF MANGANISM AND PARKINSON'S DISEASES

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Manganism, a human neurodegenerative disease caused by high brain manganese levels has similar symptoms as Parkinson's Disease (PD). Both interfere with the dopamine system originating in the substantia nigra. Manganism impairs dopamine postsynaptic signal transduction (PST), while PD destroys dopamine neurons. Impairment of PST decreases response to stimulation. Neuronal degradation results in postsynaptic denervation supersensitivity. Treatment for PD does not benefit people with Manganism. This study contrasts neurotoxic actions of manganese and 6-hydroxydopamine on the presence of dopamine D2R receptors in gill of *Crassostrea virginica*. *C. virginica* has a cilio-inhibitory dopamine innervation from its ganglia to gill lateral cells (GLC).

Mn and 6-hydroxydopamine decrease dopamine neurons effectiveness to slow down GLC cilia; however, direct application of dopamine to GLC reduces cilia beating after 6-hydroxydopamine, but not after manganese. To test the hypothesis if manganese treatment decreases the presence or sensitivity of gill D2R receptors, and if 6-hydroxydopamine treatment increases their presence or sensitivity, the D2R of animals treated 5 days with 500 µg of manganese or 6-hydroxydopamine were quantified using PAGE and Western Blotting (WB) with D2R-HRP conjugated antibodies, then viewed and analyzed with an iBright Fl1500 image analyzer. Band intensity for 6-hydroxydopamine treatment was slightly more intense than controls, but less intense for manganese treatment. The study shows the two neurotoxins have different mechanisms of action. This can be helpful in designing appropriate therapeutic treatments for these similar neurological disorders. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

THE MANGROVE EPIGENOME (MANGROVEENCODE) PROJECT: A ONE HEALTH APPROACH TO CONSERVING MANGROVES BIODIVERSITY

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Mangrove ecosystems are highly productive and biologically diverse wetlands that serve as nurseries and habitats to many juvenile fishes, molluscs, and crustaceans, including shrimp, which are the most consumed by people worldwide. They sequester large quantities of carbon that become significant sources of greenhouse gases when disturbed through land-use change. They also support diverse species of microorganisms such as fungi, and bacteria associated with biogeochemical transformations of nutrients. They trap sediments and assimilate nutrients along with associated sediment contaminants such as antibiotics, endocrine disrupting chemicals (EDC) like metals, PCB, PAH, BPA, glyphosate-based herbicides. Mangroves began disappearing due to ozone depletion, freshwater diversion, ocean acidification, atmospheric aerosol pollution and the introduction of exotic chemicals and modified organisms in the shrimp farms nearby mangrove habitats. Current regulatory approaches have failed to protect animal and human health, collaborative science through the 'One Health approach' could help to address these gaps.

The long-term goal of the MangroveENCODE project is to study the epigenetic mechanisms with the interactions of CO_2 uptake, EDC in sentinel species (shellfish), and microbial communities considering environmental degradation-related health issues. The plan is to obtain baseline information for future studies to test mechanism-driven hypotheses to examine the interactions of CO_2, EDC, and microbial diversity using computational ecology tools. The short-term goals are to characterize the microbiome (bacterial communities), CO_2 uptake, and EDC concentrations in mangrove sediment and shrimp. A review of (a) the best technologies to assess the microbiome and CO_2 stocks from >1-meter-deep mangrove sediment, and (b) the genome sizes, microbiomes, and transposable elements of mangroves and shrimp.

MANGROVE SHELLFISH: FROM CARBON STORAGE TO EPIGENETICS - RECOGNITION TO STUDENTS AND "2024 OUTSTANDING ONE HEALTH RESEARCHERS IN AQUACULTURE AND FISHERIES" AWARDEES

Acacia Alcivar-Warren[1,2]* and Karin Tome[2]

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The speakers of the Mangrove Shellfish session will address topics that support conservation of mangrove biodiversity and a sustainable shrimp aquaculture industry including: The mangrove epigenome (MangroveENCODE) project, carbon storage capabilities of shellfish; identification of new *Vibrio campbellii* strains harboring the *p*VA1 plasmid isolated from *Penaeus vannamei* postlarvae affected by outbreaks of AHPND in Mexico; the "One Health Approach" into endocrine disrupting chemical research; a critical assessment of microplastics in molluscan shellfish; citizen science approach to mitigate the effects of harmful algal blooms in Costa Rica; and how Rotary works for shellfish. The session will end with a workshop discussing how to write effective global grants for funding by Rotary International (https://my.rotary.org/en/take-action/develop-projects/developing-effective-projects).

Two senior researchers and four junior researchers will be recognized as '2024 Outstanding ONE HEALTH Researchers in Aquaculture and Fisheries' by the FUCOBI Foundation of Ecuador: Christopher Puttock USA), Sandra Shumway (USA, Jianbo Yuan (China), Sakosi Kawato (Japan), Weidong Bao (USA), and Max D. Zavell (USA). Twelve students will be recognized as winners of the 2024 'Jimmy Alcivar Arteaga Travel Awards' of the FUCOBI Foundation, representing three countries: Ecuador (9), India (1), Mexico (1), Venezuela (1).

REPETITIVE ELEMENTS FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS VANNAMEI*, PRODUCED IN THE UNITED STATES: CHARACTERIZATION OF *OUTCAST-1_LVA* NON-LTR RETROTRANSPOSON SIMILAR TO RETROTRANSPOSON NLRS PUTATIVELY ASSOCIATED WITH ABDOMINAL SEGMENT DEFORMITY DISEASE (ASDD) OF FARMED *P. VANNAMEI* FROM THAILAND

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Limited information is available on the content of repetitive elements [RE] in Penaeids. A pilot genome sequence (470 Mb) from the first SPF *Penaeus vannamei* produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP) generated 441 RE representing 237 long terminal repeat (LTR) retrotransposons, 78 non-LTR retrotransposons, and 126 DNA transposons. Ninety-five elements were also obtained from the genome assembly of *P. vannamei* farmed in China (ASM378908v1; 1.7 Gb). Some RE show similarity to *P. vannamei* microsatellites including the telomeric pentanucleotide $(TAACC/GGTTA)_n$ repeats, the site of insertion of nimavirus *Nimav-1_LVa*. Eleven families of the non-LTR retrotransposon clade are further characterized with focus on *Outcast-1_LVa* (6,180 bp), originally named as *NonLTR1_LVa*. A genomic locus [KC179708, 4101-bp] comprise 4-kb nucleotides derived from the 1,974-6,062 of *Outcast-1_LVa,* showing 96.9% identity to the consensus sequence of *Outcast-1_LVa* stored in Repbase. KC179708 locus was putatively associated with Abdominal Segment Deformity Disease (ASDD) of farmed *P. vannamei* from Thailand. Researchers suggested ASDD may be related to inbreeding and use of eyestalk ablation (EA) in female broodstock. In ASM378908v1 genome assembly 632 *Outcast-1_LVa* locus are identified in 43 scaffolds and is actively expressed in *P. vannamei* transcriptomes from various developmental stages and adult tissues. Expression changes was observed in ovaries six days after EA. Considering that the genome size of SPF *P. vannamei* was estimated at 2.87 Gb, a contiguous whole reference genome for *P. vannamei* is needed to fully characterize its repeatome, study molecular and epigenetics mechanisms involved in growth and disease susceptibility or tolerance and determine whether expression of *Outcast-1_LVa* is associated with EA and inbreeding.

TIME TO INTEGRATE THE "ONE HEALTH APPROACH" INTO ENDOCRINE DISRUPTING CHEMICALS (EDC) RESEARCH, INCLUDING EPIGENETIC MODIFICATIONS INDUCED BY NANOPLASTICS AND GLYPHOSATE-BASED HERBICIDES (GBH) PRESENT IN MANGROVE SOIL, SHELLFISH, AND PEOPLE

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Meaningful ecological (mangroves/wetlands), animal (shellfish), and human health risk assessments of endocrine disrupting chemicals (EDC) are needed. These assessments are only possible when we understand their environmental fates, exposure levels, and systemic effects. In the case of nanoplastics, the high heterogeneity and small size make them a challenging issue, and the current limitations in nanoplastic research should not delay mitigation strategies. Further research is urgently needed to fill the gaps on the scientific knowledge about the entire plastic life cycle from plastic production, mishandled plastic waste, and incidental leakage into the environment, by allowing the roles of different scientific communities, policymakers, and the public to participate. It is critical that nanoplastic data is integrated on humans, animals, and the environment. The 'One Health Approach' is particularly relevant not only for nanoplastic research but also for EDC like metals and glyphosate-based herbicides (GBH) present in mangrove soil, shellfish, and people. Herein, the impact of contaminants of emerging concern on shellfish, particularly in bivalve molluscs, examples of bio-indicators that must be used to precisely determine the effects of these pollutants on the marine ecosystem and human health will be summarized. Exposome and epigenetics research should be a priority.

SINGLE NUCLEOTIDE POLYMORPHISMS (SNP) GENOTYPING TOOLS AND THEIR APPLICATION IN SHELLFISH BREEDING PROGRAMS: PEDIGREE MANAGEMENT TO GENOMIC SELECTION

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The last few decades have seen the wide adoption of genetic tools into breeding programs across all areas of agriculture. Decreasing costs and advances in technology in both application and analysis have made these tools accessible to a wide range of users, and the aquaculture sector has been able to show significant gains.

Modern genotyping and sequencing technology provide the opportunity to address some of the many unique challenges faced in aquaculture, including tracking pedigree, inbreeding avoidance, disease resistance, increasing fecundity, and improvement of growth and meat quality characteristics. The most widely-used genetic marker in modern breeding programs are single nucleotide polymorphisms (SNP). This type of genetic variant is found abundantly in all genomes, making SNP genotyping technologies a versatile genetic tool that can be designed for any species, is adaptable for various applications, and is scalable, targeting from one to millions of SNP. Generally, SNP panels fall into three common scale categories: low density, LD (~100-500 SNP), medium density, MD (1000-5000 SNP), and high density, HD (10,000 to 100,000 SNP). Low pass Whole Genome Sequencing is also quickly becoming a valuable tool for identifying SNP and to impute to a higher number of markers. In this session, a practical approach to evaluate the range of genetic tools that are available and the value that each brings to the shellfish and aquaculture field will be discussed.

ECOLOGICAL ASSESSMENT OF ENVIRONMENTAL HEALTH AND OYSTER AQUACULTURE GROW-OUT CONDITIONS IN REHOBOTH BAY, DELAWARE

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Oyster aquaculture leases returned to the Delaware Inland Bays (Rehoboth Bay) in 2017 boosting local economies, improving water quality, and providing important habitats for fish and invertebrates. Efforts to monitor and identify relationships between cage depth, oyster condition, water nutrient levels, and pathogens responsible for oyster mortality are vital to successfully manage the re-emerging eastern oyster (*Crassostrea virginica*) industry and restoration in the area. This project will analyze targeted pathogen levels and water quality and correlate these with oyster health at a recently established aquaculture lease.

Pathogen identification was conducted using cultured water and oyster samples collected at surface and bottom depths. The polymerase chain reaction (PCR) and quantitative polymerase chain reaction (qPCR) approaches were used for the detection of oyster pathogenic vibrios—*Vibrio coralliilyticus* and *Vibrio tubiashii*—and parasites responsible for the oyster diseases MSX (*Haplosporidium nelsoni*) and dermo (*Perkinsus marinus*). In-situ water quality data and samples were collected from the same depths and further analyzed for nutrient content.

Oyster condition index (CI) was calculated using total interior volume and dry oyster meat weight; low CI indicates the oyster and potential offspring are more vulnerable to disease and environmental stressors. The data provided from this study will contribute to a greater understanding of current farming strategies and habitat suitability of study sites in this re-emerging industry.

EVALUATING ABIOTIC AND BIOTIC FACTORS INFLUENCING NORTHERN QUAHOG (= HARD CLAM) PRODUCTION IN FLORIDA, USA

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Over the last decade, *Mercenaria mercenaria* hatchery and nursery operators experienced seed losses resulting in a negative impact on the clam aquaculture industry in Florida. To better understand and alleviate seed mortality, a two-year monitoring and assessment project was conducted during 2020-2022 to monitor a comprehensive suite of water quality indicators, investigate the presence of bacterial pathogens, survey phytoplankton species and abundance, and correlate factors that contribute to successful as well as unsuccessful production runs. The project engaged twelve commercial facilities, representing 82% of the clam seed producers across the state, who operate hatchery and/or nursery systems 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. At the project's conclusion, seed producers were provided with baseline data, equipment, and protocols to implement their own water quality monitoring and health management program. Project results are provided on the *Online Resource Guide for Florida Shellfish Aquaculture* website, https://shellfish.ifas.ufl.edu/clam-seed-project-2020-22/, including information on equipment and supplies used, instructions on bacteriological, nutrient, and phytoplankton sampling and interpretation, and workshop videos. Finally, a step-by-step problem-solving guide, utilizing information generated through the project, was developed to assist seed producers in determining possible causes of poor seed growth, abnormalities, and/or mortalities of larvae, post-set, and/or juveniles and provides resources so informed management decisions can be made to improve seed health and increase production.

SETTLEMENT AND METAMORPHOSIS OF THE RIBBED MUSSEL, *GEUKENSIA DEMISSA*, IN RESPONSE TO ENVIRONMENTAL CUES

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Ribbed mussels are typically found in *Spartina alterniflora* salt marshes and can form dense aggregations along low marsh shorelines and tidal creeks. The presence of ribbed mussels within marshes is well-documented, and many studies have examined their importance in these ecosystems; however, it is not known if mussels settle preferentially in *S. alterniflora* habitat or what influences the observed aggregations. Knowing this is important for current efforts in salt marsh restoration and efforts to grow ribbed mussels for ecosystem services. Therefore, experiments were conducted with competent larvae to test whether chemical or physical cues of *S. alterniflora* or adult conspecifics stimulate settlement and metamorphosis.

More larvae settled and metamorphosed in the presence of a *S. alterniflora* leaf, although not on the leaf, and in water conditioned with *S. alterniflora* than in seawater controls. The presence of chemical or physical cues from conspecifics had no effect on settlement and metamorphosis relative to controls. Larvae settle and metamorphose in response to chemical cues from *S. alterniflora,* resulting in ribbed mussels being found predominantly in *S. alterniflora* habitat; however, because there was no response to conspecifics, other factors are likely responsible for their aggregated distribution. Further testing is required to determine the factors resulting in mussel aggregation, including movement of juvenile mussels or environmental filtering, or both.

THE OYSTER CONSERVATIONIST PROGRAM: A COMMUNITY SCIENCE EFFORT IN GREAT BAY, NEW HAMPSHIRE

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This conference presentation will highlight the collaborative efforts of The Nature Conservancy of New Hampshire (TNC) in their Oyster Conservationist (OC) Program, a community science volunteer initiative aimed at restoring the eastern oyster population in the Great Bay Estuary. In 2023, the program engaged over 100 community members across 51 sites, fostering environmental stewardship and contributing to the restoration of oyster reefs. The presentation will delve into the program's methodology, including recruitment, training, oyster spat production, and program delivery. Preliminary results indicate a lower settlement rate in 2023, potentially linked to challenges facing the entire Great Bay Estuary. Despite this, the OC Program achieved a 74% survival rate, surpassing previous years, and contributed an estimated 2,586 oyster spat to the ecosystem. The discussion will emphasize the broader impact of the OC Program in enhancing community involvement, compare the results of 2023 to previous years of the program, and address the challenges faced by the Great Bay Estuary in the context of climate change and environmental shifts. The presentation concludes by highlighting the critical role of the program in fostering resilience and promoting the overall health of this vital estuarine ecosystem.

SURVEY OF SHELLFISH AQUACULTURE MANAGEMENT PRIORITIES IN MAINE, NORTH CAROLINA, AND FLORIDA

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While U.S. domestic marine shellfish aquaculture currently accounts for a small portion of the national seafood supply, it is poised to grow, with national and state-level policy efforts working to expand the sector. This potential growth raises management-relevant questions about what values and objectives should be prioritized in managing that growth. For example, proponents often argue that marine shellfish aquaculture provides an opportunity to reduce seafood trade deficits, increase seafood security, provide a range of environmental benefits, generate economic revenue, and improve coastal livelihood options (often in places where capture fisheries have declined). Some critiques, however, have shown that aquaculture development can engender significant local resistance, displace commercial wild capture fisheries, and privatize ocean spaces for the benefit of non-local (and increasingly multinational) corporations. These considerations involve a range of stakeholders and have management implications, yet there has been little empirical analysis of 1) how stakeholders prioritize management objectives for the shellfish aquaculture industry and 2) how management priorities vary geographically, demographically, or experientially (such as experience with the industry). This study presents preliminary results of a large-scale (n=1011) survey of residents in Maine, North Carolina, and Florida, each of which features a shellfish aquaculture industry at a different stage of development. Prioritization will be assessed through a ranking question, and variability across respondents will be assessed with a series of 'predictor variables' (demographic, geographic, etc.). The presentation will discuss which predictor variables are associated with different priorities as well as the management implications of these findings.

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

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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. The IHHNV genome (AF218266.2, 3,909bp) is integrated in various chromosomes of *P. monodon* genome from China (PM-nanhai2-001_Lachesis_group23__306, JACBPZ010000025.1) and *P. monodon* from Thailand (JABERT010000007.1) both 95-97% identical. Fragments of AF218266.2 are also present in two genomes of *P. vannamei* farmed in China [(QCYY01000759.1, *Penaeus vannamei* breed Kehai No.1 LVANscaffold_759, nucleotides 87-1851 and 936-2058, 95-96% identity) and *P. vannamei* isolate Guihai-1-2017-001_HiC_scaffold_2, JANIEY010000002.1, nucleotides 1294-2575, 68% identity).

Three IHHNV sequences have been reported from *P. vannamei* of Ecuador (AY362548.1 3,775bp; OL598344.2 3,203bp; OM728642.1, 3,902bp) and portions of these genomes are also integrated in the genomes of *P. monodon* from Thailand (GCA_015228065.1, isolate SGIC_2016 chromosome 7) and *P. vannamei* from China (GCA_003789085.1, breed Kehai No.1 LVANscaffold_759). IHHNV isolates from Peru like OM728641 (4,122bp) are also integrated in *P. monodon* chromosomes 7 and 35, the number of fragments varying, 10 and 51, respectively. Researchers concluded that the currently farmed *P. vannamei* lines in Ecuador are tolerant to circulating IHHNV genotypes, prompting the industry to request delisting of IHHNV from the OIE. This is an issue that should be addressed carefully because of the interaction with a transposable element (*RTE-2_PMon*, (3,656-bp) from *P. monodon* from Thailand that contains pieces of microsatellites, and potential for re-emerging of IHHNV via horizontal gene transfer. 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. More data on a new genome sequence for *P. vannamei* is needed in order to determine the integration sites and evolution of IHHNV-EVE, their association with SSR and noncoding RNA potentially associated with slow growth and disease resistance/tolerance.

COMPARISON OF *PERKINSUS MARINUS* AND *HAPLOSPORIDIUM NELSONI* PREVALENCE AND INTENSITY IN OYSTERS ACROSS FOUR SITES ON SAPELO ISLAND, GEORGIA

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Eastern oysters, *Crassostrea virginica*, are 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 due to the combined effects of stressors such as habitat loss, climate change, and disease. Oysters along the Atlantic and Gulf coasts of the United States are commonly infected by two lethal diseases, Dermo and MSX, caused by the protozoan parasites *Perkinsus marinus* and *Haplosporidium nelsoni*, respectively. Dermo and MSX have been linked to poor oyster health and mass mortality events in the past driving incentives for management, restoration, and reestablishment of aquaculture industries. For these efforts to be successful, it is important to investigate factors that currently influence oyster disease dynamics 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 associated host-parasite interactions. 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 used to examine seasonal and long-term trends in water quality conditions. Oysters were haphazardly collected from each site biweekly and processed to measure condition index then screened for parasites using a TaqMan probe based quantitative real-time PCR from extracted gill tissue. Generally, sites exhibited the greatest variation in salinity and temperature, both important drivers of oyster populations and protozoan parasites.

ASSESSING EASTERN OYSTER *CRASSOSTREA VIRGINICA* PREDATION UTILIZING REAL-TIME MONITORING AND EDNA ANALYSIS IN DELAWARE INLAND BAYS

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Eastern oysters (*Crassostrea virginica*) are keystone species that are recognized for their ecological and economic benefits in Delaware. Predation is a stressor that can hinder both the recruitment and distribution of oysters. Species such as fish, crustaceans, and gastropods prey upon *C. virginica*. In order to assess oyster predation and species diversity, real-time monitoring and environmental DNA (eDNA) analysis are conducted at different locations around Rehoboth Bay, Delaware. The sites include pilot artificial reefs, private aquaculture farms, and control sites without any oysters or habitat structure.

Underwater cameras are deployed every two weeks from June to October. Once retrieved, the camera footage is reviewed for any signs of aquatic life and all documented species are identified and recorded for comparisons between sampling sites. Environmental DNA analysis serves as a complimentary method for species identification and to assess the potential for eDNA as a tool for environmental monitoring.

On-site water quality monitoring along with collected water samples are also used to perform nutrient analysis and assess chemical and physical water quality conditions which will be used to determine the aragonite saturation state. The aragonite saturation state will help to assess the impacts of ocean acidification on the calcification process of *C. virginica* and how this may impact predation. This study will help to promote oyster restoration efforts and sustainable aquaculture in the Delaware Inland Bays.

INFLUENCE OF POLYCYCLIC AROMATIC HYDROCARBONS (PAH) ON CONCENTRATIONS OF HUMAN-PATHOGENIC *VIBRIO* SPP. IN OYSTERS AND SEDIMENTS UNDER *IN SITU* CONDITIONS

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Polycyclic aromatic hydrocarbons (PAH), a class of hydrophobic organic contaminants, and human-pathogenic *Vibrio* species, a genus of naturally occurring bacteria, both accumulate in oyster tissues and are a concern for public health when these oysters are consumed. The observed degradation of PAH by some *Vibrio* species raises the question of a potential exacerbation of *Vibrio* associated health risk when PAH occur in oysters or in the environment. This study further explored this question in the Elizabeth River, an estuary located in southeast Virginia, USA, known for historically high levels of PAH. Eastern oysters, *Crassostrea virginica,* were deployed at sites characterized by exposure to similar water temperatures and salinities but contrasting concentrations of PAH in their sediments. This experimental design enabled examination of the influence of this pollutant while minimizing the impact of other environmental factors known to affect *Vibrio* concentrations. PAH concentrations were measured in oyster interstitial fluid and sediment porewater samples using an antibody-based biosensor. Concentrations of total *Vibrio vulnificus*, and total and pathogenic *Vibrio parahaemolyticus* were measured in the same oyster and sediment samples using a most-probable number approach followed by quantitative PCR. The relationships between PAH and *Vibrio* concentrations were examined using general linear models, which indicated that there was either an absence of association, or a negative association between PAH and human-pathogenic *Vibrio* spp. concentrations. These *in situ* results suggest that the presence of PAH occurring in oysters and sediments does not increase the risks associated with human-pathogenic *Vibrio* spp. in these matrices.

TRACE METAL CONCENTRATIONS IN *PENAEUS VANNAMEI* FROM ECUADOR AND EL SALVADOR, AND A REVIEW OF METALS AND PESTICIDES CONTAMINATING MANGROVE SEDIMENT AND RED MANGROVE CRABS (*UCIDES OCCIDENTALIS)* AT THE GUAYAS ESTUARY OF ECUADOR

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Natural populations of Pacific whiteleg shrimp, *Penaeus vannamei,* are threatened by habitat loss, pollutants, and diseases, which may impact genetic diversity and disease resistance characteristics. To protect the habitat of shrimp populations and help develop a sustainable aquaculture industry, baseline information on status of mangroves ecosystems, contaminants, disease prevalence, and genome diversity of wild shellfish is needed. This study examines the concentrations (µg/g) of 15 metals (Al, Ag, Ba, Cd, Cr, Cu, Fe, Hg, K, Mn, Ni, Pb, S, Se, V) in *P. vannamei* broodstock from Ecuador and El Salvador maintained for breeding purposes under similar environmental conditions in a culture pond in Salinas, Ecuador. A literature review on metals and pesticides contaminating mangroves and shellfish is also presented. Muscle from ten individuals from three Ecuadorian provinces (Esmeraldas, Manabi, Guayas) and eight broodstock from El Salvador were analyzed. Guayas shrimp ranked first in number of metals with highest concentrations followed by El Salvador and Esmeraldas. Manabi shrimp ranked the lowest in metal concentrations. El Salvador shrimp had highest concentrations of four metals (Cd, Hg, Cr, Ni) that could impact reproduction, immune response, genetic diversity. Other studies indicated consumption of shrimp from Ecuador does not pose a human health risk. Accumulation of metals in mangrove crab (*Ucides occidentalis*) and sediment in Guayas Estuary were reported. Ni in sediment is a warning for ecological caution. As in crabs raised concerns on the consumers' health, a maximum intake of eight crabs/month for adults advised. They also reported 35 active compounds in the Guayas estuary, pyrimethanil was the most detected and had the highest concentrations. Prohibited pesticides were also detected in mangroves. Butachlor, carbendazim, fludioxonil could cause adverse effects in aquatic organisms. High potential acute and chronic risks of cadusafos residues on aquatic invertebrates and of diuron on algae in the Guayas wetlands reported. These data provide a useful baseline for local water managers and environmental conservation groups to act and reduce the usage of pesticides to avoid threatening aquatic and human health.

STRATEGIES FOR CO-CULTURING SEAWEED AND BIVALVES: SCIENTIFIC AND INDUSTRY PERSPECTIVES

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GreenWave is a 501(c)(3) nonprofit organization that works across coasts in North America to train and support regenerative ocean farmers growing kelp. The work of the nonprofit grew out of co-culturing sugar kelp (*Saccharina latissima*), a brown macroalgae, or seaweed, that grows in temperate regions throughout the northern hemisphere, and eastern oysters (*Crassostrea virginica*) on a commercial ocean farm in Long Island Sound. The benefits of co-culturing seaweed and bivalves are well-documented, but strategies for integrating kelp and other seaweed into a bivalve operation vary depending upon site and species. This presentation will pull from recent scientific research and industry examples to explore different models for co-culturing kelp and bivalves–including strategies piloted the GreenWave farm in Long Island Sound–and will highlight the pros and cons of different models, with attention toward cost, scalability, and operational efficiencies.

DNA TRANSPOSONS FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS VANNAMEI*, PRODUCED IN THE UNITED STATES

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A total of 178 DNA transposons families and one integrated large DNA virus were identified in the genome of Pacific whiteleg shrimp, *Penaeus vannamei,* and are deposited in Repbase (www.girinst.org). Of these, 126 are initially identified in a small-scale genomic sequence (479 Mb) obtained from the specific pathogen-free (SPF) *P. vannamei* Kona Line produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP). These DNA transposons set consist of 42 *DNA*, 1 *DNAV*, 1 *EnSpm*, 11 *Harbinger*, 2 *Kolobok*, 10 *Mariner*, 12 *Merlin*, 1 *MuDR,* 1 *P*, 3 *Polinton*, 2 *Transib*, 13 *hAT*, 8 *piggyBac*, 5 *Sat*, and 8 uncharacterized *TE* families. From the genome assembly of *P. vannamei* breed Kehai No.1 farmed in China [ASM378908v1; 1.7 Gb), additional 60 DNA transposons were also identified, including 4 *DNA*, 1 *Merlin*, 1 *hAT*, 1 *piggyBac*, 33 *Sat*, 2 *TE*, 1 *Zator* and 17 uncharacterized *REP* families.

The integrated complete genome of the DNA virus (*Nimav-1_LVaI*) is reconstructed to be a consensus sequence totaling ~279 kbp in length, which is designated as *DNAV-1_LVa* and is stored separately in seven segments in Repbase (*DNAV-1a_LVa* to 1g). Homology searches using the five Nimaviridae databases in GenBank showed *DNAV-1_LVa* with 65-75% sequence identity to *Marsupenaeus japonicus* endogenous nimavirus DNA (BFCD01000001, 217,415 bp). Using the three whole genome sequence (WGS) databases available for *P. vannamei*, *DNAV-1_LVa* shows ~95% identity to 974 matches in ASM378908v1 (QCYY01003664, 990,704 bp). Some *Sat* transposons show similarity to microsatellite sequences published from the SPF *P. vannamei* Kona Line including the telomeric pentanucleotide repeat $(TAACC/GGTTA)_n$. These repeats are also the insertion site of *Nimav-1_LVa.* Information on the chromosome locations of the 186 DNA transposons in the ASM378908v1 assembly will be presented.

A MULTIFACETED APPROACH TO STUDY THE NORTHERN RANGE EXPANSION OF ATLANTIC BLUE CRABS, *CALLINECTES SAPIDUS*, IN THE GULF OF MAINE

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Warming ocean temperatures have resulted in a northward range expansion of many species. Historically, the northern range extent of the Atlantic blue crab (*Callinectes sapidus*) was the south shore of Cape Cod, Massachusetts; however, increased observations of blue crabs in recent years suggest a growing population in the Gulf of Maine. To understand the distribution and abundance of blue crabs in their newly expanded range, Manomet deployed a multifaceted monitoring approach that includes trap surveys, a mark recapture study, and crowdsourcing observations.

From 2022-2023, Manomet trapped 76 blue crabs in the New Meadows Ponds in West Bath, Maine and conducted a mark-recapture study that tagged 63 crabs and recaptured 4. To better understand blue crab distribution outside of the trapping locations, Manomet developed and distributed an online survey targeted towards fishermen, harvesters and other ocean users in the Maine, New Hampshire, and Massachusetts region, who are frequently on the water and key to identifying changes in the ecosystem. Since 2022, 248 blue crabs were found across 105 individual reports in waters from Cape Cod to the Gulf of St. Lawrence. Observations were reported year-round and included life stages and behaviors not seen in the trap study, such as ovigerous females, soft-shells, and mating crabs. Together, these efforts provide both detailed population dynamics at a fine scale and a broader picture of blue crab distribution and habitat use in the Gulf of Maine.

USING THE INTERTIDAL ZONE AS A NURSERY FOR JUVENILE CULTURED SOFTSHELL CLAM: A COMPARATIVE EXPERIMENT FROM THREE MAINE COMMUNITIES

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Juvenile softshell clams, *Mya arenaria* L., 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 local field-based nursery 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 are designed to produce the largest clams possible for enhancement efforts and 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. During 2022, a concept of using the mid-intertidal at three intertidal locations in 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) was tested. Results demonstrated no significant density effect on survival ($P = 0.61$), and overall mean of 36.1 ± 7.8% ($n = 15$). Final mean SL varied inversely with increasing density ($P < 0.001$; $SL_{1,667}$ = 26.1 ± 0.9 mm vs. SL33,333 = 17.1 ± 0.9 mm). These results were used to inform additional tests during 2023 at three intertidal locations across the Maine coast from Sipayik (east), Gouldsboro (mid-coast), and Freeport (south) where clams were deployed on four dates (early June to mid-July).

GENOMIC SELECTION FOR GROWTH TRAITS OF THE EASTERN OYSTER IN EAST MAINE

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Enhancing growth traits is a key breeding objective for eastern oyster aquaculture in east Maine, due to the region's year-round cold temperatures. Genomic selection (GS), leveraging the association between phenotypes and desired traits, offers a expedite method for genetic improvements in complex traits. A 66K high-density single nucleotide polymorphisms (SNP) array developed by Eastern Oyster Breeding Consortium now enables the application of GS in Eastern oyster breeding.

In this project, an oyster line produced by the Downeast Institute in spring 2020 and deployed in a cold-water site near the institute were used as training population. In October 2022, 1,235 oysters were collected randomly, measured for growth metrics (shell height, length, width, whole weight, meat weight) and genotyped using the 66K array. Additionally, 301 broodstock from the same cohort of the training population's parents were biopsy-sampled and genotyped. After evaluating several GS models, a multi-trait genomic best linear unbiased prediction (GBLUP) model was chosen for its highest accuracy in cross-validation (56% for shell height). The broodstock of the top, middle and bottom 30 genomic estimated breeding values were selected respectively to create three lines, representing three different growth speeds – the fast, average, and slow. The spawning was performed in 2023 April and the three lines have been deployed in August at the three cold-water sites of east Maine with 20 floating bags (2,000 seed/bag) per site for field test.

INTERACTIVE EFFECTS OF SIZE AND INTRASPECIFIC DENSITY ON GROWTH AND SURVIVAL OF CULTURED JUVENILE ARCTIC SURFCLAM, *MACTROMERIS POLYNYMA,* IN TWO EASTERN MAINE INTERTIDAL FLATS

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The efficacy of culturing Arctic surfclams, *Mactromeris polynyma*, in eastern Maine has been investigated to diversify shellfish species for harvesters, shellfish buyers, and the public as direct and indirect effects of warming waters have pushed stocks of wild, commercial bivalve species such as soft-shell clams, sea scallops, and blue mussels to historic low levels. A fishery for Arctic surfclams in offshore waters of Atlantic Canada is worth >$100 million annually; however, no Gulf of Maine fishery exists although surfclams are found there. A 415-day trial was initiated at two low intertidal sites in eastern Maine: Gouldsboro and Beals from mid-June 2022 to August 2023. Surfclams (small: 9.6 ± 0.4 mm SL; large: 12.4 ± 0.4 mm) at three densities unique to clam size were added to two sizes of protected experimental units (EU:2 ft^2; 4 ft^2) in a completely factorial design at both locations (N = 60). Samples from January 2023 (~220 days) revealed live surfclams in only 45% (Gouldsboro) vs. 100% (Beals) of EU, due primarily to differences in crab densities between locations (crabs were removed from boxes in January). Surfclam growth varied with initial size at both sites, but larger clams of both sizes were recovered at Beals where maximum seawater temperature was 15.6°C vs. 18.5°C at Gouldsboro. August 2023 samples revealed < 5% survival in Gouldsboro vs. 38% in Beals.

EXPANDING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP) IN THE SOUTHEAST US AND ACROSS THE GULF OF MEXICO

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The Regional Shellfish Seed Biosecurity Program was created to reduce uncertainty and provide clarification concerning the biosecurity of moving molluscan bivalve shellfish among states and bodies of water in support of the growing shellfish aquaculture industry. The program began with a focus in the mid-Atlantic and northeast regions where shellfish aquaculture was well-established, yet disease concerns were impeding development as a result of limited access to information on shellfish pathogen distributions and impacts. Interest in developing and expanding shellfish aquaculture has increased substantially in the southeast and across the northern Gulf of Mexico (NGOM) with similar regulatory concerns. Simultaneously, shellfish restoration and their application in nature-based solutions such as living shorelines is increasingly limited by a lack of access or understanding of the same information on. This session will describe efforts to expand the RSSBP into the southeastern United States and NGOM and solicit feedback on progress and any additional needs.

UPDATE ON THE CONNECTICUT OYSTER DISEASE MONITORING PROGRAM

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Long Island Sound (LIS) has sustained an active shellfishing industry for hundreds of years. Currently, more than 60,000 acres of shellfish farms are cultivated in Connecticut coastal waters of LIS with harvests exceeding 24,300,000 oysters annually. Much of this production is supported by natural recruitment from wild populations before cultivation, making Connecticut industry practices relatively unique along the East Coast. Recognizing the importance of this natural resource, Connecticut has routinely monitored oyster diseases since the late 1990s.

The Department of Agriculture Bureau of Aquaculture (DoAg BA) is tasked with collecting, analyzing, reporting, and storing these data. *Haplosporidium nelsoni* (MSX) was monitored using histology from 1997 to 2016 and then using qPCR from 2019-2023, along with a co-occurring parasite *Haplosporidium costale* (SSO). *Perkinsus marinus* (Dermo) was monitored using Ray's fluid thioglycolate medium (RFTM) with histology from 1997 to 2016 and then using qPCR from 2019-2023. A summary of this data will be presented noting nuances of annual prevalence and intensity in timing of sampling, location, sampling techniques, and year.

While *H. nelsoni* has had a declining impact on local oyster populations since 1998 and *P. marinus* has never reached epizootic proportions in Connecticut waters, the DoAg BA remains committed to the sustainable and healthy management of this important natural resource. For future directions, the DoAg BA will restore its histology-based monitoring program and plans to expand by developing qPCR capabilities. As aquaculture continues to grow, maintaining robust monitoring programs will increasingly be valuable to a variety of stakeholders.

EXPLORING THE RECOVERY AND SPATIAL DISTRIBUTION OF PISMO CLAMS (*TIVELA STULTORUM*) ON PISMO BEACH, CALIFORNIA

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Pismo clams (*Tivela stultorum*) supported a once abundant recreational fishery on the California Central Coast until their populations declined in the 1980s. Pismo clam abundance on Pismo Beach, the historic epicenter of this fishery, remained low until clams began reappearing in the intertidal zone in larger numbers in 2015. The population grew steadily for the next few years, and then increased dramatically in 2021. The recovery of this species has presented the opportunity to better explore their spatial ecology and habitat preferences and requirements, and how these factors influence their distribution and abundance. This study analyzed clam abundance data at three sites along the length of Pismo Beach to determine how abundance and size structure differ over this range. At each of these three field sites, the spatial distribution of the clam bed was explored, documenting how much of the beach the clams occupy and how it changes over time. Within this rage along the length of the beach, the location of clams within the vertical intertidal zone was assessed based on size class of clams to illuminate how position on the beach varies by size. Lastly, sediment grain size along the length of the beach was analyzed to explore how physical habitat may be used to predict clam presence and abundance. These data collectively build understanding of the habitat requirements of Pismo clams and how they are distributed within their ideal habitat.

WORKSHOP: THE FUTURE OF AQUACULTURE AT THE NOAA FISHERIES SERVICE

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The National Oceanic and Atmospheric Administration (NOAA) Fisheries Service is developing a future outlook that will outline how the agency would be able to implement the NOAA aquaculture mission and vision under various funding scenarios. To inform this effort, the NOAA Fisheries Service is hosting a series of regional and national workshops with stakeholders to better understand your needs. This is one of the opportunities to provide input and help the NOAA Fisheries Service define the different future scenarios. In this workshop, participants will use instant response technology to take part in prioritization discussions of existing aquaculture related services the NOAA Fisheries provides, and brainstorm additional work that can be done to further aquaculture mission of NOAA and support the growth and resilience of the U.S. aquaculture sector.

RECOVERY MECHANISMS OF EELGRASS (*ZOSTERA MARINA*) FOLLOWING MECHANICAL HARVEST OF PACIFIC OYSTERS (*CRASSOSTREA GIGAS*)

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In Washington State (WA), Pacific oysters have been cultured within and alongside eelgrass beds for over a century. Oysters that are cultured directly on the sediment ("ground culture") often involve use of a hydraulic dredge to maintain optimal growing conditions and to harvest oysters. As a byproduct, this process can remove and damage eelgrass, resulting in a disturbance event. Eelgrass serves several ecosystem services, such as providing nursery habitat for ecologically and commercially important estuarine species, so understanding eelgrass recovery following disturbance is of management interest. Here, six adjacent oyster beds containing eelgrass in Bruceport, WA over three years were studied. The beds were each dredged during different times of the year, allowing for the study of disturbance timing on eelgrass recovery. The recovery of eelgrass via clonal growth and development of seedlings was tracked. Factors including season of disturbance and frequency of disturbance affect the mechanisms of recovery, as well as the degree to which eelgrass recovery is possible. Findings from this study will inform management of eelgrass on oyster culture beds to support the resilience of these habitats.

A NUMERICAL INVESTIGATION OF SIZE SELECTIVITY IN A MODIFIED SCALLOP DREDGE

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The US Atlantic sea scallop fishery, valued at $670M in 2021, faces challenges due to unintentional capture of non-target species, particularly undersized scallops with high discard mortality rates. Improving size selectivity is crucial for economic gain and healthier populations. Recently, a modified dredge was developed by Atlantic Capes Fisheries, LLC to improve size selectivity. The geometry is derived from the standard New Bedford dredge, but features a novel cutting bar, capable of rotating along the transverse axis and can be set to angles of 45° or 60° relative to the seabed. This study complements concluded field research and delves into the detailed flow field in the wake of the modified dredge in the context of size selectivity. The NASA FUN3D computational fluid dynamics solver models the unsteady viscous flow field using an unstructured body-fitted mesh, resolving the boundary layer on the dredge frame. The resulting time-dependent velocity field drives scallop trajectory simulations in MATLAB, employing a Runge-Kutta integration scheme. These simulations account for scallop particles' drag and negative buoyancy forces, offering realistic insights into their responses to the flow field. The study examines scallop trajectories across a range of sizes (50-150mm shell height), revealing size-dependent effects on particle behavior. Preliminary results suggest that particle trajectories are strongly dependent on scallop size and the initial release location. Future work will focus on experiments specifically aimed at evaluating size selectivity as a function of cutting bar angle, further enhancing our understanding of this critical aspect of scallop fishing.

EDNA METABARCODING TO SURVEY SHELLFISH IN THE GULF OF MAINE

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Environmental DNA (eDNA), which is DNA left in the environment through the defecation or shedding of organic material (fur, skin, feces) from organisms, has proven to be an efficient and cost-effective tool in biomonitoring and biodiversity assessment in several ecosystems. Metabarcoding of eDNA was used to survey wild populations of fish and shellfish such (e.g., longfin squid *Doryteuthis pealeii*, shortfin squid *Illex illecebrosus*, scallops, and sea urchins), in the Gulf of Maine (GOM) during the Maine Department of Marine Resources (DMR) inshore trawl surveys in the spring and fall 2023. Specifically, traditional trawl survey results were compared to those from two eDNA collection methods: passive metaprobes attached to the codend of the trawl or by filtering slush water from the trawl. From eDNA samples, fish, invertebrate, and cephalopod eDNA were amplified with general primers and sequenced the amplicons to infer species distribution. The goal of this study was to compare traditional trawl and eDNA surveys in terms of species composition and abundance of key shellfish species and determine whether and how eDNA surveys can be used to survey wild shellfish populations in the GOM. Results of this comparative study, as well as applications to aquaculture of cephalopods, bivalves, and urchins, will be discussed.

DIFFERENCES IN TOLERANCE AND RESPONSES TO THERMAL STRESS BETWEEN DIPLOID AND TRIPLOID EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) FROM THE NORTHERN GULF OF MEXICO

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Most eastern oysters (*Crassostrea virginica*) harvested from aquaculture production for the half-shell market are triploid, single-set oysters. Oyster growers typically prefer triploids due to their faster growth rates and superior meat quality during the spawning season compared to diploid oysters; however, triploid oysters experience higher mortality rates compared to diploids potentially related to a lower tolerance to environmental stressors. To investigate links to temperature, the physiological and behavioral responses of diploid and triploid oysters were compared to acute thermal stress, their ability to recover from sublethal stress, and their upper thermal limits.

Diploid and triploid half-sibling oysters were subjected to increasing temperatures from a baseline of 25°C at a rate of 2°C/h. As temperatures increased, physiological response was measured via intermittent respirometry, and behavioral responses were measured via observations of closing, gaping (sublethal), and mantle retraction (lethal). There were no significant differences observed between ploidies in metabolic peak temperature (~33°C) and onset of sublethal (~43°C) and lethal (~44.5°C) behavioral reactions. Diploids showed a significantly higher metabolic demand compared to triploid oysters at peak metabolic temperature but at no other time during the temperature ramp. Both ploidies exhibited 100% recovery from sublethal stress. Results of this study suggest that, while thermal stress may play a role, it is unlikely the sole factor contributing to the observed mortality differences between diploid and triploid oysters in the nGOM.

ANALYSIS OF GENETIC DIVERSITY OF A NEWLY DISCOVERED TREMATODE PARASITE OF THE BAY SCALLOP (*ARGOPECTEN IRRADIANS*) IN NORTH CAROLINA

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Parasitic infections have the potential to hinder aquaculture by increasing mortality and degrading product quality. In 2012, a novel parasite was observed infecting bay scallops, *Argopecten irradians*, and in subsequent years infected scallops have been identified in North Carolina (NC) and Florida (FL). A 28S rDNA fragment was used to confirm that the parasites from scallops collected at these locations are members of the same species belonging to the family Didymozoidae (Superfamily Hemiurodea), and that they form a well-supported clade with a recently described Australian species (*Saccularina magnacetabula*). In this study, a 913bp fragment of the cox1 mitochondrial gene was used to investigate the genetic diversity of trematodes collected from scallops originating from five NC locations (Back Sound, Core Sound, Chadwick Bay, Becky's Creek, and Masonboro Sound). The results of this study indicate a recent population expansion, low genetic diversity, and a lack of genetic structure for this trematode within North Carolina.

ONTOGENETIC STAGE INFLUENCES ON SURVIVORSHIP DISPARITY BETWEEN DIPLOID AND TRIPLOID EASTERN OYSTERS

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Triploid oysters now constitute the predominant farm-raised oyster product in numerous regions with some hatcheries currently producing >90% triploid oyster spat. Triploid popularity is primarily driven by significant growth advantages and more consistent meat quality, with most prior work reporting comparable adult survivorship. Though adult performance is similar, some evidence suggests that triploids may be frailer during earlier age classes particularly to bacterial infections. Anecdotal reports from local farmers endorse this view.

To assess these claims, two cohorts of half-sibling diploid and triploid eastern oyster lines were produced in 2020 and 2021. A subset of larvae and juveniles from both spawns were then exposed to a cocktail of *Vibrio* pathogens and monitored for viability. Separate oysters from the same spawns were maintained at a hatchery for ~ 3 months before being deployed in either the Peconic Bay NY (2020), or Patuxent River MD (2021) and monitored for a year. Survivorship was significantly higher in diploids than triploids at both the larval and juvenile stages, however differential mortality decreased as oysters aged, with nearly identical adult performance after a year in the field. These trends were consistent across spawns and lines. Overall, the results support that triploids are more frail at younger age classes, but these differences decrease over time. Therefore, farmers may benefit from purchasing larger or older triploid seed, and hatcheries should have heightened biosecurity measures when raising triploids due to increased risk of bacteria-related mortalities.

ASSESSING BEHAVIORAL CHANGES IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, WHEN EXPOSED TO *MARGALEFIDINIUM POLYKRIKOIDES*

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The marine dinoflagellate, *Margalefidinium polykrikoides* (Mp), is responsible for algal blooms known as "rust tide" (RT), named so due to the brown-red discoloration of affected waters. Through production of toxic compounds, Mp is harmful and often lethal to both wild and cultured marine organisms, including *Crassostrea virginica*. To better understand the relationship between RT and oysters, exposure experiments were conducted with Mp concentrations similar to bloom densities (~ 5000 cells/mL) on different oyster life stages. Adult oysters were exposed once to either Mp alone, Mp with the algal diet *Tisochrysis lutea* (Tiso), seawater with Tiso (control), or seawater only (control). Video recordings of each tank were taken for 4 days following exposure for 9 hrs/day. Behavior analysis was based on two criteria: number of times each oyster opened and closed, and proportion of time spent open. Preliminary results show a higher open/close count in oysters exposed to Mp with Tiso than the Tiso control. Following the experiments, animals were sacrificed with whole bodies collected for histologic evaluation and gill, gut, and rectal tissue were collected separately for qPCR analysis. A Mp-specific singleplex qPCR assay was performed on the separate tissues to identify and differentiate ingestion vs egestion of the dinoflagellate. Feces and pseudofeces from adult oysters exposed individually to the treatments were assessed using the Mp qPCR to further understand oyster filtration of Mp. While no conclusive results have been shown yet, it is predicted that the oysters will reject the dinoflagellate, leading to higher concentrations of Mp in pseudofeces vs feces.

CLIMATE CHANGE AND INFECTIOUS DISEASES: THE *VIBRIO* MODEL

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Members of the genus *Vibrio* are natural inhabitants of the aquatic environment and are commonly associated with aquatic invertebrates, notably crustaceans, zooplankton, and bivalves. This species is known to cause disease in humans and marine animals, resulting in significant public health burden and aquaculture loss. Infections cause by *Vibrio* spp. have historically been linked to consumption of raw/undercooked seafood, namely oysters, but non-foodborne cases, namely wound infections, have recently outpaced foodborne infections in the United States. Incidence of vibriosis is rising globally, with evidence that changing climatic conditions are influencing environmental factors that enhance growth of pathogenic strains in aquatic ecosystems. Over the past few decades, both Maryland and Florida have reported long-term increases in *Vibrio* spp. infections. Herein, occurrence of pathogenic *Vibrio* spp. was surveyed in water and oyster samples collected from the Chesapeake Bay and Gulf Coast of Florida, the latter of which was significantly impacted by Hurricane Ian in September 2022 resulting in a spike in vibriosis. Results confirm environmental predictors and provide evidence of a long-term increase in *Vibrio* populations in the Chesapeake Bay. In addition, DNA sequencing and metagenomics suggested multiple clonal populations present in the environment post Hurricane Ian and provided insight with respect to human health-related factors, such as antibiotic resistance genes and virulence factors. By coupling genetic analysis with remote sensing, namely in context of identifying environmental conditions favorable to growth of pathogenic *Vibrio*, these data can aid in development of predictive risk intelligence models for *Vibrio* incidence, critical to public health and aquaculture.

INFECTION WITH *SACCULARINA* SP. REDUCES EGG QUANTITY BUT NOT EGG QUALITY OF THE BAY SCALLOP, *ARGOPECTEN IRRADIANS*

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Among infectious threats faced by bivalves, perhaps none pose a greater risk to an individual's fitness than do digenean trematodes. The production of millions of cercariae in a first intermediate host potentiates the trematode life cycle but requires vast amounts of energy which must be stolen from the host. In stealing host energy, however, a parasite risks killing its host, thereby eliminating its own fitness - the classic virulence tradeoff. Parasitic castrators such as trematodes solve this conundrum by stealing energy that the host would have otherwise devoted to reproduction, thereby avoiding a decrease in host viability. Most trematodes inhabit the gonad of their first intermediate host – a logical target for eliminating reproduction; however, in *Saccularina* sp., a newly-discovered trematode infecting bay scallops (*Argopecten irradians*) in North Carolina, histological analysis indicates that sporocysts primarily occupy afferent vessels of the host's gill, rather than the gonad. Despite its unconventional tissue tropism, does *Saccularina* sp. still reduce host fecundity? To assess effects on egg quantity, infected and uninfected scallops were individually spawned and egg output was quantified. To assess effects on egg quality, infected and uninfected scallops were spawned in groups of four, resulting larvae were reared for 48h, and conversion rate to D-stage larvae was quantified. Results indicate that infection reduced egg quantity, but when infected scallops spawned successfully, there was no significant difference in egg quality. These results could have important implications for aquaculture facilities and presently-depleted wild bay scallop populations.

MAXIMIZING OYSTER AQUACULTURE YIELD ACROSS DIVERSE DISEASE DEFENSE TRAITS

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Disease is a primary constraint on oyster aquaculture production. Hatcheries and selective breeding programs have responded by producing oyster lines that perform well in regions and under environmental conditions where numerous pathogens are known to be endemic. Because it is difficult to directly assess resistance to specific pathogens in an aquaculture setting, many commercially available oyster lines demonstrate tolerance to disease impacts with true resistance unknown; that is, oyster lines that perform well in pathogen-endemic regions grow sufficiently fast to survive to market size, but do not necessarily resist infection with disease-causing pathogens. Using coupled epidemiological models that consider diverse and covarying disease defense traits, including pathogen resistance, tolerance to disease impacts, growth to market size, and pathogen shedding to the environment, no singular trait emerges as a primary focus for maximizing aquaculture yield. Instead, yield is maximized when all traits and their interactions are collectively considered. These results highlight considerations for multi-trait breeding programs and target trait profiles for maximizing production in disease endemic areas.

KNOWLEDGE IS POWER: RESOLVING THE GEOGRAPHIC DISTRIBUTION AND HOST RANGE OF OsHV-1 ON THE EAST AND GULF COASTS TO MITIGATE IMPEDIMENTS ON SHELLFISH AQUACULTURE COMMERCE

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Disease outbreaks and associated mass mortality events have plagued many of our shellfish fishery and aquaculture industries over recent decades. Critical to managing disease outbreaks are not only strong biosecurity practices and key knowledge of existing, but also potential pathogen distributions, both geographically and regarding potential hosts. An emerging pathogen of concern for bivalve aquaculture is the viral pathogen Ostreid herpesvirus 1 (OsHV-1), variants of which have caused major shellfish mortalities around the world. Of particular concern are the OsHV-1 µvars which have spread globally in Pacific oyster aquaculture since 2008. OsHV-1 variants have been detected in >40 species to date primarily in disease endemic areas. OsHV-1 is not routinely monitored in potentially susceptible Atlantic and Gulf of Mexico species, with the last survey conducted well prior to emergence of the OsHV-1 µvars. Beginning in 2023, a survey was conducted to determine OsHV-1 distribution in US East and Gulf Coast species including eastern oysters (*Crassostrea virginica*), northern quahogs (= hard clams) (*Mercenaria mercenaria*), and bay scallops (*Argopecten irradians*). Thus far, academic and State and Federal government hatcheries in nine states have provided samples of 1-2 cm bivalves (each n=150) for testing with OsHV-1-specific qPCR, with no detection of the pathogen in samples analyzed to date. Results are expected to be negative as there has been no indication of disease or mortality in cultured shellfish along the East and Gulf Coasts that would be characteristic of OsHV-1 epizootics.

WORKSHOP: ADVANCING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP)

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The Regional Shellfish Seed Biosecurity Program (RSSBP) is a collaboration of industry members, scientists, regulators, and extension personnel working to minimize risks associated with interstate seed transfers of bivalve shellfish for aquaculture, enhancement, and restoration. The RSSBP has created a hatchery biosecurity compliance program with multiple participating hatcheries now recognized by several states to facilitate rapid permitting of biosecure products. The Program has built a geographic database that can be queried to assess risks of disease transfers. A Pathology Working Group provides expertise to advise and guide the Program while an advisory council provides general oversight. This workshop will provide brief presentations on various aspects with ample opportunities for discussion to resolve existing hurdles and identify needs for advancing the Program further.

DYNAMICS OF BAY SCALLOP MAROSPORIDA (BSM) IN THE HOST AND ENVIRONMENTAL SAMPLES FROM THE PECONIC BAYS, NEW YORK

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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. Since 2019, bay scallop populations in the Peconic Bays (NY) have been suffering large-scale summer mortalities resulting in over 95% reduction in population densities of adult, market-size, scallops. Previous investigations showed that these mortality events were associated with outbreaks of an apicomplexan parasite infecting kidney tissues, and provisionally named Bay Scallop Marosporida (BSM).

In this work, a specific quantitative PCR method was used to monitor parasite abundance in scallop tissues and environmental samples, including seawater and sediments. Results showed that BSM has a strong tropism for scallop kidney but was also found in scallop biodeposits and in environmental samples. Field surveys demonstrated a strong seasonal signature, as infection intensity and scallop mortality worsen as summer progresses. The peak in parasite abundance in environmental matrices generally matched infection intensities in scallop tissues. Interestingly, results of preliminary transmission experiments showed that BSM can be acquired by naive juvenile scallops when exposed to kidney tissue homogenates suggesting that dead scallops, and possibly BSM cells released in biodeposits, may mediate transmission. Overall, these results strongly suggest that BSM can be released to the environment by live (e.g., via the excretory system) or dead (via tissue degradation) infected scallops, particularly during summer when new scallop recruits reach the benthos.

DEVELOPING A PILOT SCALE SHELLFISH HATCHERY IN DELAWARE – FIRST YEAR PROGRESS UPDATE

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The Delaware (DE) oyster aquaculture industry has grown since the initial lottery opened in 2017; however, barriers to entry and the COVID-19 pandemic have hampered industry growth. Presently, ten active commercial farming operations exist in the Inland Bays, with farmers purchasing seed from out of state hatcheries. The importation of out of state seed adds an additional hurdle for growers when seed supply is already constrained along the coast. To address an industry wide bottleneck of seed availability, Delaware Sea Grant, the University of Delaware, and Delaware State University have partnered to develop the infrastructure needed to supply Delaware growers with oyster larvae and seed. The pilot shellfish hatchery was established in 2022 on the University of Delaware Lewes campus, finishing an inaugural growing season in 2023. The pilot hatchery conducted a total of eight spawning events in 2023, producing viable oyster larvae for industry, and surpassing planned goals and expectations. One batch of 105,000 remote-set, locally produced spat on shell was supplied to a commercial operation in Port Mahon, DE, marking a historical moment for the Delaware industry; however, the hatchery faced many challenges that resulted in multiple brood crashes, poor set rates, and equipment malfunction. The hatchery team aims to address facility issues and production bottlenecks in 2024 to establish a reliable source of seed for Delaware growers and ecological restoration practitioners alike. Results from our inaugural year, and challenges will be shared.

QUANTIFYING HABITAT PROVISION SERVICES OF OYSTER (*CRASSOSTREA VIRGINICA*) AQUACULTURE AND PERFORMANCE AMONG TWO FARMED STRAINS GROWN ALONG A TIDAL GRADIENT

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Balancing optimization strategies for eastern oyster aquaculture production while understanding the ecological ramifications of these activities in coastal ecosystems is needed to manage sustainable production strategies in the U.S., thereby enhancing management and policy efforts. Oyster aquaculture is often celebrated for a suite of positive ecological benefits, yet many of the parameters touted remain openly contested or are understudied, including habitat provision services. The structure associated with caged aquaculture provides habitat for local communities – improving local diversity and supporting nurseries for commercially and recreationally important fisheries. While these concepts are identified in previous studies, few have attempted to quantify the biomass and radius-of-effect that these structures have on local communities. Further research regarding the ecological role of shellfish aquaculture would assist policymakers in making regulations that encourage sustainable farming practices while providing information to the farming community on the services rendered. This research follows two primary goals: 1) quantify habitat provision services of rack-and-bag oyster aquaculture along the southern coast of Delaware Bay, U.S. across a gradient of bottom types, and; 2) compare the performance of two hatchery-produced oyster strains grown along a tidal gradient over one growing season. This talk will discuss the findings from recent field efforts and describe planned interests in modeling ecosystem function and habitat suitability to determine optimal locations for oyster aquaculture and oyster restoration that optimize ecological function and culture efficiency. Together, this project aims to examine the potential application of aquaculture efforts to restoration projects attempting to augment shoreline resilience.

A COMPARISON OF SETTLEMENT PLATE MATERIAL FOR MONITORING OYSTER SPAT RECRUITMENT

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Settlement plates or recruitment plates are commonly used in assessing the natural recruitment of oyster spat and species abundance of other marine organisms. Historically, a wide range of materials have been utilized for settlement plates including asbestos board, porcelain tile, limestone, and polyvinyl chloride (PVC). This study assessed the effectiveness of material types on the settlement of eastern oyster (*Crassostrea virginica*) pediveliger larvae in a controlled environment.

Six types of settlement plate materials were selected for testing: acrylic, PVC, cement board (HardieBacker™), ceramic, slate, and oyster shell. Four substrate selection trials were conducted over the summer of 2023 at the Auburn University Shellfish Laboratory. Each trial consisted of placing 60,000 pediveliger oyster larvae in a nursery tank with the settlement plate materials randomly distributed ($n = 20$/trial). Additionally, settlement on each material was tested in the absence of material choice by placing individual units of material in beakers and adding 200 pediveliger larvae per beaker ($n = 4$/trial). The larvae were allowed to set for a minimum of four days before determining the overall set rate. There was variation in the results over the four trials. In material preference trials, the spat set was highest on oyster shell with an average set rate of 3.6 spat/cm^2 ($p < 0.05$). Slate, ceramic, and cement performed significantly better than acrylic and PVC. In beaker trials of individual materials, ceramic tile exhibited the highest spat set with an average set rate of 1.0 spat/cm^2 ($p < 0.05$).

GROWTH AND SURVIVAL OF TETRAPLOID EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*, IN DIFFERENT SALINITY ENVIRONMENTS IN THE GULF OF MEXICO

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Off-bottom oyster farming is heavily reliant on triploid oysters produced by mating male tetraploid with female diploid broodstock. Triploid oysters often exhibit reduced gametogenesis, faster growth, and higher meat yield compared to diploid oysters, but may exhibit higher mortality in stressful environmental conditions. Understanding how tetraploid broodstock lines respond to varying environmental conditions is important in producing a more resilient triploid oyster.

Two tetraploid broodstock lines used in the Gulf of Mexico region, GNL20 (Louisiana origin) and APCK20 (Florida origin), were spawned to produce four experimental tetraploid cohorts: two pure lines (GNL22 and APCK22) and two reciprocal crosses (APCK-GNL22 and GNL-APCK22). The GNL line originated from the Louisiana Sea Grant Program Oyster Research Laboratory and the APCK line originated from the Auburn University Shellfish Laboratory (AUSL) in conjunction with 4Cs Breeding Technologies, Inc. All lines are currently maintained by AUSL. Four replicates (n=400) of each experimental cohort were deployed at three sites of differing salinity in Alabama: Mobile Bay (low salinity), Grand Bay (moderate/high salinity), and Dauphin Island (high salinity). Survival and size metrics were assessed monthly over one year. At Mobile Bay and Dauphin Island, there was no significant difference in the survival of the APCK22 and the GNL22 lines ($p < 0.05$). At Grand Bay, the GNL22 line survived significantly better than the APCK22 line. Most of the mortality observed at Grand Bay and Dauphin Island occurred in the spring/early summer during periods of high salinity fluctuation and extreme turbidity events.

INCREASING SHELLFISH AQUACULTURE INTERSECTIONS WITH OYSTER RESTORATION: IMPLICATIONS FOR SHELLFISH HEALTH MANAGEMENT

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As commercial oyster aquaculture has greatly expanded in the eastern and southern USA in recent decades, so too has oyster restoration via substantial public and private investment. These activities can effectively occur side-by-side in many areas, but the ways in which they interact on different levels deserve more attention. It is assumed they can be harmonious in providing ecological benefits, as the concept of "restorative aquaculture" suggests. Intensive oyster aquaculture may even provide benefits of reducing disease pressure on natural and restored oyster populations. The question is, however, whether large-scale oyster restoration may affect aquaculture in ways that are not beneficial: not necessarily in local ecology, but rather at a higher level in the realm of social dimensions. In the mid-Atlantic, large-scale oyster restoration relies substantially on hatchery production, on the long-standing assumption that broodstock supplementation is necessary. Dedication of hatchery production to the restoration realm, while economically beneficial to hatcheries, can constrain local access to hatchery product by the aquaculture industry, forcing growers to go farther afield to acquire seed, increasing pathogen introduction risks—this is counter to interests in increasing aquaculture biosecurity. Hatcheries producing for restoration objectives may also allocate production to seed varieties undesirable for aquaculture, limiting seed choice by industry, which likely contributed to a disease outbreak at farms in the Chesapeake Bay in 2023. As both aquaculture and restoration grow, it is important to understand the intersections between these realms, and to manage them purposefully to ensure sustainability on both fronts.

ADVANCING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP)

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The Regional Shellfish Seed Biosecurity Program continues to develop to meet the needs of industry and regulators working to expand shellfish production safely and effectively. This final session will run across the remainder of the workshop block as a facilitated discussion. Questions, comments, or recommendations concerning any of the specific areas previously presented are welcome. Additional topics may include:

- Expansion of the Hatchery Compliance Program to nurseries
- Issues confronting the Pathology Working Group
    - Expanding or limiting the list of pathogens of concern (e.g., OsHV1)
    - Proficiency testing of shellfish pathology laboratories
    - Standardization of pathogen tests
- Structure and terms of the Advisory Council and others within the RSSBP structure
- Long-term funding mechanisms
- Coordination with the USDA CAHPS, NOAA Aquaculture initiatives, the Bivalve Hatchery Health Consortium and shellfish breeding consortia

6-HYDROXYDOPAMINE TREATMENT CAUSES SUPERSENSITIVITY OF DOPAMINE D2R RECEPTORS IN GILL LATERAL CELLS OF *CRASSOSTREA VIRGINICA*

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Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by dopamine and serotonin nerves from their ganglia. Dopamine decreases while serotonin increases cilia beating. 6-Hydroxydopamine, a neurotoxin destroying dopamine neurons, induces Parkinson's Disease in animals. In *C. virginica,* 6-hydroxydopamine decreases the cilio-inhibitory actions of dopamine when applied to VG on GLC cilia beating. Denervation supersensitivity is a phenomenon observed after nerve cell damage. It is due to increased postsynaptic receptor sensitivity to the neurotransmitter. Manganese causes the neurodegenerative disease Manganism, which has similar symptoms as Parkinson's Disease but affects dopamine postsynaptic signal transduction (PST). Manganese decreases cilio-inhibitory actions of dopamine on GLC cilia beating in *C. virginica*. To test the hypothesis that treating *C. virginica* with 6-hydroxydopamine causes supersensitivity of dopamine on GLC cilia beating, 500 µg of 6-hydroxydopamine was injected into posterior adductor muscles. After 5 days dose responses of dopamine on GLC cilia beating were conducted. 6-hydroxydopamine treated animals demonstrated supersensitivity compared to controls. The dopamine dose response curve of 6-hydroxydopamine treated animals was shifted 1 log dose to the left. In contrast, earlier work with manganese treatments reduced dopamine potency, shifting the dose response curve to the right. The study shows 6-hydroxydopamine produces a supersensitive response to dopamine postsynaptic receptors present in GLC. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

SIGNATURES OF POSITIVE SELECTION TO OCEAN ACIDIFICATION RESILIENCE IN LARVAL MEDITERRANEAN MUSSELS *MYTILUS GALLOPROVINCIALIS*

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Southern California is home to only a handful of commercial aquaculture farms, most of which are relatively small in comparison to their East Coast and Pacific Northwest counterparts. In recent years, the coastal waters of Southern California have been designated by the National Oceanic and Atmospheric Administration (NOAA) as an Aquaculture Opportunity Area, an area that has been identified as a potential location for sustainable commercial aquaculture and targeted for industry expansion and federal funding. While this news is exciting for local farmers, industry partners, and researchers alike, it is jeopardized by rapid ocean acidification chronicled in the Southern California current system. The utilization of genetic selection and breeding strategies for traits of economic interest can support the longevity and productivity of the aquaculture industry, specifically in rapid adaptation and domestication of stocks to climate change and variable environmental conditions. To address this challenge, a cohort of locally sourced Pacific Southwest (PSW) Mediterranean mussels was bred and underwent an experimental ocean acidification exposure for the entirety of the larval stage before being out-planted in ambient farm conditions for grow out to adulthood. The whole genome of larvae from both treatment and control cohorts from before and after the exposure period was sequenced in order to investigate molecular differences between treatments. Significant differences in genetic parameters between treatments and tests for positive selection across regions of interest suggest several regions within the larval Mediterranean mussel genome under positive selection for ocean acidification resilience.

NEW INSIGHTS INTO THE LIFE HISTORY OF *HEMATODINIUM PEREZI* (DINOFLAGELLATA: SYNDINIALES) IN JUVENILE BLUE CRABS (*CALLINECTES SAPIDUS*)

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The parasitic dinoflagellate, *Hematodinium perezi,* occurs with high prevalence in the hemolymph of juvenile blue crabs. Upon completion of its development in the crab, two spore types (macro- or micro-dinospores) are released into the water column in high density, up to 10^6 cells/mL. Each crab releases only one type of dinospore and dies soon thereafter. In the laboratory, transmission has been successful through cohabitation of infected and non-infected crabs; however, transmission using dinospores directly has never been successful. Thus, the functions of the two different dinospore types, along with the sexual cycle of *H. perezi*, remain unknown, as with most syndinid dinoflagellates. To understand this long-standing question, multiple approaches were attempted. Sporulation methodologies were established in the laboratory to generate large quantities of high quality dinospores. Ameboid trophont stages from the hemolymph of the host were also collected. The ploidy of each stage was investigated with flow cytometry and both dinospore types appeared to be diploid compared to the haploid ameboid trophont. Moreover, laboratory transmission using only the micro-dinospores was successful, suggesting that the two dinospore types are not gametes. In addition, transcriptomic analysis was done on the different life history stages using RNASeq and each stage showed clear differences in the transcriptome profiles with highly differentially expressed genes. These findings provide novel insights into the unique life history of *H. perezi* with an internal sexual cycle and different infection strategies.

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

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Polyaromatic hydrocarbons (PAH) are major contaminants in aquatic ecosystems, particularly in coastal marine areas contaminated by fishing vessels, oil spills, and drainage from multiple sources. The green mussel, *Perna viridis*, inhabits estuaries and coastal marine regions, the primary gateways for terrestrial pollutants. To mitigate pollution risks, animals enhance their defense mechanisms by increasing enzyme levels, such as hepatic cytochrome P450-associated enzyme activity. A study measured the ability and activity of certain enzymes in the hepatic S9 fraction of *P. viridis* from three different sites: a highly oil-polluted site, a moderately polluted off-shore site, and the least oil-polluted site, serving as a reference site. The study investigated the effects of different concentrations of ethyl-naphthalene (PAH) on *Perna viridis*, a marine species. The hepatic S9 fraction of the animal was used to measure the inducibility and activity of various enzymes, including phase I reduction nicotinamide adenine dinucleotide phosphate, reduced cytochrome c reductase, cytochrome c oxidase, and three CYP450 isoforms. The samples were also treated with ethyl-naphthalene at different concentrations for 24 hours. The enzymes showed a dose-dependent activity hierarchy in response to oil contamination in the studied locations. Samples from highly oil-contaminated locations showed significantly higher enzyme activity than those from less contaminated areas. MROD activity strongly correlates with hydrocarbon pollution extent, making it a reliable indicator for petroleum hydrocarbons in *P. viridis.*

IDENTIFICATION OF MOLECULAR BIOMARKERS AGAINST XENOBIOTICS IN THE MARINE GREEN MUSSEL, *PERNA VIRIDIS*

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Coastal marine areas are frequently contaminated by pollutants from fishing vessels, oil spills, and other sources. The green mussel, *Perna viridis*, lives in estuaries and coastal marine beds, which act as pathways for pollutants. To limit pollution, animals use defensive systems with heightened enzyme levels. Enzymes like hepatic cytochrome P450-associated enzymes are used as biomarkers. A study assessed the capacity and function of certain enzymes in the liver S9 fraction of *P. viridis*. This study collected samples from three locations: Kasimedu fishing harbor, Rayapuram, Chennai, a moderately polluted offshore site, and the least oil-polluted site, Velar estuary, Parangipettai. It also examined the effects of administering different amounts of PAH to the pernavirdis in a controlled laboratory environment. The study measured BROD, MROD, and EROD levels in green mussel tissues using a Spectro-Fluorometer. The MFO enzymes showed a hierarchical pattern of activity in response to oil contamination, with greater activity in highly oil-contaminated sites (Kasimedu Station-1 and Station-2) compared to the little oil-contaminated reference area (Vellar Estuary). The laboratory treatment of hepatic tissue showed enhanced MROD activity, which strongly correlates with hydrocarbon contamination levels, making it a reliable biomarker for detecting petroleum hydrocarbons in *P. viridis*. Antioxidant enzymes like superoxide dismutase, catalase, and glutathione reductase increased in activity within a 24-hour period, indicating their potential as antioxidants. The study found that *P. viridis* is protected by a cellular enzyme defense mechanism, which includes the production of antioxidant enzymes like GSH, SOD, and CAT, which neutralize reactive oxygen species.

APPLYING NOVEL MOLECULAR WORKFLOWS TO MONITOR POTENTIAL AGENTS OF DISEASE

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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 disease and resulting oyster mortality, field assessments were conducted across six oyster leases throughout the state of North Carolina. Water and oyster samples were collected bi-weekly from each lease for five months throughout the growing season of 2022 while temperature and salinity data were continually recorded via HOBO. A multifaceted approach combining a variety of analyses was employed by coupling histological data with novel droplet digital PCR (ddPCR) assays to identify oyster-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. All sites experienced some level of mortality, though at different scales with the onset of mortality being variable across locations. For the leases with the most severe cases of mortality, losses at the lease primarily occurred in mid-May with pathogen concentrations coinciding with an increase in degradation of digestive tubules as determined via histopathology. Amplicon sequencing also revealed evidence of dysbiosis within the visceral mass microbiome during disease onset in times of stress. By integrating all the data, a stress framework was developed to describe the progression of disease with the goal of offering predictive power for future monitoring efforts.

CALLING ALL CLAMS: COORDINATING PARTNERS TO MAXIMIZE PROJECT IMPACT AND PRIORITIZE RESEARCH OBJECTIVES FOR CLAM RESTORATION INITIATIVES IN FLORIDA

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Degraded water quality in coastal systems is of growing concern throughout the U.S. This is especially true in Florida, where water quality restoration has been identified as an important funding priority for government leaders from local municipalities to state and federal levels. As filter feeders, bivalves are championed as potential tools to improve water quality, with the hope that their addition will enhance water clarity, reduce nutrient levels, and remove harmful phytoplankton. To this end, millions of dollars have been pledged to support directed clam deployments in estuaries in Florida. Multiple projects are currently being implemented by a variety of stakeholder groups, including research institutions, non-profit organizations, and local governments. Examples include All Clams on Deck, A Billion Clams for Charlotte Harbor, Sarasota Bay Watch, and Indian River Lagoon clam restoration efforts. Often, these localized projects are instigated independently, and may be restricted to specific geographic regions and funding periods, but the current groundswell of efforts to plant clams make this an ideal opportunity for coordination across sectors to address fundamental research priorities and evaluate outcomes of restoration endeavors. Florida Sea Grant aims to facilitate communication across groups to consolidate research, maximize data collection and collaboration, and better evaluate overall impact of restoration activities to inform future efforts.

CHARACTERIZING THE TISSUE-SPECIFIC RESIDENT AND TRANSIENT MICROBIAL COMMUNITIES OF THE QUAGGA MUSSEL, *DREISSENA BUGENSIS*

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Research into bivalve microbiomes has identified distinct microbial communities across tissue types, including the hemolymph, gills, and gut complex. The consistent presence of these microbial communities likely indicates that bivalve microbiomes play crucial roles in host physiology and have a functional role similar to those in vertebrates. The bivalve suspension-feeding strategy exposes these animals to a number of microbes, both free-living and particle associated. Some of these microbes are unlikely to become established as members of a particular community. Most research in this field has focused on marine bivalves, with little focus on freshwater species. The purpose of this study was to characterize the resident gill and gut microbial communities of the freshwater quagga mussel. Quagga mussels were collected from natural populations in the Niagara River. One subset of mussels was dissected immediately to isolate both resident and transient microbes associated with the gill and gut tissues. A second subset of mussels was placed into individual depuration chambers for 24 hours to allow animals to egest feces and transient microbes. After 24 hours egested feces were collected, and gill and gut tissues isolated to characterize the resident microbial communities. Water samples were taken from the Niagara River to examine the pool of microbes from the natural water. All samples underwent DNA extraction, PCR, and 16S rRNA sequencing to identify the associated microbial communities. Data from this experiment will provide essential baseline knowledge of the quagga mussel microbial communities and inform future work investigating the dynamics of freshwater bivalve host-microbe interactions.

INVESTIGATING THE INFLUENCE OF PHYTOPLANKTON SIZE DISTRIBUTION ON THE SUCCESS OF EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) LARVAE IN THE MISSISSIPPI SOUND: A MODELING STUDY

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Eastern oyster (*Crassostrea virginica*) populations in the Mississippi Sound are declining due to habitat degradation and recent mass mortality events. Phytoplankton assemblages are the main food source for larvae and fluctuate in quality with environmental conditions. These fluctuations, in turn, impact the settlement and growth of oyster larvae. A biochemically-based model for oyster larvae has been applied to evaluate the influence of food quantity and quality on larval performance in Mississippi Sound. Application of this model suggests that in 2021 and 2022 food quality may have limited larval success. Plankton size distributions in these two years also suggest that plankton of appropriate size for larval feeding may be limited during crucial periods of the spawning season. Previous analyses of plankton lipid, protein, and carbohydrate composition analyses enables the investigation of the impact of food quality on the growth, metamorphosis, and settlement of larvae; however, the influence of phytoplankton size distributions in limiting food resources was not considered. This modeling approach is expanded here to evaluate the influence of plankton size distribution and consequences of relative food quantity and quality in supporting successful larval survival. Investigating whether larvae face nutritional limitations due to the size of available food will provide insight into the effect of food supply on larval survival, growth, and successful metamorphosis. The goal of this study is to examine how variations of phytonutrient characteristics defined in terms of quantity, quality, and size of food will impact the settlement and survival of oyster larvae.

PANGENOME ANALYSIS OF *PHAEOBACTER INHIBENS*, A MARINE PROBIONT FOR OYSTERS

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Phaeobacter inhibens S4, recognized as a promising marine probiotic for larval *Crassostrea virginica*, holds potential in maintaining larval oyster health and survival when exposed to bacterial pathogens. Other *P. inhibens* strains have also shown probiotic activity in marine larviculture. Our study presents a comprehensive pangenome analysis of 37 *P. inhibens* strains isolated from diverse habitats, aiming to elucidate their genomic diversity and functional adaptations crucial for probiotic activity. Utilizing long-read sequencing we completed the assembly for *P. inhibens* S4. The pangenome for S4 and 36 additional unique *P. inhibens* strains with complete genomes on NCBI was analyzed using comparative genomics. Our analysis mapped conserved genomic elements that may be pivotal for probiotic success, including genes associated with biofilm formation, quorum sensing, antimicrobial compound production, and stress tolerance mechanisms, showing differences in distribution amongst the different strains. S4 clusters most closely with another probiotic strain, BS107, isolated from Spain, and strains from Denmark being investigated for probiotic activity, while strains isolated from China tended to group more distantly. Moreover, our investigation delineates S4 strain-specific genomic features contributing to adaptability and host-specific interactions within the oyster holobiont. This comprehensive pangenome analysis offers insights into the functional genomic landscape of *P. inhibens* strains, unraveling their adaptive strategies and potential applications as a probiotic for aquaculture. Understanding the genomic basis of *P. inhibens* diversity and its interplay with oyster health is pivotal for harnessing its beneficial properties to optimize larval *C. virginica* cultivation practices.

MONITORING TEMPORAL TRENDS IN THE DISTRIBUTION OF THE RANGE EXPANDING BLUE CRAB (*CALLINECTES SAPIDUS*) IN SOUTHERN MAINE ESTUARIES

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The rapidly warming Gulf of Maine has led to the northward range expansions of multiple marine species including the commercially and ecologically important blue crab, *Callinectes sapidus*. While *C. sapidus* has historically occurred south of Cape Cod, recent observations suggest the establishment of populations in the Gulf of Maine. Weekly trapping surveys were conducted 2020-2023 (Spring through Fall) to investigate the occurrence, persistence, and spatiotemporal distribution of *C. sapidus* in salt marsh habitats (salt pools, tidal creeks, estuary channels) in two southern Maine estuaries. Environmental data were collected year-round in trapping locations and at nearby long-term monitoring sites to help explain seasonal and annual variability in catch data trends. Crab abundance and distribution varied greatly across years and seasons, with the timing of peak catch varying annually. Captured crabs (n = 353) included adult and juvenile males and females, including several mating pairs and post-molt individuals, providing evidence for mating and molting within this system. A complimentary acoustic telemetry study demonstrated the fine-scale, seasonal movements of blue crabs (n = 22) and provided evidence of a blue crab overwintering in the system. This ongoing study provides early evidence for the establishment of *C. sapidus* populations in southern Maine and sheds light on the environmental drivers influencing blue crab distribution, capacity to overwinter, and persistence at northern latitudes.

DECADAL POPULATION VARIABILITY IN SUBTIDAL BAY CLAMS IN TILLAMOOK BAY, OREGON, USA: IMPLICATIONS FOR MANAGEMENT OF COMMERCIAL BAY CLAM DIVE FISHERY

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Tillamook Bay hosts the largest commercial bay clam dive fishery in Oregon. This fishery has been growing rapidly with a 5-fold increase in landings since 2006. The Oregon Department of Fish and Wildlife (ODFW) Shellfish Program conducts comprehensive randomized subtidal surveys in Tillamook Bay with a focus on the four bay clam species targeted by the commercial fishery: gaper (*Tresus capax*), butter (*Saxidomus gigantea*), cockle (*Clinocardium nuttallii*), and native littleneck (*Leukoma staminea*) clams. These decadal surveys were designed to complement intertidal clam population surveys to manage the commercial and recreational clam fisheries in the bay. The ODFW subtidal clam survey was first conducted in 2012 and the results of this survey were used to establish annual landing limits for the commercial dive clam fishery in 2016. The ODFW recently repeated the survey in 2023 to identify any shifts in bay clam distribution and abundance and identify habitat associations for the target species. Overall, bay clam biomass has decreased in Tillamook Bay relative to the 2012 survey although the population size structure does not differ between the surveys. The largest decreases were found for cockle and butter clam populations where biomass estimates showed an approximately 50% decrease relative to 2012. Clam population distribution was comparable between the surveys with high clam biomass associated primarily with gravel/cobble substrates. The ODFW will use these results to adjust annual landing quotas for the subtidal dive fishery and aid in the management of both these important bay clam resources and associated habitats.

SHELLFISH RESTORATION AND ECO-ENGINEERING - CONVERGENT EVOLUTION?

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Incorporating ecology into the design of built structures or "eco-engineering" is becoming increasingly common worldwide to mitigate impacts from coastal development and help restore biodiversity to urban seascapes. Habitat forming species can be a large driver of biodiversity and biogenic habitat, particularly shellfish reefs support significant biodiversity throughout Australasia; however, globally shellfish reefs have experienced significant global declines. This study investigates eco-engineering as a tool to facilitate recruitment of native bivalves and support shellfish restoration efforts. Specifically, the 3D complexity of native mussel reefs were surveyed and scanned to create mimic substrates and then investigated mussel settlement preferences to microhabitats in the lab. Mussel distributions and demography among eco-engineered habitats with different complexities in the field were also investigated. Replicating habitats as similarly as possible to their original substrates and tailoring these with biogenic species in mind, marries eco-engineering and restoration principals. Using these strategies together gives the highest chance of ecosystem restoration success in altered environments.

IMMORTALIZED MARINE INVERTEBRATE CELL LINES FOR BIOMEDICINE AND BIOTECHNOLOGY

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To date there are few to zero immortalized cell lines for marine invertebrate species. This hampers basic and translational research with these species. What are the barriers? How do we remove them? What are the driving reasons to do so?

While several cell-cultivated seafood companies may have immortalized or continuous cell lines for species of commercial interest, they are not readily available to researchers and likely not fit for purpose due to their tissue of origin. Although there is a rich history of research using marine invertebrate primary cell lines including the squid (*Loligo pealei),* purple sea urchin (*Strongylocentrotus pupuratus*), eastern oyster (*Crassostrea virginica*) and American lobster (*Homarus americanus*), work with these cells is habitually a race against senescence. Development of hybrid cell lines, such as PmLyO-Sf9, a fusion of shrimp lymphoid organ cells with with Sf9 cells, is a potential workaround but introduces new complexity. Only in 2023, was the first continuous marine sponge cell line with 98 population doublings reported in the peer-reviewed literature, rekindling hope that progress is at hand. Currently, available options fail to meet the needs for marine invertebrate research. This session will begin with a brief summary of the status quo then shift discussion-based identification of key needs and barriers in order to identify key action items for tackling this issue. Technology will assist with realtime capture of inputs and a draft report will be provided to the NSA.

IMPACT OF BACTERIAL COMMUNITY AND ACCLIMATION ON MORTALITY OF JUVENILE PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) CAUSED BY OSHV-1 INFECTION

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Current understanding on host-pathogen interactions hypothesizes that Oyster Herpes Virus (OsHV-1) alters host physiology and disrupts microbiota homeostasis leading to mortality. To understand microbial role in host-pathogen interactions and to investigate the impact of acclimation on infection outcome, this study challenged juvenile Pacific oysters with OsHV-1 µVar at 22°C with- and without-antibiotic treatments after two days (Assay-1) or 16 days of acclimation (Assay-2) in laboratory condition.

During Assay-1, challenged oysters treated with Streptomycin (200 ppm) and Ampicillin (200 ppm) together had a significantly greater mortality rate 83.8% compared to that of the without-antibiotics group at 44.9% at 10 days post-challenge (DPC). Subsequently, Assay-2 oysters were treated with only Ampicillin (200 ppm) which significantly lowered mortality to 19.9% than the without-antibiotic group at 40.6% after 16 DPC. Although, mortality in without-antibiotic group in both assays were comparable, daily morality rate was slower in the longer acclimated oysters (44.9% by 10dpc vs 40.6% by 16dpc). The control oysters in both assays, despite antibiotics exposures and handling without OsHV-1, remained healthy and did not suffer any mortality. The results indicate Streptomycin and Ampicillin negatively impacted oyster survival in presence of OsHV-1 µVar. Ampicillin alone improved survival but did not eliminate mortality. Longer acclimation might have altered host physiology which led to slower mortality rate observed in Assay-2. Nonetheless, results show evidence and support the hypothesis that microbial community may play a role in the mortality of oysters infected with OsHV-1.

OYSTER SURVIVAL IN RESPONSE TO A LABORATORY CHALLENGE WITH *PERKINSUS MARINUS* IS A POLYGENIC TRAIT

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Eastern oyster producers consistently identify resistance to dermo disease, which is caused by the protozoan parasite *Perkinsus marinus*, as a top priority for selective breeding. Genetic architecture of survival to a laboratory challenge with the parasite was investigated to inform breeding program design. Three year-classes of juvenile oysters from a family-based selective breeding program were challenged with *P. marinus* by injection following a standardized methodology. A total of approximately 6,000 individuals representing 109 full-sibling families were challenged and genotyped with a SNP array containing 65,893 loci.

A genome-wide association study was performed to identify loci that affected survival to the challenge. After quality control filtering, a total of 32,876 SNP remained and were assessed with a linear mixed model while controlling for relatedness. Six SNP on four chromosomes had statistically significant effects with a Bonferroni corrected $\alpha = 0.05$ ($p < 1.52e\text{-}6$). All SNP were estimated to individually explain 0 - 4% (mean 2%) of the genetic variation for the trait. The absence of individual SNP explaining a large fraction of the genetic variation suggests that survival to the *P. marinus* challenge is a polygenic trait. Marker assisted selection is unlikely to result in efficient genetic improvement but pedigree-based and genomic selection for this trait could be effective.

GENETICS AND ONTOGENY: TWO KEY FACTORS INFLUENCING THERMAL RESILIENCE IN A CULTURALLY AND ECONOMICALLY IMPORTANT BIVALVE SPECIES

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Increasing seawater temperatures coupled with more intense and frequent heatwaves pose an increasing threat to marine species. In this study, the New Zealand green-lipped mussel, *Perna canaliculus*, was used to investigate the effect of genetics and ontogeny on thermal resilience. Six selectively-bred full sibling families and four different ages, from early juveniles (6, 8, 10 weeks post-fertilisation) to sub-adults (52 weeks post-fertilisation), were used for experimentation. At each age, each family was exposed to a three-hour heat challenge, followed by recovery, and survival assessments. Gill tissue samples from sub-adults were collected after the thermal challenge to quantify *hsp70* gene expression. Results showed that genetics, ontogeny, and size influence thermal resilience in *P. canaliculus*, with LT_{50} values ranging between 31.3-34.4°C for all studied families and ages. Juveniles showed greater thermotolerance compared to sub-adults, while the largest individuals within each family/age class tended to be more heat sensitive than their siblings. Sub-adults differentially upregulated *hsp70* in a pattern that broadly correlated to net family survival following heat challenge, reinforcing the perceived role of inducible *hsp70* protein in molluscs. This study provides insights into the complex interactions of age and genotype in determining heat tolerance of a key mussel species. As marine temperatures increase, equally complex selection pressure responses may therefore occur. Future research should focus on transcriptomic and genomic approaches for key foundation species such as *P. canaliculus* exposed to multiple relevant stressors, allowing for better predictability of the response of this species in the context of climate change.

THREE-DIMENSIONAL REEFS: MOVING OYSTER RESTORATION OUT OF THE STONE AGE

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Resource intensive oyster restoration approaches based on settlement of spat on rocks, shells and fabricated concrete structures limit scale and hinder progress. Transport and handling of heavy substrates for restoration is expensive and inefficient with an ultimate oyster mass far less than the substrate. Deployment of heavy substrates in a two-dimensional layer on the sea floor also exposes spat to hypoxia and predation resulting in poor survival.

Settlement and colonization of hatchery produced eyed larvae on wire mesh was investigated as an alternative matrix for creating three-dimensional reefs (Reefers). Spools of crab trap wire (46m X 60cm) were conditioned 14 days in 206 L plastic drums containing filtered (20 µm) natural seawater (salinity of 25). Eyed diploid larvae (100,000) were dispersed into the drum and fed algal paste for a 3-day settlement period followed by 14-day flow-through period with natural seawater. The wire spool was then suspended from a dock for further growth. After ~three months, it was largely encapsulated with wire layers fused together with oysters (~100Kg). Unwinding the spool resulted in detachment of most oysters and high mortality rate. Sections with remaining viable oysters were deployed on edge from the sea floor up 60 cm both linearly between pilings and encircling individual pilings in Mobile Bay. Within 30 days no oysters remained on the linear sections, presumably from predation. Most oysters on the circular sections survived for several months until they were killed by a hard freeze. These results inform further optimization of setting and deployment protocols for establishing three-dimensional reefs.

EXPANDING INDUSTRY APPLICATIONS OF BIPHASIC ASSAYS FOR *VIBRIO* ENUMERATION IN OYSTERS

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Miniaturized biphasic *Vibrio* kits correlate well with National Shellfish Sanitation Program (NSSP) approved polymerase chain reaction (PCR) assays for enumeration of *Vibrio parahaemolyticus* (*Vp*) and *V. vulnificus* (*Vv*) in oysters. Biphasic kits are simpler, faster and far less resource intensive than PCR. Taylor Shellfish Company established in-house *Vp* testing capability with a biphasic kit in 2022 to evaluate the effectiveness of their refrigerated wet storage for reducing risk. Over the past two *Vp* seasons ~3000 oyster samples have been analyzed. These data demonstrate ~95% reduction of *Vp* levels after a 3-day wet storage period and a similar reduction in *Vp* illnesses linked to their oysters.

Auburn University has a grant to replicate the Taylor Shellfish in-house *Vibrio* testing model with Gulf Coast oyster industry. Participating firms will be provided with equipment, supplies and training for enumeration of *Vp* and *Vv*. Analyst proficiency will be verified periodically by comparing their results to those obtained by NSSP approved methods. Preliminary results indicate that naturally occurring *Vp* levels in oyster mantle fluid remain relatively stable after extended storage and would be a suitable matrix for proficiency determinations that could be shipped to Taylor Shellfish or other laboratories. A data quality system based on verification fits industry needs better than the lengthy and expensive NSSP process of method validation and laboratory certification. Establishing widespread *Vibrio* analytical capability to additional species (*Vv*) and regions will further empower the oyster industry to understand best handling and harvest practices to reduce their *Vibrio* risk.

EFFICACY OF REFRIGERATED WET STORAGE TO REDUCE *VIBRIO PARAHAEMOLYTICUS* AS DEMONSTRATED BY A NOVEL TEST KIT

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Sporadic illnesses and occasional outbreaks associated with the naturally occurring *Vibrio parahaemolyticus* (*Vp*) bacteria in oysters consumed raw has plagued the United States shellfish industry for years. Despite strict harvest controls adopted by States, sporadic *Vibrio* illnesses continue to plague the industry.

In an effort to reduce the risk of *Vibrio* illness, Taylor Shellfish Company and their British Columbia (BC) business, Fanny Bay Oyster Company have experimented with temperature controlled wet storage. Since 2020 in BC, and 2021 in Washington State, they have been holding oysters in closed recirculating temperature controlled wet storage systems. In 2022 and 2023 Taylor Shellfish confirmed the efficacy of the *Vibrio* purging testing 3,019 samples using a novel, biphasic test kit for *Vp*. Replicate sampling identified unexpected variability within some harvest lots in addition to seasonal lot to lot variability. *Vp* levels at harvest informed wet storage protocols. Typically, three days in a tote-based recirculating wet storage system at 11°C reduced *Vp* levels by 95%. *Vp* illnesses attributed to Taylor Shellfish oysters have dropped by a similar percentage.

Unfortunately, due to the inherent variability associated with purging *Vp* using a biological process it is unlikely this method could be validated for doing so under current NSSP protocols. Regardless, temperature controlled wet storage coupled with industry implemented testing using the biphasic test kit to verify *Vibrio* reduction can result in dramatic illness risk reduction. This approach could be incentivized by providing waivers from harvest restrictions to companies adopting it.

CONSERVATION PALEOBIOLOGY: PUTTING THE DEAD TO WORK

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Long-term data are essential to habitat management and restoration because they provide a means to establish baseline conditions, document the environmental impacts of anthropogenic activities, and track trends in populations and habitat condition. In practice, however, for many species and habitat management interventions, long-term monitoring is rarely done, or is limited to short temporal intervals (< 10 years). An underutilized solution to this lack of temporal data is molluscan death assemblages (DA), which are time-averaged accumulations of dead, identifiable shell remains preserved in the sediment on the seafloor. Here, the utility of molluscan DA to provide historical data relevant to resource managers with two examples will be discussed. The first case concerns the use of DA of oysters (*Crassostrea virginica*) from reefs in Florida to add historical context for existing monitoring of live oyster body size, revealing how trend assessments using the live-oyster monitoring data alone can differ after considering the longer-term perspective provided by the DA. The second case concerns assessment of benthic habitat condition in Long Island Sound and shows how the remains of dead mollusc shells can be used to evaluate the success of a recent management intervention strategy designed to improve water quality by reducing the nitrogen pollution load in the Sound. Molluscan DA that are collected using standard sampling protocols for living molluscs provide a cost-effective and efficient means of retroactively acquiring historical data to supplement monitoring data for many other species and estuarine and coastal habitats.

SHELLFISH MICROBIOMES: CHALLENGES AND OPPORTUNITIES FOR AQUACULTURE AND ECOLOGY

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Microbes that live on and within shellfish (i.e., their microbiomes) play an important role in their ecological success and economic potential as a sustainable food source. In this talk, an overview of known and potential roles of shellfish microbiomes with particular reference to other topics of interest discussed at the 2023 NSA Meeting will be presented. This includes interactions between shellfish microbiomes and disease, the response of shellfish microbiomes to external factors (e.g., environmental stressors, pollution, shellfish food), and the beneficial potential of individual members of the shellfish microbiomes. Current and emerging methods for investigating shellfish microbiomes and challenges that should be addressed in this research field will also be discussed. By highlighting ongoing research efforts of the NSA presenters in the context of the broader field of microbiome research, this session hopes to facilitate collaborations and identify future research priorities that benefit shellfish both in industry and the wild.

EXPANDING THE ECOSYSTEM SERVICES OF OYSTER FARMS WITH THE CO-CULTIVATION OF SUGAR KELP, *SACCHARINA LATISSIMA*: MAXIMIZING NITROGEN BIOEXTRACTION

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Sugar kelp (*Saccharina latissima*) is an emerging mariculture crop in the United States that can provide a means of crop and market diversification for shellfish farmers, as well as expand farm ecosystem services. Like bivalves, kelp and other seaweeds are non-fed, extractive aquaculture crops that sequester nutrients from surrounding waters to grow. These nutrients are removed from marine systems when bivalves and seaweeds are harvested, a process known as bioextraction. This project sought to directly quantify nitrogen removal rates obtainable through sugar kelp farming across a range of water quality in the coastal waters surrounding Long Island, New York (NY). Kelp growth differed significantly among eight sites, with yields at peak biomass ranging from 0.06 to 11.8 kg m^{-1}. Tissue nitrogen content also significantly varied among sites, ranging from 0.85 to 2.66 percent of dry tissue biomass, with higher tissue nitrogen content found in locations with greater kelp growth. These site differences in kelp growth and nitrogen content largely paralleled ambient nitrate concentrations and suggests high N environments are ideal for maximizing bioextraction of N by kelp. Extrapolating the growth and nitrogen data obtained here using realistic farm designs, it is estimated that kelp farming can remove 0.04 to 58.11 kg N per acre per year in NY waters, depending on location. These nitrogen removal rates will be compared to that found for oyster aquaculture, and the combined ecosystem services of oyster and kelp co-cultivation will be discussed.

ANTIFOULING SURFACE TEXTURING OF EQUIPMENT AND BIOFOULING MONITORING BENEFITS FOR SHELLFISH AQUACULTURE

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Biofouling impairs animal welfare and economic viability in the shellfish industry when stock species, equipment and infrastructure become fouled. Biofouling on equipment and infrastructure can increase weight, lead to material fatigue, corrosion, and interfere with stock quality. National legislation may not allow or limit the use of biocidal antifouling products on shellfish farms, protecting the product, the consumer, and the environment. The aim is to demonstrate environmentally-friendly biofouling control measures, current and in development, for aquaculture.

The approach of husbandry and cleaning is an example of a traditional, very effective, environmentally- and economically-friendly method to control biofouling. In the EU funded SME led FP6 project Collective Research on Aquaculture Biofouling (CRAB; 2004-2007; 11 farms, cold temperate to subtropical) farmers monitored biofouling spatfalls with scientific guidance to inform their cleaning schedule (baseline monitoring). Spatfalls were found to be mostly different in time, quality, and intensity, demonstrating site- and species-specific biofouling issues and timings for cleaning, thus validating the baseline monitoring. Newly-developed sensor technology may allow monitoring of biofouling in real-time, on equipment or infrastructure of concern in the future, contributing to streamlining husbandry and cleaning in combination with baseline monitoring. Antifouling surface textures are adding to the control efficacy of baseline and sensor monitoring of biofouling. Textures are laser-machined and may reduce the incidence of biofouling by 90%. Biofouling monitoring and the environmentally friendly antifouling approach may be an option to support the shellfish industry and the consumer. The biofouling issue is not controlled with one approach.

THE IMPACTS OF TWO MACROALGAL SPECIES, *ULVA* SP. AND *GRACILARIA* SP. ON THE GROWTH AND SURVIVORSHIP OF EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Seaweeds can be considered a nuisance organism by shellfish farmers since they often bio-foul cages and other gear, potentially restricting water flow to the shellfish, and necessitating an increase in general farm upkeep and care. Seaweeds, however, also produce oxygen and sequester CO_2, deterring ocean acidification. The purpose of this study was to evaluate the impacts of two common macroalgae species, *Ulva* sp. and *Gracilaria* sp., on the survivorship and growth of the eastern oyster, *Crassostrea virginica*, in an aquaculture setting. Oysters were cultivated in floating mesh bags with and without the addition of these seaweed species in two embayments on the north shore of Long Island, NY with contrasting water quality: Northport Harbor and Mount Sinai Harbor. Experiments were conducted from two to five weeks. Overall, experiments in both locations and with both seaweed species found no negative impacts on oyster growth and survivorship. In several experiments, oyster growth was significantly enhanced in the presence of seaweeds ($p<0.05$). Surface water mapping of large-scale *Ulva* arrays in Northport Harbor demonstrated the ability of this seaweed to regionally raise levels of DO and pH, suggesting *Ulva* sp. improved water quality stimulating bivalve growth. The results suggest that the co-cultivation of these seaweeds with shellfish may help improve commercial shellfish yields and help protect shellfish crops from coastal acidification. Additionally, since many seaweeds have commercial value, including *Ulva* and *Gracilaria*, the co-cultivation of seaweeds with shellfish may provide additional revenue streams for shellfish farmers.

EXPOSURE TO PLASTIC DEBRIS ALTERS EXPRESSION OF BIOMINERALIZATION, IMMUNE, AND STRESS-RELATED GENES IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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The degradation of marine plastic debris poses a threat to organisms by fragmenting into pieces and releasing a complex chemical leachate. Numerous studies have investigated individual dangers such as microplastic ingestion or exposure to single chemicals; however, few studies have examined the holistic threat of plastic exposure. The objective of this study was to measure changes in gene expression of gill and gonadal tissue of the eastern oyster (*Crassostrea virginica*) in response to plastic debris exposure during their first year. Shell and polyethylene terephthalate plastic were used as substrate for the metamorphosis of larvae in a settlement tank. Substrate pieces were then transferred to metal cages and outplanted in pairs onto restoration reefs in the St. Mary's River, Maryland, USA. After 10 months of growth, the oysters were collected, gill and gonadal tissue removed, and sex identified. The tissues of six oysters from each sex and substrate type were then used in RNA-seq. Plastic exposure altered the expression of immune and stress-response genes in both gill and gonadal tissue. Genes upregulated in response to plastic were enriched for gene ontology functions of proteolysis and fibrinolysis. Downregulated genes were involved in shell biomineralization and growth. One male oyster exposed to plastic had "feminized" gene expression patterns despite developing mature sperm, suggesting plastic leachate can alter gene expression and shift protandric individuals to develop as females. Plastic pollution may therefore reduce shell growth, initiate immune and stress responses, alter sex differentiation, and impact reproductive output of eastern oysters through changes in transcription.

EXPLORING RESILIENCE IN THE OYSTER FARMING INDUSTRY OF NORTH CAROLINA

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Shellfish farming, specifically oyster farming, is a rapidly growing industry in North Carolina (NC). Similar to finfish aquaculture and commercial harvest industries, oyster farming is subjected to a wide range of economic, regulatory, environmental, and anthropogenic stressors that layer upon the industry. Specifically, the NC shellfish industry has withstood immense pressures in the past five years including increased tropical events and regulatory pressures, a changing business climate, and increased mortality events. Understanding these pressures can improve both industry and farm level resilience through behavior modification, collaboration, improved site selection, and grow-out practices.

The purpose of this study is to establish a resilience framework for both individual growers and the industry itself that identifies and defines the most important stressors affecting oyster farming in NC. The framework will contextualize these stressors over different temporal scales at the individual and industry level through qualitative interviews with individual growers, industry stakeholders, and regulatory groups. Lastly, the authors will identify key drivers of resilience at the individual and industry levels. This goal will be accomplished through quantitative surveys developed from analyzing the preceding interviews and identifying commonalities. As the oyster farming industry continues to grow, this work is essential for assessing and identifying strategies to improve resilience, especially in the face of climate change. Commercial fisheries are often top heavy and favor capital, but the oyster farming industry is currently flush with small-scale operations. Through collaboration across stakeholders, regulatory bodies, and farmers, the industry has the potential to increase its value, and create enabling industries.

TIDES OUT: WASHINGTON SHELLFISH CREW AND MANAGER TRAINING PROGRAM

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Washington State is the largest producer of farmed bivalves in the nation and is currently facing a substantial decline in aquaculture workforce recruitment and retention. With a lack of employee recruitment, the already challenging working conditions (i.e., unpredictable work schedule, poor weather conditions) become more difficult with current employees having to increase their work capacity causing a lack of retention, which creates a negative feedback cycle. Therefore, an informal needs assessment funded by the National Sea Grant Office was conducted by Washington Sea Grant (WSG) and Oregon Sea Grant to determine the specific workforce needs of the local shellfish industries. The survey concluded two predominant needs in Washington: 1) to learn new approaches to recruit, mentor, and manage the next generation of increasingly diverse workers; and 2) to develop a training program that prepares future employees for unpredictable working/weather conditions, demanding physical duties, and essential skills for being a safe and successful worker on the tide flats. To approach this, WSG created an Advisory Committee composed of shellfish aquaculture and seafood industry experts that are focused on integrating diversity, equity and inclusion priorities in the manager and crew training programs. These programs will provide hands-on learning by current industry representatives and will be conducted simultaneously to provide a networking opportunity between current and potential future employees.

ENHANCING BLUE MUSSEL SEED COLLECTION THROUGH LARVAL-SPECIFIC ENVIRONMENTAL RNA (ERNA) TOOLS

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One of the most significant challenges for the blue mussel aquaculture industry is reliably capturing wild mussel seed from the water column. Recently, the increasing spatiotemporal unpredictability of mussel larvae has led to failed seed recruitment and, consequently, severe financial and production hardships for farmers. To increase the probability of successful seed collection, reliable methods to detect, quantify, and map the distribution of mussel larvae are urgently needed. Molecular tools that leverage environmental RNA (eRNA) within the water column provide promising solutions to this problem, as they are capable of: (1) specificity beyond the species level, allowing for identification of living organisms of a distinct developmental stage and (2) high spatiotemporal resolution due to the rapid degradation rate of RNA. Here, the development of eRNA-based biomonitoring tools that are capable of specifically detecting and quantifying live blue mussel larvae will be described. In addition, preliminary results obtained from testing field samples collected from an active blue mussel farm in Maine and recent RNA-seq efforts to characterize the blue mussel developmental transcriptome will be discussed. It is envisioned that the eRNA-based assays and accompanying toolkits resulting from this work will transform mussel farmers' ability to rapidly monitor seed around their farms or seed collection sites. Moreover, regular monitoring with these tools will allow farmers to gain a more comprehensive understanding of the changing phenology of mussel larval supply. Finally, while these tools focus on mussels, similar eRNA-based tools can readily be developed for other economically-important shellfish species.

VALUES, PROBLEM DEFINITIONS, AND POLICY PREFERENCES IN MAINE AQUACULTURE

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As aquaculture's footprint grows in state waters, so too does social conflict related to diverse values and competing policy priorities, suggesting the need for more research about the social dimensions of the industry and community perspectives about how aquaculture development should proceed. The purpose of this research is to understand the role of competing values and priorities in inciting social conflict related to aquaculture development, using the state of Maine as a case study. This presentation will present research about the values and beliefs underlying competing portrayals of aquaculture. It will then present findings from a Q-method study with diverse stakeholders in the aquaculture industry of Maine—both proponents and opponents—to explore how competing values shape policy preferences for aquaculture development. This research revealed five distinct perspectives, each of which defines the "problem" of aquaculture differently and holds competing policy preferences for industry growth moving forward. These findings suggest divergent priorities between these groups, as well as areas of relative consensus that may serve as reasonable starting points for constructive policy dialogue. This study also highlights the inadequacy of "aquaculture" as a blanket term and supports the need to differentiate between species and cultivation practices (e.g., finfish and shellfish) in both discourse and management practices.

IMPACTS OF GENTRIFICATION, LOSS OF ACCESS, AND A CHANGING COASTAL ENVIRONMENT ON THE SOFTSHELL CLAM FISHERY IN MAINE

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The wild clam fishery is the second most valuable fishery in the State of Maine and is an important part of the coastal communities of Maine; however, shellfish harvesters face an increasing loss of access to intertidal mudflats, driven largely by changing coastal property ownership and gentrification. Concurrent with this loss of upland access, sea level rise and extreme weather events pose threats to mudflat habitats. Efforts to better understand how these multifaceted issues impact mudflats, shellfish, and harvester livelihoods are crucial for proactive and adaptive management of the fishery.

From 2022-2023, Manomet collaborated with six towns in Casco Bay, Maine to inventory harvester access sites. Results showed that 66% of access points were across private property, mostly through informal agreements with landowners, underscoring the precarious nature of access to the coast. The vast majority (78%) of all identified access points were footpaths to the shore, rather than physical infrastructure. This inventory informed strategies taken by each town to protect or enhance access, including outreach to landowners and collaboration with land trusts. The loss of coastal access is further exacerbated by sea level rise and extreme weather, which impact the extent and productivity of the mudflats, and pose jurisdictional questions for management of the resource. In 2023, Manomet launched a project that brought together harvester knowledge, drone survey data, LiDAR data, and archival imagery to develop tools and resources for towns to prepare for climate change impacts. Together these efforts are supporting co-management and adaptation in the clam fishery of Maine.

USING AN OBJECTIVES HIERARCHY TO SUPPORT SUSTAINABLE AND HEALTHY OYSTER PRODUCTION IN MISSISSIPPI

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Research for the Mississippi Based RESTORE Act Center of Excellence (MBRACE) has emphasized production of eastern oysters (*Crassostrea virginica*) in Mississippi Sound as a healthy and sustainable food product. The MBRACE program uses an objectives hierarchy, a tool of decision science, to inform and guide program direction by identifying logical connections between research and program goals. The process of developing an objectives hierarchy reduces confusion and generates a common vision for what is valued in a decision context. Programs use the tool to clarify and justify objectives to funding agencies; and research proponents use it to demonstrate how their efforts address those objectives. Simple questions are used to organize objectives into a hierarchy, yielding a comprehensive list of decision/action options and interdependencies. Two objectives of the MBRACE program are to increase oyster production and to reduce human illness from oyster consumption. These two objectives are specified by asking 'how' or 'what do I mean by that', leading to an inclusive listing of decision options. Values of an objective are defined by asking 'why', which leads to ultimate program goals that can be measured through specific performance indicators. At the top of an objectives hierarchy is a 'fundamental objective', a directed preference for an objective that requires no further explanation, such as maximizing ecological, economic or social benefits. The objectives hierarchy framework benefits organizational success by fostering critical thinking, comprehensive decision/action alternatives and transparency, which is crucial for any organization with a diversity of stakeholders and stakeholder values.

WHY MUSSELS CAN SURVIVE WITHOUT OXYGEN, BUT ARE SENSITIVE TO ANOXIA

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Mussels survive low tide by closing the shells and switching to an anaerobic metabolism and can survive for multiple days with closed shells. Yet when placed in water that becomes anoxic mussels do not survive long. By combining measurements of shell movement, heartrate, and oxygen levels inside the shell, the behavioural mechanism that explains this was identified.

DIVERSITY, EQUITY, AND INCLUSION IN THE OYSTER AQUACULTURE AND RESTORATION SPACE

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Together in partnership, The Nature Conservancy and The Pew Charitable Trusts launched the Supporting Oyster Aquaculture and Restoration (SOAR) program in October 2020, with the purpose of supporting the oyster industry and leveraging aquaculture as a means of reef restoration on a nation-wide scale. This program features partnerships between growers, state regulatory agencies, NGO, and industry associations. SOAR 2.0 was relaunched in 2023 to continue to provide support for the oyster aquaculture industry and oyster restoration, demonstrate the effectiveness of the program, secure long-term support for a continuing restoration market, and work towards creating a diverse, equitable and inclusive ecosystem within the shellfish aquaculture and restoration communities. SOAR 2.0 DEIJ work will start with a focus on race and ethnicity with the overarching goal of advancing the leadership of underserved communities in the aquaculture space, co-creating opportunities if none exist, and cultivating and retaining a more diverse oyster aquaculture workforce. To accomplish the work, four objectives have been set: completing an assessment to better understand and identify underserved communities in oyster aquaculture and restoration, conducting outreach to understand challenges for underserved communities, creating a SOAR DEIJ strategic plan to guide future SOAR work and funding opportunities, identifying, and funding a select number of projects starting in fall 2024, and developing a pipeline of potential projects for future funding.

LEVERAGING AQUACULTURE FOR RESTORATION: AN OVERVIEW OF THE SUPPORTING OYSTER AQUACULTURE AND RESTORATION PROGRAM

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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, the National Oceanic and Atmospheric Administration and United States Department of Agriculture Natural Resources Conservation Service. The program features two components, an oyster purchase for restoration and a Shellfish Growers Resiliency Fund. The program has generated cooperation and support from all participants, primarily growers, regulators, and the restoration community. Since its inception, SOAR has seen great success, to date 3.5+ million oysters have been purchased and 125 growers participated. This resulted in 450+ jobs being sustained and around 40 acres of oyster reefs being rebuilt at 25 restoration sites. As a result, SOAR 2.0 was launched in early 2023 to continue to provide support for the oyster aquaculture industry and oyster restoration, demonstrate the effectiveness of the program at scale, secure long-term support for a continuing conservation market, and work towards creating a diverse, equitable and inclusive ecosystem within the shellfish aquaculture and restoration communities. SOAR 1.0 program successes and challenges will be described, as well as an overview of SOAR 2.0.

THE EFFECTS OF BIVALVE SHELLFISH AQUACULTURE ON SEDIMENT DENITRIFICATION IN FLORIDA

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Bivalve shellfish aquaculture provides economic and environmental benefits. Nitrogen (N) is an important nutrient in coastal ecosystems, however, in excess it can cause algal blooms and dead zones. There is growing evidence that shellfish aquaculture enhances sediment denitrification, a microbially mediated process that converts harmful N to harmless N2 gas. Yet, data representing Floridian shellfish and their growing conditions are lacking. To address this gap, sediment denitrification (Net N_2 production) and other biogeochemical properties (sediment organic matter and dissolved inorganic nitrogen fluxes) were measured at four aquaculture shellfish leases along the Gulf Coast of Florida near Tampa and Cedar Key in the wet and dry seasons. Sediments were compared from northern quahog (= hard clam) (*Mercenaria mercenaria*) and eastern oyster (*Crassostrea virginica*) aquaculture leases to reference sediments without shellfish. In Tampa, both types of shellfish aquaculture enhanced denitrification in the wet season (clam=304.21± 84.67; oyster=139.57±45.52); however, there was little to no enhancement in the dry season. Regardless of season, in Cedar Key, neither clam nor oyster culture enhanced denitrification. Differences in the effects of shellfish on denitrification may be caused by local hydrology and water depth, husbandry practices, age of operation, and shellfish species. For instance, Cedar Key maintains more leases than in Tampa. The amount and proximity of leases potentially creates a larger "footprint" that makes it difficult to isolate the effect of shellfish. Our results highlight the need to account for site specific variability when evaluating shellfish aquaculture as a tool for water quality restoration through N removal.

THE HOLOGENOME OF THE CHILEAN BLUE MUSSEL, *MYTILUS CHILENSIS*, EXPOSED TO HYPOXIA

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The Chilean blue mussel, *Mytilus chilensis,* is a key socioeconomic species inhabiting the southern coast of Chile. This endemic marine mussel supports a booming aquaculture industry, which entirely relies on artificially collected seeds from natural beds that are translocated to diverse physical-chemical ocean conditions for farming. Furthermore, various microorganisms, pollution, and environmental stressors threaten mussel production, eventually impacting its survival and growth. Herein, the hologenome concept is pivotal to developing sustainable shellfish aquaculture. A high-quality reference genome of *M. chilensis*, comprising a genome size of 1.93 Gigabases assembled into 14 chromosomes will be presented. The genome annotation showed 34,530 genes and 4,795 non-coding RNA. A total of 57% of the genome contains repetitive sequences with predominancy of LTR-retrotransposons and unknown elements. To explore the hologenome interactions of *M. chilensis,* genome expression analysis, and microbiota survey were also conducted in mussels experimentally exposed to hypoxia conditions. The results suggested high modulation of the hologenome, revealing tissue-specific molecular interplays between the bacterial community and mussels under physiological stress. The hologenome of *M. chilensis* provides pivotal molecular knowledge to understand how climate change can impact mussel biology.

NON-ZOONOTIC TISSUE PARASITES IN THE EASTERN OYSTER

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Oyster reefs of Galveston Bay, Texas, are primarily constructed by the eastern oyster (*Crassostrea virginica*). These are a high-functioning habitat for coastal ecosystems, and economically important for fisheries and aquaculture businesses. Oyster survival is challenged by multiple stressors, including parasites and associated disease outbreaks. Therefore, the intensity of *Perkinsus marinus* ("dermo disease") and the abundance of a variety of tissue parasites was assessed, and their influence on oyster morphometrics and soft tissue production was examined. Oysters were collected from low and mid-bay regions during October of 2022. It was found that *P. marinus* intensity differed across regions, likely related to salinity differences, and that infection influenced oyster tissue mass. Prevalence of *P. marinus* ranged from 22% to 90% with higher prevalence in the low bay. Abundance of other parasites affected oyster condition and differed across regions in ways that also suggest higher salinity supported higher parasite abundances. Their prevalence ranged from 50 to 100% also with more prevalence in the low bay. Turbellaria and Copepoda were the most abundant; these are known for causing lesions in the gills and altering mucus composition. Regional differences could have important implications for managers, wild fisheries, and newly legalized oyster aquaculture businesses, due to their effect on the quality of the shellfish product. Further assays are strongly recommended as higher levels of *P. marinus* and a variety of tissue parasites were detected when compared with prior surveys. The present research suggests that parasite intensities may be an important factor for current oyster survival in Galveston Bay.

OYSTERS AS AN ECOLOGICAL INDICATOR FOR EVERGLADES RESTORATION

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Progress on the restoration of the Florida everglades and the greater south Florida ecosystem is communicated to Congress and the State of Florida funding agencies through two periodic reports: the System-wide Ecological Indicators for Everglades Restoration report and a System Status Report. Eastern oysters (*Crassostrea virginica*) have been monitored as an important biological indicator informing those reports since 2000 (Caloosahatchee River) and 2005 (St. Lucie Estuary, Loxahatchee River, and Lake Worth Lagoon). The principal metric, or performance measure, for oysters is acres of oyster habitat, but comprehensive surveys are time consuming and costly. Interim metrics that are monitored include monthly assessment of water quality, disease, settlement and reproduction, growth and mortality, and semi-annual surveys for abundance and size.

Recent reports indicate oysters are failing to meet restoration targets, primarily due to declining oyster density and settlement. In Lake Worth Lagoon and the Loxahatchee River persistently high salinity results in elevated levels of *Perkinsus marinus*. In the St. Lucie Estuary, density is declining despite relatively stable conditions in recent years. In the Caloosahatchee River, a combination of high freshwater releases combined with the passage of tropical weather systems is also contributing to declining oyster metric scores. In each of the estuaries, the largest oysters are a smaller proportion of the population than was common when the study began. Results of a preliminary randomized survey will be discussed as a means of relating the monthly and semi-annual metrics to less frequent wide-scale surveys.

GROWTH AND PHYSIOLOGICAL RESPONSES OF FRESHWATER MUSSELS (*UTTERBACKIANA IMPLICATA* AND *SAGITTUNIO NASUTUS*) RECIPROCALLY TRANSPLANTED BETWEEN A POND AND STREAM SITE

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Hatchery propagation and pond grow-out are useful tools for freshwater mussel restoration. The translocation of hatchery-sourced mussels from eutrophic grow-out ponds to restoration sites may expose mussels to appreciable differences in seston composition, which may influence growth and survival. Mussels adjust their physiological processing to compensate for natural fluctuations in particulate matter (PM), particulate organic matter (POM) and the organic fraction of particulate matter (PPOM). The physiological responses of mussels were investigated in response to rapid artificial fluctuations in seston composition through translocation.

The physiological plasticity of mussels responding to seston change was assessed by reciprocally transplanting hatchery-produced mussels from the Delaware River Basin (*Utterbackiana implicata,* N = 60; *Sagittunio nasutus*, N = 60) between a stream (PM = 3.06 mg/L, PPOM = 78%) and hydrologically-linked pond (PM = 10.68 mg/L, PPOM = 42%). Four physiological experiments were conducted post-transplantation to measure feeding responses at days 0, 4, 11, and 28. Growth and survival was monitored for 401 days post-transplantation. Greater PPOM (i.e., food quality) is associated with greater mussel growth, even at significantly lower POM (i.e., food quantity) concentrations. Both species rapidly adjusted absorption efficiencies when exposed to new environments, while condition index and clearance rates acclimated slowly. Growth rates lagged in transplanted mussels until condition indices stabilized to match those of the control mussels. Understanding physiological responses to changes in environmental condition will guide best practices for translocation, set expectations for the growth of mussels post-transplantation, and provide tools to accurately assess ecosystem services provided by freshwater mussels.

VARIABLE TO THEIR CORE: BIVALVE MICROBIOMES HAVE CORE BACTERIA BUT ARE ALTERED BY ENVIRONMENT

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Many factors affect the microbiome of an organism including its environment, proximity to other organisms, and physiological condition. As filter feeders, bivalves have highly plastic microbiomes that are especially influenced by the surrounding seawater, yet they also maintain a unique core set of microbes. The bacterial microbiomes of four bivalve species native to the mid-Atlantic east coast of North America were characterized using 16S ribosomal RNA sequencing: *Crassostrea virginica, Macoma balthica, Ameritella mitchelli,* and *Ischadium recurvum.* Significant differences were found in bacterial amplicon sequence variants (ASV) across species, with each species harboring a core ASV present across all individuals. It was also found that some *C. virginica* co-cultured with *I. recurvum* had high abundances of the *I. recurvum* core ASV. ASV associated with infection by the parasites *Perkinsus marinus* and *Zaops ostreum* were identified as well as others associated with bivalve size. Several of these ASV are candidates for further investigation as potential probiotics, as they were found positively correlated with bivalve size and health. These results show that all four species have highly plastic microbiomes, while maintaining certain core bacteria, with important implications for growth, health, and adaptation to new environments.

CAN MICROBIOME DATA BE USED TO IMPROVE PREDICTIVE MODELS OF CRITICAL ESTUARINE HABITATS? A CASE STUDY IN CHESAPEAKE BAY

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Microbial processes play a critical role in shaping marine environments, yet computational models of these environments generally limit explicit representation of microbes to photosynthesizers. One challenge in representing decomposer communities within such codes is a lack of observations to show which functional groups of decomposers exhibit environmental control. Results are presented from a recent series of studies in Chesapeake Bay. Microbial community structure was analyzed using 16S sequencing of 236 samples during the summer of 2016 and spring/summer of 2017. The distribution of functional genes using shotgun metagenomics of 38 samples during the spring/summer of 2017 was also examined, with over 8000 genes found in at least 30 sites. The distribution of genes was compared to results from a newly developed computational model that includes sulfur cycling. Key results from this series of studies include: 1) although the abundance of many phytoplankton taxa (including *Vibrio*) show a strong sensitivity to salinity, functional genes show much less sensitivity; 2) sulfur-oxidizing organisms are common and show a strong response to low levels of oxygen; 3) sulfur-oxidizing genes associated with these organisms are moderately predictable both from observed and modeled oxygen and modeled hydrogen sulfide; 4) many of the closest matches to these genes are found in known molluscan endosymbionts.

ACHIEVING CARBON NEUTRAL BIVALVE AQUACULTURE VIA THE CULTIVATION OF SEAWEEDS

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As climate changes accelerates, a global effort is underway to reduce the emissions of CO_2 to the atmosphere. Beyond a source of revenue for farmers, bivalve aquaculture provides a wealth of ecosystem services including enhancement of wild bivalve populations via spawning and filtration pressure on plankton, which in turn improves water clarity and removes nitrogen and carbon (C) from the water column. While some of the C consumed by bivalves is ultimately incorporated into tissue, shell, and biodeposits, this sequestered C is small relative to the C produced by bivalves as they calcify and respire. As a consequence, bivalve farms are net sources of CO_2 to estuaries and the atmosphere. In contrast, as photosynthetic organisms, seaweeds are capable of sequestering vast quantities of CO_2 as they grow. Hence, the co-culture of seaweeds with bivalves represents an opportunity to transform aquaculture into a carbon sequestering activity. During the past decade, our group has documented the ability of temperate seaweeds including sugar kelp (*Saccharina latissima*), *Gracilaria* spp., and *Ulva* spp. to sequester significant amounts of C, often to the great benefit of bivalves. Highlights have included the ability of fast-growing seaweeds, *S. latissima*, and *Ulva* sp., to cause the lysis of harmful algal blooms and to transform acidified waters to supersaturated with regard to aragonite, leading to significantly increased growth rates of bivalves. This talk will review these benefits as well as detail the level of seaweed cultivation needed to transform bivalve farms into carbon sequestering operations.

ENVIRONMENTAL DNA EARLY-WARNING SYSTEMS FOR BIOFOULING: PROMISES AND PITFALLS

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Biofouling of unwanted organisms on aquaculture gear is a problem for most farms and limits sustainable growth of the industry globally. Major barriers to biofouling management include the diversity of biofouling organisms and the unpredictability of their arrival and growth over time and space. Whether environmental DNA (eDNA) surveys of aquaculture farms can contribute to early-warning systems that could lead to more effective biofouling mitigation was explored. To do this, traditional and eDNA surveys for three common biofouling organisms were conducted in an experimental scallop farm in the Damariscotta River, Walpole, ME from summer to fall: blue mussel *Mytilus edulis*, barnacle *Semibalanus balanoides*, and solitary ascidian *Ciona intestinalis*. Settlement plates represented our traditional survey method and eDNA surveys included three methods: water sample filtration, scallop shell swabs, and passive eDNA "metaprobes" hung from the scallop lines for variable number of days. Results of each method will be compared in terms of sensitivity, accuracy, labor, and cost, and the general promises and pitfalls of using eDNA for biofouling forecasts will be discussed.

CONCERNED OYSTERMEN RESTORING ESTUARIES

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The massive disruptions to the oyster industry caused by the Covid-19 pandemic creates an opportunity to rethink how oyster habitat can be restored and created. Oyster reef restoration and enhancement projects have focused on replacing or supplementing cultch material in the hopes of gaining a natural spat set. Despite these considerable efforts, oyster reproduction has varied wildly over the last 5 years from Florida to Texas causing nearly catastrophic consequences to the Gulf oyster community. The use of aquaculture as a tool for restoration or enhancement has been limited, with any efforts primarily focused on the use of spat on shell. We seek to determine the ecosystem service benefits provided using large, single oysters, obtained from the private commercial aquaculture sector.

Participating oyster farmers are providing oysters to the appropriate state agencies (AL MRD and MS DMR) for deployment at designated sites. Working in cooperation with the state agencies, oysters stocked will be monitored by Auburn University Shellfish Lab (AUSL) personnel to assess oyster growth and survival, natural recruitments, and estimates of associated ecosystem services. In addition to the direct support to oyster farmers during the pandemic by paying a net price of up to $0.40 per oyster, this project will also provide critical ecosystem services through improved water quality, increased biodiversity, creation of more diverse habitat and cultural services provided by productive oyster reefs.

OYSTER FARMING RESILIENCE INDEX

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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, significant environmental events to COVID 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 their 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.

SELECTIVE CAPTURE OF PROKARYOTES BY MUSSELS AND ASCIDIANS AS DETERMINED THOUGH MICROBIOME SEQUENCING IN INHALANT AND EXHALANT WATERS

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Capture efficiency of plankton (from <1 µm to >500 µm) by suspension-feeding animals varies widely as a consequence of the anatomy of capture organs, size of plankters, and other physicochemical factors. Research in tropical systems indicates that particle shape and surface properties likely contribute to patterns of capture success for micrometer- and submicrometer-scale plankton, but little work has been done with temperate species living in mesotrophic environments. In this work, the patterns of selective capture of prokaryotes by four abundant suspension-feeders common in Long Island Sound were examined. Two species of mussels (*Mytilus edulis* and *Geukensia demissa*) and two species of solitary ascidians (*Ciona intestinalis* and *Styela clava*) were sampled over a range of seasonal and environmental conditions. Inhalant and exhalant seawater samples were collected *in situ* using a modified VacuSIP apparatus and then filtered to collect plankton. Filter pads were subjected to DNA extraction, PCR amplification of the 16S gene, and high-throughput sequencing. Microbiome analyses included comparisons of alpha- and beta-diversity, and several metrics of selective capture. Of the four species examined, *M. edulis* had a relatively low degree of prokaryotic capture, whereas *G. demissa*, *C. intestinalis*, and *S. clava* performed much more selective capture. These results suggest that particle size alone does not fully explain prokaryotic capture because certain taxa (e.g., Bacteroidia and Cyanobacteriia) were preferentially removed by the filtration activities of these animals. It is possible that differential capture is related to taxon-specific cell surface properties and lectins in the mucus of capture organs.

COMPREHENSIVE GENOMIC ANALYSIS OF *ARGOPECTEN IRRADIANS* ACROSS THE UNITED STATES: REVEALING POPULATION DIVERSITY AND EVOLUTIONARY HISTORY

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The bay scallop, *Argopecten irradians*, has significant commercial and recreational value and thrives in estuarine and coastal environments along the U.S. coastline from New England to the Gulf of Mexico. Understanding the genetic and genomic diversity of this species is critical for its conservation, effective population management, aquaculture, and restoration strategies. This study presents a comprehensive genomic analysis of *A. irradians*, including large-scale sequencing of 864 samples from various U.S. locations (Massachusetts, New York, New Jersey, North Carolina, Florida, Texas), as well as historical museum specimens.

Using genotyping-by-sequencing (GBS) and whole-genome resequencing techniques, a detailed genetic distribution map of *A. irradians* populations in these regions was constructed. Generated data reveal a remarkable diversity in the genetic makeup of bay scallops, highlighting distinct population structure. The analysis indicates significant variation between populations in different states, which can be attributed to adaptations to unique environmental conditions and possibly historical events leading to genetic divergence. In addition, comparison with museum specimens provides insight into the evolutionary trajectory of this species over time. The study reveals evidence of genetic admixture and possible recent hybridization events contributing to the current genetic diversity. These findings provide a deeper understanding of the evolutionary history of *A. irradians* and underscore the importance of preserving unique genetic lineages. Overall, this research provides a foundation for targeted conservation efforts, enabling the identification of key populations and aiding in the development of informed management strategies to sustain, and potentially propagate, bay scallop populations throughout the United States.

ACUTE AND LONG-TERM RESPONSES OF JUVENILE OYSTERS TO DYNAMIC MULTIPLE COASTAL STRESSORS

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Coastal stressors (e.g., exaggerated diel cycling of pH and DO in urbanized estuaries) are impacting the long-term survival and health of juvenile *Crassostrea virginica* oysters. These stressors could ultimately influence wild population longevity and ecosystem function in addition to affecting growth and success in aquaculture nurseries. This study aims to describe the acute and long-term phenotypic plasticity of juvenile oysters in a dynamic multi-stressor environment and whether stress priming improves oyster response to subsequent stress. An experimental aquarium system was used to mimic a eutrophic estuary diel cycle (cycling between pH 7.15-8 and DO 1.5-8 over a 24 hr period). The experiment was split into two phases: (1) 2-wk initial exposure and (2) a ~9-wk secondary exposure with a week of ambient recovery in between. During the ambient recovery, half of the oysters from the control and stress tanks were reciprocally crossed to the other tank to look at the effects of stress priming. Mortality was very low over both phases of the experiment (avg % mortality < 3.3% across all treatments at the end of phase 2). Size and respiration measurements were taken at multiple timepoints throughout both exposures to access and compare growth and physiological response to stress across treatment groups over time. Juveniles were also sampled for later gene expression analysis at both ambient and stressful conditions in the diel cycle. These data will provide insight into juvenile oysters' plastic stress response to realistic, dynamic stressors and whether pre-exposure to stressors could improve outcomes in nurseries.

GENETIC IMPROVEMENT OF THE EASTERN OYSTER AND PROSPECTS OF GENOMIC SELECTION

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The eastern oyster, *Crassostrea virginica*, supports an important aquaculture industry in the United States that faces threats from two major diseases: Dermo (caused by *Perkinsus marinus*) and MSX (caused by *Haplosporidium nelsoni*). Rutgers University has selectively bred eastern oysters since 1960 and produced strains that have shown strong disease resistance and improved growth. Breeding occurs along the Cape Shore region of lower Delaware Bay where both MSX and Dermo are endemic, and oysters are subjected to stressful intertidal conditions. After three years of exposure to disease and intertidal stress, the largest survivors with desired shell characteristics (top 10-20%) are selected to produce the next generation. Selection over time produced two strains, the Haskin NEH® (Northeast High survival) strain derived from Long Island Sound and the DBX strain derived from Delaware Bay, each represented by several sublines and maintained by progressive rotational crossing. Both strains show improved growth and survival compared with unselected controls. Tetraploid oysters were developed from the disease-resistant strains to produce triploids that grow significantly faster than diploids. The combination of disease resistance and triploidy increased yield. Genomic selection was recently implemented to improve Dermo resistance and field survival. For both traits, survivors and fatalities were classified as resistant (live) and susceptible (dead) phenotypes and genotyped with a 66K SNP array to predict genomic estimated breeding values (GEBV) in the breeding population. Genomic selection utilizes whole genome information and is expected to enhance selection efficiency for traits such as Dermo resistance.

A CONTROLLED FLOW-THROUGH SYSTEM FOR STUDYING THE EFFECTS OF OCEAN ACIDIFICATION ON BIVALVE LARVAE

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Navigating the intricacies of oyster larvae culture in flow-through systems includes carefully managing water flow, algal supply, and providing appropriate turbulence within the culture vessels. Development of the Hatfield Ultra Density Larval System (HUDLS) has focused on the enhancement of spat production while concurrently reducing labor demands in bivalve larval culture; however, an additional layer of complexity is introduced with the integration of such systems with accurate manipulation of seawater carbonate chemistry.

This presentation describes the integration of systems for flow-through and manipulation of carbonate chemistry in studies on the effects of ocean acidification (OA) on Pacific oyster larvae (*Crassostrea gigas*). By incorporating a two-stage CO_2 injection design, the desired carbonate chemistry was maintained in flow-through larval culture chambers. The carbonate chemistry of the reservoir supply of seawater was adjusted based on pH measurements, followed by finer adjustment in the flow-through chambers by bubbling with a precisely controlled CO_2/air gas mixture. The pHt, pCO_2, and aragonite saturation values and percent coefficients of variation for OA conditions in the flow-through chambers over a 14-day period averaged 7.53 ±0.93%, 1548.9 ± 16.8%, µatm, and 1.17 ± 16.8%, respectively. Culture vessels holding larvae in OA conditions produced significantly less spat compared to those in ambient conditions (ANOVA; $p = 0.0167$). This novel flow-through system significantly contributes to the development of methodologies to accurately manipulate OA and other culture conditions in studies with the planktonic life stages of bivalves and other aquatic species.

LEVERAGING THE R-STRATEGY AND UNMANNED AERIAL VEHICLES TO OVERCOME PREDATION IN SHELLFISH RESTORATION PROJECTS

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Restoration of shellfish, such as oysters and clams, has become a very popular activity in estuaries and other coastal areas suffering from periodic or past water quality degradation. As shellfish are often affected by algal blooms, hypoxia events, and other water quality problems, efforts to reestablish or bolster impacted populations are necessary to restore filter feeding capacity and overall ecosystem health. In Florida, significant resources have been dedicated to restoring oysters and clams in areas of reduced water quality such as the Indian River Lagoon, Charlotte Harbor, Sarasota Bay, and Tampa Bay. Most shellfish restoration efforts rely heavily on traditional aquaculture techniques for growing stock and out-planting, hence the popularity of restoration aquaculture as a new direction for the industry. One aspect of traditional grow-out techniques poses is the use of cover netting or bags in areas that prohibit use of such gear. To overcome this, heavy lift drones are being tested to determine the efficacy of dispersing large quantities of juvenile organisms, instead of adults, to overcome predation pressure experienced without protective gear. Initial results suggest the technique is viable and provides additional benefits such as project cost reduction and wholistic ecosystem lift.

THE EFFECTS OF WATER CHEMISTRY ON THE SURVIVAL AND GROWTH OF EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, LARVAE IN CULTURE

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The eastern oyster provides essential ecosystem and economic services; however, oyster populations have declined significantly due to various natural and anthropogenic stresses. Aquaculture has the potential to meet the seed demand for both commercial and restoration purposes, but hatcheries have yet to consistently meet demand due, in part, to water quality/chemistry problems. This project assessed the effects of salinity, temperature, pH, dissolved oxygen (DO), and carbonate chemistry on the growth and survival of oyster larvae.

Water quality data, larval survival, and larval growth were monitored at four hatcheries along the Gulf coast during April-October from 2022-2023. Water quality will be compared among the hatcheries, and associations with larval performance (growth, percent hatch, survival) will be assessed. The 2022 data from Auburn University Shellfish Laboratory (AUSL), a flow-through hatchery, and the University of Southern Mississippi (USM), a recirculating hatchery, showed that, on average, USM produced 298-µm pediveligers in 14 days; AUSL produced 239-µm pediveligers in 18-19 days. The USM percent hatch and survival were 49.5% and 34.9%, respectively; the AUSL were 51.1% and 26.8%, respectively. Average alkalinity and calcium results for USM were 4683.42 µmol/kg and 5.92 mmol/kg, respectively; AUSL were 1789.43 µmol/kg and 5.85 mmol/kg, respectively. USM had an average temperature of 25.95°C, salinity of 20.67, pH of 8.47, and DO of 6.95 mg/L; AUSL had an average temperature of 27.65°C, salinity of 20.02, pH of 7.86, and DO of 6.90 mg/L, respectively. Further analysis will determine the significance of these findings and how they can be managed to improve larval production.

EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) CIS-DEFENSIN ANTIMICROBIAL PEPTIDES: GENE STRUCTURE, EXPRESSION, AND DIVERSITY

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A bioinformatic and molecular approach, including a custom profile hidden Markov model, was applied to identify a multigene cluster of cis-defensins in the *C. virginica* genome that includes the gene encoding American Oyster Defensin, an antimicrobial peptide isolated in 2005 using a protein chemistry approach that had eluded mapping until now. The predicted peptide structures indicate that seven of the defensins contain three disulfide bonds and one defensin has four disulfide bonds, and all show strong sequence and structural homology with known antimicrobial defensins including those from *C. gigas.* Gene structures vary, and the defensins also exhibit high and variable sequence diversity within some genes among individuals. Quantitative gene expression analyses confirm different patterns of expression among tissues for the different defensins, with some showing greater tissue specificity. The diversity of cis-defensin sequences in the eastern oyster and high sequence and structural polymorphism may be important for the oyster's adaptation and resistance to multiple potential pathogens. These data support the hypothesis the production of a combination of peptide isoforms is an evolutionary strategy to increase the spectrum of antimicrobial activities of these innate immune effectors.

RAZOR CLAM GROWTH RATES IN RELATION TO SEDIMENT TYPE

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Atlantic razor clams, *Ensis leei*, are endemic to the northeastern coast of the United States and are a potentially valuable but untapped resource for shellfish growers. Although they command a good price in the market, wild harvests are sporadic because razor clams dig deep burrows, are mobile, and found in the low intertidal and subtidal, limiting harvest to negative tides. Recent efforts with razor clams in the hatchery have had success in spawning and early larval culture; however, the post-settlement nursery culture of razor clams to produce seed (spat) of an appropriate size for field planting remains a significant bottleneck with respect to the adoption of razor clam aquaculture.

This project addressed this bottleneck by testing the use of a "dockside-raceway" system for remotely setting razor clams and subsequent nursery culture. The experiment included three replicate raceways each with partitions containing one of three different sediment types, fine sand, coarse sand and a 50:50 mix of sand and natural mud. After three months of nursery culture, substantial differences were found in the total number of clams recovered from each raceway. Even so, the final density of clams in the sand/mud mix sediment was consistently higher in the sand/mud mixed treatment than in the other two treatments. There were only subtle differences in the average size of clams recovered from the three sediment types. Potential limitations and challenges in scaling up the experiment will be discussed, but results suggest this approach to razor clam nursery culture is promising.

MULTIFACETED STUDY OF AN ONGOING RANGE EXPANSION OF BLUE CRABS (*CALLINECTES SAPIDUS*)

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Blue crabs (*Callinectes sapidus*) historically ranged from Cape Cod, Massachusetts (USA) to Uruguay, though in recent years have had an increased presence within the Gulf of Maine. Understanding this natural range expansion is crucial for getting a glimpse into how marine crustaceans may respond to the impacts of ongoing anthropogenic climate change, particularly regarding their complex, multi-step life cycles. Reports of blue crabs within the Gulf of Maine date back to the 1860s, primarily during warmer years, though from 2016 onward, their presence in southern Maine has been more consistent. This project seeks to understand the temporal dynamics and trophic impacts of blue crabs within this novel environment. To understand blue crab temporal dynamics, both environmental DNA (eDNA) and traditional survey methods were used in southern Maine. To understand trophic impacts, DNA-based gut content analyses were used to understand whether these crabs are likely to impact key shellfish species (e.g., softshell clams, lobsters), and stable isotopes to characterize their trophic niche. This presentation will demonstrate the methods used for understanding this ongoing range expansion, determine likely impacts of blue crabs on key Gulf of Maine shellfish, and what long-term outcomes could arise from a warming world for marine crustaceans.

SHRIMP SCAMPI: A CITIZEN SCIENCE PROJECT - EDUCATING ABOUT MICROBES AND HORMONE DISRUPTORS LIKE METALS AND GLYPHOSATE IN SHRIMP USING FOLDSCOPES

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Shrimp Scampi was initiated by students from Trottier Middle School, Southborough, Massachusetts (MA) and Algonquin Regional High School, Northborough, MA to assess the adverse health effects to the environment, wildlife, pets, seafood, and people, caused by exposure to the antimicrobial and herbicide glyphosate, glyphosate-based herbicides (GBH), Roundup, and other endocrine disrupting chemicals (EDC) like metals and Bisphenol A (BPA). These EDC appear associated with obesity, diabetes, cancer, antimicrobial resistance, and congenital malformations.

Shrimp is the favorite seafood worldwide. In the United States, 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 citizens about hormone disruptors present in seafood using foldscopes (paper microscopes). In addition to monitoring EDC in muscle of shrimp sold at MA supermarkets and wild shrimp from Ecuador, another goal is to perform in-depth reviews of the scientific literature about EDC and their generational epigenetic inheritance. Preliminary results of 21 metals analyzed in shrimp sold in five MA supermarkets in 2023 will be presented [n=5 pooled samples (15-30 shrimp tails/sample). All metals were detected in all samples. The epigenetic marks (DNA methylation, histone modification, non-coding RNA) reported for shrimp and fish exposed to EDC are summarized. The foldscopes were distributed in Pastaza and Manabi provinces, Ecuador. They were donated by friends of the FUCOBI Foundation and the Rotary Club of Southborough, MA (https://fucobi-english.weebly.com/portovelo.html).

A BIOINFORMATIC SEARCH FOR VIRUSES IN THE BLUE CRAB, *CALLINECTES SAPIDUS,* ACROSS THE U.S. GEOGRAPHICAL RANGE OF THE SPECIES

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In the United States, the Atlantic blue crab, *Callinectes sapidus*, supports culturally and economically important fisheries. Episodic declines in blue crab numbers in the mid-Atlantic highlight the need to better understand the factors that drive variation in abundances, including infectious diseases. Shifts in supply and market demand for blue crabs mean that interstate transport is common, and as the species' range expands northward, blue crabs are being harvested in new areas. Pathogens can spread through commercial animal transport and have devastating consequences on shellfish, thus, addressing disease prevention is of particular interest in managing the blue crab fishery. Yet, a comprehensive assessment of viral pathogens in blue crabs has not been undertaken. This research utilizes high-throughput metagenomic sequencing to identify and characterize the RNA viral communities in crabs from six U.S. states, from New York to Texas. An ongoing challenge in the field of 'viromics' is the lack of a universally conserved region in viral genomes. Therefore, bioinformatic analyses rely on sequence similarity to previously-described viruses and machine-learning models to identify 'viral-like' signatures, among other techniques; nevertheless, there is little consensus on best practices for analyzing viromes from metagenomic data. In this study, a wide range of bioinformatic tools were used to search for both previously-described and novel blue crab viruses. This work aims to establish a baseline understanding of the viral communities in the blue crab across the United States and can be applied to a wide range of studies regarding shellfish disease ecology and biosecurity.

ASSISTED SEAGRASS RECOVERY USING CO-PLANTINGS OF THE NATIVE SOUTHERN HARD CLAM (*MERCENARIA CAMPECHIENSIS*) IN SOUTHWEST FLORIDA, USA

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Seagrass extent in southwest Florida has contracted sharply in recent years, with estuaries reporting up to a 28% loss since 2016. To reverse declines, managers should continue to improve local water quality, but also explore novel approaches to seagrass restoration. This study tested whether the reported facilitation of seagrass by bivalves could be used to enhance habitat recovery at management relevant scale. A total of 48, 8×8-m plots were established in early 2023 within a recovering *Halodule wrightii* bed that suffered a near complete die-off in 2018. Experimental plots varied in initial seagrass coverage and half were randomly assigned co-plantings of the native southern hard clam (*Mercenaria campechiensis*; 30 clams m^{-1}). In plots with hard clams, tethers were deployed to non-destructively assess bivalve performance. Monitoring included sediment characterization, assessments of seagrass aboveground cover, and mark-recapture of tethered hard clams at the beginning and end of the seagrass growing season (March-October). Preliminary findings indicate that seagrass aboveground coverage increased at the experimental site, but *M. campechiensis* co-plantings did not significantly enhance the rate of recovery during the first growing season. Tethered hard clam survivorship increased non-linearly with seagrass percent occurrence, with a threshold level of cover identified at ~50% occurrence. These initial findings suggest that although additions of *M. campechiensis* do not accelerate seagrass habitat recovery after one growing season, the presence of a minimum seagrass aboveground cover does influence the success of bivalve co-plantings, as assessed by mark-recapture methods.

WORKSHOP: ART AND DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS

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Scientists, researchers, and innovators have two jobs – do the science and communicate the science. We receive a great deal of training and experience to conduct research and innovation, but, except for journal publications, little to no training in communicating science, especially to divergent groups of stakeholders or audiences. While graphics design is a full-time pursuit, there are a number of core ideas and techniques that can help all of us create more engaging power point slides and posters that will in turn help us communicate more effectively to all audiences.

MODELS IN SHELLFISH BIOLOGY - WHAT CAN THEY TELL US?

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The models used for simulating shellfish populations represent a progression from correlative models to deterministic process-based models to coupled circulation-population models. These varied modeling approaches have been used to investigate the effects of environmental conditions, disease processes, fishing, and other factors, in controlling population dynamics for a range of shellfish species. The simulation results from these models highlighted the importance of interactions of biological and physical processes in structuring shellfish population dynamics. Marine shellfish now are experiencing an environment that is becoming warmer, more acidic, and industrialized, such as the development of the offshore wind energy industry. Simulating and projecting the competing effects of stressors from long-term climate change and those from short-term industrial development on marine shellfish populations and distributions, and the dependent economic and social systems requires linked systems of models that are grounded in experimental and field observations and include stakeholder input during model specification and validation. This presentation will overview the status of shellfish models and consider advances needed to move to the next generation of linked environmental-shellfish-economic-social models.

OPTIMIZATION OF LOW-DENSITY SNP PANELS FOR GENOTYPE IMPUTATION IN OYSTERS

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It has been demonstrated that a combination of low- and high-density genotyping, combined with genotype imputation, can be a cost-effective strategy for genomic selection in aquaculture species.; however, the effectiveness of this strategy depends on the accuracy of imputation and its subsequent effect on the accuracy of breeding value predictions. While measures of genetic diversity and genomic spacing are often considered in the design of SNP panels, choosing a subset of markers that will maximize imputation accuracy is more challenging, especially when there is a variable landscape of recombination throughout the genome. Here, a strategy for designing imputation-optimized SNP panels using evolutionary algorithms will be presented and demonstrated for oysters, and the potential benefits of optimized genotyping panels for oysters and other species will be discussed.

IMPROVING RESILIENCE OF HATCHERY-REARED BLUE MUSSELS (*MYTILUS EDULIS*) TO OCEAN ACIDIFICATION WITH DIET AND SEAWATER BUFFERING

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As wild blue mussel seed declines in the Gulf of Maine, mussel growers are relying increasingly on hatchery production to stock their farms. While mussel populations are currently under pressure from predation by the invasive European green crab, ocean acidification (OA) is expected to be another stressor – especially among earliest life stage mussels – as climate change progresses. Traditionally, shellfish hatcheries have implemented seawater buffering to mitigate low pH in their incoming seawater. Here, live microalgae diet optimization is proposed as an alternative strategy for rendering blue mussel larvae inherently more resilient to OA in a hatchery scenario. Following an initial microalgae growth and nutritional analysis phase, 4 diets – each consisting of a flagellate and a diatom species – were created to emphasize different nutritional parameters (industry standard, high calorie, high DHA, high EPA/protein). A first experimental trial tested larval/early juvenile response (survival and growth) to a 2-level seawater pH treatment (7.80/present day, 7.30/year 2100) and a 4-level diet treatment, and a second experimental trial tested response to the pH treatment, a reduced 2-level diet treatment, and a 2-level seawater buffering treatment (soda ash buffering, no buffering). Each trial was followed by a field deployment of experimental mussels at each of 2 mussel farms in different locations along the Maine coast (Blue Hill Bay Mussels and Bangs Island Mussels) to reanalyze mussel responses after they achieved market size. The experimental trials tested the efficacy of diet optimization for improving blue mussel resilience to OA, as well as its interaction with seawater buffering.

RISK OF PATHOGEN TRANSFER FROM BIRDS IS UNKNOWN

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Bird presence on shellfish farms has drawn increasing attention due to perceived potential fecal contamination; however, the risk of pathogen transfer from birds to humans from shellfish consumption remains unknown. 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, but the NSSP standard assumes a correlation between pathogens and fecal coliform in wastewater, not from birds. No correlation exists between pathogens carried by birds and the risk of illness from enteric pathogens (i.e., *Campylobacter, Escherichia coli, Listeria, Salmonella, Shigella*) through shellfish consumption. In fact, birds are often poor hosts of pathogens which cause illness in humans and 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”. If birds are implicated as the source of fecal coliform contamination in shellfish growing waters, existing growing area certification data are insufficient to understand risk to humans from shellfish consumption. No risk assessment has been attempted, yet some shellfish authorities in the U.S. and Canada are suggesting, and in some cases requiring, risk management. This approach is not consistent with human health risk assessment because dose-response is unknown for fecal coliform from birds. Furthermore, the absence of a risk assessment means that any risk management strategy cannot be evaluated for effectiveness at avoiding human illness from enteric pathogens from shellfish consumption.

STATUS, PARTICIPATION, AND PROGRESS OF THE HATCHERY COMPLIANCE PROGRAM OF THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP)

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A core component of the Regional Shellfish Seed Biosecurity Program is the Hatchery Compliance Program (HCP). This program provides biosecurity guidance for hatcheries through twelve best management practices (BMP) designed to prevent pathogen contamination within hatchery production systems. Hatcheries can participate at various levels that meet their specific needs and use that participation to assist customers with meeting permit requirements. State and Federal regulatory agencies can use the HCP to help facilitate reviews of importation requests. A brief overview and status will be followed by an extensive Q&A session.

THE BIVALVE HATCHERY HEALTH CONSORTIUM: A COLLABORATIVE APPROACH TO IDENTIFYING AND MANAGING CAUSES OF DECREASED LARVAL PERFORMANCE IN HATCHERIES

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The goal of the "Bivalve Hatchery Health Consortium (BHHC): Managing Larval Mortalities in Hatcheries" is to support the growth of the bivalve shellfish industry by providing access to diagnostic tools helping hatcheries ensure reliable production of bivalve seed. The objectives for this consortium are: (1) identify the causes of bivalve hatchery larval mortalities and crashes along the east coast of the U.S. through an integrated, collaborative, and proactive approach to sample collection and analysis; and (2) develop strategies and protocols to manage and minimize larval crashes in hatcheries. During the upcoming hatchery seasons, work will begin with private and public hatcheries wishing to participate in the project to collect algae, water, and larvae from a variety of larval runs, including "good" (successful performance) and "bad" (lower performance or crashes). Hatcheries will also provide data relevant to larval performance. All individual hatchery information collected will remain confidential. The consortium will provide all supplies for the sample collections, cover shipping fees, and cover the cost of disease diagnosis. The goal of this workshop is to enlist researchers interested in larval performance in hatcheries and other interested parties (e.g., hatchery managers, extension specialists) to participate in the BHHC, discuss the collaborative approach for sample and data sharing, and strengthen the experimental approach for sampling collection and analysis. Members of the BHHC coordinating team, including pathologists, ecologists, hatchery managers, and extension specialists, will answer questions and gather feedback from those interested in the program on how to address this critical issue of larval crashes.

THERMAL TOLERANCE OF *MERCENARIA* SPP. DURING A SIMULATED MARINE HEATWAVE IN SOUTHWEST FLORIDA, USA

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As marine heatwaves become increasingly more frequent and intense with climate change, physiological stress should begin exceeding species' tolerance limits, especially for relatively sessile ectotherms, such as bivalves. In Florida, northern quahogs (= hard clams) (*Mercenaria* spp.) comprise an ecologically and economically valuable group of bivalves, including a $14.3 million aquaculture industry. This study examined the lethal and sublethal effects of a simulated marine heatwave, coupled with salinity stress, on *M. mercenaria* and southern hard clam (*Mercenaria campechiensis*). In each trial, clams (n = 15 species^{-1}) were stocked in 151.4 L aquariums for one week at one of two salinities (18 or 30) and one of five maximum daily temperatures (28°C, 31°C, 33°C, 35°C, or 37°C). Marine heatwave conditions were simulated within each aquarium by increasing temperatures stepwise from 28°C to the assigned thermal maximum over three days and allowing temperatures to drop by 1.7°C overnight to mimic the diurnal cycle. Clam survival was reported daily and temperatures within each tank were continuously monitored. Across nine replicate trials, high maximum temperatures coupled with lower salinity were found to adversely affect hard clam survival, but responses were species specific. *M. mercenaria* demonstrated higher heat tolerance but was more susceptible to low salinity relative to the native *M. campechiensis*. These findings suggest that hard clams in Florida are susceptible to increasingly severe marine heatwaves, especially when concurrent with other stressors, such as periods of low salinity. These results could inform site selection for aquaculture and restoration efforts throughout Florida.

SITE-SPECIFIC DIFFERENCES IN UPPER THERMAL TOLERANCE AND TRANSCRIPTOMIC RESPONSES OF ATLANTIC CANADIAN BLUE MUSSELS (*MYTILUS EDULIS*)

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Rising sea surface temperatures and prolonged marine heat waves threaten the sustainability of the blue mussel (*Mytilus edulis*) farming sector in Atlantic Canada. Therefore, to enhance the survival of mussels grown in the warming ocean, it is pivotal that the industry identifies sources that may be more thermally tolerant. In this study, the thermal biology of mussels from Sober Island Pond, Nova Scotia (NS) were compared with mussels grown in St. Peters Bay, Prince Edward Island (PEI). Mussels from these two distinct sites were held at four temperatures (20°C, 25°C, 30°C, or 35°C) to compare lethal thermal thresholds (LT_{50}). Neither location survived as temperature was raised to 35°C (all individuals perished at 33°C) and minimal/negligible mortality was recorded in the 20°C control group. Interestingly, LT_{50} values significantly differed between sources at 25°C (73.2 d NS vs. 40.8 d PE) and 30°C (4.9 d NS vs. 4.4 d PE). Given these differences in survival between sources, gill samples collected at the start of the LT_{50} trial and then again when mortality reached ~50% in mussels reared at 25°C were RNA-sequenced. Comparing between sources, several key environmental stress responsive transcripts were differentially expressed, such as *hsp70*, *hsp90*, *grp94* and *hif1a*, at various temperatures/time points. This study not only provided fundamental information on how mussels respond to acute and chronic thermal stress, but also identified several putative biomarkers of upper thermal tolerance for this species. This research aims to support the sustainable growth of blue mussel aquaculture industry and actively combat the negative effects of anthropogenic climate change.

WINDOW TO AN UNDERWATER WORLD: SHARING THE HABITAT VALUE OF SHELLFISH FARMS WITH A BROAD AUDIENCE

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The NOAA Milford Lab first set out with GoPro cameras in 2017 to investigate reports from oyster growers that they were seeing wild fish in and around their gear. In the six years since, "Team GoPro" has collected and analyzed more than 1,600 hours of underwater footage from farms and naturally-structured comparison habitats in Long Island Sound from Norwalk to Noank, Connecticut. Twenty-one fish species associated with the cages have been documented, including commercially and recreationally important species, as well as a wide variety of fish behaviors associated with habitat use. The project has resulted in considerable evidence that fish use oyster gear in a similar way as they use natural structured habitat.

The underwater videos collected throughout this project are a powerful and compelling outreach tool, in addition to data. They can demonstrate to coastal residents and regulators who make decisions concerning aquaculture that local farms are providing habitat. They are also useful to engage K-12 students and the public in discussions about local marine ecosystems, aquaculture, and science. Analytics demonstrate the popularity of the videos on the project website. The team worked with a production company to make a short video about the project called "Home Sweet Oyster Cage". Partnering with a non-profit, the team developed a STEM education activity. The project has also been highlighted by two ArcGIS StoryMaps, NOAA Fisheries feature stories, social media posts, and media coverage. The presentation will share what the team has learned about how different outreach products reach different audiences, as well as the value of underwater video to demonstrate the ecosystem services provided by aquaculture.

eDNA: CASTING A NEW NET FOR MONITORING SEA SCALLOP (*PLACOPECTEN MAGELLANICUS*) FISHERIES

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Environmental DNA (eDNA) can offer a non-invasive, cost-effective, and efficient method for monitoring aquaculture and commercial fisheries populations to inform sustainable fisheries management practices; however, eDNA tools must be thoroughly groundtruthed to determine best practices for their appropriate application. While quantitative eDNA assays for sea scallops (*Placopecten magellanicus*) have been developed and calibrated for sperm and dockside conditions, information is lacking on the quantification rates of scallop eDNA generation and degradation, calibration for other life stages, e.g., eggs and larvae, and evaluation of field applications. These challenges are addressed through a combination of laboratory experiments and field observations. Using a controlled mesocosm experiment, the eDNA generation and degradation rates of scallops at different biomass densities over a 48-hour period are quantified. Positive linear relationships between eDNA generation rates and biomass and a negative linear relationships between eDNA degradation rates and biomass over time are expected. Using a vertically-stratified sampling design above a wild scallop bed, the spatial and temporal variability in scallop eDNA presence over a 6-month period is evaluated. During spawning and larval transport seasons, the eDNA signal is expected to be distributed throughout the water column. Outside of these seasons, the eDNA signal is expected to be limited to the benthos. Results from this work may inform the use of carefully constructed sampling designs to conduct adult stock assessments or to estimate recruitment potential and will identify benefits and shortcomings of eDNA as a tool for assessing commercially important species.

GONADS AND GOURMET: UNVEILING FARMED SCALLOP'S PLUMP TREASURES AND AQUACULTURE'S BOUNTY POTENTIAL

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The Atlantic sea scallop (*Placopecten magellanicus*) fishery ranks among the most economically valuable marine fisheries in the United States (~$426M in 2022). With recent declines in catch and projections indicating that demand for sea scallops may surpass the supply from traditional fisheries, the scallop aquaculture industry has been on the rise; however, the ecological consequences of raising sea scallops in aquaculture remain largely unexplored. Here, biological and ecological impacts of sea scallop aquaculture by comparing the morphometrics of farm-raised sea scallops to those of wild scallop populations in Penobscot Bay, Maine, are assessed. In 2020-2022, researchers sampled farm-raised scallops from lantern nets at three aquaculture sites in Penobscot Bay, Maine, and collected wild scallops via SCUBA from beds adjacent to each farm. Shell height and masses of adductor, gonad, total viscera and shell were collected. Farmed scallops have larger adductor, gonad, and viscera masses compared to their wild counterparts within size classes 80 - 110mm. Conversely, wild scallops have larger shell masses. Preliminary results estimating potential larval spillover from aquaculture farms will also be shared. Larger meat yields from aquaculture-raised scallops offer a significant return on investment for scallop growers. Additionally, larger gonads in aquaculture-raised scallops suggest an increased potential for reproductive output, which has ecological ramifications for both aquaculture and wild harvest industries. These results shed light on the complex interplay between aquaculture and the natural environment, highlighting the need for further investigation into the ecological consequences of sea scallop cultivation.

DEVELOPMENT OF IDENTIFICATION AND DETECTION METHODS FOR EMERGING CAUSES OF VIBRIOSIS

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The infection incidence of domestically acquired human vibriosis increased 54% in 2022, as compared to the baseline years of 2016-2018. Food safety efforts have focused during this time on reducing illnesses associated with *Vibrio parahaemolyticus* and *V. vulnificus*; however, over the years other species are increasingly being recognized as causes of foodborne vibriosis, many associated with consumption of raw bivalve molluscan shellfish. These emerging causes of human vibriosis include *V. fluvialis*, *V. cholerae* (non-O1/non-O139), *V. mimicus*, *V. alginolyticus*, and *Grimontia hollisae*. As all *Vibrio* spp. are naturally occurring organisms in the shellfish harvest environment, it is critical for us to understand the prevalence, distribution, and environmental drivers of these emerging human pathogens to be able to effectively evaluate the risk posed to public health. The first step is having appropriate methods to detect, isolate, and identify these organisms from shellfish and the surrounding marine and estuarine environments. As such, this presentation will cover recent progress in developing real-time PCR detection methods for *V. fluvialis*, *V. mimicus*, *V. alginolyticus*, and *G. hollisae*, as well as evaluation of chromogenic agars to isolate and differentiate vibriosis-causing species.

OYSTER ENHANCEMENT FOR NEW HAMPSHIRE OYSTER GROWERS AND ESTUARIES

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The National Sea Grant Program funded a project to provide relief to aquaculture operations in New Hampshire (NH) due to COVID-19 impacts. Ten NH oyster farmers participated in oyster population and ecosystem service enhancement studies using up to 10,000 unmarketable oysters sold to New Hampshire Sea Grant at market price. The purchased oysters were moved by the farmers, to pre-selected non-producing areas of their farm license areas to create State permitted experimental oyster reefs. Sea Grant funds supported the initial condition of the oysters (fall 2020) and ensuing assessments (spring and fall 2021) of ecosystem impacts. Measurements of average shell growth, mortality, and recruitment of young oysters showed experimental oysters exhibited growth trends, mortality, and evidence of recruitment that varied by site but were in ranges consistent with previous studies of farmed oyster beds in the experimental areas. The average growth was 19.8%, average mortality was 9.1%, and evidence of recruitment occurred at 9 of 10 farms. Evidence of habitat provision included colonization of oysters by *Gracilaria, Ulva* and *Ascophyllum* and observation of mud crabs (xanthids), green crabs, hermit crabs, ribbed mussels, blue mussels, and hard clams at the reefs, while the growth data are evidence of filter feeding associated water filtration of food and other suspended particles. The study suggests that construction of "restoration areas" on farms or other sites can sustain oysters in the short and long-term based on the findings of this study focused on factors related to restoration success.

LONG-TERM SEASONAL ECOLOGY OF *VIBRIO PARAHAEMOLYTICUS* IN THE NORTHEAST US

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Shellfish-borne illnesses from pathogenic *V. parahaemolyticus* (*Vp*) in the northeast US have increased over the past 15 years. Tracking and forecasting the population dynamics of this environmentally transmitted pathogen is key to informing risk assessment and providing for a better understanding of ecological mechanisms underlying human illness potential and expansion.

Previous studies in the Great Bay Estuary (GBE) of New Hampshire and Maine suggested a range of ecosystem targets (pH, ecosystem conditions, plankton communities, nutrients) as drivers of *V. parahaemolyticus* concentration variation in estuarine ecosystems as potential tools that complement management strategies to provide for improved pre-harvest risk management. The current database for *Vp* and ecosystem drivers in GBE now spans 17 continuous years at two sites. A combination of descriptive and predictive modeling and multivariate community analysis representing sites and the harvest-area were again used to re-analyze *Vp* concentrations in water, sediments, oysters, phytoplankton, and zooplankton in relation to water quality, plankton community and meteorological factors. This presentation focuses on findings that describe temporal trends and relationships that reflect the seasonal and long-term trends of *Vp* populations, including shifts in potentially pathogenic *Vp* strains, in oysters at one of the study sites. Continued analysis of the full *Vp* database, along with continuous databases for *V. vulnificus* and *V. cholerae* is underway to provide for expanded risk assessment and ecological comparisons of these pathogenic *Vibrio* species in the GBE as a model approach for shellfish harvesting areas in the northeast US.

FIC DOMAIN-CONTAINING ENZYME GENES IN INVERTEBRATES: A TALE OF TRANSPOSONS, PATHOGENIC, AND INTEGRATED VIRUSES

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Many gene families are shared across the tree of life between distantly related species because of horizontal gene transfers (HGT); however, the frequency of HGT varies strongly between gene families and biotic realms suggesting differential selection pressures and functional bias. One gene family with a wide distribution is the FIC domain-containing enzymes (FicD). FicD catalyze AMPylation, a post-translational protein modification consisting in the addition of adenosine monophosphate to accessible residues of target proteins. Beside the well-known conservation of FicD in deuterostomes, the presence of a conserved FicD gene ortholog was reported in a large number of protostomes and microbial eukaryotes. Additional FicD gene copies were also reported in the genomes of some rotifers, parasitic worms and bivalves. A few dsDNA viruses of these invertebrates, including white spot syndrome virus, Cherax quadricarinatus iridovirus, ostreid herpesvirus-1 and the beetle nudivirus, carry copies of FicD, with phylogenetic analysis suggesting a common origin of these FicD copies and the duplicated FicD of their invertebrate hosts. HGT and gene duplications possibly mediated by endogenous viruses or genetic mobile elements seem to have contributed to the transfer of AMPylation ability from bacteria and eukaryotes to pathogenic viruses, where this pathway could have been hijacked to promote viral infection.

SELECTION RESPONSE OF GULF OF MEXICO EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) BRED FOR PERFORMANCE IN LOW SALINITY ENVIRONMENTS

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The decline of natural reefs of the eastern oyster (*Crassostrea virginica*) in the northern Gulf of Mexico (Gulf) has stimulated the development of aquaculture to support the market demand and restoration programs. Gulf habitats feature diverse salinity environments that may require oysters bred for habitat-specific optimal genetic characteristics. This presentation will report on the performance of eastern oyster bred in low-salinity environments after one generation of selection.

Selective breeding employed a common-garden approach where families were pooled at fertilization for communal rearing and molecular pedigrees were used a posteriori to determine parentage and estimate breeding values in a walk-back selection process. The F1 generation pool was bred in 2020 and included 202 full and half-sib families that were deployed on three low salinity sites for growth challenge. Breeding values (BV) for height were estimated at harvest size in fall 2021. Parents with highest BV were bred in 2022 to generate 102 full sib and 51 half sib families with a selection differential of +3.10 mm (5.7%). A control pool was also generated using 25 full sib families with the BV averaging +0.089 mm. The F2 generation (selected and controls) was reared at the Grand Bay Oyster Park and Mobile Bay site, where growth and survival were monitored via bi-monthly sampling. Selected oysters had significantly greater survival at peak mortality and shell height 10-months post deployment than control oysters at both sites, indicating positive response on growth and correlated increase in survival.

THE EVOLUTION OF CUSTOMIZABLE, WIRE-BASED REEF-BUILDING SUBSTRATE FOR OYSTER (*CRASSOSTREA VIRGINICA*) HABITAT RESTORATION IN COASTAL SOUTH CAROLINA, USA

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Biologists at South Carolina Department of Natural Resources (SCDNR) Marine Resources Division have been using three-dimensional wire mesh structures to create oyster-based living shorelines in substrate-limited intertidal environments since 2011. The early years of these efforts (2011-2016) focused on the repurposing of derelict crab traps (DCT) both to create reef habitat but also to reduce the negative impacts of this form of marine debris via ghost fishing and mortality of both target and non-target species. Derelict traps have also recently been acquired from other states. Recognizing that wire mesh frames provide a large surface area that supports oyster recruitment in the substrate-limited environments that characterize much of the coastal nearshore region of South Carolina, USA, in 2016 researchers began to explore pre-fabricated alternatives in the form of manufactured wire reefs (MWR).

Recent research at the SCDNR Marine Resources Division indicates that these relatively light and highly customizable MWR are successful at creating new oyster reefs and protecting shorelines from erosion in many South Carolina intertidal settings and have hence been incorporated into living shoreline research projects. Key design considerations have included the physical shape of individual MWR units, the inclusion and orientation of additional interior mesh panels, the application of thin-set cement, and the most recent modification of the inclusion of clean loose oyster shell within the units in so-called "shell-infused" MWR. These findings indicate that multiple wire-based living shoreline designs perform well, affording restoration practitioners multiple, customizable options across a range of material availabilities and environmental settings.

POTENTIAL IMPACTS OF THE PARASITIC TREMATODE, *BUCEPHALUS CUCULUS*, IN A COLLAPSED OYSTER FISHERY

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The digenetic trematode, *Bucephalus cuculus,* is a well-known parasite of the eastern oyster, *Crassostrea virginica,* with varying degrees of prevalence within its range. This trematode primarily affects *C. virginica* in the United States from the Gulf of Mexico and north along the east coast of the U.S. to the Chesapeake Bay region. The infection effectively castrates *C. virginica* and eventually leads to mortality. Throughout much of its range impacts of *B. cuculus* are very low, however there are areas where much higher infection rates are observed.

Oysters from the Apalachicola Bay region have recently been observed with increased infection rates of *B. cuculus*. The parasite may be a contributing factor inhibiting recovery of the historically famous Apalachicola Bay oyster fishery which collapsed in 2012. Despite restoration efforts which began in 2015, the fishery was officially closed to harvest in 2020. The causes and impacts of such high infection rates of *B. cuculus* are not completely understood. Infection rates are regularly above average in *C. virginica* populations surviving in the Apalachicola Bay study sites monitored by Florida Fish and Wildlife Research Institute scientists. A better understanding of the underlying cause of such high infection rates and overall impacts may help contribute to *C. virginica* recovery in this estuary.

COMPARING PERFORMANCE OF VARIOUS TRIPLOID OYSTER (*CRASSOSTREA VIRGINICA*) SEED LINES AND STOCKING DENSITIES IN NOVEL SUBTIDAL AQUACULTURE GEAR

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Oyster aquaculture in deep (>6 m) Delaware Bay waters is becoming increasingly popular to enhance production, although expansion into offshore zones prevents use of traditional nearshore growing technologies, such as rack and bag techniques. Additionally, challenges imposed by rough water conditions, rapid oyster growth, and prolific *Polydora websteri* prevalence require intensive husbandry to maintain gear, regulate oyster growth and shell shape, and minimize biofouling to retain high product value in half shell markets. One Delaware Bay oyster farm patented a bottom-deployed gear design to exploit the strong extant tidal energy by autonomously rotating gear and tumbling oysters. The novel design is comprised of three cylindrical drums, each containing 40 traditional longline baskets holding oysters, attached to a rail frame sitting on the seafloor. A steel plate extending from each drum is pushed by tidal flow, thus rotating the drum twice daily, and redistributing the oysters within baskets, ultimately reducing husbandry frequency, and enhancing operation efficiency. Performance of various triploid seed lines (DEBY, NEH, and LOLA) at low and high basket stocking densities (150 and 200 oysters per basket, respectively) were compared to optimize production in the recently developed subtidal gear. Primary performance metrics included growth, condition, shell shape (fan and cup ratios), and mortality. Preliminary statistical analyses indicated that seed line imposed a greater effect on performance than stocking density, and that the DEBY line generally outperformed NEH and LOLA lines. Further statistical modeling will reduce uncertainty from experimental design and emphasize the effects of seed line and stocking density.

RELATIONSHIP BETWEEN GAPING BEHAVIOR OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, AND *VIBRIO* SPP. LOAD

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The eastern oyster, *Crassostrea virginica*, is an economically important species for human consumption worldwide. Oysters draw water through their mantle cavity when open, but periodically reduce their gape or close - reducing or eliminating water flow through the mantle cavity. Patterns in gaping activity may influence the exposure of oysters to *Vibrio* in the water column and the accumulation of *Vibrio* in the mantle fluid. This study investigates factors affecting gaping behavior, variability in gaping among individuals, and effect of gaping behavior on *Vibrio* concentrations in the mantle cavity. Gaping was quantified using a MosselMonitor® (AqaDect, Netherlands) suspended in a flow-through trough receiving filtered (50 µm) seawater. Percent gape was recorded every 60s for six days. *Vibrio* counts in mantle cavity fluid were obtained on the initial and final days of each trial. Percent gape was highly variable, with the majority of oysters spending between 14 and 56% time closed. Variability in time closed was higher among trials than within trials, and differences among individual oysters were more evident over a 24-hour period than when averaged across multiple days. Data are currently being analyzed to assess the effects of diel, temperature, and tidal cycles on gaping behavior, and the relationship between time closed and changes in *Vibrio* counts in the mantle fluid. Results will help determine factors influencing time spent open and actively feeding and respiring, as opposed to closed, and whether gaping behavior affects accumulation of *Vibrio* in oyster mantle fluid.

SALINITY AND FOOD SUPPLY INFLUENCE OYSTER LARVAL PERFORMANCE AND RECRUITMENT LIMITATION IN THE WESTERN MISSISSIPPI SOUND: A MODELING STUDY

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Consequent to repeated mass mortality events over the last decade, the oyster population in Mississippi Sound is recruitment-limited, indicating that local population growth and recovery is constrained by the influx of new individuals capable of establishing themselves into the extant population. Therefore, recovery requires an abundant larval stock capable of timely growth, development, and successful metamorphosis. In turn, ambient temperature, salinity, food quantity, and food quality governs larval performance. Total food content (quantity) is important for sufficient larval performance, but more so is food quality, as larvae require a biochemically balanced diet of lipids, protein, and carbohydrates for effective somatic growth and energy accumulation to overcome the metabolic demands of development through successful metamorphosis. Here, *in situ* environmental data and food (seston) measurements were collected at seven historic oyster reefs in western Mississippi Sound through the 2021 and 2022 spawning seasons. Observations were integrated into an established biochemically based larval performance model, whereby larvae and food are defined by their biochemical constituents, to estimate time periods conducive to metamorphic success and larval survivorship. Prolonged extreme low salinity (<5) regimes and protein depauperate food supply suppressed modeled larval survivorship in 2021. Conversely, enhanced estuary-wide salinity and food quality improved 2022 estimated larval performance and survivorship, despite lower overall food content, suggesting the fate of larvae largely depends on the quality of available food when environmental conditions are satisfactory. Model-estimated settlement windows in 2022 aligned well with concurrent monitoring surveys of recruitment, further validating the predictive power of the model.

EXTREME POPULATION DENSITIES IMPACT OOCYTE PRODUCTION IN ATLANTIC SEA SCALLOPS, *PLACOPECTEN MAGELLANICUS*

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The Atlantic sea scallop, *Placopecten magellanicus*, supports one of the most valuable fisheries in the United States. The fishery is managed through a suite of innovative strategies, including rotational area management which protects juvenile sea scallops to increase both yield-per-recruit and spawning potential. While generally successful, area management was challenged by two extremely high-density recruitment events which did not respond as expected to fishing protection. Juveniles at both sites, the Nantucket Lightship Closed Area and the Elephant Trunk Closed Area, persisted at high population densities and initially exhibited varying degrees of impacted performance. The effect of sea scallop population density on reproduction was investigated through quarterly sampling during 2018–2020 in high, medium, and low-density portions of both areas. Female sea scallop gonads were retained to directly investigate the effects of population density on oocyte development. Using histological methods, the volume fraction of developing, mature, and resorbing oocytes was determined for each gonad sample. Preliminary results indicate higher rates of oocyte resorption at high population densities, suggesting fewer oocytes were developed to maturity or released during spawning by sea scallops in high-density areas. Total oocyte production will be estimated both for individual scallops and per m^2 of ocean bottom to investigate differences in fecundity across study areas and population densities. A secondary goal is to assess the agreement between reproductive stages assigned at sea with those assigned through histological examination to improve the accuracy of future sea scallop survey efforts.

REMOVAL OF NOCTURNAL HYPOXIA INCREASES JUVENILE BIVALVE GROWTH

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Bivalves are an economically and ecologically important species. Oyster and clam aquaculture in the US is worth $219 and $122 million respectively, while ecological value for services has been estimated at $3-19 thousand hectacre^{-1} year^{-1}. Many estuarine systems experience diel fluctuations in dissolved oxygen (DO) and pH as a result of the shifting balance between photosynthesis and respiration. During warmer summer months, these fluctuations are often intensified, exposing local populations to brief but repeated episodes of co-occurring hypoxia and acidification. For this study, an experimental flow through system was created that preserved natural diel cycles but also eliminated nocturnal hypoxia by vigorously aerating in situ water in a maze. Juvenile bivalves (*M. mercenaria*, *C. virginica*, *A. irradians*) were subjected to both natural diel cycles and DO amended conditions during the peak cycling season (summer). Growth and survival were quantified. Across all bivalves, amelioration of nocturnal hypoxia yielded a mean increase in growth of ~20%. The percent increases in growth rates of the aerated treatments for *C. virginica* and *A. irradians* were significantly correlated with hours of hypoxia during experiments (p<0.005) and were significantly negatively correlated with average nocturnal DO concentrations in control treatments (p<0.05). In contrast, *M. mercenaria* were more resistant to hypoxia and did not show significantly improved growth when provided relief. Since slower growth can leave juvenile bivalves more vulnerable to predation, these results demonstrate that nocturnal estuarine hypoxia may be an ecosystem threat to populations of *C. virginica* and *A. irradians*.

USE OF DIRECT-FED MICROBES TO ENHANCE SHRIMP RESISTANCE TO A *VIBRIO PARAHAEMOLYTICUS* STRAIN CAUSING EARLY MORALITY SYNDROME (EMS)

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Early Mortality Syndrome (EMS) or Acute Hepatopancreatic Necrosis Syndrome (AHPNS) is an epizootic bacterial infection of shrimp that has negatively impacted the global shrimp aquaculture industry. This disease is largely attributed to pathogenic *Vibrio parahaemolyticus* EMS strains (VP-EMS). Application of probiotics was examined for control of pathogenic VP-EMS infections in Pacific white shrimp (*Litopenaeus vannamei*) under laboratory-scale conditions. Two probiotic products, a single strain (O14VRQ) of *Bacillus subtilis* and a blend (Plus10) of five strains of *Bacillus* from four different species (*B. amyloliquifaciens*, *B. megaterium*, *B. brevis,* and two distinct strains of *B. subtilis*), were evaluated at various concentrations as feed additives (applied as a top coat on commercial feed) or dosed directly into the culture water. Two trials were conducted in which shrimp were fed either a control feed (no probiotics) or probiotic-coated feed for seven days prior to be being challenged with VP-EMS. Shrimp were observed for clinical signs of disease and mortalities during the disease challenge study. These experiments demonstrated that while both *Bacillus* probiotic products were shown to significantly (p<0.05) improve shrimp survival, the O14VRQ strain provided the most consistent protection across the trials in top coated feed. Overall, better efficacy was observed with probiotic coated feeds. Findings were directly and positively correlated with concentration for top-coated and even more so for direct in-tank applications. The mode of action of the *Bacillus* strain against *Vibrios* is under investigation. Collectively, these findings provide insights about how probiotic strains could be applied to enhance shrimp health in aquaculture.

ASSESSING THE EFFECTS OF HUSBANDRY DECISIONS ON MORTALITY, GROWTH, AND TIME-TO-MARKET IN OFF-BOTTOM OYSTER AQUACULTURE

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Off-bottom oyster aquaculture is a labor-limited industry with slim profit margins. Production inefficiencies can amplify the economic strain on a company. Therefore, any technique that improves production and reduces operational costs has tremendous potential to increase the economic sustainability of shellfish aquaculture. While previous studies have highlighted the benefits of low stocking densities (which presumably increases water flow and food availability), less is known about the effects of densities that trigger the practice of splitting or thinning into lower densities. This project addresses this gap by investigating the effects of splitting oysters at three different triggering densities (25%, 50%, and 75%) on growth metrics, yield, and time-to-market.

In April 2023, 27 FlipFarm baskets were stocked with ~25 mm oysters at 10% of total basket volume and deployed across three lines on the VIMS Research Farm in the York River, Chesapeake Bay (9 baskets per line). Baskets were haphazardly assigned one of three thinning densities, and regularly observed for growth, split once a treatment level reached the trigger volume, and restocked at 10% by size class (creating additional baskets). To date, the 25% treatment has been split three times, the 50% treatment split twice, and the 75% treatment split once. Preliminary data show oysters in the 50% treatment grew faster than the 25% treatment over the second half of the sampling period. The cumulative mortality of these treatments has not differed. Anticipated splits in the coming months will provide further insights into yield, time-to-market, and estimated labor-related cost-benefit scenarios.

IMPROVING SPAWNING SUCCESS OF THE SUNRAY VENUS CLAM, *MACROCALLISTA NIMBOSA*

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Interest in the commercial production of alternates to hard clams has remained high for the past two decades as the industry has considered the need for diversification. The sunray venus clam, *Macrocallista nimbosa*, has held the most promise of the alternative species examined, and is well received by consumers due to its large meat size and unique shell pattern; however, consistent seed production has proved to be an issue. To that end, a series of trials was conducted to examine the impact of various maturation conditions, such as conditioning time, season, temperature, feed and feed rate. Multiple spawns were attempted that compared conditioning times (6, 9 and 12 weeks), temperature (18, 21 and 24°C), feed rate (2, 4, 6 and 12%), and season, using *T. lutea*, *C. neogracile* or a combination of the two. Successful spawns were associated with longer conditioning times, higher temperatures, higher feed rates, and a combination diet. Although successful spawns were achieved in all four seasons, fewer spawns occurred during winter.

IN SITU VALVE OPENING RESPONSE OF EASTERN OYSTERS TO ESTUARINE CONDITIONS

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High-frequency recording of valve opening behavior (VOB) in bivalves is often used to detect changes in environmental conditions. Generally, though, focus is put on a single variable such as temperature or the presence of toxicants in the water. Description of routine VOB under non-stressful conditions is also important to interpret responses to environmental changes. The first detailed quantitative investigation of the *in situ* VOB of eastern oysters (*Crassostrea virginica*) to environmental variables typically not considered stressful will be presented. The VOB of eight individuals was monitored for seven weeks in a Louisiana estuary. The relationship between VOB metrics (inter-individual variability, the probability of an oyster being closed, and the rate of valve closure), and temperature, salinity, chlorophyll-*a* (chl-*a*) concentration, the rate of change in those environmental variables, and the rate of change in water depth were examined. Relationships were analyzed through statistical models including rates of change over 0, 0.25, 1, 6, 12, and 24-hours. All responses were best explained by the 12-hour time step model. The interaction between salinity and the rate of change of salinity had the most impact on inter-individual variability. Oysters closed faster at higher salinities and were more likely to be closed at lower chl-*a* concentrations. Significant interactions were found between many environmental variables, indicating the high level of complexity of oyster behavior in the natural environment. This study contributes to the better understanding of the impact of environmental conditions on oyster behavior and can help inform predictive tools for restoration initiatives and fisheries practices.

PREDICTING RESTORATION AND AQUACULTURE POTENTIAL OF EASTERN OYSTERS THROUGH AN ECO-PHYSIOLOGICAL MECHANISTIC MODEL

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On-going and predicted changes in precipitation and river flow impact key coastal species such as the eastern oyster, *Crassostrea virginica*. Identifying suitable locations to ensure resilient oyster populations and to support future production remains a challenge for managers. To explore potential outcomes for oyster restoration and aquaculture development, an individual bioenergetic model based on DEB theory was used to derive an aquaculture index, based on survival and time to market size, and a restoration index, based on survival and reproductive output. The model was run across six major Texas and Louisiana estuaries under current (2014–2020) and future (2041–2050) projected environmental conditions. Aquaculture scores under current conditions reproduce an observed gradient of oyster growth increasing from the upper to lower estuary (Texas) or offshore areas (Louisiana), with lower variation occurring in Texas estuaries. Restoration scores under current conditions showed similar trends with more variability due to spawning potential, which is important for reef sustainability. In general, Louisiana estuaries showed higher growth rates and reproduction than Texas estuaries, but due to the higher variability and more frequent extremes in salinity, were more likely to experience mortal conditions in any given year. Comparison between current and future conditions indicated that oyster aquaculture and restoration potential in presently occupied areas might decrease in the future; however, the spatial resolution of available climate model outputs limits planning information. This represents a necessary improvement to better evaluate the physiological response of oysters to future conditions. This work also demonstrates the potential of mechanistic modeling to inform future planning under environmental conditions not currently experienced.

EXPLORING WHETHER CARBONATE CHEMISTRY SHOULD BE CONSIDERED FOR SITE SELECTION FOR EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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The focus of this study was quantifying temporal and spatial environmental variability impacting eastern oyster (*Crassostrea virginica*) growth and calcification (pH, dissolved inorganic carbon (DIC), and saturation indices (Ω)) across two southeast salt marshes, Galveston Bay, Texas, and Wassaw Sound, Georgia. Influences from tidal action and biological productivity in the estuary can result in low saturation states creating potentially poor conditions for oyster growth. It was hypothesized that oysters grown in optimal calcifying conditions would be less energetically challenged, maximizing growth rate and delivery of ecosystem services. In Georgia, oyster growth studies were conducted to draw connections between water quality and oyster growth. Daily pH variability was similar (~0.5 units/day) among all sites in Texas and Georgia, except for Prairie Preserve recording higher daily pH variability ($p < 0.05$). DIC and TA were higher in Texas than in Georgia, leading to higher saturation indices. In Georgia, saturation indices fell below nominal calcification threshold ($\Omega<1$) at most sites, however, oysters actively recruited and grew (Coffee Bluff $\Omega = 0.4 \pm 0.1$, yet recruitment was highest at 17 ± 0.7 spat m^{-2} d^{-1}). Ontogenetic differences in growth suggest optimum growing conditions may not be the same at all life stages. The current study provides evidence for increased larval recruitment and early growth in the upper estuary but increased adult growth in the lower estuary. These results may assist stakeholders by informing target locations within the local estuary that provide highest likelihood of successful growth, sustainable aquaculture and/or restoration.

THE PROS AND CONS OF LONG-TERM DATASETS: A CASE STUDY OF EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) REPRODUCTION IN SOUTH FLORIDA ESTUARIES

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When long-term datasets align in area and time of study, they can present unique opportunities to answer questions in novel ways. Extensive datasets can also present unique challenges in their maintenance and analyses as protocols evolve and researchers change. Eastern oysters in south Florida have been used as an indicator species for assessing the health of the Everglades. Oyster reproduction and recruitment have been monitored monthly in the Caloosahatchee River Estuary since 2000 and in the St. Lucie Estuary and the Loxahatchee River Estuary since 2005 as part of the Comprehensive Everglades Restoration Plan (CERP). Oysters in Lake Worth Lagoon have also been monitored monthly from 2005 through 2015 as part of the CERP monitoring program and since 2015 as a regionally similar population. With this long-term dataset, potential changes in basic biological characteristics, such as size at and timing of maturity, can be assessed. Size at maturity of south Florida oysters will be determined directly through reproductive staging and indirectly through alignment of oyster die-offs, recruitment, and reproductive development. The timing and extent of maturity will be compared among estuaries to determine if intensity or duration of reproductive activity has changed since the initiation of the dataset. Challenges presented by long-term datasets and methods to adapt will be considered.

EXTREME HEAT EVENT INFLUENCES THE TOXIC IMPACTS OF TIO$_2$ NANOPARTICLES WITH DIFFERENT CRYSTAL STRUCTURES ON THE MUSSEL, *MYTILUS CORUSCUS*

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Because of the wide use and unintentional emission of TiO_2 nanoparticles (TiO_2 NP), coastal habitats are inevitably exposed to increasing pressure of nano-pollutants. In addition, extreme climate events, such as marine heatwaves (MHW), have been verified to have a more profound impacts to the marine life than persistent ocean warming. Temperature not only regulates the physiological rhythms of marine life, but also alters the physical and chemical properties of TiO_2 NP, changing their toxic mechanism to marine life. As an essential role in coastal ecosystem, mussel's attachment life and filter feeding make them have to face the great ecological risk of TiO_2 NP. Here, mussels were exposed to 100μg/L TiO_2 NP, represented environmental concentration, with different crystal structures (Anatase and Rutile) under 22°C or 28°C for 14 days, and the physiology of defense and digestion are researched to evaluate the ecological risk of TiO_2 NP.

This study showed that:1) the agglomerations of TiO_2 NP were more serious at 28°C than those at 22°C, 2) MHW and TiO_2 NP led to the significant changes in antioxidant system and immune system of mussels, respectively, 3) integrated biomarkers response (IBR) reflects the influences of Anatase to mussels were greater than Rutile, 4) regardless the crystal structures, MHW aggravated their effects to mussels, 5) the composition and function of the intestinal microbiome in the mussel were significant altered by MHW or TiO_2 NP. This study provides an important reference for analyzing the physiological and ecological effects of nanomaterial pollution on bivalves under global climate changes.

ANALYSIS AND VARIABILITY OF METAPOPULATION CONNECTIVITY IN OYSTER RESTORATION

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Restoration strategies for native oyster populations rely on an understanding of patterns in population connectivity and metapopulation source-sink dynamics. In addition to genetics, a prevailing method to investigate connectivity involves biophysical modeling of larval dispersal and statistical analysis of the resulting connectivity matrix. This study evaluated variation in connectivity of eastern oyster (*Crassostrea virginica*) metapopulations undergoing restoration in lower Chesapeake Bay. Metapopulations ranged widely in geomorphic and hydrodynamic conditions, including (i) a western shore tributary assumed to be a semi-closed system, (ii) a river system comprised of multiple interconnected rivers and bays, and (iii) an open system of two large sounds associated with the Bay mainstem. The biophysical modeling involved release of virtual larvae from multiple potential reef patches in the metapopulation, advection for two weeks, larval mortality, and settlement on reef patches for one week. Simulations were run under differing environmental conditions. Connectivity matrices were analyzed using multivariate statistics and network modeling. Connectivity patterns were diverse and varied significantly among the metapopulations, but could be classified by statistical analyses according to the construct of source-sink dynamics. Populations in a metapopulation could be sources, sinks, pseudo-sinks and stepping-stones, among others. Populations were characterized by their value to restoration, 'bet-hedging' strategies, resilience to climate change, and as linked harvest grounds subsidized by protected source populations.

HIGH-PRESSURE PROCESSING (HPP) AS AN EMERGING TECHNOLOGY: MICROBIAL AND PHYSICOCHEMICAL EFFECTS ON PRECOOKED BLUE CRAB MEAT

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Crab is a highly sought-after shellfish. The blue crab (*Callinectes sapidus*) is native to the Atlantic Coast of the Americas from Nova Scotia to Argentina, including the Gulf of Mexico. It is the most valuable fishery species in the Chesapeake Bay, and it offers significant culinary and economic value in the U.S., particularly in the states of Maryland, Virginia, North Carolina, and Louisiana. Fresh crabmeat is a perishable ready-to-eat (RTE) product and usually has one week of shelf life under refrigeration. High-pressure processing (HPP), as an emerging non-thermal green technology, was applied to extend the shelf life of precooked crab meat and its effect on product quality were investigated for 4 weeks of storage at 4°C. The microbiological and physicochemical quality attributes of precooked RTE fresh crab meat with and without HPP treatment are presented. The parameters for evaluating microbiological quality included total aerobic bacteria, sanitary indicator bacteria (coliform and *E. coli*), and spoilage microorganisms (yeast, and mold). The tested physicochemical parameters were pH, color, drip loss, water holding capacity, texture, lipid oxidation, and fatty acid composition. The results showed that HPP is an effective non-thermal processing technology that can enhance the microbiological quality and extend the shelf life of fresh RTE blue crab meat without significantly affecting the product's physicochemical quality.

A PANEL DISCUSSION ON HIGH-PRESSURE PROCESSING (HPP) TECHNOLOGY: CHALLENGES AND OPPORTUNITIES FOR BETTER QUALITY AND CLEAN LABEL SEAFOOD PRODUCTS

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High hydrostatic pressure or ultra high-pressure processing (HPP) is a non-thermal, green technology that subjects food to a high pressure using cold water as the pressure transfer medium. The major advantage of using HPP technology is that it inactivates bacteria and viruses, and slows the growth of spoilage microorganisms without adding any chemical preservative or food additives. Using HPP can enhance food safety and quality but does not appreciably affect nutritional and sensory properties. This panel discussion will address major challenges and opportunities associated with HPP applications for seafood processing. A diverse group of panelists from academia and industry will join and share their research results and experiences on HPP applications for enhancing the safety and quality of oyster and blue crab meat. Discussion topics will include but are not limited to: (1) proper packaging and processing parameters for HPP treatment, (2) the effects of HPP treatment on the survival and growth of pathogenic and spoilage microorganisms, (3) microstructure, sensory quality, and consumer acceptability of HPP treated seafood, and (4) advantages and disadvantages of HPP applications in the seafood industry. Through these presentations and discussion, scientific information will be conveyed, and useful solutions and potential opportunities will be elaborated.

EFFECTS OF HIGH-PRESSURE PROCESSING (HPP) ON THE SENSORY QUALITY AND CONSUMER ACCEPTABILITY OF PRECOOKED READY-TO-EAT (RTE) ATLANTIC BLUE CRAB MEAT

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High pressure processing (HPP), as an emerging clean-label technology, was applied to enhance the microbiological quality and shelf life of precooked ready-to-eat (RTE) fresh Atlantic blue crab meat. This presentation focuses on the effects of HPP on the morphological properties, sensory quality, and consumer acceptability of the HPP-treated product. Live blue crabs were pressure-cooked in a retort (≥115°C for 4–6 min). The crab meat was then hand-picked, packed in plastic containers (polypropylene cups), sealed with an oxygen permeable barrier film (with an oxygen transmission rate of at least 10,000 cc/m^2/24 h at 24°C), and subjected to HPP treatment at 600 MPa for 3 min. A consumer taste survey (IRBNet Package: 1933295-2) was conducted in three states (Maryland, North Carolina, and Louisiana) to assess the sensory quality and consumer acceptability of HPP-treated crabmeat. The survey results showed that sensory quality of the HPP-treated crab meat was well-accepted throughout the 3-week storage period. Throughout the entirety of the sensory study from week 1 to week 3, the sensory attributes (appearance, smell, texture, and flavor) were scored predominately 5-7 on a 7-point liker scale, indicating good to excellent ratings. Commentaries from participants were mostly positive while negative comments, such as the yellow color of the meat and the presence of shell fragments, were due to factors unrelated to the HPP process. In addition, morphological and microstructural results generated by using scanning electron microscope and hyperspectral imaging will also be discussed.

DEVELOPMENT OF THE SOFTSHELL CLAM AQUACULTURE IN MARYLAND WATERS

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The softshell clam (*Mya arenaria*) has been an important fishery in Maryland; however, the stock collapsed around 2000 for a variety of complex reasons. Maryland aquaculture leases are primarily located in the upper/middle Chesapeake Bay region, where is characteristic of low salinity waters, leading to a monoculture – the eastern oyster. Given the economic potential and the low-salinity suitability of *M. arenaria*, development of *M. arenaria* aquaculture practice may unlock a new shellfish aquaculture sector in Maryland and have a perspective of restoration.

Addressing this goal, PEARL started a program in 2021, focusing on breeding success, development of subtidal culture methods, and how to cope with severe summer mortality. So far, the team has been able to produce seed annually and have created five lines including a selected heat-tolerance line. Several subtidal culture gear types were designed and were tested at two sites of Patuxent River from October 2022 to May 2023. Among these methods, a floating-sand-tray-based method and a polyculture method raised the clams up to 1.8 inches and 1.6 inches respectively with 100% survival during about 7.5 months' culture. A heat shock experiment in the ambient waters in the summer 2023 showed that the *M. arenaria* seed are much more tolerant than 1-year-old or adult *M. arenaria* (survival rate 97% vs 0%) when the temperature is over 30°C. The seed deployed in Augst 30, 2023 reached average 1.4 inches on Nov 29, 2023, which is highly possible to reach 2 inches - the market size by the following May.

GENOME SEQUENCING REVEALS GENOMIC BASIS FOR DOMESTICATION AND ENVIRONMENTAL ADAPTATION IN KUMAMOTO OYSTERS, *CRASSOSTREA SIKAMEA*

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The Kumamoto oyster, *Crassostrea sikamea,* is a species naturally found in southern China, southern Japan, and there is also a hatchery population in the U.S. which was introduced from Japan in the 1940s. It is relatively slow growing with small, but deeply cupped shells, and more resilient to harsh environmental conditions as compared to other *Crassostrea* oysters. The genomic basis for these attributes of *C. sikamea* has not been well studied.

In the present study, a high-quality reference genome of *C. sikamea* was assembled with a Contig N50 of 4.21M and a Scaffold N50 of 62.25M (assembly size 616Mb). Phylogenetic inference indicated that *C. sikamea* diverged from the *C. angulata* and *C. gigas* clade about 9.9 million years ago. Genomics analysis of *C. sikamea* individuals separately representing geographic populations of wild oysters from China and Japan and hatchery populations from the U.S. were resequenced to identify genomic regions affected by domestication. PCA analysis classified three distinct clusters for the American, Japanese, and Chinese populations, although the American populations was closer to the Japanese population and more spread due to its breeding history. In total, 118 shared genes were enriched between US&CN and US&JP, which might be related to domestication and adaptation to the new environmental conditions in Northwest coast of the U.S. (cooler and less variable water temperature). Most of these candidate genes are involved in cytoskeleton, cell cycle regulation (two actins, two fibrillin-1 and two KDM1B) and immune/stress response (C1q domain containing protein, C-type lectin, and hsp70-binding protein).

ADAPTING AQUACULTURE TECHNIQUES TO ENHANCE OYSTER POPULATIONS, *CRASSOSTREA VIRGINICA*, IN REEF RESTORATION

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Oyster reef restoration often involves large logistical efforts that include planting of shell cultch and seeding of fresh set spat on large shell that subsequently exhibit high mortality. The Auburn University Shellfish Lab (AUSL) is conducting a three-year (June 2021-May 2024) oyster reef restoration project in Little Dauphin Bay (LDB), Alabama utilizing aquaculture techniques to improve survival and growth of seeded oysters while removing logistical concerns by using smaller setting material.

Six paired plots were cultched with recycled oyster shell. One plot per pair was seeded with oyster clusters while the other plot remained unseeded. Oyster clusters were produced by setting pediveliger larvae on small shell and then nursed in aquaculture baskets on an adjustable long-line system at the AUSL oyster farm to increase initial growth and survival prior to planting. Additionally, three sets of paired plots were trapped for oyster drills to analyze predator mitigation. Settlement plates were utilized to assess recruitment throughout LDB. To date, seeded plots have been planted with 1,931,393 oysters (mean shell length=25.78mm). Recent sampling of plots indicates a bi-modal size distribution suggesting two recruitment classes since project initiation. Seeded plots consistently had higher oyster populations throughout the study but were not significantly different from unseeded plots. Oyster drills appeared on reefs in March 2022 with trapping efforts showing little effect on oyster populations. Recruitment plates indicate larval sources from outside of LDB contributing to oyster populations. Final sampling in Spring 2024 will determine the overall interaction of seeding and trapping on restored oyster populations.

THE ROLE OF PROBIOTICS IN SHRIMP AQUACULTURE: A COMPREHENSIVE REVIEW IN THE ECUADORIAN CONTEXT

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Shrimp aquaculture in Ecuador plays a vital role as one of the main sources of income. Ecuadorian shrimp is a major product in the global seafood market; however, it faces a variety of challenges, mainly disease outbreaks. Probiotics are beneficial living microorganisms that can promote the host health and mitigate pathogenic risks when they are added in adequate amounts. A review of the use of probiotics in Ecuadorian shrimp aquaculture as a promising preventive method against diseases is presented. The probiotic mechanisms of action and their further impact on shrimp health is mainly through competitive exclusion or stimulation of a defense reaction in the host and plasmids carrying transposon-like elements. The Ecuadorian government invests a great amount of effort on epidemiological prevention, but the research done about probiotics is relatively scarce. A literature review using university libraries in Ecuador and NCBI databases (www.ncbi.nlm.nih.gov) revealed most publications were about acute hepatopancreatic necrosis disease (AHPND) caused by *Vibrio parahaemolyticus*. An isolate of *V. campbelli* from Ecuador also harbors pirAB genes responsible for AHPND and the plasmid exhibits Tn3 transposon-like elements, suggesting horizontal plasmid transfer. The diversity of probiotics used in the Ecuadorian shrimp industry is mainly as a water quality enhancer and as a therapeutic natural product use against pathogenic outbreaks. The main strain is *V. alginolyticus*, also *Vibrio* P62 and Bacillus P64. Data indicates that probiotics use in Ecuadorian farms is increasing, avoiding antibiotics. More research is needed to clarify research gaps such as the influence of prebiotics or the isolation of new prebiotics strains.

IMPROVED RESISTANCE TO *VIBRIO CORALLIILYTICUS* AND OSTREID HERPESVIRUS 1 MORTALITY IN JUVENILE PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) SELECTED FOR A SINGLE NUCLEOTIDE POLYMORPHISM ON CHROMOSOME 8

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Selective breeding of *C. gigas* in the western USA has been shown to improve survival against pathogens. Selection for a SNP on chromosome 8 of the Pacific oyster genome has led to increased survival of spat in Tomales Bay, California, where ostreid herpesvirus 1 (OsHV-1) is endemic. To evaluate whether this improved survival is due to increased resistance to OsHV-1, and to determine if selection for this SNP confers increased resistance to other pathogens, 12 biparental crosses of *C. gigas* that were either heterozygous for the putatively protective variant or homozygous for the reference allele (i.e., control families) were produced. Larvae from the families were challenged with *V. coralliilyticus* RE22 at two days post-fertilization (dpf) and with the Tomales Bay OsHV-1 variant at six dpf. After metamorphosis, spat were reared for five months before undergoing a second challenge with RE22 and for six months post-fertilization before performing two challenges with a European microvariant of OsHV-1.

In larval oysters, the heterozygous genotype was found to significantly increase survival compared to the control families when challenged with *V. coralliilyticus* RE22, showing a 5.44% increase; no significant improvement in survival was observed against OsHV-1. Challenges with spat found that improved survival in oysters with the heterozygous genotype against RE22 was maintained, showing a 28.12% increase in average survival of juveniles. In spat challenged with OsHV-1, crosses with the heterozygous genotype had an average of 38.9% greater survival than the control families across two trials.

ASSESSING SHORT-TERM EFFECTS OF MARINE HEAT WAVES AND HYPOXIA ON JONAH CRAB (*CANCER BOREALIS*) FEEDING BEHAVIOR AND SURVIVAL

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Historically, New York (NY) has harbored some of the most productive fisheries in the nation, with shellfish landings consistently among the most valuable. Prior research has demonstrated how climate change induced warming and persistent hypoxia have increased the vulnerability of several NY shellfisheries to collapse. The Jonah crab holds economic significance in the northeastern U.S. as a newly emerging fishery, though little is known about the effects of warming temperatures and hypoxic conditions on Jonah crab behavior and physiology. This project exposed Jonah crabs to extreme and ideal temperatures (26°C and 15°C) and normoxic and hypoxic conditions (>90% and <35% dissolved oxygen (DO) saturation) as individual and co-stressor conditions in a two-by-two experimental design. In each treatment, crabs were kept in individual cages to prevent intraspecific interactions and were gradually acclimated to treatment conditions for one week. Results showed significantly reduced survival rates caused by elevated temperature (64% vs 100% at ambient temperatures; $p<0.05$). Time to initiate successful foraging was significantly delayed three-fold by elevated temperatures (14 vs 53 minutes; $p<0.05$). Food consumption was also greatly reduced at elevated temperatures with 93% of crabs consuming all mussels provided at ideal temperatures and less than 30% doing so at elevated temperatures ($p<0.05$). While the future effects of climate change on habitat suitability for economically important shellfish species remains uncertain, these preliminary results suggest bottom marine heat waves could have detrimental impacts on the emerging Jonah crab fishery in the U.S.

AN OVERVIEW AND DISCUSSION ON THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP) DATABASE AND MAPPING TOOL

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The Regional Shellfish Seed Biosecurity Program (RSSBP) has been collating molluscan bivalve disease data from the East and Gulf Coasts of the United States and built a database with a mapping tool that can be queried to understand disease distributions and make comparisons among locations of interest to the user. The tool can be used by shellfish farmers and restoration practitioners to identify biosafe transfers, hatcheries and nurseries to understand customer needs regarding biosecurity of potential sales, and resource managers to evaluate transfer requests. This session will provide a brief overview of the database followed by an extended Q&A on its use, needs, and further development.

METHODS AND RESULTS OF APPLYING LOW-COST GENOMIC TOOLS FOR SELECTIVE BREEDING OF *CRASSOSTREA VIRGINICA* IN TEXAS

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Depending on the scale of production, a breeding program may only be economically viable if operating costs and investment in infrastructure and personnel are relatively low. Methods of breeding oysters that produce substantial genetic improvement and maintenance of genetic variation while maintaining low operating costs could broaden accessibility of programmatic oyster breeding. In addition to the advantage of increasing breeding value accuracy, application of certain genomic tools could reduce operating costs and the required investment in infrastructure, personnel, and genotyping. Methods of DNA collection, spawning, early-life rearing, and sib-testing applicable to effective, low-cost breeding of oysters are being developed in Texas to fulfill the demand of a regional breeding program for *Crassostrea virginica.* Goals, strategies, and results of applying low-cost genomic tools for oyster breeding programs will be discussed.

SEABIRDS, *CAMPYLOBACTER*, AND OFF-BOTTOM OYSTER AQUACULTURE

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Campylobacteriosis, caused by bacteria in the genus *Campylobacter*, is the most common source of human bacterial gastroenteritis worldwide. A Department of Health investigation traced a 2021 outbreak in Rhode Island to the consumption of raw oysters. Indigenous to the gastrointestinal tract of birds, indirect transfer of *Campylobacter* to oysters during bird interactions with commercial oyster farming gear may be responsible. Due to these concerns, oyster farmers must maintain an operational plan describing mitigation strategies to minimize risks associated with bird interactions; however, data on *Campylobacter* transfer from seabirds to oysters is lacking. Goals of this study include: 1) test the effectiveness of a non-lethal bird deterrent; 2) enumerate *Campylobacter* in seabird species found in the northern Gulf of Mexico, and 3) survey oysters for *Campylobacter* and describe the similarity between isolated strains from oysters and seabirds.

Six experimental floating cages were deployed at a farm site in coastal Alabama, three equipped with bird deterrents (zip ties) and three controls. Cameras monitored the efficacy of the deterrents. *Campylobacter* incidence in seabird fecal matter was determined using a selective and differential media. An enrichment procedure was used to detect *Campylobacter* in oysters. Deterrents decreased bird interactions with gear 8-fold. Approximately 7.5% of bird feces were positive for *Campylobacter*. Sequencing of the 16S rDNA identified the isolates as *C. lari* subsp. *concheus*. This species has not been confirmed as a human pathogen.

NUTRIENT REMEDIATION CAPACITY OF THREE NEW ZEALAND KELP SPECIES: CONSIDERATIONS FOR IMTA APPLICATIONS WITH *PERNA CANALICULUS*

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Shellfish aquaculture produces a significant amount of nitrogenous waste products, resulting in potential localized eutrophication in marine systems. Solutions to this problem include the introduction of assimilatory species, such as macroalgae, to create Integrated Multitrophic Aquaculture systems (IMTA) to reduce nitrogen loading, particularly ammonia (NH_3) and ammonium (NH_4^+), associated with conventional bivalve monoculture systems. In the current study, the assimilatory capacity of three economically promising species of brown macroalgae were explored (*Ecklonia radiata*, *Macrocystsis pyrifera*, and the non-native *Undaria pinnatifida*) for IMTA applications in New Zealand with *Perna canaliculus* (the green-lipped mussel). The experiment compared assimilatory capacity across three laminarian species, under light vs dark treatments at three temperatures (10, 14 and 18°C) using a closed chamber incubation system. The aims of the study were: 1) to compare the nutrient remediation capacity of three large brown algal species and, 2) to compare performance resilience across the annual temperature range experienced in the Otago region. Initial winter observations (10°C) found that the presence of all kelp species significantly reduced NH_3/NH_4^+ efflux produced by *P. canaliculus* when treatment and photic condition were held as fixed effects ($p < 0.01$); however, assimilatory capacity was statistically similar across kelp species at 10°C ($p > 0.05$), suggesting that in cold-water, all species would be similar in nitrogenous reduction capacity. Further investigation into remediation capacity at warmer temperatures will test for differences in performance among species, which with continued projections of oceanic warming will be important to consider for the application of IMTA systems.

SCIENCE TO SUPPORT MANAGEMENT OF INVASIVE GREEN CRAB: A WASHINGTON STATE CASE STUDY

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Effective management of marine bioinvasions frequently hinges on rapid deployment of best available science to address urgent concerns. To do so, managers and scientists must work together closely, and infrastructure and processes should be aligned for efficient implementation. The example of European green crab (*Carcinus maenas*) management in Washington State was used as a case study. The green crab was first detected in Washington waters in 1998 after warm El Niño currents spread larvae of California populations as far north as Vancouver Island. Because of perceived risks to coastal resources, the green crab was designated a deleterious species in Washington State, which among other actions, mandated monitoring, and control of the species in state waters. Over the past decade, green crab abundance and distribution has increased throughout the region, as has coordinated management in many jurisdictions. In this presentation, how knowledge transfer and collaboration have developed among managers, scientists, and other stakeholders and how management has evolved to build regional response capacity will be highlighted. In particular, the importance of integrating new scientific understanding into management will be emphasized. This has enabled a robust and responsive regional strategy, rooted in effective communication and science-informed decision-making.

INTERACTING CLIMATE CHANGE STRESSORS AND CARRYOVER EFFECTS IN OYSTERS

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Oysters are facing threats to their well-being with increases in anthropogenic changes to the environment. Because of their sessile and long-lived nature, oysters are unable to escape unfavorable conditions and will likely experience variation in environments throughout their lifetime. Therefore, it is critical to understand how early life experiences will affect oysters' response in the future to better prepare for a changing environment. Within-generation carryover-effects (CE) describe how experiences early in life affect phenotypes later in life; however, the mechanisms of CE are largely unknown. In a fully factorial experiment, eastern oysters (*Crassostrea virginica*) were exposed to two interacting climate change stressors (hypoxia and warming) early on in their life and again three months later. In order to identify possible underlying mechanisms of CE, whole-body tissue samples were used for DNA methylation and microbiome analyses. Evidence shows strong methylation patterns associated with early exposure to warming. In contrast, early exposure to hypoxia altered the microbiome. These results support these two pathways as possible interacting mechanisms of CE and demonstrate the importance of investigating multiple stressors simultaneously. Enhancing our understanding of these processes can provide insights to efficient and effective management practices to ensure the persistence of oyster populations through a changing climate.

CROSS-GENERATIONAL EFFECTS OF OCEAN ACIDIFICATION ON A THIRD GENERATION OF BAY SCALLOPS

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Ocean acidification (OA; elevated pCO_2) is accelerating in coastal ecosystems and threatens many organisms, especially during early larval development. Transgenerational plasticity is a possible mechanism conferring resilience to rapid environmental change. To better understand the effects of OA exposure across generations, and the potential for transgenerational plasticity, bay scallops were continuously grown, from embryogenesis to sexual maturity, under one of three OA conditions (pCO_2 = 500, 800, 1200 µatm) for two generations. The third-generation offspring of these scallops were grown in a full factorial design (parental history × larval exposure) under the three OA conditions. Survivorship, growth rate, and larval physiology were measured from prodissoconch I to metamorphosis. Shell abnormalities in D-stage larvae and the number that had successfully metamorphosed by day 19 post fertilization were quantified. Respiration rates were also measured from prodissoconch I to metamorphosis to assess changes in metabolism related to growth and survivorship. Differences were found among treatments that will be discussed in the context of acclimation to rapid environmental change. Graphical trends suggest that transgenerational plasticity may confer some resilience to OA under some conditions and additional transcriptomic analysis is underway.

MACHINE LEARNING AND COMPUTER VISION TECHNIQUES TO IDENTIFY AND MONITOR OSTREIDAE NONDISRUPTIVELY

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Oysters are growing in importance both as a food source for a rising population and a natural filtration system for waterways. Yet despite the importance of oysters, the aquaculture sector in the United States has failed to see modernization like the rest of the agriculture industry. To help modernize this aging sector, the goal was to use deep learning image recognition software to train computer vision models to detect, classify, and track these oysters. These models allow for remote monitoring and counting, making it easier for farmers and environmental groups to assess the health, prevalence, and extent of oysters in an area. By utilizing YOLOv8 and its new features, it is possible to train and test oyster detection, classification, and segmentation models with far better precision and tracking than the project last year. The work completed so far has shown great promise in being adapted into use in the field and in oyster hatcheries as a way to monitor and track oysters, which should prove useful in the modernization of the aged aquaculture industry.

HOW REPRESENTATIVE IS YOUR SAMPLE? DEMOGRAPHIC DATA IN THE US SHELLFISH AQUACULTURE INDUSTRY

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In research and extension involving human subjects or participants, the utility and value of resulting data depend upon how representative the sample is of the target population. This is a challenge with any data poor setting, including basic demographic data. Demographic data may be lacking on specific target research populations such as individual commercial fisheries or aquaculture sectors. With this data gap in mind, in 2020, a survey targeting the US shellfish aquaculture industry sought general demographic information to create a baseline dataset that could help understand overall demographics and representation as well as track changes in industry make-up over time. This anonymous survey was shared with industry associations, local extension specialists, state resource managers, and directly to growers and received 388 responses spanning 22 states. The majority of respondents were oyster farm owners; thus, the results may provide a demographic snapshot of a subsector of the industry but cannot be used to infer patterns for the industry at large. Survey results will be presented and discussed with a broader charge for continued and more on-the-ground efforts to better capture industry demographics.

SHELLFISH AND SEAWEED AQUACULTURE ECOSYSTEM SERVICES HORIZON SCAN: PROJECT UPDATE

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Shellfish and seaweed aquaculture are increasingly recognized for their role in ecosystem services production, and a growing body of peer-reviewed science documents their connections to all categories of ecosystem services: cultural, provisioning, regulating, and supporting. This project aims to assess the state of the science and utilize the knowledge of experts throughout the United States to identify key next steps for advancing the field of bivalve shellfish and seaweed aquaculture ecosystems services research. Framed as a horizon scan, this project seeks to identify not only research gaps and needs, but potential areas where policy or management has yet to operationalize well-documented aquaculture-associated benefits and services.

In 2023, research scientists, industry leaders, resource managers, extension personnel, and others well-versed in aquaculture ecosystem services were invited to contribute to this aquaculture ecosystem service horizon scan. Synthesized findings of that information call will be presented to introduce an initial prioritization and discussion of related research and management needs. This presentation will be one of several opportunities for project participants and others to provide feedback on this synthesis.

UNDERSTANDING REPRODUCTIVE DEVELOPMENT IN FEMALE WHITE SHRIMP, *PENAEUS SETIFERUS*, IN SUPPORT OF SUSTAINABLE FISHERIES MANAGEMENT IN SOUTH CAROLINA, USA

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Accurate assessments of female reproductive development are an important component to the sustainable management of the white shrimp (*Penaeus setiferus*) fishery in South Carolina (SC). Reproductive development is commonly assessed macroscopically based on ovary appearance; however, few studies have quantitatively assessed the reliability of macroscopic determinations of whether female white shrimp have spawned. The detection of prior spawning and its prevalence of occurrence have been crucial for estimating reproductive output and informing the timing of commercial seasonal openings in SC. The objectives of this study were to: 1) characterize female white shrimp reproductive development and spawning activity, as observed through histology; and 2) compare microscopic observations with macroscopic observations to determine the efficacy of macroscopic assessments. Weekly samples of female white shrimp were collected in the Charleston Harbor, SC from March to June, 2022, and ovarian tissues were processed through histology for microscopic assessments. A detailed framework for distinguishing microscopically observed development stages is provided, along with explanations of oocyte atresia, a marker of prior development. Reproductive development and spawning phenology observed microscopically were then compared with macroscopic observations to assess agreement in detection of prior spawns, assuming that microscopic approaches are accurate. The finding of an average percent agreement of 49% across the 8 weeks when spawning was taking place and a low of 25% agreement suggests that macroscopic detection of spawning activity may be an unreliable tool for fisheries management as currently applied. Alternative methods should consider broadening the reproductive stages and parameters used in fisheries management.

INVESTIGATING SUSPENSION-FEEDING INVERTEBRATES AS BIOINDICATORS OF MICROPLASTICS

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Suspension-feeding animals interact with microplastics of different shapes and sizes suspended in the water column. Bivalve molluscs have been suggested as potential bioindicator species for microplastics as they are known to consume microplastics in the natural environment, are widely distributed, sessile, and easy to collect; however, these molluscs are selective suspension feeders and, thus, do not consume all particles to which they are exposed. This study investigated how two indiscriminate suspension feeders, the Atlantic slippersnail, *Crepidula fornicata* (gastropod), and the sea grape, *Molgula manhattensis* (tunicate), interact with microplastics of different sizes, shapes, and polymers to determine their suitability as bioindicator species for microplastics. The data were compared to that of previous experiments with oysters (*Crassostrea virginica*) and mussels (*Mytilus edulis*). Animals were offered aged polyester or nylon microfibers of different lengths, nylon and polyester microfibers of similar lengths, or polyethylene and polystyrene microspheres of similar diameters during a 2-h exposure. Feces and pseudofeces collection during and after the exposures revealed that slippersnails and sea grapes both exhibited size-based rejection of nylon fibers, rejecting longer fibers at higher proportions. Polymer type did not influence ingestion of fibers or spheres. Sea grapes were the most indiscriminate feeders when compared with slippersnails, oysters, and mussels, but were able to egest microplastics just as quickly. Although sea grapes rejected proportionally fewer microplastics than slippersnails, neither species will make an ideal bioindicator because they do not ingest all plastic particles they encounter, they egest the particles quickly, and do not accumulate microplastics in their tissues.

CITIZEN SCIENCE APPROACH TO MITIGATE THE EFFECTS OF HARMFUL ALGAL BLOOMS IN COSTA RICA

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Marine biotoxins are poisons that are produced by certain kinds of microscopic algae that are naturally present in marine waters, normally in amounts too small to be harmful. Biotoxins accumulate in shellfish to levels that can cause illness or death in humans and other mammals that ingest them. Of critical concern is the neurotoxin, saxitoxin, and related derivates. Ingestion of saxitoxin contaminated shellfish and finfish is responsible for the illness known as Paralytic shellfish poisoning (PSP). Saxitoxin is produced by the dinoflagellates *Alexandrium*, *Pyrodinium*, and *Gymnodinium*. Along the coast of Costa Rica, blooms of *Pyrodinium* and *Gymnodinium* have been reported since 1981. During 1999, blooms of these species caused 70 cases of PSP with 6 fatalities, leading to a shellfish closer for over two years because of consecutive blooms and a lack of resources to analysis these toxins in Costa Rica. Commercially important shellfish such as thorny oyster (*Spondylus calcifer*), Panama pearl oyster (*Pinctada mazatlantic*), mangrove cockle (*Andara turculosa*), and Guiana swamp mussel (*Mytella guyanensis*) are all known vectors for human intoxication.

The NOAA National Phytoplankton Monitoring Network is a community-based volunteer science approach to monitor harmful algal blooms and their associated toxins. Founded in 2001, the network has trained over 600 volunteers across 36 U.S. states and 4 countries including Costa Rica. Since 2022, the network has partnered with Innoceana, a global marine conservation organization that works to preserve the ocean for future generations by empowering coastal communities through access to education and innovative tools, to monitor potential harmful algae along Isla Violin. This project will expand the initial sampling conducted by increasing the number of sites and involve local schools and community groups to monitor the entire coast of Costa Rica.

PARTICIPATORY SCIENCE APPROACH TO MONITOR HARMFUL ALGAL BLOOMS, AND CHANGES IN ENVIRONMENTAL CONDITIONS WITH THE AQUACULTURE INDUSTRY

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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, PMN enhances the National ability to respond to and manage the growing threat posed by HAB by collecting important 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 harmful algal blooms, 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 participatory science approach of PMN to include the partnership of 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 take action to protect or harvest. This presentation will cover the methods used to monitor aquaculture sites and progress made by AQPMN to establish a national participatory science approach to monitor ichthyotoxic HAB, co-developed by the shellfish and finfish industries.

THE FUTURE OF FISHERIES AND RENEWABLE ENERGY: MODELING POTENTIAL IMPACTS OF U.S. OFFSHORE WIND ENERGY DEVELOPMENT ON THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSMIA*, FISHERY IN THE MID-ATLANTIC BIGHT

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The approval of offshore wind energy projects in the mid-Atlantic Bight (MAB) could have adverse impacts on the future of the Atlantic surfclam, *Spisula solidissima,* fishery. The current and future areas designated for offshore wind energy development overlap with Atlantic surfclam fishing grounds and could restrict fishing efforts. The possible restrictions that may confront the Atlantic surfclam fishery were simulated using a spatially explicit fishery model (SEFES). Simulations were implemented to investigate transit rules to fishery grounds, including whether fishing vessels will be able to transit through current and planned lease areas. The distribution of catch, hours fished, landings per unit effort (LPUE), sea time, fishing mortality, and fishing trips were projected between 2016-2055, consisting of five time periods, each with four-year average time spans. Across all fleetwide scenarios a significant decline in the mean of all parameters was observed (with the exception of LPUE) for the fishery when future wind energy lease areas were included relative to established lease areas. Case simulations were also run for five specific fishing areas designated in the MAB, each showing similar trends to the fleetwide observations. These simulations suggest that the addition of future windfarm leases will increase the overall impact on the Atlantic surfclam fishery in years to come. The progression of offshore wind development and the clean energy industry must consider the long-term impacts it will have to surrounding sedentary benthic species, and the sustainability of commercially important marine fisheries that rely on these species, for successful coexistence.

GREENING AQUACULTURE: CULTIVATION OF NATIVE SEA LETTUCE (*ULVA* SPP.) FOR POLYCULTURE RESEARCH

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The Georgia (GA) coast has shown great potential for large-scale oyster aquaculture, and the rate at which the sector has grown demands implementation of novel techniques to ensure sustainability and success in the face of climate change. One practice - integrated multi-trophic aquaculture (IMTA) - is known to have positive effects on the health and quality of farmed organisms and the surrounding environment through low pH/alkalinity amelioration, while also being a unique and viable way for a farming operation to diversify its products. To date, there has been no such attempt at investigating or demonstrating macroalgae culture in Georgia before. One native species, sea lettuce (*Ulva* spp.), is widely cultivated around the world for its many useful applications. Before any large-scale polyculture can occur, there is a need to investigate the feasibility of farming sea lettuce in Georgia. Native *Ulva* specimens were collected from Tybee Island, GA for use in spore settlement and ocean grow-out trials. Seeded ropes were placed at two experimental small-scale plots on Skidaway Island, GA and growth was monitored over time. A 5-week lab experiment was conducted in which eastern oysters (*Crassostrea virginica*) and *Ulva* were cultivated together and separately to determine any influences on water quality. Total alkalinity and pH were higher in *Ulva* and polyculture treatments than controls and oyster-only treatments. The results of this study can lay the groundwork for future research in IMTA in the southeastern US.

USING DNA METABARCODING TO UNDERSTAND THE FEEDING ECOLOGY OF THE ATLANTIC SEA SCALLOP, *PLACOPECTEN MAGELLANICUS*

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The composition of Atlantic sea scallop (*Placopecten magellanicus*) diet and how diet relates to reproductive success is not well understood. Studies of other scallop species have correlated prey availability during gonadal development to spatfall density, suggesting that this could be a predictor of subsequent recruitment and an important consideration for both spatial management of the resource and the development of a stock enhancement program. DNA metabarcoding involves simultaneously amplifying the same genetic locus from a multispecies sample, followed by high-throughput sequencing and comparison of recovered DNA sequences to reference sequences for taxonomic identification. This study aimed to establish a DNA metabarcode sequencing approach for the identification of prey diversity in the digestive glands of sea scallops collected off the U.S. Atlantic coast. Environmental DNA (eDNA) from sediment and water samples collected concurrently with scallop samples were also sequenced to investigate potential prey selectivity and how prey availability varies temporally and spatially. Methods were selected and optimized for the extraction, amplification, and sequencing of DNA from the three sample types. Initial focus was on the identification of diatoms, a known component of scallop diet. Preliminary identifications and comparisons of species composition between sample types are presented. Future objectives of this study include analyzing how diet composition varies with environmental parameters and during gonadal development to investigate potential correlations between prey and scallop productivity. A better understanding of sea scallop feeding ecology can inform and help predict future habitat suitability and recruitment.

ESTABLISHING A FRAMEWORK FOR UNDERSTANDING RISKS ASSOCIATED WITH BIRDS ON SHELLFISH AND CO-CULTURE OPERATIONS

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Existing regulatory frameworks established to protect public health associated with shellfish consumption were originally developed based upon pathogen information from sewage. Dramatic growth in near-shore and mid-shore floating bag shellfish aquaculture, along with concomitant increases in human activities that promote bird recruitment, have increased the risk of bird feces to public health. This is evidenced by a recent (2021) outbreak associated with *Campylobacter* sp., associated with oyster aquaculture. On one hand, bird feces can contain pathogenic bacteria and parasites, that go beyond *Campylobacter* sp., including *Salmonella*, *E. coli,* and *Cryptosporidium*; however, there is relatively little quantitative data available on the strain-specific bacterial pathogens. The loads of each of these pathogens are highly variable in bird feces. On the other hand, risk-based relationships previously observed among pathogens in human sewage and acceptable levels of fecal coliforms, are very different from those related to bird fecal contamination. One example is according to infectious dose. Birds are more likely to be a risk to human health because of bacterial pathogens, but infectious doses of pathogenic forms of *Salmonella* and *Campylobacter* range from 100-10,000 and 500-10,000 cells, respectively, depending on the consumer. This contrasts to norovirus with lower infectious doses (ca. 10-20 viruses). This presentation will categorize approaches for quantifying the risk of bird fecal contamination on shellfish and co-culture operations. A discussion on new technologies, including long-read sequencing, and microbial source tracking will be presented toward development of assessments that protect both the reputation and economics of our shellfish growers, and the consumer.

HIGH-RESOLUTION MONITORING OF AVIAN COMMUNITIES AT MARICULTURE OPERATIONS YIELDS INSIGHTS INTO COMMUNITY DYNAMICS, BIOGEOCHEMISTRY, AND SANITATION RISKS

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The high mobility and sociality of seabirds, along with their trophic position as secondary consumers, make this group important in shaping coastal ecosystem structure and nutrient dynamics. How these species move within and across ecosystems is influenced by habitat availability and quality, with large multispecies aggregations often forming in areas with high assumed value. The rise of shellfish mariculture in coastal waters and associated floating structures has provided a novel and presumably valuable habitat for seabirds, potentially rewiring avian movement in these systems and generating conflict for those tasked with implementing and enforcing bird mitigation at shellfish farms. The avian community was characterized and quantified utilizing these farms and examine the environmental variables responsible for explaining biomass movement. A camera trap network was deployed alongside environmental loggers at three floating shellfish farms for an entire year, with all instruments capturing data hourly. Such high-resolution monitoring has allowed analysis of temporal patterns of abundance and composition and demonstrated the role of sea level in driving avian movement. Camera imagery was also utilized to estimate site-specific guano inputs, with results challenging the idea of these farms as sites of net nitrogen removal and highlighting when bird-related sanitation risks may be greatest. The diverse and dynamic avian community described by this work points to the power of high-resolution monitoring in revealing important ecological patterns and processes and surveilling the potential negative consequences of seabird-aquaculture interactions.

A NEUROPHYSIOLOGICAL ROLE OF GLUTAMATE IN GANGLIA OF THE BIVALVE *CRASSOSTREA VIRGINICA*

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Glutamate neurons (GN) are excitatory neurons in mammals and various invertebrates. GN disfunctions are associated with Parkinson's and Alzheimer's diseases. GN have not been reported in *Crassostrea virginica*; however, NMDA glutamate receptors are reported involved in metamorphosis in some bivalves. GABA is synthesized from glutamate. In *C. virginica* and other studied bivalves, gill lateral cells (GLC) are innervated by cilio-excitatory serotonin and cilio-inhibitor dopamine nerves from their visceral ganglia (VG). GABA has been detected in *C. virginica*, having a neurophysiological function inhibiting serotonin neurons. To test the hypothesis of GN function in VG of *C. virginica,* the effects of glutamate application to VG on GLC cilia beating rates were studied. Applying glutamate to VG increased GLC cilia beating from 5 to 20 beats/sec. When repeated in the presence of dextromethorphan hydrobromide (DMT), a NMDA receptor antagonist. DMT reduced cilia beating to 0 beats/sec. Applying glutamate after DMT did not increase beating rates. The study revealed a neurophysiological role for glutamate as an excitatory neurotransmitter in VG, possibly exciting serotonin neurons. DMT results are inconclusive and need to be further investigated. DMT does have side effects, including decreasing reuptake of catecholamines. If DMT is decreasing reuptake of dopamine in VG, that could cause the deceased beating rates observed, as the cilio-inhibitory actions of dopamine, a catecholamine, would be increased. The work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0537231071 of the NYSDoE-CSTEP program, P120A210054 of the DoE-MSEIP Program and K12GM093854 of the NIH IRACDA Program of Rutgers University.

ASSESSING THE FEASIBILITY OF RENTING SMART SUSTAINABLE SHELLFISH AQUACULTURE MANAGEMENT (S^3AM) AS A SERVICE FOR SMALL OYSTER FARMS

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Smart Sustainable Shellfish Aquaculture Management (S^3AM) is an advanced technology that aims to enhance shell-on bottom oyster production efficiency through guided crop planting, inventory development, and targeted harvest. Assessing its profitability for adopters is crucial, given previous ex-ante analyses indicating economies of scale and profitability for medium to large-scale oyster farms, but not for small-scale ones. In this study, farms producing 200 bushels/year are small, 2000 bushels/year are medium, and 6000 bushels/year are large. This study focuses on exploring the feasibility of providing S^3AM as a renting service to small farms. Various performance metrics, such as net return, input cost ratio, break-even price above total and variable costs, and break-even yield above total and variable costs, will be evaluated. The analysis will encompass different scenarios, including renting technology once per crop year during planting or harvesting, twice per crop year (planting and harvesting), and thrice per crop year (planting, inventory development, and harvesting). The results of this study are anticipated to provide valuable insights for shell-on bottom oyster growers, enabling them to make informed decisions about adopting or renting the novel technology as a service.

INVESTIGATING THE INTERACTIONS BETWEEN MICROPLASTICS AND FRESHWATER BIVALVES

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Suspension-feeding bivalves interact with microplastics (MP) (< 5mm) in a manner similar to that of the planktonic organisms they typically consume. While extensive research has explored the interaction of marine bivalves with MP, there is a notable gap in knowledge concerning freshwater bivalves. The present study addresses this research gap by investigating the interaction between freshwater bivalves and MP. The eastern elliptio (*Elliptio complanata*), a native North American freshwater bivalve, was exposed to polyester (PET) microfibers of 75µm, 500µm, and 1mm in size (with a width of 15µm), as well as polystyrene (PS) microspheres of 20µm, 500µm, and 1mm in diameter, in a 2-hour exposure experiment. Collection of biodeposits, pseudofeces (indicative of rejection), and feces (reflecting ingestion) occurred at intervals of 3 hours, 24 hours, and 48 hours. The proportion of MP rejected and egested within the initial three hours was also determined. Regardless of the polymer types and shapes, a discernible trend emerged where larger MP were more frequently rejected than smaller MP, indicating a size-based rejection pattern. Furthermore, post-ingestive selection was observed within the bivalves' gut, as smaller MP of both polymer types exhibited an extended retention period in the gut compared to larger MP. Consequently, the size of the plastic particle was the primary factor influencing ingestion and rejection of MP by *E. complanata*.

RESTORING NATIVE SHELLFISH COMMUNITIES FOR IMPROVED WATER QUALITY AND ECONOMIC RESILIENCY IN THE INDIAN RIVER LAGOON, FLORIDA

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Restoration aquaculture is a relatively new arena in the aquaculture industry of Florida, and as such, has enabled the myriad projects occurring around the state that are aimed at restoring shellfish populations and function. Coastal and estuarine ecosystems have been especially hard hit there due to harmful algal blooms, eutrophication, hypoxia, and other effects of degraded water quality. In the Indian River Lagoon, eutrophication from developed landscapes has contributed to devastating large scale algal blooms that have left the northern quahog (= hard clam) population (*Mercenaria mercenaria*) almost entirely extirpated from the system. Without the filtration capacity of a once thriving population of hard clams, turbidity now threatens recruitment of seagrasses, a foundational species in the lagoon. In an effort to restore seagrasses and improve water quality overall, large scale restoration efforts are underway to repatriate native clams. Over the last four years, over twenty-eight million clams have been repatriated to the lagoon and fate tracked. Results suggest that 1) clams are well suited for improving water quality as evidenced in high survival rates and successful growth, and 2) large variability in salinity, ostensibly form stormwater inputs, is the single most detrimental factor for success of restoration in the lagoon.

INVESTIGATING THE RELATIONSHIP BETWEEN SEAWATER NUTRIENTS AND HARMFUL ALGAL BLOOMS AT RHODE ISLAND SHELLFISH FARMS

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Shellfish aquaculturists along the northeast of the U.S. have been experiencing rising concerns over the increasing presence of harmful algal blooms, specifically *Margalefidinium polykrikoides* (Mp), an ichthyotoxic dinoflagellate that causes localized rusty colored tides. Ninigret Pond is the largest coastal salt pond in Rhode Island and houses several expanding shellfish farms. Harmful algal blooms can heavily impact farm production both by causing direct mortality to shellfish as seen with Mp blooms, to other severe impacts like closing shellfish harvest areas due to potential domoic acid toxin presence.

Beginning December 2022, monthly sampling was conducted for one year through western Ninigret Pond. Water samples were collected in triplicate and used for both seawater nutrient analysis and determining Mp concentrations via qPCR assays correlating nutrient spikes to farmers' bloom observations to better understand Mp behavior. Varying lower levels of Mp were found via qPCR, however, no rust tide bloom was visually observed. Farmers noted other unidentified algal blooms occurring throughout the sampling period instead. The water quality and nutrient results from this study will be compared to historically collected data from the pond throughout the past ten years to investigate any relationships (both Mp and non-Mp related), recorded algal bloom presence, and yearly water quality consistency for the pond. Analysis will take into account any changes from being dredged mid-2023 as well. This data collective will assist farmers in understanding potential patterns of algal bloom occurrence in Ninigret Pond.

GASTROPODS - THE OTHER SHELLFISH

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Gastropoda is the largest class in the Mollusca. They are ecologically important and include important suspension feeders that can rival bivalves. They have also proven to be important model systems for physiology, neurobiology, morphology, life histories and evolution. Many species are commercially important, while others have emerged as invaders, impacting other important. They are also commercially important, but are often overlooked. It is time to shine a light on this wonderful group.

STREAM – A SATELLITE-BASED WATER-QUALITY MONITORING SYSTEM FOR EFFECTIVE ASSESSMENT OF AQUACULTURE OPERATIONS

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Coastal resources are prone to intertwined effects of climate variability and anthropogenic stressors. With their massive societal and economic benefits through fisheries, aquaculture, and recreation, it is imperative for decision-making entities to integrate the highest-quality data and observations into decision support systems, thereby enhancing coastal management and monitoring. To further enrich existing observational capabilities, an expedited data processing system was developed that ingests, processes, and displays water quality (WQ) maps (i.e., chlorophyll-*a*, Secchi, total suspended solids) from high-resolution imagery (10 – 30 m) of Landsat and Sentinel-2 missions. This web-based platform, STREAM (a satellite-based analysis tool for rapid evaluation of aquatic environments), offers globally validated WQ products developed using a processing engine that relies on a machine-learning model. For its interface, various tools and capabilities that have already been developed as part of the NASA near-real-time data processing systems (e.g., Fire Information for Resource Management System) are harnessed. It allows end-users to visualize WQ maps, identify pixel values, and view time-series plots for a given pixel or a region. STREAM will enable low-latency (< 6 hours) detection of anomalous WQ conditions for robust and timely decision-making. The system is currently live and supports processing at select regions.

EFFECTS OF PERFLUOROOCTANOATE AND NANO TITANIUM DIOXIDE ON MALE GONADS OF THE THICK-SHELL MUSSEL, *MYTILUS CORUSCUS*

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Perfluorooctanoic acid (PFOA) and nano-titanium dioxide (nano-TiO_2) are widely used as surfactants, and their release into the environment can cause toxic effects on Marine organisms. To study the effects of these pollutants on the gonadal development, male thick-shell mussels (*Mytilus coruscus*) were exposed to varying PFOA concentrations alone or combined with nano-TiO_2 for 14 days. The results revealed significant interactive effects of PFOA and nano-TiO_2 on multiple parameters related to the gonadal function in male mussels. Co-exposure to PFOA and nano-TiO_2 led to a decrease in the gonadosomatic index, the testicular spermatic area and sperm resorption in male mussels. Furthermore, in the presence of both PFOA and nano-TiO_2, there was a decline in the lipid and protein content of the gonads, paralleled by a downregulation of lipid metabolism genes, fatty acid synthase (FASN) and stearoyl-CoA desaturase (SCD), and a pronounced upregulation of the steroidogenic factor 1 (SF-1). Notably, genes essential for gonadal maturation, wingless-type Mouse Mammary Tumor Virus integration site family member 4 (Wnt-4) and Wnt-7b, showed substantial downregulation, while beta-catenin (β-catenin) was upregulated. Moreover, apoptosis was evident in the gonads, accompanied by a downregulation of the apoptosis inhibitor gene B-cell lymphoma 2 (Bcl-2), and the upregulation of caspase-8 and transforming growth factor beta (TGF-β). Thus, PFOA and nano-TiO_2 can disrupt the gonadal function in the male mussels by interfering with Wnt family signaling pathways, modulation of steroid and lipid metabolism and induction of apoptosis. Therefore, a mixture of organic and nanoparticle contaminants poses a significant risk to thick-shell mussels.

PRESENCE OF GLUTAMATE NEURONS AND GLUTAMATE RECEPTORS IN GANGLIA OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Mammals and invertebrates have glutamate neurons in their nervous systems. Glutamate dysfunction is associated with Parkinson's and Alzheimer's diseases. Glutamate is synthesized into GABA. GABA neurons recently were found in *Crassostrea virginica* that inhibit serotonin neurons. To test the hypothesis that glutamate is a neurotransmitter in *C. virginica,* immunohistofluorescence (IHF) along with PAGE and Western Blotting (WB) were used to view glutamate neurons and the glutamate GluR-1 receptor in visceral ganglia (VG) and adductor muscle (PAM) of *C. virginica*. VG and PAM were dissected and prepared for IHF or PAGE and WB. For IHF, VG and PAM were frozen, cryostat sectioned, fixed with EDAC and incubated with GluR-1 FITC antibodies. Sections were viewed and photographed on a fluorescence microscope. VG and PAM also were prepared for PAGE and WB, incubated with GluR-1 HRP antibodies and viewed with an iBright Fl1500 image analyser. IHF showed the presence of glutamate nerves and GluR-1 receptors in the VG cortex and neuropile. PAGE and WB showed GluR-1 receptor bands in VG and to a lesser extent in PAM. The study shows glutamate neurons and GluR-1 type receptor present in VG of *C. virginica*. This study complements other lab work showing a neurophysiology function of glutamate as an excitatory neurotransmitter. The work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0537231071 of the CSTEP program of the NYSDOE, P120A210054 of the MSEIP Program of the DoEd, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

MAPPING IMPACT RISKS ASSESSMENT OF NAVIGATION NOISE ON GIANT SCALLOP BEDS IN THE GULF OF ST. LAWRENCE, CANADA

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Underwater acoustic environments have been significantly altered by human activities since the industrial revolution. Among these emerging anthropogenic disturbances, navigation-related noise is the most widespread spatiotemporally, covering the widest range of sound frequencies among anthropogenic noise sources. Given the physical characteristics associated with sound wave propagation in aquatic environments, these waves serve as a means of long-range directional perception for numerous aquatic organisms.

Results associated with the sound perception thresholds of two developmental stages (1-year juveniles and 3-year adults) of the giant scallop (*Placopecten magellanicus*) were integrated with an existing three-dimensional physical model aimed at estimating marine traffic noise in the Gulf of Saint Lawrence on an annual basis, with daily resolution (https://soundscape-atlas.uqar.ca). Behavioral responses linked to giant scallops (1-year juveniles and 3-year adults) sound sensitivity have been assessed through laboratory experiments. These results emphasize potential impacts associated with increased valve movements caused by navigation noise on this valuable marine resource, both ecologically and economically. Building on these findings, existing knowledge about the auto-ecology of giant scallops, and acoustic modeling, the risks of maritime traffic noise impacts on scallop fishing grounds in the Gulf of Saint Lawrence were mapped. These theoretical outcomes will lay the groundwork for conducting additional *in-situ* experiments, ultimately contributing to the development of management measures aimed at safeguarding fragile and economically significant marine ecosystems.

IMPACTS OF OYSTER AQUACULTURE ON ADJACENT NATURAL REEFS

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As in many other areas, there are ongoing efforts to increase shellfish aquaculture within North Carolina, especially oyster culture. An effort to maintain oyster culture operations within a segment of the North Carolina Estuarine Research Reserve led to reconsideration of potential impacts of oyster aquaculture on adjacent natural oyster reefs. As part of a larger study, oyster demographics and faunal utilization of these systems were examined in natural reef patches near and distant from culture operations. There were minimal differences observed for oyster demographics, associated resident fauna, and associated nekton on natural oyster patches at varying distances from aquaculture. Strongest impacts were observed for structure / non structure (bare sandflat) comparisons. The unexpected passage of Hurricane Florence over the study area also offered the opportunity to observe resiliency to storm disturbance. There was a surprising increase in oyster spat settlement immediately after the passage of the hurricane and differential impacts on associated fauna.

CREATING A HISTOLOGICAL ATLAS FOR MARYLAND FRESHWATER MUSSELS

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Freshwater mussels provide a variety of ecological services. These include nutrient cycling, biofiltration, and structural habitat. There are over 300 species of freshwater mussels in North America yet nearly all of these are declining. Recent evidence of a virus connected to a mortality event of pheasant shells (*Actinonaias pectorosa*) suggests that disease is likely contributing to this decline along with other environmental factors. Aquaculture efforts to restore freshwater mussel populations are underway in Maryland and having a species-specific histological knowledge base will be critical if disease issues arise. There is already an excellent published histology atlas covering all the organs in three species of freshwater mussels, but none of those are found in Maryland. It is important to document the histology of healthy mussels on a species-by-species basis since there can be differences between species. To this end, the objective of the current study is to use histology to document each organ in 5 of the 17 species of known freshwater mussel species in Maryland (*Utterbackiana implicata* – alewife floater, *Lampsilis cardium* – plain pocketbook, *Elliptio producta* – Atlantic spike, *Alasmidonta varicose* – brook floater, *Elliptio complanate* – eastern elliptio). This will allow for the detection of both emerging and species-specific pathogens in Maryland freshwater mussels.

DIRECT MEASUREMENT AND GENETIC PARAMETER ESTIMATION OF DERMO RESISTANCE TRAITS IN AN EASTERN OYSTER BREEDING POPULATION

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Dermo disease, a chronic condition caused by the protozoan parasite *Perkinsus marinus*, impacts nearly every region where eastern oysters are cultured in the U.S. A recent industry survey ranked Dermo resistance as the most desirable target for genetic improvement; however, phenotype measures that form the basis for selection have been limited to field performance trials with uncontrolled pathogen exposure in space and time. Furthermore, genetic parameters that quantify the capacity for selection of Dermo resistance within a breeding program have not been calculated.

Here results from controlled laboratory disease challenge experiments are reported that enable direct measurement of disease response phenotypes and estimation of genetic parameters for Dermo resistance. Nearly 6000 individual one-year-old pedigreed oysters representing three-year classes (2019, 2020, and 2021) and 109 unique full-sibling families from the Aquaculture Genetics and Breeding Technology Center (ABC) were injected with a consistent concentration of cultured parasite and monitored for survival for 42 days. Parasite load of each oyster was quantified at either the time of death or the end of the experiment. Siblings of the challenged oysters were also evaluated for survival in the field. Survival in response to laboratory challenge was estimated to be moderately heritable (0.14 ± 0.03 on the observed scale, 0.24 ± 0.05 underlying liability scale) but the genetic correlation between challenge survival and survival at a field site with moderate Dermo disease pressure was low. Implications of these findings for incorporating Dermo resistance traits in the ABC selective breeding program will be discussed.

USING THE DRIVER-PRESSURE-STATE-IMPACT-RESPONSE (DPSIR) FRAMEWORK TO SUPPORT SUSTAINABLE AND HEALTHY OYSTER PRODUCTION IN MISSISSIPPI

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The eastern oyster (*Crassostrea virginica*) provides significant cultural, ecological, and economic benefits for coastal Mississippi. Historically, oyster landings in Mississippi have fluctuated due to overfishing, natural and man-made disasters, variability in salinity regimes, and harvest closures due to sewage pollution. In recent history, the fishery has been decimated following Hurricane Katrina, the Deepwater Horizon oil spill, and multiple Bonnet Carré Spillway openings. Restoration and recovery of the oyster resource is a top priority for the state of Mississippi but requires an understanding of the complex interactions between management decisions and factors that affect oyster health, survival, and harvest. The Driver-Pressure-State-Impact-Response (DPSIR) framework is structured to organize the cause-and-effect relationships between human activities and the environment. The DPSIR framework was applied as a conceptual model to illustrate the existing knowledge and challenges to facilitating healthy and sustainable oyster production with economic, ecological, and social co-benefits for the citizens of Mississippi. Major challenges for the Mississippi oyster industry are the effects of freshwater discharges from the Bonnet Carré Spillway and water quality improvements in shellfish growing areas. The Mississippi Based RESTORE Act Center of Excellence (MBRACE) uses the conceptual model to identify knowledge gaps and guide current and future research. MBRACE research focuses on maximizing sustainable oyster production in the Mississippi Sound and minimizing human health risks from oyster consumption. The DPSIR framework allows MBRACE researchers to better communicate scientific findings to state resource managers and policy makers to inform oyster restoration and management decisions.

ASSESSING THE EVOLUTIONARY RESPONSE OF THE EASTERN OYSTER TO EXPOSURE TO COASTAL ACIDIFICATION AND SEWAGE EFFLUENT: A CASE STUDY

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Although coastal organisms experience natural and anthropogenic stressors simultaneously across multiple spatial and temporal scales, the synergistic effects of multiple stressors are largely unknown. In urbanized estuaries, coastal acidification (CA) can be caused by eutrophication (i.e. nutrient loading). CA is strongly associated with a second anthropogenic stressor, sewage effluent (SE). SE can cause acidification locally by increasing nitrogen (N) loads and stimulating algal and microbial production of CO_2. Even treated SE can cause CA because excess N is often removed with microbial treatments, leading to effluent that is low in N but has decreased pH and increased concentrations of CO_2. The physiological effects of CA and SE have been well characterized separately but have never been examined together in early life history stages when organisms are most sensitive to stressors. Additionally, results from many studies have not been examined in a mechanistic framework, such as identifying the genes that provide resistance to multiple stressors. Here, multiple factorial exposures were used on eastern oyster larvae to characterize the effects of CA and SE on larval mortality and use expressed exome capture sequencing to detect which genetic variants lead to resistance and potential adaptation. Preliminary results indicate that CA, SE, and CASE induce clear changes in the allelic composition of larval pools and that the CASE treatment did not represent a composite of the CA and SE treatment. Higher gene ontologies for outlier loci appear to be related to chemical and stress response, supporting the possibility of adaptive resistance to multiple stressors.

WHAT IS ROTARY AND HOW DOES ROTARY WORK FOR SHELLFISH?

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Rotary as an organization is an integral part of 36,000 local communities worldwide. Rotarians for the past 118 years have engaged with their local communities providing "service" and "doing good" wherever there is a recognized need with humanitarian and now environmental projects. The Rotary Foundation has spent more than $24 million on Environmental Projects worldwide since 2014. But how much or little has been spent on shellfish restoration? How you can get involved in shellfish projects to increase efforts 100-fold will be discussed.

WORKSHOP: HOW TO WRITE EFFECTIVE GLOBAL GRANTS FOR FUNDING BY ROTARY INTERNATIONAL

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Rotary is a global network of 1.4 million neighbors, friends, leaders, and problem-solvers from 36,000 local communities and 46,000+ clubs around the world. Rotarians see a world where people unite and take action to create lasting change – across the globe, in local communities and in themselves. Rotary clubs work together to promote peace, fight disease, provide clean water, sanitation, and hygiene, save mothers and children, support education, grow local economies, and protect the environment (https://www.rotary.org/en/about-rotary).

Rotary mission is to provide service to others, promote integrity, and advance world understanding, goodwill, and peace through fellowship of business, professional, and community leaders. Rotary provides service wherever there is a recognized need with humanitarian and now Environmental Projects. The Rotary Foundation has spent more than $24 million on Environmental Projects worldwide since 2014 and would like to increase the amount spent on shellfish restoration projects. This workshop will discuss how to develop projects and write effective global grants for funding by Rotary International (https://my.rotary.org/en/take-action/develop-projects/developing-effective-projects).

OCEAN ACIDIFICATION MAY INCREASE THE BIOLOGICAL IMPACT OF METAL POLLUTION ON COMMERCIAL BIVALVES, A CASE STUDY FROM MINE WASTE DEPOSITS IN ARCTIC NORWAY

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Historically, Norway has used fjords for the disposal of waste including mine-tailings, fine grained waste material produced by mining activity which is often contaminated with metals. 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. Little is known about how metals associated with these mine tailings will interact with climate change and ocean acidification to possibly effect coastal fisheries and aquaculture. Recent studies of commercial bivalve species (*Arctica islandica, Venerupis corrugate*) show that elevated pCO_2 leads to adjustments in coelomic acid-base balance, with increased bicarbonate concentration buffering pH in response to elevated pCO_2; however, this bicarbonate compensation is not observed in bivalves exposed to mine tailings resulting in significant acidosis, elevated metabolic costs, and increased mortality. To further investigate the mechanisms and breakpoints behind these physiological responses. The bivalves, *A. islandica,* and *V. corrugate,* were exposed to sediments collected from historic mine-tailing deposits (Repparfjorden, Norway) for five weeks in combination with five different pH/pCO_2 treatments (pH 7.4 to 8.2). When exposed to mine-tailings the activity of gill enzymes (Na^+/K^+-ATPase) involved in ion-regulation and critical for bicarbonate up-take was reduced. Combined with effects on energetics and electron transport chain activity, and the increased bioavailability of metals under more acidic conditions, metal contamination may further exacerbate the negative effects of climate change. Showing the importance of considering future predicted environmental conditions when understanding and regulating for the possible legacy effects of proposed, present, and historic mining activity.

EVALUATION OF THE 2022-YEAR CLASS EASTERN OYSTERS SELECTED FOR DISEASE RESISTANCE AND FAST GROWTH

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Eastern oyster (*Crassostrea virginica*) aquaculture is a significant and growing industry in the United States. Selective breeding is essential for the sustainable development of eastern oyster aquaculture. Established by Dr. Harold Haskin in 1960, the Rutgers University oyster breeding program has continued breeding eastern oysters for disease/stress resistance and fast growth. Different sublines are produced by mass selection, outcrossed with wild stocks to maintain genetic diversity, and crossed in rotation to maximize diversity in the production line. In June 2022 eleven diploid sublines of various genetic lineages were produced and deployed in four replicate bags on an intertidal flat for evaluation. All groups were sampled (25 per replicate, 100 per group) over 18 months, with the most recent sampling being November 2023. The production line (22N7), a hybrid cross between two selected sublines of Haskin NEH® (19N7 x 19N3), showed significantly lower cumulative mortality, 18.2%, than the wild control (22DW) and Maine outcross (22N6). The pure NEH line (22N5) had a significantly larger mean height, 74.1mm, and whole weight yield, 49.1g, compared to 22DW and 22N6. These results indicate that the NEH® strain continues to have improved growth and survival, and hybrid crossing between selected sublines is an effective way to produce a robust oyster.

AQUACULTURE COMMUNICATIONS RESOURCES AND INITIATIVES PROVIDED BY NOAA NATIONAL SEA GRANT

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For over 50 years, Sea Grant has been a leader in promoting safe, strategic and sustainable aquaculture through research, education and extension. Whether it is studying the scientific and social aspects of aquaculture or providing training and community support, Sea Grant's efforts bring people together around American seafood. Many of these Sea Grant-supported efforts also create resources and opportunities related to communications. This presentation will focus on aquaculture-related communications resources and initiatives that are currently accessible to industry and other public audiences. Specifically, the following will be presented in detail:

Communications Resources

- NOAA Sea Grant Aquaculture Webpage
- NOAA Sea Grant Seafood Resources Webpage
- Social Media
- News Stories Related to Aquaculture

Communications Initiatives

- Sea Grant Program Aquaculture Supplemental Funding
- Aquaculture Collaboratives (current opportunity open for funding Regional Aquaculture Communications/ Aquaculture Literacy Collaboratives)
- National Aquaculture Initiatives Supporting Aquaculture Education and Literacy
- Aquaculture Information Exchange

UPDATE ON LABORATORY CHALLENGES TO *CRASSOSTREA VIRGINICA* FAMILIES AND LINES WITH OsHV-1 MICROVARIANTS

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The potential impact to the shellfish industries of the spread of OsHV-1, particularly the highly virulent OsHV-1 microvariants (µvars), to the US East and Gulf coasts is concerning. Laboratory trials were conducted exposing spat and juveniles of the eastern oyster, *Crassostrea virginica*, to OsHV-1 mvars. Through a bath challenge, spat from 30 eastern oyster families and two popular broodstock lines were exposed to a French µvar. Spat mortalities ranged from 0-50% with a mean mortality of 15.1±2.5%. Juveniles from eight of the families representing a range of mortality in the spat challenges were exposed via injection to the San Diego and French µvars separately. Mortality ranged from 0-86.7% with a mean of 23.3±6.9%. Performance was highly correlated between the spat and juvenile challenges (Pearson R~0.90 for each virus and $p<0.05$). Viral loads (using qPCR as a proxy of infection) were high in families with higher mortality and low in those with no or low mortality. Viral DNA also was detected in tissues of surviving oysters; at high levels in poorer performing families and at very low levels in families demonstrating little or no mortality. Results suggest that although some lines and families are susceptible, there is strong evidence for a high degree of genetically-based tolerance in *C. virginica*. Heritability analyses will be done once qPCR data is available for all families. These results indicate that selective breeding could be important for combatting OsHV-1 should it spread to the East and Gulf coasts of the US.

BEST PRACTICES HELP GROWERS IMPROVE SOCIAL LICENSE

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The East Coast Shellfish Growers has recently revised the 2010 Best Practices for Shellfish Aquaculture. The update was based on dozens of workshops and meetings and has added new sections to address new floating gear technologies and updating sections on storm planning, record keeping, anchoring, site selection fouling control, bird issues, and much more. The lion's share of the Best Practices (BP) address concerns raised by the public and help growers be good neighbors in the commons. BP help growers minimize concerns such as noise, odors, marine debris, and aesthetics while minimizing environmental impacts and maximizing the ecosystem services that shellfish farms provide.

Many BP are simply common-sense ways to improve public relations. Implementing some BP may require a fair amount of effort, but most BP are already being used by smart growers and will help new growers improve productivity and efficiency. The BP manual includes a tool that allows growers to develop farm-specific plans that can be used for employee training, marketing, or permitting.

MANAGEMENT OF BIRD-RELATED PATHOGEN RISK IN SHELLFISH AQUACULTURE

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The National Shellfish Sanitation Program (NSSP) describes the minimum standards for shellfish harvest, handling and distribution. The FDA, working with the Interstate Shellfish Sanitation Conference has devised a uniform set of regulations and guidance to be followed by all of the states designed to ensure that shellfish distributed in the U.S are safe and wholesome. When the Aquaculture Chapter of the NSSP was revised, a mandate was added to require that if aquaculture gear may attract birds or mammals, that operators must provide a written operational plan to describe how to address possible contamination of shellstock and potential adverse impacts to water quality. The 2023 revision of the NSSP contains guidance on how states can address these concerns and the variety of approaches states can consider to minimize health risks to consumers. This presentation will describe some of the measures and regulations that state regulators have adopted to address public health concerns related to bird waste on the East Coast.

ASSESSING THE RISK OF PATHOGEN CONTAMINATION FROM ROOSTING BIRDS ON AQUACULTURE GEAR

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Floating oyster cages provide attractive roosting sites for waterbirds. The abundance of roosting waterbirds often changes seasonally, and this may relate to levels of fecal coliform and *Campylobacter* measured in water and oysters at farms. Weekly land-based surveys were conducted in Rhode Island from Dec 2020 to April 2023 to assess seasonal variation in waterbird distribution and abundance in relation to shellfish aquaculture operations. 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 cages during late summer coincided with when harmful bacteria may proliferate. Based on these findings, samples of seawater, bird feces, and oysters were collected weekly from six floating gear farms in Rhode Island and Massachusetts from August to September 2023. In 2023, when bird abundance was relatively low as compared to previous years, *Campylobacter* was not detected in the oyster meats and sea water. Fecal coliform levels measured were below the action level for water samples (geometric mean < 14 MPN/100mL). Current studies that directly assess the extent to which bird abundance on floating aquaculture gear is related to disease-risk indicators in water, bird feces, and oysters are discussed.

HOST SPECIFICITY OF PREDATORY BACTERIA AGAINST HUMAN PATHOGENIC STRAINS OF *VIBRIO PARAHAEMOLYTICUS*: POTENTIAL INTERVENTION STRATEGIES FOR *VIBRIOS* IN MARKET OYSTERS

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Predatory organisms are nature's way of maintaining bacterial balance in the marine environment. Vibrio predators include bacteriophages and bacteria, like *Halobacteriovorax* (*HBx*) and *Pseudoalteromonas* species. This presentation describes the effectiveness of four *HBx* strains isolated along the Delaware, Alabama, and Hawaiian coasts to infect and kill 23 strains of human pathogenic *V. parahaemolyticus* (*Vp*). The *Vp* consisted of 6 different sequence types and 12 serotypes. Vibrios containing the well-known hemolysins *tdh* and *trh* were also evaluated to determine if either hemolysin could protect *Vp* from *HBx* infection. The ability of *HBx* to reduce *Vp* in market oysters was also evaluated.

Results showed that each of the four *HBx* strains readily killed at least 21 of the 23 *Vp* strains regardless of their sequence type, serotype, hemolysin status, or geographical origin. The Hawaiian and Alabama *HBx* strains together killed all 23 *Vp* strains. The effectiveness of these two *HBx* to reduce *Vp* in market oysters was evaluated over a 3-day period in either control tanks (oysters only) or treatment tanks containing oysters + high-titer *HBx* added on day 1. Daily tests of *Vp* and *HBx* in the oysters revealed unexpected swings in natural *Vp* levels and high numbers of background predatory bacteria, especially *Pseudoalteromonas,* and occasional bacteriophages. Negative control oysters also contained many predators, thus preventing a clear assessment of the effectiveness of *HBx* treatment on *Vp* levels. Research is continuing to characterize some of these newly discovered and naturally occurring *Vp* predators by scanning electron microscopy and DNA sequencing.

MODIFICATIONS TO A SCALLOP DREDGE TWINE TOP TO REDUCE FLATFISH CATCH

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The sea scallop (*Placopecten magellanicus*) dredge fishery has annual catch limits for windowpane flounder (*Scophthalmus aquosus*) and yellowtail flounder (*Limanda ferruginea*) stocks on Georges Bank in the Northwest Atlantic. The fishery has limited access to parts of Georges Bank during a year as well as gear restrictions to mitigate catches of these flatfish and minimize the possibility of exceeding the catch limits. There is a need to further reduce bycatch, as the annual catch limit for windowpane flounder has been exceeded since 2020, and the yellowtail flounder stock is in poor condition. Sea trials were conducted in 2022 and 2023 to test square mesh escape panels and SafteyNet's Pisces LED light system installed in the twine top of a scallop dredge to reduce the catch of these flatfish. In 2022, three Pisces light colors, two flash rates, and two brightness levels were tested with and without a square mesh escape panel. The escape panel was also tested in two locations in the twine top. In 2023, a two-row and a three-row escape panel configurations were tested. Catch data indicated reductions in flatfish catch across all light colors, flash rates, and brightness levels. The location of the square mesh panel was also determined to be important, with greater reductions in catch observed when the panel was lower in the twine top. Less flatfish escaped the twine top with a three-row escape panel compared to the two-row panel. No reductions in sea scallop catch were observed for any experimental gear configuration.

BLUE CRAB (*CALLINECTES SAPIDUS*) POPULATION CHARACTERISTICS AND *CALLINECTES SAPIDUS REOVIRUS* 1 (CSRV1) IDENTIFICATION

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The blue crab (*Callinectes sapidus*) population in the Delaware Inland Bays, particularly Rehoboth Bay, holds significant economic and ecological importance. The blue crab is a key contributor to the seafood industry in Maryland and Delaware. This ongoing study focuses on areas associated with oyster aquaculture and pilot oyster reefs. The primary objective is to evaluate the blue crab population and identify a potential pathogenic virus affecting them. The study specifically targets *Callinectes sapidus reovirus* 1 (CsRV1), analyzed in the lab using PCR (polymerase chain reaction) and qPCR (Quantitative polymerase chain reaction) methods. Notably, no prior research has comprehensively examined both the *C. sapidus* population and CsRV1 within the Delaware Inland Bays. CsRV1 primarily affects the gills, impacting the respiratory system, and is associated with elevated mortality rates in aquaculture settings. In natural habitats, infected crabs exhibit symptoms such as lethargy, behavioral changes, and respiratory distress. Study sites were selected based on distinct characteristics, including areas with oyster aquaculture, artificial reefs, and control sites. The research involved deploying 18 traps across six sites, each equipped with two large commercial cages and one small lobster pot. During the summer and fall of 2022, the research team collected data from over 1,000 blue crabs. Findings indicate stable populations of adult females at natural control sites throughout the season, with an increase in adult male abundance during the cooler months at aquaculture and reef sites. In 2023, CsRV1 was identified in the lab using PCR and qPCR techniques.

MULTIPLE OMICS TO DISENTANGLE NEW FACETS OF THE ENIGMATIC FAMILY OF MOLLUSC HERPESVIRUSES

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The family Malacoherpesviridae is currently represented by only two viruses infecting molluscs, Ostreid herpesvirus-1 (OsHV-1) and Haliotid herpesvirus-1 (HaHV-1), both causing detrimental infections in aquaculture species. The origin of malacoherpesviruses remains obscure as well as the molecular details of their infection cycles due to a limited functional similarity to the replication of mammalian herpesviruses. Innovative research approaches can, therefore, contribute to untangle new facets of this enigmatic viral family.

To extend the knowledge on malacoherpesvirus diversity, searches were performed in genomic, transcriptomic and metagenomic datasets, including from the Tara Oceans expedition, and resulted in four novel malacoherpesvirus-like genomes, with gastropods and bivalves as the most probable hosts. This reveals that malacoherpes-like viruses are circulating in the aquatic environment, representing possible emerging viruses under changing environmental conditions. Long-read sequencing and proteomics of *Anadara broughtonii* infected with OsHV-1 was applied to gain insights into the biology of malacoherpesviruses. The annotation of the viral genome and its dynamic modulation over infection revealed preferential transcription and independent translation of the capsid scaffold protein as an isoform of the OsHV-1 capsid maturation protease, a feature reported for vertebrate herpesviruses and resembling an important process during viral replication. The integration of long- and short-read transcriptomics was used to determine the extension of RNA editing during infection, a key process able to modulate antiviral processes, revealing a transcription-based viral counter defence mechanism. In conclusion, the integration of different 'omics can provide new instruments for a better understanding of bivalve antiviral immunity and interactions with pathogens.

COMPARING RIBBED MUSSEL SETTLEMENT IN NATURAL FRINGING MARSHES VERSUS LIVING SHORELINES IN THE CHESAPEAKE BAY

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Ribbed mussels (*Geukensia demissa*) are important biotic components of salt marsh ecosystems along the U.S. Atlantic Coast. The use of nature-based approaches to shoreline protection, living shorelines, instead of traditional shoreline hardening, is being encouraged to help conserve coastal ecosystems, such as salt marshes. Living shorelines often combine engineered features with natural elements, like native wetland plants, to stabilize shorelines and restore marsh ecosystems. Ribbed mussels increase resilience, productivity, and stability of a marsh but are rarely incorporated directly in living shorelines; rather, mussels are expected to recruit naturally to these constructed marshes; however, created marshes in the Chesapeake Bay lag behind their natural marsh counterparts in terms of ribbed mussel populations. Factors affecting juvenile settlement in living shorelines are understudied but may include reduced settlement cues and interrupted access due to hardened shoreline structures. Quantifying juvenile settlement in natural and constructed marshes may aid in understanding how recruitment is affected by restoration design, such as rock sills and clean sand fill. Collection devices deployed in four natural marsh and living shoreline site pairs in the southern Chesapeake Bay were compared to determine differential settlement of post-larval mussels. Preliminary data suggest that mussels are settling in living shoreline marshes in lower numbers as compared to natural marshes. Understanding factors affecting juvenile recruitment and survival will improve restoration design and create more resilient living shorelines by supporting a robust population of ribbed mussels.

THE NEW JERSEY SHELLFISH AQUACULTURE EXCHANGE—A CROSS-CUTTING APPROACH TO HABITAT RESTORATION AND RESILIENCY

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The COVID-19 pandemic had an unprecedented impact on economies around the world and severely disrupted food supply chains. Relying heavily on sales to restaurants, New Jersey oyster farmers were particularly hard hit, reporting lost sales exceeding 90% in the second quarter of 2020. Farmers were forced to pivot to direct sale opportunities. In addition to the direct loss of revenues, the lost sales led to crop management challenges as oysters destined for spring markets remained on farms, out growing premium market size, taking up limited farm space and precluding gear cycling. While no longer suitable for prime markets, the large oysters were ideal for habitat restoration purposes. A program was developed to purchase these unsold oysters for habitat restoration. Seventy-six thousand farm raised oysters were purchased and planted on four New Jersey oyster enhancement areas in fall 2020 and a model shellfish exchange program fostering the direct planting of farm-raised oysters was developed. The model shellfish exchange program paved the way for subsequent restoration efforts employing farm-raised oysters and provided ecological and economic uplift. A secondary project objective was the development of a directory of New Jersey shellfish farms designed to connect consumers to New Jersey shellfish farms and their products and educate them about the methods and benefits of shellfish aquaculture. Both efforts supported market diversification of shellfish farm businesses, not only better enabling farms to weather the COVID-19 “storm”, but also creating a path supporting long-term resilience and sustainability of the New Jersey shellfish aquaculture sector.

INVESTIGATING THE LEVELS OF *PERKINSUS MARINUS* IN HATCHERY SEED FROM THE US EAST COAST

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Limited sources and supply of shellfish seed along the East Coast restricts growth of the aquaculture industry. It increases requests for interstate transfers, which come with uncertainties regarding pathogens and risks. Few laboratories conduct shellfish pathology, which can delay an already lengthy process of seed certification transfers. During this time, rapidly growing seed can double in size and may have been exposed to additional pathogens circulating in the waters in which they are held. The situation highlights the growing need for biosecure aquaculture products that can facilitate the decision-making process for regulators while providing producers a mechanism to promote the quality of their product and bolster buyers' confidence in such products.

Larvae and seed are the least likely stages to be infected by common pathogens for eastern oysters (*Crassostrea virginica*) and northern quahogs (= hard clams) (*Mercenaria mercenaria*). In this study, oyster and clam seed certification data were analyzed for the most ubiquitous pathogen of concern, *Perkinsus marinus* (Dermo disease), to investigate the biosafety of hatchery bivalve products. Samples were collected primarily in the Delaware Bay and Chesapeake Bay areas spanning 1998 to 2023. *Perkinsus* was found in only 18 of 102 samples (~17.6%), and no infection or *Perkinsus* cells were found in animals reared in treated water nor in animals smaller than 5mm. The highest prevalence (6.7%) occurred in a group with a size range of 6.0 to 15.7mm maintained in untreated water. These results indicate that small animals, reared in sterilized water, do not pose a biosecurity risk during transfers.

A COMPARISON OF SHELLFISH IMPORTATION REGULATIONS ACROSS EAST AND GULF COAST STATES

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Interstate shellfish seed transfers are crucial for industry growth as hatcheries are unevenly distributed leaving many states without local sources of shellfish seed for aquaculture. To protect farm production and natural resources, each state has developed its own set importation regulations. A tabulation and comparison of regulations will be provided to elicit a discussion on what makes sense based on the best available science. A goal is to determine whether a uniform set of standards makes sense and can be developed to facilitate interstate commerce while maximizing biosecurity with respect to bivalve mollusc pathogens.

USING UNCREWED AERIAL SYSTEMS TO MAP INTERTIDAL EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) REEFS TO INFORM MANAGEMENT AND RESTORATION PRACTICES IN THE SOUTHEASTERN UNITED STATES

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Intertidal eastern oyster (*Crassostrea virginica*) reefs support critical ecosystem services in the southeastern United States, including habitat provisioning, shoreline protection, and improved water quality. Recent estimates, however, suggest that over the course of the last century 85% of oyster reefs have been lost globally due to habitat alteration, disease, and increased harvest pressure. In 2022, researchers and resource managers from National Estuarine Research Reserves (NERR) from North Carolina to Florida embarked on a NOAA NERRS Science Collaborative-funded project to develop standardized methods to accurately quantify changes in intertidal oyster reefs over time. Ultimately, the project aims to evaluate uncrewed aerial systems (UAS) as monitoring tool capable of remotely assessing the structural and demographic conditions of intertidal oyster reefs.

This presentation will focus on recent field efforts within the Ashepoo-Combahee-Edisto (ACE) Basin NERR of South Carolina that applied machine learning to classify intertidal oyster reefs using UAS-derived spectral and elevation data. Five UAS datasets were collected across three sites during the summer of 2023. The classification process used two machine learning algorithms available in the ESRI ArcGIS Pro Spatial Analyst Extension to detect and differentiate intertidal oyster reefs from other surrounding habitat features. Algorithm training refinements were incorporated into the classification workflow to optimize accuracy across multiple iterations, resulting in accuracy values as high as 86%. As performance improvements continue to be applied, confidence is growing in the anticipated benefits of using UAS-derived remote sensing data to enhance the technical capacity of end-users conducting intertidal oyster reef change assessments.

UPTAKE, DISTRIBUTION, AND DEPURATION OF PSP-INDUCING PHYCOTOXINS IN ARCTIC SURFCLAMS *MACTROMERIS POLYNYMA* (STIMPSON 1860)

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The Arctic surfclam, *Mactromeris polynyma* (Stimpson 1860), is a bivalve of increasing commercial interest in the United States. The surfclams *M. polynyma* and related surfclam species accumulate paralytic shellfish toxins (PST) when exposed to toxin-producing dinoflagellates such as *Alexandrium catenella*. The specific patterns of uptake, distribution, and depuration of PST have not been documented for this species. An exposure experiment was conducted in which juvenile *M. polynyma* (15-25 mm SL) were challenged with a bloom concentration (100,000 cells* liter^{-1}) of *A. catenella* in a laboratory-controlled environment for 4 days, then allowed to depurate in ambient seawater for 17 days (21 days total). Tissues were dissected and categorized as either digestive or other tissues. The PST receptor binding assay measured PST levels >100 times the FDA regulatory limit of 80µg saxitoxin equivalents* 100g tissue^{-1} in clams exposed to *A. catenella*. The PST levels continued to rise after the conclusion of the 4-day exposure period, reaching a peak at day 7 in all tissues. The surfclam tissues depurated 46% to 75% of the maximum PST burden by the end of the depuration period, but levels remained in excess of the regulatory limit. Approximately 80% of the PST was localized in the digestive tissues for the duration of the study. The Arctic surfclam has the capacity to accumulate PST in excess of the FDA regulatory limit, partially depurate the PST, and localize a majority of the PST in digestive tissue.

ADOPTING PRINCIPLES OF FOOD JUSTICE FOR EQUITABLE OYSTER AQUACULTURE INDUSTRY DEVELOPMENT

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The food justice movement is growing, amplifying the need for equity and social justice within the food system. To date, the movement has predominantly focused on terrestrial food systems, excluding ocean food systems. At the same time, the Atlantic coastal region is experiencing an expansion of non-industrial aquaculture production, especially oysters, benefitting coastal environments and communities. While Black oystermen played critical roles in developing the wild catch oyster industry, which drove economic development of Eastern coastal communities, barriers to advancement and wealth accumulation prevented many Black oystermen from experiencing the full array of compensation, benefits, and legacy that the booming oyster industry often provided to white oystermen. Now, there is a significant lack of racial diversity at the business ownership level in oyster aquaculture in Maryland, Delaware, and New Jersey. This presentation will discuss research that identified barriers to advancement that Black oystermen faced in Maryland, Delaware, and New Jersey, impacts on the aquaculture industry, and opportunities for industry managers and stakeholders to promote socioeconomic diversity by integrating the principles of food justice into management plans.

GROWTH AND SURVIVAL OF TRANSPLANTED SOFTSHELL CLAMS (*MYA ARENARIA*) DURING A WINTER GROW-OUT PERIOD IN THE YORK RIVER, VIRGINIA

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The softshell clam (*Mya arenaria*) is an infaunal, filter-feeding bivalve commonly found in estuarine habitats throughout its native range on the US East Coast. For the past few decades, commercial-scale aquaculture and harvest of the species has been limited to 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 across the salinity gradient of a Virginia (VA) estuary and whether clams planted in the fall could exceed market size of 50 mm before elevated summer temperatures threatened their survival. In November 2022, 24 experimental plots each with four predator-exclusion cages were deployed across three areas with distinct salinity regimes in the York River, VA; softshell clams (n = 4,128, mean initial shell length = 13.3 mm ± 0.03 SE) were planted at a density of 650 clams per m^2. One cage per plot was harvested monthly from April to July 2023 to assess clam survival and growth across the winter-to-summer grow-out period. Planted clams grew significantly over the winter and spring before experiencing a mass mortality event as temperatures reached a critical threshold for the species (28°C). Clams exhibited distinct survival and growth patterns at each of the three river locations, likely related to compounding effect of multiple stressors (e.g. temperature, salinity, and competition). Results suggest conditions in Virginia support softshell clam aquaculture as long as such ecological stressors are considered and mitigated.

TRANSGRESSIVE GENE EXPRESSION AND EXPRESSION PLASTICITY UNDER THERMAL STRESS IN HYBRID *MYTILUS* MUSSELS

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Interspecific hybridization can lead to myriad outcomes, including transgressive phenotypes in which the hybrids are more fit than either parent species. Such hybrids may display important traits in the context of climate change, able to respond to novel environmental conditions not previously experienced by the parent populations. While this has been evaluated in an agricultural context, the role of transgressive hybrids under changing conditions in the wild remains largely unexplored; this is especially true regarding transgressive gene expression. The effect of hybridization on temperature-induced changes in gene expression (expression plasticity) was investigated using the *M. edulis* species complex as a model system. Transcriptomic profiles for the cool-temperate *M. edulis*, the warm-temperate *M. galloprovincialis*, and their hybrids were compared after a two-week, sub-lethal thermal challenge. Hybrid expression plasticity was most often like one parent or the other; however, a large fraction of genes showed transgressive expression plasticity (i.e. the change in gene expression was either greater or lesser than both parents), while very few were intermediately plastic in hybrids. Despite their close phylogenetic relationship, there was limited overlap in the differentially expressed genes responding to temperature indicating interspecific differences in the responses to high temperature in which responses from hybrids are distinct from both parents. Differentially expressed long non-coding RNA (lncRNA) were also identified, suggesting they may contribute to species-specific differences in thermal tolerance. This work suggests transgressive hybrids may play an important role in population persistence under future warming conditions.

PHENOLOGY OF *PERKINSUS MARINUS* AND CLIMATE CHANGE

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Dermo (*Perkinsus marinus*) is a disease that causes mortalities in the eastern oyster, *Crassostrea virginica*. Its current range extends from the Gulf of Mexico to Massachusetts. It became endemic in the Delaware Bay in the 1990s as temperatures warmed and the range of the disease expanded. The disease exhibits a positive correlation with the temperature and salinity of its environment. This results in a seasonal cycle that varies in strength throughout its range, from a small dip in prevalence in the colder months on the gulf to a period of complete dormancy in the Delaware Bay. The latitudinal gradient in temperature along the Atlantic and Gulf coasts is not correlated with annual salinity levels or patterns in any given location, complicating the relationship of these two environmental factors to dermo mortalities. This project is an investigation of changes over time in seasonal dermo patterns in the Delaware Bay and its relationship to the latitudinal gradient of dermo intensity along the Atlantic coast and the Gulf of Mexico.

ASSESSING THE ABUNDANCE OF *VIBRIO PARAHAEMOLYTICUS* AND *V. VULNIFICUS* IN CULTURED OYSTERS ASSOCIATED WITH MACROALGAE FROM RHODE ISLAND

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The pathogen *Vibrio* spp. are gram-negative, halophilic bacteria abundant in the marine environment. Two species of *Vibrio*: *V. parahaemolyticus* and *V. vulnificus*, are pathogenic to humans who consume raw or under-cooked shellfish. With increasing water temperatures, the concentration of *Vibrio* sp. bacteria increases in estuarine environments and can accumulate in the tissues of eastern oysters, *Crassostrea virginica,* as part of their filter feeding process. Macroalgae is commonly found near oyster aquaculture sites, frequently fouling gear. Previous studies have suggested that macroalgae may be a reservoir for pathogenic *Vibrio* spp.

To understand the relationship between oysters, macroalgae, and *Vibrio* spp. in Rhode Island, oysters, water, sediment and macroalgae samples were collected in triplicate from two aquaculture sites. Samples were collected twice monthly from June 2022 to October 2022. Levels of *Vibrio* spp. were enumerated using the FDA-MPN method for oysters and colony forming units (CFU) from two *Vibrio*-selective media for seven genera of macroalgae. Quantitative PCR was used to confirm levels of total *V. vulnificus* along with total and pathogenic (*tdh*$^+$ and *trh*$^+$) *V. parahaemolyticus.* In oyster tissues, *V. parahaemolyticus* was generally found at higher concentrations than *V. vulnificus* from both sites with peaks in late August/early September. A similar trend was noted for pathogenic *Vibrio* colonizing macroalgae. Of the seven macroalgal genera, *Fucus* and *Ulva* had the highest concentrations of *V. parahaemolyticus* and *V. vulnificus*, respectively. Further relationships of *Vibrio* spp. will be explored between oysters, water, sediment and macroalgae samples.

INCREASED MACROFAUNAL SECONDARY PRODUCTION WITH OYSTER ARTIFICIAL SUBSTRATES IN THE YORK RIVER, VIRGINIA

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Recently, major restoration efforts in the Chesapeake Bay have focused on the eastern oyster (*Crassostrea virginica*), but studies examining the effects of oyster reefs on the benthic infaunal communities the reefs replace is lacking. Limited availability of natural oyster shell for restoration has led to widespread use of artificial oyster substrates for restoration. The goal of this experiment was to determine the effects of five artificial oyster reef types (granite stone, oyster castle, concrete diamond, concrete c-dome, and concrete x-reef) and natural oyster shell on macrofaunal community metrics (density, diversity, biomass, and secondary productivity) compared to bare sand using a before-after, control-impact (BACI) approach. Two control and three impact sites in the York River, Virginia, were surveyed to examine the benthic community before and after the installation of artificial oyster reefs in subtidal areas. Two replicates of each of six reef types were deployed in a randomized block design at the three experimental sites. One-year post-deployment, all reef sites performed better along every community metric than bare-sediment control sites. Specifically, all reef structures had successful macrofaunal recruitment, biomass, and productivity. Granite reefs had highest densities and biomasses, granite and shell reefs had highest productivity, and diamond reefs had significantly lower densities and biomasses than all other reefs. Macrofaunal communities were dominated by amphipods, xanthid crabs, and polychaetes (in addition to oysters). Understanding the effects of artificial oyster reefs on benthic communities is crucial to promote long-term ecological success of restoration efforts.

SEEING THE LIGHT, TASTING THE OCEAN: HOW BIVALVES SENSE THEIR ENVIRONMENT

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Many marine organisms have a biphasic life cycle that transitions between a swimming larva and a more sedentary adult form. At the end of the first phase, larvae must identify suitable sites to settle and undergo a dramatic morphological change. Environmental factors, including photic and chemical cues, appear to influence settlement and trigger metamorphosis, but in adults, a completely new sensory system is used to detect cues necessary for survival and reproduction. What sensory receptors are involved in these two phases of life are largely unknown. The protein receptor, opsin, which belongs to large superfamily of transmembrane receptors that detects environmental stimuli, hormones, and neurotransmitters was examined. While opsins are well-known for light-sensing, including vision, a growing number of studies demonstrate light-independent functions, such as taste. Opsin expression in Pteriomorphia, a large, diverse clade of marine bivalves, that include commercially important species, such as oysters, mussels, and scallops, was examined. Results from opsin expression studies show: 1) more opsins and opsin types are expressed in larvae than adults; 2) opsin evolution is dynamic and lineage-level gene expansions have resulted in species having very different opsin repertoires; and 3) opsin expression patterns are more similar between closely related species and highly divergent across deeper evolutionary distances. The next steps to test light-independent modalities of opsin through bioinformatic methods and protein expression studies will be discussed. Linking these data to species life history can help to understand the biological relevance of the opsin receptors.

OYSTER INSURANCE OPTIONS FROM USDA RISK MANAGEMENT AGENCY

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The United States Department of Agriculture (USDA) Risk Management Agency (RMA), created in 1996, serves agricultural producers of America through effective, market-based risk management tools to strengthen the economic stability of agricultural producers and rural communities. The RMA is committed to increasing the availability and effectiveness of Federal crop insurance as a risk management tool. Beginning with the 2024 crop year, the RMA began offering a pilot Shellfish Crop Insurance Program for oysters. The Program is available in 28 counties across 12 states. This session will include a presentation on the role of the USDA RMA, the current Shellfish Crop Insurance Program, and possible future enhancements to the Program.

A SNAPSHOT OF NOAA RESOURCES FOR SEAFOOD COMMUNICATIONS AND ENGAGEMENT

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From the sustainability of products and industry processes, to food safety and security, the aquaculture sector is faced with many challenges in communicating complex topics to the communities they serve. Topics that require expertise from a variety of disciplines for more effective communication. One way that NOAA supports efforts to enhance aquaculture communications is through the National Seafood Strategy, released in August of 2023. The strategy underscores the strong commitment of NOAA to seafood sector resilience, and the growing importance of seafood—including aquaculture products—in meeting global needs.

New methods and innovative approaches for aquaculture communications are increasingly highlighting the value of connecting across sectors to co-develop aquaculture communication efforts. This presentation will provide a tour of National Seafood Strategy-supported communications and engagement resources that are increasing public awareness of the availability, sustainability, and nutritional value of U.S. aquaculture products. Join this session to learn more about (1) resources that are currently available to the shellfish industry, and (2) efforts that are seeking input from industry in their development.

WORKSHOP: HOW TO USE SOCIAL MEDIA TO COMMUNICATE YOUR SCIENCE TO THE PUBLIC AND WHY YOU SHOULD

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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.

DISTRIBUTION OF OYSTER SETTLEMENT ON NOVEL REEFENSE MODULES AND IMPLICATIONS FOR ARTIFICIAL REEF COLONIZATION

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This study supported a Defense Advanced Research Projects Agency (DARPA) Reefense project aimed at developing reefs to support coastal protection. It is part of a collaborative effort to protect both civilian and Department of Defense infrastructure against sea level rise and climate change impacts by designing oyster reef breakwaters using novel concretes and unique modular units. Experiments were conducted to test how eastern oyster (*Crassostrea virginica*) larvae settled onto the modular units under flow. Three different arrays of 1/10th scale units were tested in an annular flume along with an array of solid, truncated cones that served as the control. Replicate trials (n=4) contained one of each array spaced evenly around the flume and were run for five days once larvae were added. Oyster settlement on each module was mapped and quantified. Reef module arrays had higher overall oyster densities than the solid controls. Oyster distributions varied among array configuration with higher relative densities on the downward slopes or back sides of the arrays relative to flow. Computational Fluid Dynamic models are under development that may inform the interpretation of oyster settlement patterns. Resulting data could improve artificial reef designs to maximize oyster colonization or aid in the prediction of highest recruitment and predator protection zones on newly-installed reefs.

ALGAL TOXINS IN CULTURED OYSTERS ACROSS DIVERSE COASTAL SITES

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Intensive off-bottom oyster aquaculture has expanded throughout estuaries across much of the world. Expansion into new estuary margins, particularly areas that have not historically supported extensive wild harvest fisheries, opens questions about human exposure to naturally occurring toxins and toxicants from oyster consumption. Algal toxins such as microcystins, produced by predominantly freshwater cyanobacteria, and domoic acid, produced by the marine diatom *Pseudo-nitzchia*, have received considerable attention, particularly in shellfish. Here, a field survey of microcystins and domoic acid in farmed oysters sampled across diverse coastal sites in North Carolina was conducted. Monthly sampling showed the consistent presence of microcystins, even in high salinity estuary margins, particularly in sites downstream of larger rivers. Domoic acid was more consistently found in more marine influenced sites, particularly in the late fall and winter. These results highlight the spatiotemporal variability in human exposure to algal toxins from oyster consumption and underscore the potential for local to regional management of human health risks.

SUMMER MORTALITY IN 2N AND 3N VIRGINIA- AND NORTH CAROLINA-DERIVED OYSTER LINES

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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 described simply as summer or triploid mortality. To investigate pathology associated with these events, as well as causal links with ploidy, 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 farms across North Carolina in the summer 2022, two of the North Carolina sites experienced near complete mortality (>90%) with another experiencing more moderate mortality (>50%). Ploidy was not associated with mortality, but the North Carolina sites universally saw the diploid and triploid North Carolina lines perform best. The mortality events 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 like that observed through summer mortality events in past years, highlighted by persistent sloughing of absorptive cells within digestive tubules preceding mortality. These results suggest that oyster aquaculture in coastal sounds, which has seen recent expansion, requires specific attention in aquaculture breeding programs. The results here will therefore be discussed in the context of existing oyster hatchery and breeding programs and regional aquaculture industry growth.

COMPARISON OF THE NEUROTOXIC ACTIONS OF 6-HYDROXYDOPAMINE AND MANGANESE ON GILL LATERAL CELL DOPAMINE D2R RECEPTORS OF *CRASSOSTREA VIRGINICA*

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Parkinson's Disease (PD) and Manganism are human neurodegenerative diseases with similar symptoms but different neurophysiological causes. PD degenerates dopamine neurons in the substantia nigra. Manganism, caused by elevated manganese levels in the brain, does not degenerate dopamine neurons, but rather impairs postsynaptic signal transduction (PST). Neuronal degradation can cause denervation supersensitivity at the innervated cells. PST impairment causes decreased response to stimulation. 6-Hydroxydopamine, a neurotoxin selectively destroying dopamine neurons, induces PD in animal models. In *Crassostrea virginica*, 6-hydroxydopamine and manganese reduce dopamine neurons ability to slow down gill lateral cell (GLC) cilia beating. The present study contrasts neurotoxic actions of 6-hydroxydopamine vs manganese on GLC dopamine D2R receptors using immunohistofluorescence. To test the hypothesis that animals treated with 6-hydroxydopamine will have increased D2R fluorescence intensity, while manganese will decrease fluorescence intensity, animals were treated 5 days with 500 µg of 6-hydroxydopamine or manganese, then gills were processed for immunohistofluorescence with D2R/FITC conjugated antibodies. Photomicrographs were taken and fluorescence intensity measured using ImageJ from NIH. 6-Hydroxydopamine increased D2R fluorescence by 40%, while manganese decreased it by 35%, compared to the controls. These results are consistent with physiological data observed measuring GLC cilia beating rates in similar experiments. The study shows the two neurotoxins have different mechanisms of action. This can be helpful in differentiating the cause and designing the appropriate potential therapeutic treatments for these neurological disorders. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

FEASIBILITY OF USING SHELLFISH AQUACULTURE FOR WATER QUALITY IMPROVEMENT INITIATIVES IN FLORIDA

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Nitrogen (N) pollution threatens coastal ecosystems health, and excess N can lead to eutrophication and harmful algal blooms. Because shellfish remove N through assimilation and enhanced denitrification, there is interest in using shellfish aquaculture and restoration as a nutrient best management practice; however, data from Florida, where many estuaries suffer from N pollution, are noticeably absent. Florida recently approved the creation of restoration leases, where shellfish can be planted exclusively for water quality restoration. If incentives are reasonable enough to compensate shellfish farmers to produce additional products for restoration, this development in state rule could pave the way for a secondary "restoration market" and increase profitability for the shellfish industry. In addition, if existing commercial production of shellfish results in N reduction, there could be a mechanism to pay or otherwise incentivize farmers for environmental benefits. To assess the feasibility of such a program, N removal measurements at shellfish farms were combined with results from a survey of local water treatment facilities to quantify the amount and economic value of shellfish-enhanced N removal services. A survey of shellfish producers was used to gauge interest in such a program. If scientifically, legally, and economically feasible, this alternate source of revenue for farmed shellfish will contribute to ecosystem restoration, industry stability, and workforce development. This project represents a critical step in moving forward with a payment for ecosystem services plan in Florida, which would provide an alternate revenue stream and encourage the growth of this important industry.

IDENTIFICATION OF NEW *VIBRIO CAMPBELLII* STRAINS HARBORING THE *p*VA1 PLASMID ISOLATED FROM *PENAEUS VANNAMEI* POST-LARVAE AFFECTED BY OUTBREAKS OF ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) IN MEXICO

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Acute hepatopancreatic necrosis disease (AHPND) continues to cause significant losses in Mexican shrimp farms, with no scientific reports on mortality in commercial hatcheries available. In this study, clinical symptoms, histopathological anomalies, bacteriological analyses, and the identification of isolates through whole-genome sequencing in three natural AHPND outbreaks affecting *Penaeus vannamei* post-larvae from local hatcheries were investigated. Within three to four days of acclimation, post-larvae exhibited mortality alongside clinical signs such as empty digestive tracts, whitened hepatopancreas, anorexia, and lethargy. Presumptive diagnoses of AHPND were established using histopathological analysis and the PCR AP4 method to detect pirAB genes after sample enrichment. Higher *Vibrio*-like densities ($p = 0.045$) and green colonies ($p = 0.021$) were observed in the hepatopancreas of affected post-larvae in outbreaks 1 and 2 compared to seemingly healthy specimens. Additionally, 29 isolates from the hepatopancreas and stomachs of shrimp were sequenced, both with and without clinical AHPND signs, identifying two new *Vibrio* species closely related to the Harveyi and Orientalis clades. *Vibrio campbellii* was the predominant species, followed by *V. parahaemolyticus*. Six *V. campbellii* genomes carried *p*VA1-like plasmids harboring pirAB genes responsible for AHPND. The *p*VA1 plasmid exhibited Tn3 transposon-like elements, similar to the *V. campbellii* strain from Ecuador but absent in the Chinese strain, suggesting horizontal plasmid transfer between coexisting *Vibrio* species within a specific geographic region. This study represents the first report of *V. campbellii* strains harboring a *p*VA1-like plasmid causing AHPND in post-larvae from Mexican commercial hatcheries, underscoring the importance of active genomic disease surveillance.

PROJECTED RANGE SHIFT OF THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA*, FROM CLIMATE-INDUCED BENTHIC WARMING: FORECASTING FISHERY INFLUENCE IN THE MID-ATLANTIC BIGHT THROUGHOUT THE 21ST CENTURY

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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 Bight (MAB) that brings in roughly $30 million in revenue per year. Rapid climate change is expected to continue modifying the geographical range distribution of Atlantic surfclam populations, with consequences for the surfclam fishery. This study projected fishery-based indicators from the years 2020-2095 related to simulated biomass distributions of the Atlantic surfclam, using a Spatially Explicit, agent-based Fisheries and Economics Simulator (SEFES). Simulations generally showed a positive trend in Atlantic surfclam biomass throughout the next three-quarters of the century as distributions continued offshore and northward movement along the continental shelf. A general decrease in fishing mortality is projected given present quota caps throughout the MAB, with a simultaneous increase in catch and LPUE (landings per unit effort), signaling future potential growth in the surfclam fishery. Regionally, forecasts show biomass expanding into deeper waters particularly off New Jersey, Long Island, and southern New England starting in the early 2050s, potentially occupying offshore regions designated for offshore wind energy development. Conversely, Georges Bank and Delmarva populations gradually declined over the simulation. Trends in time spent fishing, catch, and LPUE were forecast to parallel those of biomass in each region. These results will inform industries that rely on this fishery and other competing coastal resources and provide a basis for development of anticipatory management for the socio-ecological and economic impacts that may result from future changes in range distribution.

A LONG AND WINDING ROAD: 20 YEARS INTO HARD CLAM RESTORATION IN CENTRAL GREAT SOUTH BAY, NEW YORK

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This past year marked the 20th anniversary of the acquisition by The Nature Conservancy of 13,425 acres of privately-owned, bay bottom, formerly held by the Bluepoint Oyster Company in central Great South Bay, NY. Before this acquisition, the area was intensively managed for shellfish production and endured decades of extensive mechanical harvest. The estuary also suffers from land-derived pollution and coastal habitat conversion among other stressors.

Following the acquisition, an ecosystem-based restoration approach was enacted following a multi-pronged, partner-driven process that focused on rebuilding the once-renowned northern quahog (= hard clam) (*Mercenaria. mercenaria*) population in the Bay. Using an adaptive management approach, guided by consistent monitoring, this work focused on rebuilding the population's reproductive potential, identifying population bottlenecks, implementing more sustainable harvest management, and identifying and addressing the sources of eutrophication.

Over the past two decades, there has been a sporadic but gentle increase in the abundance of wild-born hard clams as well as an increase in macrofauna diversity and abundance. This increased diversity is helped in part by a steady increase in Atlantic razor clams (*Ensis leei*) and a very robust population of stout razor clams (*Tagelus plebeius*), first observed in the most recent survey. These observations raise the question of whether the cessation of disturbance from intensive mechanical shellfish harvesting has created enabling conditions for a transition in benthic community structure. These findings highlight the importance of long-term monitoring efforts and the challenge of defining restoration success within timescales of years as opposed to decades.

EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, POPULATION GENOMICS IN A WELL-MIXED ESTUARINE SYSTEM (GREAT BAY ESTUARY, NEW HAMPSHIRE, USA)

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Eastern oysters, *Crassostrea virginica*, are economically and environmentally important organisms for the habitats in which they reside, including Great Bay Estuary (GBE), New Hampshire, USA, where they aid in nutrient cycling, reef habitat, and shoreline protection. Native oyster populations in GBE are on the decline and restoration efforts have been implemented to restore dying reefs through planting of large, MSX-tolerant aquacultured oysters with the goal of increasing larval output. The extent of any existing population structure in GBE and the movement throughout the estuary of oyster larvae of native and aquaculture strains is unknown. This study compared population genetic characteristics of oysters at three native reefs, two farms, a restoration site, and an intertidal native population to examine genetic connectivity and estimate effective population sizes. Population structure characteristics will help to determine if eastern oysters in GBE follow a classic metapopulation structure with source-sink populations, data that are essential to inform the current restoration approach.

MULTISTRESSOR LABORATORY EXPERIMENTS WITH THE ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*): OCEAN WARMING AND ACIDIFICATION

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The Atlantic surfclam (*Spisula solidissima*) supports a large commercial fishery in the mid-Atlantic region of the United States, where ocean conditions are subject to the effects of climate change. To examine how changing ocean conditions may impact surfclam growth and survival, laboratory experiments were used to observe surfclam performance at ambient and manipulated levels of temperature and carbonate chemistry (reflective of ocean warming and ocean acidification, respectively). Two laboratory experiments were conducted, both using flow-through unfiltered seawater with natural fluctuations in water quality. In the first experiment, surfclams were exposed to one of three experimental conditions (ambient, medium, or low pH) for 6 weeks, and physiological measurements were taken after 24 hours, 2 weeks, and 6 weeks. Results indicated that after 2 weeks, decreasing pH levels resulted in lower feeding rates; however, after 6 weeks, physiological rates were lowered for clams in all treatments, hypothesized to be the result of naturally increasing temperatures over the course of the experiment (>25°C). To further examine the interactive effects of pH and temperature, a second experiment was conducted where clams were exposed to one of 9 treatments, with three levels of pH and temperature in a fully crossed design. After 6 weeks, growth, feeding physiology, shell strength, and gene expression of clams were measured. The design of this experiment highlights the importance of integrating natural environmental variability into laboratory studies and studying multiple environmental stressors concurrently. These results will help to inform models of surfclam growth and distribution under different climate change scenarios.

THE UNITED STATES SEA SCALLOP RESOURCE: ITS HISTORIC SUCCESS AND PRESENT DECLINE

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The sea scallop (*Placopecten magellanicus*) resource in the United States experienced an unprecedented increase from 1999 to 2004. Several factors led to this including revised management approaches, investments in improved survey technologies, data-rich stock assessments, favorable environmental conditions, and some luck. These conditions may have led to two extremely large scallop recruitment events. In 2003, about 12 billion recruits were observed in the mid-Atlantic, while the total population was about 21 billion scallops. This resulted in the Elephant Truck closed area, which sustained the fishery for the next 6 years. The scallop resource remained stable until 2014. In 2014, about 31 billion scallops recruited in Georges Bank, the largest abundance ever recorded, and the total population increased to 39 billion scallops. Recently, despite the data rich surveys and well-funded scientific efforts the scallop resource has undergone a substantial decline. The possible reasons for this decline include over-optimistic model projects for the biological reference points, poor harvesting practices, inaccurate spatially specific growth models, increased predation, and no comprehensive understanding of density-dependent relationships. Understanding these factors may help halt and reverse this decline.

A FARMS APPROACH TO ADDRESS OYSTER MORTALITY IN THE OFF-BOTTOM OYSTER AQUACULTURE INDUSTRY IN FLORIDA

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In recent years, Florida growers have experienced unexplainable oyster mortalities in late spring and early summer, with reported losses at some lease areas of 50-90% of adult oysters reaching harvest size. To begin to understand these events, a pilot study was conducted in 2020-21 to monitor oyster growth, mortality, and health, along with basic but key water quality parameters, over a production cycle at "sentinel" farms within two aquaculture lease areas. In 2022, the study was expanded by increasing the number of participating farms to nine water bodies across the state providing greater replication and environmental gradients. A FARMS (Farms for Aquaculture Research and Monitoring of Shellfish) applied research approach provides growers with equipment, supplies, and guidance to obtain experimental data at commercial farms. Loggers placed inside culture gear monitor water temperature and salinity continuously; data are downloaded via a mobile app and posted to a dashboard, https://shellfish.ifas.ufl.edu/farms-2023/. Triploid and half-sibling diploid seed are cultured by growers to determine how oysters respond to various gear types and management practices during the period when mortalities typically occur. Histology-based health assessments are also conducted with quantification of inflammatory response, tissue degradation, and parasitic infections. This ongoing study responds to industry concerns by working with growers to monitor water quality parameters and interpret relationships with oyster survival, ploidy, health, and production efficiency. Determining the effects of environmental and culture conditions on population responses will provide resources for growers to refine management practices and mitigate drivers associated with oyster mortalities.

ADVANCES IN OYSTER PRIMARY CELL AND ORGAN CULTURES

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Although molluscs are not widely regarded as model laboratory organisms, they have contributed significantly to the fields of evolutionary biology, ecology, neurobiology and biomineralization. Despite their importance, no immortalized cell lines have been established from marine invertebrates and as such, primary cell culture techniques play a crucial role in advancing marine mollusc research. This talk will highlight novel insights into the maintenance and characterization of primary cell cultures originating from the European flat oyster, *Ostrea edulis*.

Haemocyte circulatory cells, vital to molluscan immune responses, prove challenging to culture long-term as they are usually terminally differentiated when extracted from the oyster. To overcome this challenge, culture techniques were improved for the maintenance of gill and mantle tissue explants and whole heart organ cultures. These improvements have not only extended the viability of haemocyte cells but have also facilitated the discovery of novel cell types and behaviours. Additionally, whole organ heart cultures have opened opportunities for studying cardiac function *ex vivo*, allowing for heart rate measurements in cultured explants for up to four months. The optimization of cell and tissue culture methods across molluscan species, especially those acting as hosts for pathogens, will significantly advance our understanding of molluscan immune responses, expediting the creation of robust disease management solutions for aquaculture and ecological restoration.

THE MITIGATION OF HARMFUL ALGAL BLOOMS (*ALEXANDRIUM CATENELLA*, *PSEUDO-NITZSCHIA* SPP., *DINOPHYSIS ACUMINATA*, *MARGALEFIDINIUM POLYKRIKOIDES*) BY CULTIVABLE SEAWEEDS

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While many macroalgae have been shown to inhibit and lyse HAB phytoplankton, there has been a lack of data on the macroalgae/HAB pairs most relevant for the growing global aquaculture industry. Here, results from a collection of studies that demonstrate mitigating effects from relevant macroalgae/HAB pairs – predominantly, the effects of *Ulva* spp. on warmer-water HAB species *Dinophysis acuminata* and *Margalefidinium polykrikoides*, and the effects of sugar kelp (*Saccharina latissima*) on cool-water HAB including *Alexandrium catenella* and *Pseudo-nitzschia* spp. will be presented. Algicidal activity was present for all pairs; for example, in bloom water incubations, *Ulva* significantly reduced (92% reduction) bloom populations of wild *M. polykrikoides* compared to control ($p < 0.05$), *S. latissima* significantly reduced bloom populations of *A. catenella* (73-95% reduction, $p < 0.005$) and bloom populations of *Pseudo-nitzschia* species assemblies (69-75% reduction, $p < 0.05$). Mitigation potential was also demonstrated in many of these pairs using multiple strains of each species in culture. The presence of sugar kelp in shellfish enclosures significantly decreased toxin accumulation in shellfish fed toxic HAB phytoplankton; kelp significantly lessened saxitoxin accumulation ($p < 0.05$) from *A. catenella* in blue mussels (*Mytilus edilus*) and domoic acid accumulation ($p < 0.05$) from *Pseudo-nitzschia multiseries* in razor clams (*Ensis* spp.), demonstrating the efficacy of seaweeds to inhibiting both HAB and the trophic transfer to HAB toxins.

TRANSCRIPTOME SEQUENCING OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) IN STRESSFUL SALINITY CONDITIONS

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Oysters are a vital part of the Florida estuarine ecosystem and commercial fisheries industry. They protect estuarine environments by preventing erosion from storms, and they provide essential habitat and structure for other marine species. Oysters comprise the largest portion of the United States' aquaculture production and they offer a way to address global food insecurity. Despite these benefits, the eastern oyster (*Crassostrea virginica*) faces multiple ecological and anthropogenic threats, including pollution, climate change, overharvesting, and salinity change, ultimately leading to an 85% decline in global oyster reef distribution. Few studies have used transcriptome sequencing to analyze variable gene expression and for pathway analysis in eastern oysters as a response to stressful salinities as an isolated variable. This project utilized transcriptome sequencing to examine how extreme low and high salinity events influence the expression of genes and alter pathways related to stress response in eastern oysters. It is hypothesized that when eastern oysters are exposed to stressful salinity conditions, molecular pathways related to stress response, including the ER associated degradation pathway and the unfolded protein response pathway, will be upregulated. Further understanding of these molecular pathways will provide insight into the eastern oyster's stress response system and help guide future work in oyster sustainability.

ISSUES RELATED TO THE DELISTING OF INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS (IHHN) AS A NOTIFIABLE DISEASE BY THE WORLD ORGANIZATION FOR ANIMAL HEALTH (WHOA)

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Infectious hypodermal and hematopoietic necrosis (IHHN) is one of the major diseases of cultured penaeid shrimp and has been listed as a notifiable crustacean disease by the World Organization for Animal Health (WOAH) since 1995. This virus was first detected in *Penaeus stylirostris* from Hawaii in 1981. It caused severe mortalities in cultured populations of *P. stylirostris* and caused slow growth in other penaeid species. However, penaeid shrimp, including the predominate farming species *P. vannamei*, have become more tolerant to IHHNV infection. No significant mortalities in farmed shrimp have been noted in recent years. In 2020, a South American country X requested WOAH to consider delisting IHHN as a notifiable disease because it has become widespread and is of little consequence to production. The disease is found in many shrimp farming countries in Asia and Latin America, including country X, where it has been endemic since the late 80's. Some countries reject the importation of IHHNV-positive shrimp even though IHHNV is endemic in the importing country. There are no criteria or processes for delisting a disease; WHOA uses the listing criteria to evaluate the request for delisting. The assessment showed that IHHNV disease still meets the listing criteria: 1) IHHNV is still spreading; 2) there are IHHNV-free countries, zone, or compartment; 3) a case definition is available, and a reliable means of detection and diagnosis exists; 4) IHHNV has caused significant economic losses in some countries. In this presentation, we will discuss the pros and cons of delisting aquatic diseases that are very widespread and no longer cause any consequential production losses.

A YEAR IN REVIEW: THE COMMERCIAL OYSTER AQUACULTURE SECTOR TRAINING (COAST) PROGRAM

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One of the hurdles for a sustainable off-bottom oyster aquaculture industry, not only in the northern Gulf of Mexico but across the United States, is limited availability of skilled employees. As such, workforce development has become a primary initiative throughout the industry.

In 2023, the Commercial Oyster Aquaculture Sector Training (COAST) Program for the northern Gulf of Mexico was launched. This program is a workforce development initiative aimed to recruit workers to the oyster aquaculture industry and provide them with training to meet industry demand. Current funding allows for the teaching of 10 apprentices over the course of two years in various aspects of oyster farming, including production and rearing, business management, food safety, and serving. Participating businesses from Alabama and Mississippi receive a portion of the apprentice's wages to support training efforts. This presentation will provide a one-year update on the COAST program, including plans for program development and enhancement, general logistics, business and apprentice recruitment, an update on participants, and challenges encountered.

MICROHAPLOTYPES BOOST POWER FOR RELATEDNESS ANALYSIS FROM SNP-BASED AMPLICON SEQUENCE PANELS IN THE PACIFIC OYSTER

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Amplicon sequence panels have become a staple of modern genetic analysis workflows. Numerous advantages to amplicon panels exist, including the ability to interrogate target SNP and other variation within each amplicon. This type of data is not accessible using array genotyping methods. Yet oftentimes amplicon panels are designed and optimized for SNP and do not harness the extra statistical power that is available from using multi-nucleotide alleles. In this study, a recently designed SNP panel using three Pacific oyster populations from the USDA POGS breeding program was used to evaluate if microhaplotypes provided higher statistical power for likelihood-based relationship reconstruction than target SNP and highest Minor Allele Frequency SNP. The microhaplotype data set used the smallest number of loci (n = 358), yet due to the high number of alleles per locus within each population (average 4.88 alleles per locus) resulted in the highest statistical power for relationship reconstruction. The main difference between target SNP, highest MAF SNP and microhaplotype analyses was a compression of the log likelihood distributions between relationship types in the SNP analyses compare to the microhaplotype analysis. Remarkedly little difference existed between MAF-SNP and target-SNP analyses suggesting that there is little to be gained from optimizing bi-allelic loci compared to microhaplotypes. Overall, these results are promising for the use of microhaplotypes in a number of aquaculture applications including simple parentage analysis to enable more complex breeding designs, as well as for pedigree imputation based genomic selection methodologies which hinge upon infallible relationship assignments.

PROBIOTIC-INDUCED PROTECTION OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*) LARVAE FROM VIBRIOSIS IN HATCHERY SETTINGS

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Bacterial pathogens of shellfish have caused mass mortality events worldwide. The species *Vibrio coralliilyticus* specifically has been linked to mass mortality events of *Crassostrea gigas* larvae in hatcheries on the U.S. Pacific Coast. These mortality events can create a bottleneck in production as oyster farmers rely on a steady supply of healthy oyster larvae from hatcheries. *Vibrio* are found ubiquitously in aquatic environments and, in addition to shellfish, *V. coralliilyticus* has been identified as a pathogen to fish and corals. Developing non-antimicrobial protocols, such as supplementation with probiotics, to control pathogenic bacteria in hatcheries is of growing interest to improve hatchery supply.

Probiotics are defined as live microorganisms that confer a health benefit to the host when administered in adequate amounts. Previously, at the Oregon State University Hatfield Marine Science Center in Newport, Oregon, three marine bacteria were identified as highly beneficial to oyster larvae when supplemented exogenously. Applied in combination, the three bacterial strains significantly reduced acute mortalities of *C. gigas* larvae from exposure to *V. coralliilyticus* compared to each strain independently. This study further investigates the feasibility and efficacy of this probiotic combination under different formulations to prevent *V. coralliilyticus* induced mortalities. In axenic larval culture, 80-90% of larvae treated with these probiotics within 24 hours of fertilization survived a lethal dose of *V. coralliilyticus* at 48 hours post fertilization. In addition, preliminary data indicates that dead or recently lysed probiotics promote a similar improvement in oyster larvae survival compared to the controls after pathogen exposure.

OCEAN ACIDIFICATION AND OCEAN DUMPING: COMPARING PAST AND PRESENT CARBONATE CHEMISTRY AND DISSOLVED OXYGEN CONDITIONS OF SEA SCALLOP AND SURFCLAM HABITAT ALONG A COASTAL SHELF

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Coastal systems provide benthic habitat that sustains valuable shellfisheries but are subject to dissolved oxygen (DO) and/or carbonate chemistry impairment from anthropogenic pressures such as eutrophication and increasingly, climate change. Through a series of cruises and assessments of historical cruise records, this study documented the magnitude and extent of seasonally low pH, high pCO_2, low Ω_{Ar}, and low DO in the coastal shelf bottom waters of the New York Bight at present and before/during an episodic hypoxic event in 1976 that resulted in mass mortality of surfclams and other profitable shellfish species. From 2019-2020, seasonally low pH_T (as low as 7.73), high pCO_2 (as high as 874 µatm), and low Ω_{Ar} (as low as 0.91) were observed, with more severe conditions typically in regions near New York City (25-50 m depth). In 1974, two years before the extreme event, the most severe DO (2.39 mg L^{-1}) and carbonate chemistry (pH_N: 7.39 and Ω_{Ar}: 0.45) conditions occurred in August as a halo around a sewage disposal site. During the mass mortality event of 1976, extremely low DO (< 1 mg L^{-1}), pH_N (< 7.5), and Ω_{Ar} (< 0.5) levels were observed in parallel across the region. Direct comparisons of 2019 and 2020 subsurface chemistry to that of 1974—a year with ocean dumping but no mass mortality—over a spatially congruous area indicated significant increases in bottom water DO over time but not Ω_{Ar}, with evidence to suggest the influence of ocean acidification on subsurface Ω_{Ar} over the intervening half century.

DEVELOPMENT OF NOVEL MOLECULAR TECHNIQUE TO DIAGNOSE PRESENCE AND SEVERITY OF HEMOCYTIC NEOPLASIA IN NORTHERN QUAHOGS (= HARD CLAM) (*MERCENARIA MERCENARIA*)

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Disseminated neoplasia is a transmissible cancer observed in marine bivalves across the temperate and tropical oceans of the world. A similar disease termed hemocytic neoplasia (HN) has been identified in populations of northern quahogs (= hard clams) (*Mercenaria mercenaria*) along the eastern United States, in both farmed and native clams. The disease appears to spread readily through the water column resulting in significant mortality in some populations of cultured hard clams. Identifying the presence and severity of HN cells in an individual is typically best performed with histological analysis; however, histological processing and evaluation of the resultant slides is resource intensive and takes significant time. Additionally, low levels of infection (few neoplastic cells in the hemolymph) may be missed in histological sections. Using reverse transcriptase quantitative polymerase chain reaction (RT-qPCR) assays on hemolymph samples provides a non-lethal diagnostic method that is representative of an entire animal without the use of histopathological examination. RT-qPCR provides insight into the relative quantity of specific genetic sequences present in a given sample. In this case, RNA expression of target genes observed to be upregulated within neoplastic cells are normalized to a reference gene to determine disease severity. Thus far, RT-qPCR has detected an increase in neoplasia presence in individuals marked as negative by histology, supporting the proposition that RT-qPCR is a more sensitive and comprehensive diagnostic method. Thresholds will be established in order to develop a HN severity staging system using this new method.

THE SYNERGISTIC EFFECTS OF HARMFUL ALGAE AND OCEAN ACIDIFICATION ON LARVAL BIVALVE SURVIVAL

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Bivalves are an economically important resource whose populations have been declining in recent years. Historically, there have been multiple stressors impacting these populations including overharvesting, pollution, and disease. As climate change accelerates, it will bring additional stressors including ocean acidification (OA) and more frequent and intense harmful algal blooms (HAB). OA can reduce bivalve larval development, metamorphosis, growth, and survival. Bivalve larvae exposed to toxic HAB can have reduced growth development, motility, and survival. While HAB and ocean acidification can individually affect larval survival, the manner in which these stressors will act and interact to impact early life stage bivalves is unknown. This study exposed larval bivalves (*M. mercenaria, C. virginica*) to a range of pCO_2 levels representative of current and future oceans and three harmful algal bloom species found globally: *Alexandrium catenella, Dinophysis acuminata* and *Margalefidinium polykrikoides*). During experiments, there was decreased hard clam larval survival in OA and increasing densities of *M. polykrikoides* (1,000, and 2,000 cells mL^{-1}) treatments with the lowest survival in OA and *M. polykrikoides* combined treatments ($p < 0.01$). There was reduced oyster larval survival ($p < 0.01$) in separate OA and increasing densities of *D. acuminata* (1,750 and 5,000 cells mL^{-1}) treatments, with the combined OA and *D. acuminata* treatment showing similar levels of mortality. Collectively, these findings demonstrate that species specific studies must be done to understand how bivalve species survival will be affected by the expansion of coastal OA and prolonged, intense HAB events.

EFFECT OF CHRONIC TEMPERATURE ALTERATIONS ON DISEASE DEVELOPMENT AND MORTALITY IN THE NORTHERN BAY SCALLOP, *ARGOPECTEN IRRADIANS IRRADIANS*

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Mass mortality events of adult northern bay scallop, *Argopecten irradians irradians*, have been reported in New York (NY) every summer since 2019. These events are attributed to heavy infection by an apicomplexan parasite occurring in conjunction with warm temperature anomalies and other stressful environmental conditions. To further investigate the effect of temperature on disease development and scallop survival, two experiments were performed by holding scallops for three (April-July) to six (January-July) months in flow-through systems maintained at ambient seawater temperature or adjusted to capture past (-2.5°C) and future (+2.5°C) temperature conditions. Throughout this period, scallops were monitored for mortality and disease. Water and biodeposit samples were also collected to understand the impact of temperature on parasite release into the surrounding environment.

Parasite loads in scallop tissue peaked fastest (early to mid-June) for the "hot" treatments followed by the "ambient" treatments. Alternatively, parasite loads in the "cold" treatment peaked around the end of June. Peaks in parasite loads were closely linked to increased mortality in all treatments. Scallops in the "hot" treatment experienced the greatest and fastest mortality out of all the treatments, while the "cold" treatment displayed the lowest mortality. Parasite load also increased with temperature in the environmental samples suggesting that scallops were shedding parasite cells as the disease progressed and/or scallop mortality occurred. These results suggest that changes in temperature trends during spring and early summer may represent a major factor regulating parasite development, and consequently disease and mortality outbreaks in NY bay scallops.

TIME FOR A CHECK-UP: COMPARING LEVELS OF GENETIC DIVERSITY AND INBREEDING AMONG HATCHERY LINES WITH OFFSPRING FROM WILD POPULATIONS OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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Selective breeding of the eastern oyster (*Crassostrea virginica*) has produced genetically improved lines for expansion of the oyster aquaculture industry. The Aquaculture Genetics and Breeding Technology Center (ABC) at the Virginia Institute of Marine Science has been engaged in family breeding since 2004 and is responsible for generating elite eastern oyster brood stock made available to the oyster aquaculture industry through commercial hatcheries. The ABC currently produces five diploid selected lines (DEBY, XB, LOLA, LILY, HNRY) all with a specific selection history and with precise genetic makeup. The ABC breeding program seeks to improve genetic gains in performance traits, while balancing selection intensity to keep inbreeding low. To examine the current genetic health of the ABC five diploid selected lines, levels of genetic diversity and inbreeding were compared with first generation oysters spawned from individuals collected from wild populations in Texas, Louisiana, Florida, and Virginia. Samples from each group were genotyped using the *C. virginica* 66K SNP array, and estimates of genetic diversity, inbreeding, and genetic differentiation were examined. Overall measures of diversity indicate the ABC five selected diploid lines contain high levels of genetic diversity and appear to be healthy. Low levels of inbreeding were observed in the five selected lines, indicating that efforts to minimize inbreeding within the lines have been successful. Similar levels of genetic diversity were observed among wild and selected groups. Levels of genetic differentiation varied among the groups, with clear differentiation between wild and selected groups.

COMPARATIVE PERFORMANCE OF TRIPLOID OYSTERS, PRODUCED BY CHEMICAL INDUCTION AND MATED TRIPLOID TECHNIQUES, TO THEIR DIPLOID COUNTERPARTS

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Partial sterility of triploid (3n) oysters enables year-round harvest, improved meat quality, and superior growth. Two main techniques are used to produce shellfish triploids: 1) 'chemical induction' method, blocking the release of polar body in embryos via chemical treatment and 2) 'mated triploid' method, widely used, where tetraploid (4n) males are crossed with diploid (2n) females to produce 3n offspring. There are growing concerns however that mated 3n may be more vulnerable to diseases or climate-driven stressors.

This research aims to evaluate the long-term performance of 3n oysters (*Crassostrea gigas*) obtained using different induction methods to identify any potential trade-offs from each method. Using stock of equivalent genetic background, one diploid control (2n) and triploids derived from chemical induction (3nC) or mated triploids (3nT) were produced and fitness, reproductive potential, and tolerance to environmental stressors were assessed. Chemical induction (3nC) yielded 95% triploid D-larvae compared to 100% for 3nT. Larval performances of mated 3n and 2n were comparable, whereas 3nC had lower spat yield than 3nT. Lab-based OsHV-1 infection showed no advantages from any groups, while acute heat-stress challenge showed that 3nT were more thermotolerant than 2n and 3nC. Field-survival of the remaining oysters was high (> 85% for all groups), with 3nT being 18% larger than 3nC, and 40% larger than their 2n counterparts. Reproductive potential was higher in 3nT than 3nC, particularly in oysters grown in warmer waters. Collectively, these findings will inform stakeholders in assessing the feasibility of using tetraploidy for 3n oyster spat production moving forward.

EMPOWERING SEAFOOD SERVERS TO TELL THE STORIES OF AQUACULTURED OYSTERS: 2024 UPDATE ON THE OYSTER ESSENTIALS TRAINING PROGRAM

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Oyster aquaculture in the southern United States (especially from North Carolina to Texas) has expanded rapidly in the past decade, prompting concerns about market saturation. To address this concern, a two-year program is being conducted that targets seafood restaurant professionals to increase their understanding of the differences among oyster varieties and their ability to answer customer questions. Training sessionss are being conducted in southern US coastal states as well as 'foodie' cities across the US. In these, servers are given an 'oyster compass' as a tool to help remember how to differentiate oysters. They also participate in real-time polling to evaluate any change in knowledge due to the training. It is hypothesized that trained, more knowledgeable seafood servers will increase sales of aquacultured oysters by comparing sales pre- and post-training. In addition, interviews with participants will be conducted to assess the value of training beyond sales.

To date, 528 servers have been trained in 34 sessions with 4 training sessions in 'foodie cities', and 22 post-training interviews completed. There has been a significant increase in self-assessed comfort by servers in both answering customers' questions about oysters and explaining the differences among oyster varieties. Quantitative sales data has been more difficult to collect and analyze but there are several qualitative instances of increased sales after training. These have been conducted in Louisiana, Texas, Mississippi, Alabama, Florida, Georgia, New York, North Carolina, South Carolina, Virginia, Maryland, and Washington, DC. Additional training sessions will also be held in Denver, Colorado and Chicago, Illinois.

GENOMIC SELECTION FOR DERMO RESISTANCE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Genomic selection (GS) is a powerful approach to genetic improvement especially for polygenic traits that are difficult to measure. GS was conducted in the eastern oyster using a recently developed 66K single nucleotide polymorphisms (SNP) array to improve resistance to Dermo disease caused by *Perkinsus marinus*. Oysters from a Florida wild population (FL) and an Auburn selected population (LAFT) were challenged with *Perkinsus marinus,* separated into dead (susceptible) and live (resistant) phenotypes, and genotyped. The genome-wide association study was conducted and identified no major quantitative trait locus for dermo resistance which has an estimated heritability of 0.25. Markers were ranked according to their association with resistance, and different marker-sets and statistical models were tested for prediction accuracy by cross-validation. For LAFT, the genomic best linear unbiased prediction (GBLUP) model with top 4.8K markers produced the highest predictability and was used to calculate genomic estimated breeding values (GEBV) in survivors. A selection index was constructed with GEBV and whole-body weight, and the top 40 individuals were selected as parents for GS group (LAFTGS). For FL, same model with top 10K markers was used. The top 36 individuals with the highest GEBV were selected to produce the GS group (FLGS). The bottom 39 individuals with lowest GEBV were selected to produce the control group (FLC). A phenotypically selected group (FLP) was produced using 46 survivors from Dermo challenge. Oysters from each group were evaluated with a subsequent Dermo challenge, indicating a significant improvement in FLGS Dermo resistance (14%) comparing with FLC.

PREDICTING LARVAL DISPERSAL AND POPULATION CONNECTIVITY OF SEA SCALLOPS, *PLACOPECTEN MAGELLANICUS*, ALONG THE COAST OF DOWNEAST MAINE

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This research combines computer modeling and population genomics approaches to explore the patterns of larval dispersal and genetic connectivity among populations of sea scallop (*Placopecten magellanicus*) along the Downeast coast of Maine. Such models will aid the nascent scallop aquaculture industry and managers of the Maine scallop fishery to reduce impacts on key spawning beds that support larval recruitment critical to both groups. To date, modifications of an individual-based hydrodynamic computer model of the coastal currents in this region were made to include important aspects of larval development and behaviors such as growth and mortality rates, swimming speeds, and vertical migration patterns. Application of this model has provided three key observations. First, larvae originating from near the mouth of the Bay of Fundy typically did not reach the central Gulf of Maine within the expected ~40-day larval duration. Second, larvae spawned along the Downeast coast typically are transported long distances downstream and offshore by the Eastern Maine Coastal Current but few of these larvae reach inner bays, such as Blue Hill Bay, by the time they are competent to settle. Third, a significant proportion of larvae reaching the Jericho Bay area just west of Mount Desert Island originate from the Penobscot Bay region further to the west due to circulation patterns within Penobscot Bay. A test of these model predictions using population genomic analyses and assignment tests comparing the degree of genetic similarity among predicted source sites and settlement sites will be presented.

DEVELOPMENT OF A MICROHAPLOTYPE-BASED GENOTYPING PANEL FOR AQUACULTURE, RESTORATION, AND FISHERIES MANAGEMENT FOR *CRASSOSTREA VIRGINICA*

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The eastern oyster (*Crassostrea virginica*) is an ecologically and economically valuable species along the East Coast of the United States and within the Gulf of Mexico; however, the oyster fishery is being threatened by anthropogenic and environmental stressors such as salinity and temperature fluctuations and increased fishing pressure and an improved understanding of genetic differentiation is vital for future management of *C. virginica*. In addition, the use of low-cost genotyping in oyster breeding programs is increasing. Here, the development of a microhaplotype-based genotyping panel using genotyping-in-thousands by sequencing (GT-seq) technology is described. This panel, designed and optimized using individuals from Gulf of Mexico and east coast populations, captures a broad spectrum of genetic variations across the *C. virginica* genome. The optimization process for this genetic panel, future applications, and broader impacts will be discussed, including the value of the panel for widespread aquaculture, fisheries management, and restoration initiatives.

PHYLOGEOGRAPHY OF NORTH ATLANTIC POPULATIONS OF SEQUENCE TYPE 36 *VIBRIO PARAHAEMOLYTICUS*

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The last decade witnessed epidemiological changes in *Vibrio parahaemolyticus* illnesses in the US where a Pacific endemic strain called sequence type (ST) 36 declined in prevalence in the north Pacific but notably increased in other locations, such as aquaculture areas in the north Atlantic. A phylogeographic study was performed to better understand the ecological dynamics associated with diversification and Atlantic invasion by ST36, and especially better define the distribution of their environmental reservoirs as these could be the sources for additional translocation events. Population genomic analyses indicate diversification of ST36 occurred in the Pacific and was pre-empted by loss of an inovirus prophage that had been stably maintained for decades. Subsequently, multiple distinct lineages translocated into the Atlantic, at least some prior to 2006 without causing increased illnesses. Through careful tracing of clinical strains to environmental source location, we determined that the Atlantic ST36 population has remarkable geographic structure where distinct clones founded new populations in specific aquaculture areas. The founders of the two prevailing ST36 populations each acquired a new inovirus prohage prior to clonal expansion alluding to the potential that these phages promote successful invasiveness and persistence, though how they may do so is still under study. The established populations are remarkably genetically stable and display little migration or mixing. These analyses indicate that there may be natural barriers for persistence and translocation between locations that if better understood, could inform actions to help prevent further spread, and potentially even help eradicate persisting populations.

A ROADMAP FOR ADVANCING SOCIAL LICENSE TO OPERATE FOR AQUACULTURE: EAST AND WEST COAST USA

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The term social license to operate (SLO)—or community acceptance of a farm—is gaining traction in the aquaculture sector as public opposition has become a significant barrier to both business and sector development. As a result, aquaculture farmers have put much effort into engaging with their communities in an effort to build trust that is necessary in earning social license. While farmers are the primary actor in generating social license, as they have the most influence over public acceptance of their operation, other "secondary SLO actors" can influence social license as well. Secondary actors include town officials, trade associations, environmental organizations, chefs, educators, researchers and more. To investigate the role each of these secondary actors plays in generating social license for aquaculture farms, a series of social license workshops were held at industry meetings on the East and West Coast of the United States. During each meeting, small groups of diverse stakeholders discussed ways that primary and secondary SLO actors help generate social license for the aquaculture industry through a series of prompts. Discussions were notated on worksheets and results were collated and analyzed for themes. Workshop participants were also encouraged to continue contributing to the project through shared virtual folders where they provided additional insight, read drafts and gave feedback. The final output from the project was a report titled "A Roadmap for Advancing Aquaculture's Social License to Operate: East and West Coast USA" that outlines priorities for both primary and secondary actors for building social license for aquaculture.

FISHERMEN OR SCIENTISTS? HOW IDEOLOGY SHAPES WHO THE PUBLIC TRUSTS FOR INFORMATION ON AQUACULTURE

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It is well documented that the general public has limited knowledge of aquaculture, but when they want to know more, who do they turn to? This study expands on previous research exploring effective messaging (and messengers), by exploring what factors influence who Mainers trust for accurate information on aquaculture. While the most trusted messengers overall were scientists, stark differences were evident when broken down by political ideology. Respondents who identified as Democrats were significantly more trusting of scientists, government, and environmental organizations for accurate information on aquaculture compared to those who identified as independents or Republicans; however, Republicans were significantly more trusting of fishermen compared to Democrats. Trust also varied by respondents' views of what was most important for the coastal communities of Maine. Those who valued preserving the traditional character of coastal communities by protecting traditional marine industries were more likely to trust fishermen, while those who valued sustaining the coastal communities of Maine by encouraging new marine industries were more likely to trust aquaculture farmers, scientists, and government for accurate information on aquaculture. These findings have important implications for creating messaging campaigns that reach a diverse audience–the messenger matters, not just the message.

ANNUAL SPATIAL AND TEMPORAL DYNAMICS OF *MARGALEFIDINIUM POLYKRIKOIDES* IN RHODE ISLAND

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Estuaries and saltwater ponds in the northeastern United States have observed frequent rust tide blooms over the past few decades caused by the athecate dinoflagellate, *Margalefidinium polykrikoides* (*Mp*). Blooms are described by their rusty color, high cell densities (>10^3 cells per mL of seawater), and large area of affected water (10-100 km). The implications of these blooms include mortality events and decreased growth rates of finfish and shellfish. For juvenile oysters (*Crassostrea virginica*), inflammation and necrosis of the gills has been observed as a result of exposure to the algae.

This study characterized the spatial and temporal trends of *Mp* in the surface water and sediment in Ninigret Pond in Charlestown, Rhode Island, over the course of a year. Samples were collected from December 2022 through December 2023, with increased frequency during the summer months. An eDNA diagnostic qPCR assay was utilized to track *Mp* cell concentrations at three locations in the pond. The prevalence was correlated with environmental factors such as water temperature, depth, dissolved oxygen, and salinity to explore possible trends. Currently, samples through August 2023 have been processed and analyzed through qPCR. While a bloom did not occur in 2023, *Mp* was observed in the water column, with an initial peak in March. It has also been identified in the sediment in low levels since the beginning of the sampling period. This study intended to provide insight into the annual dynamics of *Mp* and develop a potential bloom monitoring method and protocol.

STREAMLINING REGULATION TO FACILITATE SEAGRASS AND NATIVE CLAM RESTORATION AQUACULTURE

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Although long identified as a critical resource, seagrass continues to decline in coverage across Florida estuaries. Nutrient enrichment is the primary disturbance compromising seagrass distribution in the state and can trigger a domino effect of ecological consequences that shifts a seagrass system to a state of high sediment resuspension, turbidity, and macroalgal colonization. Such habitat loss has been met with moderately successful restoration efforts across Florida. Nonetheless, the cost-benefit ratio of seagrass planting remains high and many degraded seagrass meadows remain unaided, necessitating more research and innovative, collaborative approaches around seagrass restoration. Restoration aquaculture of seagrass and native clams (*Mercenaria* sp.) are in part striving to fill these needs, with the latter founded on the hypothesis that these suspension feeders may increase water clarity and augment seagrass recolonization; however, restoration aquaculture falls under the jurisdiction of a complex, multi-agency regulatory framework that is at times unclear, conflicting, or simply incomplete and commonly acts as a barrier to research and practice. Regulatory streamlining and policy reform were identified as major stakeholder needs from the Florida Sea Grant 2022 Restoration Aquaculture Policy Workshop. The Florida Sea Grant Aquaculture Outreach and Communications Graduate Fellowship serves to address these challenges. First, an interagency workshop consisting of key state and federal representatives will be coordinated to identify gaps, ambiguity, or conflicts in permitting language; create a regulatory guidance document; and draft suggestions for rulemaking language reform. Findings and communication products from this workshop will be disseminated to the Florida Restoration Aquaculture Consortium for stakeholder feedback and use.

TRACKING SOURCES AND SINKS OF EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) METAPOPULATIONS IN SHINNECOCK BAY, NEW YORK, USA

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Globally, most wild oyster populations have collapsed, necessitating effective restoration practices. Understanding oyster metapopulation dynamics, including demographic rates and dispersal rates, is essential for the conservation of populations. In Shinnecock Bay, New York, six years of eastern oyster (*Crassostrea virginica*) reef restoration efforts have demonstrated that while outplanted spat-on-shell have high survivorship and growth, recruitment limitation prevents oyster reefs from being self-sustaining. To better inform oyster restoration, this study seeks to 1) map oyster recruitment patterns, and 2) quantify the abundance, timing, and distribution of oyster larvae, within Shinnecock Bay. Shoreline surveys in fall 2022 found the highest recruitment in the northeast bay, near the Shinnecock Canal, suggesting that oyster populations in neighboring Peconic Estuary may be an important source of larvae. Recruitment units placed at nine locations across the bay during 2023 similarly found the highest recruitment in this same region, with peak recruitment occurring in mid-summer (7/24/23 to 8/29/23). Water samples collected weekly from June to September will be analyzed for quantification of oyster larvae abundance using digital PCR techniques. Results will be compared to settlement patterns and physical circulation models. Together, this information will guide the future placement of oyster reefs in Shinnecock Bay to help build a self-sustaining metapopulation.

NOAA-SUPPORTED RESOURCES FOR COMMERCIAL SHELLFISHERIES RESEARCHERS, MANAGERS, AND OPERATORS

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Ocean acidification and other changing ocean conditions impact commercial shellfisheries across the nation. Shellfish can be directly impacted by coastal and ocean acidification and researchers, managers, and industry professionals need information on conditions, impacts and solutions at hand. The NOAA Ocean Acidification Program (OAP) mandates include delivering this information and ocean acidification data to stakeholders and rightsholders. Here, NOAA-supported resources for these users will be presented and then an interactive opportunity to receive input on priorities, concerns, and needs will be discussed. The information gleaned from this session will inform future investment with the goal of supporting our research and commercial shellfish communities better.

EXPANDING THE PHYLOGEOGRAPHY AND CONNECTIVITY OF *PERKINSUS* SPECIES ACROSS NORTH AND CENTRAL AMERICA

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Infections caused by *Perkinsus* parasites occur globally and continue to be found new hosts in new locations; expanding and reshaping knowledge of their biogeographic patterns and the factors influencing those patterns. In this study, the biogeography and genetic connectivity of *Perkinsus* spp. across North and Central America was characterized, which includes infection hot spots (e.g., Gulf of Mexico, Chesapeake Bay) and areas where these parasites have not been previously reported (e.g., along the California coast). Nine hundred thirty-three bivalves from North America were genetically screened for parasites in the genus *Perkinsus*, combined this with 752 bivalves previously screened from Panama, which combined includes 16 species from three different countries. Phylogenetic methods were used to confirm the identifications of all bivalves collected and *Perkinsus* spp. detected. These data were combined with publicly available sequence data for these parasites to create global haplotype networks to assess regional and continental genetic diversity and phylogeographic patterns. Three species were detected in North American waters: *Perkinsus beihaiensis*, *P. chesapeaki*, and *P. marinus*, with *P. olseni* not detected outside of Panama. It is reported for the first time *P. chesapeaki* detections in *Isognomon* sp. from Mexico and *P. beihaiensis* detections in *Ostrea lurida* from California. Additionally, these results indicate extremely low genetic diversity of these three parasites across continental and global spatial scales. These results add further evidence of recent or continuous long-range dispersal and global connectivity for many haplotypes of these parasites, suggesting that dispersal through anthropogenic activities, especially maritime trade, likely contribute to these phylogeographic patterns.

PUTATIVE ENDOGENOUS VIRAL ELEMENTS (EVE) IDENTIFIED IN THREE WHOLE REFERENCE GENOME ASSEMBLIES AVAILABLE FOR THE PACIFIC WHITELEG SHRIMP, *PENAEUS VANNAMEI*

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Three whole genome sequence (WGS) assemblies are available for *Penaeus vannamei* [GenBank accessions: ASM3358929v1 (1.9-Gb); ASM378908v1, 1.7-Gb) and (ASM373033v1, 96.78-Mb)]. In addition, a pilot sequence (470-Mb) of the first specific pathogen-free (SPF) *P. vannamei* produced by the breeding program of the United States Marine Shrimp Farming Program (USMSFP) generated 441 repetitive elements. Among these are DNA transposons [transposable elements and simple sequence repeats (SSR)] homologous to endogenous viruses like nimavirus *Nimav-1_LVa* (279,905-bp) and white spot syndrome virus (WSSV)-like, *DNAV-1_LVa* (279,384-bp). Some SSR show similarity to *P. vannamei* microsatellites including the telomeric pentanucleotide (TAACC)n microsatellite, the site of insertion of *Nimav-1_LVa.*

Other integrated viruses include portions of infectious hypodermal and hematopoietic necrosis virus (IHHNV, AF218266.2, 3909bp) and *P. vannamei* solinvivirus (PvSV) (OP265432, 10,447bp) identified in diseased Brazilian shrimp. BLASTN searches revealed 93% identity of OP265432 to Wenzhou shrimp virus 8 (KX883984, 10,445bp) and 91% identity to *P. vannamei* picornavirus (OK662577, 10,550bp). WGS searches identified portions of the 3'-end of OP265432 (92-93% identical) to three sequences [QWLK01003484, QWLK01003486, QWLK01003485] in the contig-level genome assembly ASM373033v1 of *P. vannamei* F1 breed from China (GCA_003730335, 96.78Mb), but is not present in the large scaffold-based genome assembly ASM378908v1 of *P. vannamei* breed Kehai No.1 farmed in China (GCA_003789085; 1.7-Gb) or in the recently published assembly ASM3358929v1 (GCA_033589295.1, 1.9-Gb). Similar results were found in the 3'end of KX883984 and OK662577, suggesting putative endogenous viral elements (EVE) of PvSV (PvSV-EVE) in *P. vannamei* genome. Considering that the estimated genome size for the first SPF *P. vannamei* is 2.83-Gb, a new, contiguous, whole reference genome for *P. vannamei* is needed to confirm presence of these endogenous viruses.

ENVIRONMENTAL DEOXYRIBONUCLEIC ACID (EDNA): DOES THE SCIENCE MAKE SENSE?

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Enthusiasm for deoxyribonucleic acid sampling in aquatic environments has accelerated because of simplicity, little to no damage to the environment (animals, plants, or habitat), declining analytical costs, declining analytical time and availability of field use analytical units. The attractive qualities to eDNA sampling have overshadowed: 1) the uncertainties (false positive inference or false negative inference) created by eDNA biotic and abiotic transport (wind, currents, animals, physical objects) and environmental longevity (sediment), 2) inadvertent but unavoidable human genetic data capture which points to ethical and legal challenges and 3) pathogen eDNA should not be interpreted as being a disease event.

WORKSHOP: CARBON STORAGE CAPABILITIES OF WILD AND CULTURED SHELLFISH

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Production of bivalve molluscs has been proposed as a method to reduce carbon emissions as: 1) a low-emission protein source, and 2) via carbon stored within their shells. To address the fate of shell carbon for the northwest Atlantic, stored oceanic carbon equivalents (Eq), released CO_2 via calcification, and hypothetical carbon credit value ($24 tCO_2), for both cultured and wild-captured bivalves for New England and Canadian Provinces on the Atlantic between 2016 and 2020 were estimated. Bivalve shells do not sequester atmospheric CO_2, instead storing oceanic CO_2 Eq and cannot be included directly in a carbon sequestration scheme. Total annual estimates of stored oceanic CO_2 Eq were approximately 202,253 and 363,243 tons, with concurrent releases of approximately 121,255 and 217,771 tons of CO_2 to the atmosphere. Even if bivalve shells sequestered atmospheric CO_2, current shellfish production levels are inconsequential with regard to current anthropogenic greenhouse gas (GHG) emissions. Stored oceanic carbon Eq for bivalve aquaculture is equivalent to 0.001% and 0.0005% of Canadian and US annual anthropogenic CO_2 emissions, whereas wild-capture would store 0.028% and 0.005% of Canadian and US emission, respectively. Bivalve shell will not solve climate change, but the expansion of bivalve production provides a protein source with the lowest GHG emissions, which provides a multitude of environmental services.

POSTER PRESENTATIONS

WESTERN BLOT STUDY OF THE NEUROTOXIC EFFECTS OF MANGANISM AND PARKINSON'S DISEASES

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Manganism, a human neurodegenerative disease caused by high brain manganese levels has similar symptoms as Parkinson's Disease (PD). Both interfere with the dopamine system originating in the substantia nigra. Manganism impairs dopamine postsynaptic signal transduction (PST), while PD destroys dopamine neurons. Impairment of PST decreases response to stimulation. Neuronal degradation results in postsynaptic denervation supersensitivity. Treatment for PD does not benefit people with Manganism. This study contrasts neurotoxic actions of manganese and 6-hydroxydopamine on the presence of dopamine D2R receptors in gill of *Crassostrea virginica*. *C. virginica* has a cilio-inhibitory dopamine innervation from its ganglia to gill lateral cells (GLC).

Mn and 6-hydroxydopamine decrease dopamine neurons effectiveness to slow down GLC cilia; however, direct application of dopamine to GLC reduces cilia beating after 6-hydroxydopamine, but not after manganese. To test the hypothesis if manganese treatment decreases the presence or sensitivity of gill D2R receptors, and if 6-hydroxydopamine treatment increases their presence or sensitivity, the D2R of animals treated 5 days with 500 µg of manganese or 6-hydroxydopamine were quantified using PAGE and Western Blotting (WB) with D2R-HRP conjugated antibodies, then viewed and analyzed with an iBright Fl1500 image analyzer. Band intensity for 6-hydroxydopamine treatment was slightly more intense than controls, but less intense for manganese treatment. The study shows the two neurotoxins have different mechanisms of action. This can be helpful in designing appropriate therapeutic treatments for these similar neurological disorders. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

TESTING THE ABILITY OF SURFCLAM SUBSPECIES (*SPISULA SOLIDISSIMA SOLIDISSIMA* AND *S. S. SIMILIS)* TO HYBRIDIZE

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There are two Atlantic surfclam subspecies. The northern subspecies (*Spisula solidissima solidissima*) supports the federal fishery and is abundant on the continental shelf north of Cape Hatteras. The southern subspecies (*S. s. similis*) is predominantly found south of Cape Hatteras, but is also found in shallow, patchy, northern areas, such as coastal Virginia, Long Island Sound, and southern Massachusetts; however, the taxonomic rankings of these clams remain controversial. Recent genetic evidence suggests they could be distinct, but closely related species. Given the surfclam's vulnerability to climate change and its economic importance to commercial fishing and aquaculture industries, the uncertainty around its taxonomic classification must be resolved. Therefore, the goal of this project was to determine whether the surfclam subspecies have the ability to hybridize. Surfclams were collected from commercial fishing grounds off New Jersey (*S. s. solidissima*) and from a known *S. s. similis* bed in Massachusetts. Gametes from one *S. s. solidissima* female, one *S. s. solidissima* male, eight *S. s. similis* females, and seven *S. s. similis* males were used to create four progeny groups: two purebred crosses and two hybrid crosses (*S. s. solidissima* female with *S. s. similis* males, and *S. s. similis* females with *S. s. solidissima* male). Genetic samples were collected from each of the parents to confirm genetic lineage. Fertilization rate across groups ranged from 95-100%. Larvae were reared in 60 L static cultures maintained at 17-22°C and a salinity of 29-32. Growth of the hybrid larvae appeared most similar to the purebred larvae with which they shared maternal parentage. Larvae from all four groups metamorphosed, reaching competency 21-28 days post fertilization. This work demonstrates that *S. s. solidissima* and *S. s. similis* are indeed capable of hybridizing. Future work will include repeating this work, rearing existing hybrids to maturity, and evaluating the ability of the hybrids to produce gametes and F1 generations.

A POTENTIAL SEX MARKER FOR *PENAEUS VANNAMEI* IS PART OF THE NON-LONG TERMINAL REPEAT (NON-LTR) RETROTRANSPOSON *RTE-3_LVA* FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) *P. VANNAMEI* PRODUCED IN THE UNITED STATES

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A non-infectious hypodermal and hematopoietic necrosis virus (IHHNV) related sequence (DQ228358, 4,655bp) was previously identified in the genome of *Penaeus monodon* from Madagascar and demonstrated integrated into an RTE-like non-LTR retrotransposon. The 3'-flanking sequence of the integrated IHHNV, nucleotides 3262-4655, shows 98% identity to nucleotides 1531-2924 of a *P. monodon* repeat family *RTE-2_PMon* (3,656-bp) which shares 85% sequence identity along the whole length with *RTE-3_LVa* non-LTR retrotransposon (3,654-bp; www.girinst.org). *RTE-3_LVa* was identified in the genome of the first SPF *Penaeus vannamei* produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP), deposited in Repbase. Thirteen microsatellites isolated from ovary of SPF *P. vannamei* are homologous to *RTE-3_LVa*, two are located onto the sex linkage group 4 (LG4, *ShrimpMap*2) of SPF *P. vannamei*. *RTE-3_LVa* has many copies in various scaffolds of the reference genome *P. vannamei* breed Kehai No.1 (assemblyASM378908v1, ~1.8-Gb). PCR amplification using DNA from muscle of SPF *P. vannamei* and primers from two microsatellites homologous to *RTE-3_LVa* showed sex-specific bands, suggesting that *RTE-3_LVa* is a potential sex marker.

RTE-3_LVa is also present in various chromosomes of other penaeid species like *P. monodon* from Thailand (NSTDA_Pmon_1, GCF_015228065, 2.39-Gb). Considering the variability in genome sizes of current penaeids assemblies [*P. monodon* from China and Vietnam (~1.4-~1.6-Gb), *P. chinensis* from China (~1.6-Gb), *P. indicus* from India (~1.6-Gb), *P. japonicus* from China and Japan (~1.7-Gb)], which are smaller than the expected ~2.87 Gb genome size of SPF *P. vannamei* from a breeding company in Florida, USA, a new continuous, whole reference genome sequence is urgently needed from the founders of the SPF *P. vannamei* breeding program of the USMSFP and wild *P. vannamei* to study organization and evolution of integrated viruses like IHHNV, expression of *RTE-3_LVa*, and mechanisms of sex determination and differentiation.

MITOCHONDRIAL DNA (MTDNA) OF PACIFIC WHITE SHRIMP *PENAEUS VANNAMEI* IS PRESENT AT VARIABLE LENGTH IN THE GENOME ASSEMBLIES OF FIVE PENAEID SPECIES

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Three complete mitochondrial genomes of *Penaeus vannamei* (EF584003.1, KT596762.1, DQ534543.1) are available in GenBank. Portions of the mtDNA reference genome (RefSeq: NC_009626.1, 15,990 bp) are included in the whole reference genome sequence (WGS) assembly of *P. vannamei* (ASM378908v1, 1.7-Gb). Information on sequence identities between NC_009626.1 and the three WGS assemblies available for *P. vannamei* (ASM378908v1; ASM3358929v1 1.9-Gb; and ASM373033v1 96.78-Mb) will be presented. The highest sequence identity between NC_009626.1 and the three WGS assemblies is with ASM3358929v1, though it includes the entire control region, D-loop (nucleotides 14996-15990), it does not include the cytochrome b (CYTB) gene (nucleotides 10983-11412), reflecting a more complete assembly in the ASM3358929v1 isolate Guihai-1-2017-001_HiC_scaffold_1094, 98% identity. The homology of NC_009626.1 to ASM378908v1 (LVANscaffold_2720, 85% identity) is only from nucleotides 8839-15268 and includes NADH dehydrogenase subunits 4 (ND4), ND4L, ND6, CYTB, ND1, large and small ribosomal RNA, and partial D-loop region. The genetic diversity [HhaI mtDNA polymorphisms (A and B)] of two *P. vannamei* populations (population 1 families 1.5 and 1.6, and population 2) from the first specific pathogen-free (SPF) *P. vannamei* stocks developed by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP) will be presented. All the animals of family 1.5 and population 2 showed type A and family 1.6 showed type B, indicating that mtDNA is useful for examining genetic diversity to follow individual stocks within a breeding program and to correlate genotypes with desirable growth and reproductive performance of SPF *P. vannamei* stocks.

OPTIMIZING THE INTEGRATION OF AQUACULTURE AND OCEAN ALKALINITY ENHANCEMENT FOR LOW-COST CARBON REMOVAL AND MAXIMUM ECOSYSTEM BENEFIT

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Removal of carbon dioxide from the atmosphere along with rapid decarbonization can help avoid the worst impacts of climate change and ocean acidification. Ocean alkalinity enhancement (OAE), which increases the storage of carbon in the ocean, offers the potential to remove carbon dioxide from the atmosphere while at the same time reducing ocean acidity, with potential benefits to aquaculture and other ecosystem services. In electrochemical OAE, alkalinity is enhanced by increasing sodium hydroxide, avoiding the introduction of trace elements common in other methods. The increase in alkalinity shifts the seawater carbonate chemistry to reduce pCO_2 and increase carbonate and bicarbonate ion concentrations. Ebb Carbon is pioneering a process capable of increasing ocean alkalinity and pH in a way that safely and flexibly improves water quality. Elevated alkalinity can be maintained to create conditions favorable to aquaculture, or the process can be completed leaving the pH slightly elevated compared to initial conditions. The process can be tuned for maximum ecosystem benefit, for example OAE could eliminate annual or interannual low pH events within an estuary or locally at a shellfish farm or could be deployed to offset the continual decrease in pH caused by carbon dioxide in the atmosphere. Pilot studies seek to understand the potential including benefits and harms, optimize the technology for low cost and maximum benefit, and seek input and collaborations needed to gain the social and regulatory license and ensure the safe deployment of alkalinity enhancement.

ONE PART OF THE NUTRIENT CREDIT PUZZLE: NITROGEN REMOVAL THROUGH ASSIMILATION BY CULTURED SHELLFISH IN FLORIDA

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The increasing interest in integrating shellfish aquaculture into nutrient trading credit programs in Florida is met with challenges stemming from diverse environmental conditions, cultivation techniques, state policies and economic dynamics. A collaborative effort, undertaken by the present authors and others, delved into the prospects and hinderances associated with developing nutrient trading programs. In the context of the comprehensive study, locally pertinent assessments were conducted of nitrogen removal linked to cultured clam (*Mercenaria mercenaria*) and oyster (*Crassostrea virginica*) harvest.

Industry partners facilitated the acquisition of harvest-sized clams, diploid oysters, and triploid oysters across the state – Alligator Harbor/Franklin County, Cedar Key, and Tampa Bay – during March, June/July, and November. Tissue samples were freeze-dried and ground to a fine powder. Shell material from the inner and outer surfaces of each shell was ground using a Dremel tool. Subsequently the sample materials were subjected to CNHS analysis for organic nitrogen content. The total nitrogen content for individual shellfish was calculated from the percent nitrogen by weight of shell and tissue, and compared across species, ploidy, size, location, and season. This research contributes valuable insights into the intricate dynamics of nitrogen removal capacity by shellfish aquaculture, shedding light on the potential integration of such practices into nutrient trading credit programs.

EXPLORING THE VIABILITY OF INTERTIDAL QUAHOG AQUACULTURE IN MAINE

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The Gulf of Maine is warming faster than the majority of the world oceans, threatening the livelihoods of thousands of Mainers who make a living from the sea. Marine resource diversification is essential for adapting to this rapid change and ultimately promoting economic resilience for the coastal communities of Maine. Quahogs, or hard-shell clams, present an opportunity for diversification within both aquaculture and wild shellfish industries as waters have warmed and conditions have become more hospitable to quahog growth and survival. Determining viable pathways for culturing quahogs in the intertidal zone will benefit existing and potential new shellfish farmers looking to diversify their crops, as well as shellfish harvesters who are increasingly dependent on the wild quahog resource.

In 2022, Manomet, in collaboration with the Brunswick Marine Resources Committee and Eros Oyster launched a project to test a new method of intertidal quahog aquaculture that could be an opportunity for sea farmers to expand their operations and diversify their crops, as well as a method for supporting municipal shellfish wild stock enhancement activities. Two methods for growing quahogs were used; soft clam bags which are commonly used in the mid-Atlantic but have not been tested in the harsher Maine winters and ADPI oyster bag which are a readily available gear type for farmers. Preliminary results will be presented from the first year of experimentation using bags to grow quahogs in the intertidal for aquaculture crop diversification and as wild stock enhancement.

PERFORMANCE OF EASTERN OYSTERS FROM LOCAL WILD STOCKS IN SOUTHERN NEW ENGLAND FARMS

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The eastern oyster, *Crassostrea virginica,* has economical and cultural significance in many New England States. The goal of this research was to compare performance (survival and growth) of regional wild oyster stocks in two Rhode Island farms. This is part of an ongoing project aiming to determine which oyster stocks could be utilized in a regional breeding program, as slow growth and disease presence have been detrimental to oyster farming. Oysters from four stocks, two commercial (CL1, CL2) and two wild (Green Hill Pond, GH, and Martha's Vineyard, MV), were deployed to two Rhode Island farms in Ninigret and Wickford in 2022. In July, August, and October of 2023, size and mortality of each stock was measured. There was low survival for all stocks at the Wickford site, with oysters from MV showing lower survival than the GH oysters. On the other hand, oysters from the GH stock performed better than those from the MV stock at the Ninigret farm (comparable to the commercial lines), suggesting this stock may be better suited to the environment of the coastal ponds. The yield was driven by survival in Ninigret while the combination of survival and size drove the yield in Wickford. The results from this study confirm that oyster performance shows strong genotype by environment interactions, resulting in differing performances of the same stocks across the two sites.

COMPARISON OF OYSTER (*CRASSOSTREA VIRGINICA*) REEFS ESTABLISHED SEASONALLY USING SET AND UNSET BAGGED SHELL AND LOOSE OYSTER SHELL IN GEORGIA

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Restoration efforts of *Crassostrea virginica* in Georgia have focused on establishing new reef by deploying bagged shell intertidally during peak recruitment (April-June). Local sentiment for oyster restoration projects is favorable but plastic mesh use in restoration has become increasingly problematic for resource managers with awareness of coastal microplastics contamination risking public support. Loose oyster shell is assumed ineffective for oyster restoration in high sediment estuaries of Georgia but the performance of loose shell is unknown. An opportunity exists to evaluate multiple restoration techniques using both set and unset oyster shell to remove plastic from the equation and extend the window for reef establishment. Objectives of this project were to evaluate oyster restoration intertidally at two sites, Blythe Island and Romerly Creek, using set and unset bagged and loose oyster shell during spring and fall. Twelve reefs were deployed at each location during June 2022, including set and unset shell treatments in bags and loose on bottom, with six additional set shell reefs (equal bagged and loose shell) deployed during October 2022. Oyster density ($0.25m^2$) was monitored quarterly. Summer 2023 oyster density data indicated (ANOVA) loose shell outperformed bagged shell ($p<0.001$) and set shell outperformed unset shell ($p<0.001$). Spring treatments had higher oyster density at Romerly Creek than Blythe, with fall densities similar between both sites. Fall densities at Blythe Island were significantly higher than spring ($p<0.001$), with a reversed trend at the Romerly Creek site. Results indicate that using loose and set shell during fall are both viable restoration techniques.

EDNA METABARCODING TO SURVEY SHELLFISH IN THE GULF OF MAINE

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Environmental DNA (eDNA), which is DNA left in the environment through the defecation or shedding of organic material (fur, skin, feces) from organisms, has proven to be an efficient and cost-effective tool in biomonitoring and biodiversity assessment in several ecosystems. Metabarcoding of eDNA was used to survey wild populations of fish and shellfish such (e.g., longfin squid *Doryteuthis pealeii*, shortfin squid *Illex illecebrosus*, scallops, and sea urchins), in the Gulf of Maine (GOM) during the Maine Department of Marine Resources (DMR) inshore trawl surveys in the spring and fall 2023. Specifically, traditional trawl survey results were compared to those from two eDNA collection methods: passive metaprobes attached to the codend of the trawl or by filtering slush water from the trawl. From eDNA samples, fish, invertebrate, and cephalopod eDNA were amplified with general primers and sequenced the amplicons to infer species distribution. The goal of this study was to compare traditional trawl and eDNA surveys in terms of species composition and abundance of key shellfish species and determine whether and how eDNA surveys can be used to survey wild shellfish populations in the GOM. Results of this comparative study, as well as applications to aquaculture of cephalopods, bivalves, and urchins, will be discussed.

INFLUENCE OF POLYPLOIDY ON THE FORMATION AND EFFICACY OF DNA-DERIVED EXTRACELLULAR TRAPS IN EASTERN OYSTER HEMOCYTES

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DNA-based extracellular traps (ET) are a highly preserved element of the innate immune system, recently discovered and observable in all metazoan organisms. Upon exposure to pathogens, cellular DNA undergoes decondensation and is expelled, weaving intricate mesh networks capable of ensnaring and neutralizing viruses, bacteria, fungi, and parasites. Consequently, the increased DNA content observed in triploid oysters may enhance the efficacy of ET in countering pathogens.

Various stimuli were appraised for their ability to induce ET in the eastern oyster, and then employed to assess the ploidy's influence on ET production and efficacy. Evaluation of ET formation and effectiveness was recorded using fluorescence microscopy (with DNA binding stain) and bacterial neutralization assays, contrasted by corresponding DNAse controls. Results illustrated that a puncture wound into the adductor muscle significantly increased the rate of ET formation in oysters, neutralizing over 60% of introduced bacteria. Furthermore, ET effectiveness correlated with the proportion of agranulocytes in the hemolymph and their production of reactive oxygen species (ROS), underscoring agranulocytes as robust immune effectors. Visual assessment of ET further revealed that triploid cells produced larger ET at a higher rate than their diploid counterparts; however, no difference in ET derived bacterial neutralization was observed between diploids or triploid cells. In essence, this study found a dependable approach for inducing ET in oysters and identifies pivotal host factors influencing ET formation, opening avenues for further exploration of this conserved immune mechanism.

UNDERSTANDING WHICH COASTAL STRESSORS HAVE THE GREATEST IMPACT ON THE SURVIVAL OF *CRASSOSTREA VIRGINICA* (EASTERN OYSTER) LARVAE

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The eastern oyster is a critical component of marine ecosystems because of its water filtration abilities and reefs, which provide a habitat for other organisms. Eastern oysters endure coastal stressors throughout their life cycle but are particularly vulnerable to these stressors during the larval stage. This study aimed to identify which coastal stressors had the most direct impact on the survival of eastern oyster larvae. Low oxygen, pH, and salinity concurrently affect eastern oyster larvae after events such as heavy rainfall, so it is important to isolate these stressors to understand their individual and combined impacts.

To conduct this experiment, 23-day-old eastern oyster larvae were exposed to four treatments (control, low pH/DO, low salinity, and a combination of low pH/DO and low salinity). Treatment bottles were stocked at 20,000 oyster larvae/bottle with 3 bottles/treatment. The oysters were exposed to these treatments for 24 hrs and a 3 mL density sample was taken following exposure. The samples were counted to determine the mean percent survival of the oyster larvae. The mean percent survivorships were as follows: 70.2% (control), 76.8% (low pH/DO), 90.5% (low salinity), and 76.7% (low pH/DO and low salinity). There was no significant relationship between eastern oyster survival and specific coastal stressors (p-value=0.4237). The difference in mean percent survival was not statistically significant and likely due to chance. The results of this experimental replicate are inconclusive, but the study is still ongoing.

FORGING PUBLIC-PRIVATE PARTNERSHIPS FOR OYSTER REEF RESTORATION FOR CARBON SEQUESTRATION AND ECOSYSTEM SERVICES IN COASTAL GEORGIA, USA

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Eastern oysters, *Crassostrea virginica*, are a commercially important species that also play a critical role in creating habitat by forming large reef structures. Oyster reefs provide a variety of ecosystem services, including food production, habitat formation, improved water quality, and shoreline protection. Unfortunately, oyster populations have experienced dramatic declines due to a combination of factors which include overharvest, disease-causing parasites, and degraded water quality. These population declines jeopardize the foundational role that oysters play in coastal ecosystems. One underexplored role of oyster reefs that has recently been examined is the role that oyster reefs might play in carbon sequestration along the coastline. As benthic-pelagic couplers, oysters contribute to the mass burial of fixed organic carbon into sediments around their reefs.

As the consequences of coastal habitat loss and impacts of climate change become more apparent, it is critical to explore how habitat restoration might be used as a tool for blue carbon. Working with Yamaha Rightwaters, the environmental arm of Yamaha, and the Georgia Department of Natural Resources, this project seeks to determine the carbon sequestration potential of oyster reef restoration projects in Georgia. Further, the project has added benefits of habitat enhancement for many important fish species and is very visible. As such, partnerships with industry leaders, such as Yamaha Rightwaters, has the potential to greatly increase the amount of oyster reef restoration projects in places like Georgia, increase public awareness and support for coastal habitat restoration, and provide valuable services to coastal communities that rely on our local estuaries.

SPATIO-TEMPORAL VARIATIONS OF COCKLE, *CERASTODERMA EDULE*, PATHOLOGIES IN THE RIA DE AVEIRO, PORTUGAL

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Bivalves hold significant ecological and socioeconomic value. They shape and sustain habitats for other species, support marine food webs and biodiversity, and make up a significant portion of the world's fishery sector. The common cockle, *Cerastoderma edule,* is one of the most abundantly found and exploited species in the estuaries of the northeast Atlantic-European coast. In Portugal, the commercial harvesting of cockles has noteworthy socioeconomic importance as *C. edule* is widely exploited, supporting vital commercial bivalve fisheries namely in the Ria de Aveiro coastal lagoon. The increasing importance of shellfish harvesting in Portugal requires a good knowledge of the health of cockle stocks; however, there is still a large gap in the knowledge of cockle pathologies in Portugal. Studying them is crucial for maintaining estuarine ecosystem health and dependent communities as understanding the spreading mechanisms of diseases and parasites can help develop mitigation strategies, effective monitoring, and identify areas vulnerable to disease outbreaks. Aiming to assess the spatio-temporal variations in cockle pathologies in the Ria de Aveiro, a one-year monitoring was conducted in 18 sampling stations covering the entire cockle distributional range. The biodiversity of parasites, assessed through histology, consisted of hemocytosis, *Rickettesia*-like organisms (RLO), disseminated neoplasia, *Trichodina* sp., *Rynchodida-like* organisms, *Gregarina* sp., *Nematopsis* sp., *Haplosporidium* sp., acoccidian, sporozoan and metazoan clades/pathologies being RLO and *Nematopsis* sp. the most prevalent. Results showed a general spatial and temporal homogeneity of the parasites communities. Nevertheless, hot spots of infection were identified with respective identification of the correlated environmental drivers.

AN OPEN-SOURCE METHOD FOR DEWATERING MICROALGAE CULTURES FOR USE IN LIVE FEED PRODUCTION

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Microalgae cultivation is a necessary component to shellfish hatchery production; however, the time, space and funds required to produce live microalgae for feeding different stages of shellfish is costly. To reduce these costs an open-source method of dewatering large-scale microalgae cultures was developed using a single-pump tangential flow hollow fiber filtration system. Microfiltration and ultrafiltration methods allow for concentration of microalgae cells with reduced shearing, where any shearing is mostly due to the pump or sharp angles in the plumbing of the filter. While there are other ways to concentrate cells, such as centrifuging, these methods can cause cell damage or an increase in effort for limited output. The goal of this filtration project is to create a live, cell-dense output that can be cold-stored but remains viable for feeding when needed. All stages of shellfish larvae, postset, seed, and broodstock require a variety of microalgae species in their diet, so common aquacultured species were tested to ensure the filtration method is transferable. Concentrates of *Tisochrysis lutea*, *Tetraselmis* sp., *Thalassiosira weissflogii*, and *Chaetoceros muelleri* were collected via ultrafiltration, and the cells were analyzed to determine viability after being cold-stored with and without aeration. Future work will include trials of feeding concentrates to various stages of shellfish, as well as other live feeds that require microalgae, such as copepods and larval fish.

TEMPERATURE STRESS HAS DIFFERENT IMPACTS ON MICROBIOMES IN DIFFERENT TISSUES IN OYSTERS

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Disease related mortalities in cultured molluscs are often associated with changes in environmental temperature. Elevated environmental temperatures are usually considered as a condition that facilitate disease development by enhancing the pathogenicity of the opportunistic pathogens and/or by depressing host physiological functions such as immunity. In the meantime, it is now believed that the transition of host and environmental microbial ecology from a symbiotic microbiome to a pathogenic pathobiome, which involves changes in compositions and ecological functions of the involved microbiota, represents a cause of diseases. Therefore, a disease and associated mortalities can be preceded by changes in host and environmental microbiomes.

To study the impact of rearing water temperature on oyster tissue microbiomes, the microbial compositions and diversities in the gills, mantles, digestive glands, and hemolymph of Kumamoto oysters, *Crassostrea sikamea,* were analyzed using 16S rRNA sequencing. Oysters placed at 20°C, 28°C, 35°C, or a gradually increasing temperature from 20°C to 35°C were sampled for tissues on 0, 5, 10, and 15 days after the placement. The analysis results indicated that the total OTU differed significantly among tissues but increased in all tissues as the temperature elevated. Differences in dominant taxa were also observed among tissues. In addition, the microbial diversity in the hemolymph of oysters treated at 35°C decreased significantly. These preliminary findings suggest that high temperature alters the microbiomes of different tissue compartments differently and the effects may favor the formation of the pathobiome in cultured oyster.

ISOLATION AND CHARACTERIZATION OF *BACILLUS* SPECIES WITH PROBIOTIC EFFICACY AGAINST COMMON AQUATIC PATHOGENS IN *PENAEUS* (*LITOPENAEUS*) *VANNAMEI*

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Shrimp aquaculture is a thriving and globally recognized industry. Shrimp culture production plays an important function in the Aquaculture industry. Shrimp export accounts for 17% of all marine foods exported globally. Bacterial infections have developed as a serious issue in culture fisheries, and they are the most significant difficulty confronting this business. Bacterial germs can also cause harmful infections, such as the illnesses produced by the *Vibrio* genus of bacteria and the bacteria that cause necrotizing hepatopancreases (NHP). These are the most common illnesses that cause infections in prawn farms.

The study aims to explore the potential probiotic bacteria isolated from white shrimp (*Penaeus vannamei*) and evaluate its effectiveness against common aquatic and human pathogens. The objective of this study is to identify new potential probiotic candidates that can be used to improve the health and growth of shrimp and potentially, other aquatic animals. The effectiveness of the selected probiotic strains were tested against common fish pathogens that are responsible for various shrimp diseases. The probiotic strains were also tested against human pathogens to evaluate their potential use in human health. Samples were collected from Thondi, Madurai District. Various types of agar medium were prepared, and the bacterial culture were serially diluted. The samples underewent different test like citrate utilization test, catalase test, indole test, methyl red test, Proskauer test, and pH tolerance test. Based on these results, two *Bacillus* sp. have high probiotic potentiality against common pathogens that affect aquatic creatures were characterized. These two bacterial strains can be used for future research in aquaculture, and they also showed activity against human pathogens so they can be also used for human research as well.

OPTIMIZING STOCKING DENSITIES FOR ENHANCED GROW-OUT PRODUCTION OF BAY SCALLOPS, *ARGOPECTEN IRRADIANS*

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The Atlantic bay scallop (*Argopecten irradians*) stands out as a highly sought-after mollusc with considerable market value. Its fast growth and capacity for successful hatchery seed production elevates its status as a viable candidate for aquaculture. Stocking density is an important aspect during the grow-out phase of aquaculture as it plays a pivotal role in ensuring each scallop has enough space to grow, feed, and access oxygen. Density has also been shown to affect parasite prevalence. Since 2012, a novel trematode parasite began infecting bay scallop populations in North Carolina, and in following years has been observed in Florida populations. This study investigated the effect density has on the growth, survival, condition, and trematode prevalence of bay scallops. Growth and survival, as related to stocking density, will be investigated for a 6-month grow-out period using 4mm mesh bags housed within 3-bay OysterGro® LowPro Plus™ (floating cages). Three stocking densities were investigated: Low = 50 scallops per bag, Medium = 150 scallops per bag, and High = 250 scallops per bag. Scallops were deployed at three locations with three replicates of each density at each location. Over the 6-month grow-out period, the three locations were sampled monthly for abundance (n) and 20 scallops of each replicate will be measured (length, width, height) and checked for trematode infection.

ESTABLISHMENT AND EVALUATION OF REGIONALLY CROSSBRED NORTHERN QUAHOG (= HARD CLAM)

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Northern quahog (= hard clam) (*Mercenaria mercenaria*) aquaculture is currently impacted by mass-mortality events caused by Quahog-Parasite Unknown (QPX). The growth of cultured clams is slow and needs to be improved. To determine if the performance in QPX resistance and growth can be improved by interstrain hybridization, the following four hybrid and pure crosses of hard clams in summer 2023 were produced: a New York hatchery (NYH) stock selected for QPX resistance, a wild stock from Barnegat and Great Bays of New Jersey (NJW), a hybrid cross (HYB) between NYH and NJW, and a hatchery stock from New Jersey (NJH). The four groups were produced by mass spawn of 12 – 23 parental clams with 4-5 replicates per group. No difference was observed in larval size among the groups from day 1 and day 14. Survival to D-stage at Day 1 was significantly lower ($p < 0.05$) in the hybrid cross than other crosses. Larval survival from D1 to Day 7 and Day 14, however, was significantly higher ($p < 0.05$) in the hybrid cross. After metamorphosis, the number of juveniles survived to 3-5 mm was 51,780 for HYB, 24,500 for NJW, 2,450 for NJH and 1,788 for NYH. While preliminary, results of this study suggest that the hybrid cross has higher larval survival after D1, which may be attributable to increased genetic diversity.

TRANSMISSIBLE CANCER AND MICROPARASITES IN *CERASTODERMA GLAUCUM* FROM THE BALTIC SEA

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The Baltic Sea possesses unique physical and chemical characteristics stemming from its confinement. Notably, 70% of benthic fauna of Polish Baltic Sea is represented by four key species: *Macoma balthica, Mya arenaria, Mytilus trossulus,* and *Cerastoderma glaucum*. While disseminated neoplasia cases have been documented in the first two species, the transmissible nature of this cancer has only been confirmed in *M. balthica;* however, extensive documentation of parasites affecting these bivalves in these particular waters remains limited, primarily focusing on studies of macroparasites like trematodes and copepods. This study is the first detailed description of microparasites affecting *C. glaucum* within the Baltic Sea. Histological preparations revealed intracellular colonies of rickettsia-like organisms in the gills and digestive tubules, along with branchial ciliates such as *Hypocomella* spp., *Sphenophrya* spp., and *Trichodine* spp., Apicomplexan coccidia and gregarines. Furthermore, this study identified the presence of disseminated neoplasia, and molecular analyses suggest a potential new lineage of bivalve transmissible cancer.

ASSESSMENT OF METHODS FOR HIGH-QUALITY DNA EXTRACTION FROM PARAFFIN-EMBEDDED BIVALVE SAMPLES

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The determination of parasites through histological sections is considered a gold standard method for many pathologies; however, the conventional tissue fixation solutions, commonly formalin-based, compromise the integrity of nucleic acids, posing challenges for using these samples in high-quality genomic studies. This study compared DNA integrity of paraffin-embedded samples of *Mya arenaria* fixed with Davidson's solution and the commercial solution Paxgene. Furthermore, DNA degradation over time has been evaluated for histological blocks stored under standard laboratory conditions. The use of Paxgene solution for tissue fixation enables the extraction of higher-quality DNA without altering tissue morphology, facilitating histological analyses. Nevertheless, this good nucleic acid integrity is not sustained over time.

DETECTION OF TRANSMISSIBLE CANCERS IN COCKLES USING MOLECULAR DIAGNOSTICS

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Transmissible cancers are a rare phenomenon in which cancer cells are passed between individuals, leading to the development of neoplasia in the host organism. Transmissible cancers have been detected in up to 10 different bivalves around the world and its transmission occurs through cancer cells that live in seawater. This study focused on the development of a PCR assay designed to identify two types of transmissible cancers detected in cockles *Cerastoderma edule* (CedBTN1 and CedBTN2). The assay demonstrated high sensitivity, detecting cancer lineages at low DNA concentrations and low percentages of circulating cells. Moreover, it exhibited high specificity, accurately identifying the targeted cancer types without cross-reactivity with other species sharing the habitat. The methodology established in this study offers a rapid, cost-effective, and user-friendly approach for early detection, monitoring, and prevention of transmissible cancers in cockles.

DESIGN OF AN EXPERIMENTAL RECIRCULATING SYSTEM TO ASSESS THE EFFECTS OF OCEAN ACIDIFICATION ON SURVIVAL AND GROWTH OF LARVAL EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*

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Ocean acidification poses significant threats for oysters. As oceanic CO_2 levels increase, carbonate saturation state decreases and impedes shell synthesis. The estuarine ecosystem is especially vulnerable to changing carbonate chemistry conditions from ocean acidification due to their generally low alkalinity levels and low buffering capacities. Oyster hatcheries, typically located along estuarine coasts, are vulnerable to the negative effects from ocean acidification. Little is known about the combined effects of suboptimal aragonite saturation, low pH, alkalinity, CO_2, and salinity on larval growth and survival.

This project examines individual and combined effects of aragonite saturation state and salinity on survival and growth of oyster larvae. Previous research usinghavecirculating larval rearing systems and altered pH has been done, however, all used large-volume systems and examined only a few parameters at a time. This project requires a low-volume, recirculating artificial seawater system that can maintain four salinities, three pCO_2 levels, and two alkalinities comprising twenty-four combinations in triplicate for a total of 72 tanks. Each water type is mixed in a sump and delivered to the respective replicate tanks using headboxes. CO_2 is dosed directly into the sumps using pH sensors and solenoids to regulate CO_2 flow to achieve the desired pH. High flow rates, bacterial loads, and CO_2 dosing rates caused mass mortalities across all tanks. The cuboid tanks also trapped and killed larvae in the corners. Cylindrical, round-bottom tanks, increased flow and CO_2 control, increased aeration to prevent larval entrapment, and increased mesh surface area to reduce clogging are being evaluated.

THE EFFECTS OF ULTRAVIOLET TREATMENT THROUGHOUT THE LARVAL REARING OF NORTHERN QUAHOGS (= HARD CLAMS) (*MERCENARIA MERCENARIA*)

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Within aquaculture and the rearing of larval shellfish, the use of ultraviolet sterilizers is often widely debated. The common thought surrounding the use of ultraviolet sterilizers is that they will severely limit the potential for harmful bacteria, pathogens, and/or other microorganisms from negatively affecting larval shellfish cultures. This in turn results in higher survivability of the animals being cultured.

This study looked to explore the use of ultraviolet sterilizers and the effects they may have during the rearing of larval northern quahogs (= hard clams), *Mercenaria mercenaria*. Two groups of larval *M. mercenaria* were reared in either ultraviolet treated water or non-ultraviolet treated water. These groups were monitored and maintained throughout their larval period, with data being collected regarding the population(s) density/mortality and average shell size of the animals. The study found that the groups reared in water not treated with the ultraviolet sterilizer largely outperformed those that were reared in the treated water. At the end of the study the average population density of the ultraviolet treated groups was 301 animals, while non-ultraviolet treated groups averaged 18,675 animals. Resulting in the non-ultraviolet treated group populations being 62 times greater. Notably, the average shell size of the non-ultraviolet treated *M. mercenaria* also out competed those that were ultraviolet treated with an average difference of 15 microns. The findings of this study suggest that *M. mercenaria* larvae cultured in untreated seawater performed better than those reared in ultraviolet treated seawater, possibly due to differences in microbiome or water chemistry.

CHROMOSOME-LEVEL REFERENCE GENOME FOR THE CHILEAN FLAT OYSTER, *OSTREA CHILENSIS*

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The flat oyster, *Ostrea chilensis* (Küster, 1844), is native to Chile and New Zealand. It occurs in a few natural beds in Chile, from the northern part of Chiloé Island (41°S) to the Guaitecas Archipelago (45°S). This bivalve is a slow-growing and brooding oyster with limited dispersal potential. The *Ostrea chilensis* fishery has been over-exploited for several decades such that in some locations, oysters no longer exist. This study aimed to report the first chromosome-level reference genome for *O. chilensis*. Using proximity ligation technology, a contig assembly using PacBio HiFi sequencing was scaffolded into the expected karyotype of 10 chromosomes. The final assembly is 789.2 Mb, with a scaffold-N50 of 90.12 Mb, with a predicted repeat landscape dominated by unclassified elements. Genome annotation integrating transcriptome data, comparative protein evidence, and ab-initio gene prediction identified 38,765 protein-coding genes. Chromosome-level synteny was explored against the European flat oyster, *O. edulis*, genome. The Chilean flat oyster genome represents pivotal knowledge for developing novel management strategies to promote the sustainable use of this valuable marine resource.

SUPPORTING THE OYSTER AQUACULTURE INDUSTRY WHILE ACHIEVING RESTORATION GOALS ON MARTHA'S VINEYARD, MASSACHUSETTS

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The Martha's Vineyard Shellfish Group (MVSG) has worked with the local shellfish departments to support, enhance, and restore the naturally occurring oyster populations of Martha's Vineyard for over 40 years. The oyster stocks are constantly challenged by dermo disease, eutrophication-driven environmental degradation, and fishing pressure. Since 2021, MVSG has partnered with the Nature Conservancy to implement the SOAR (Supporting Oyster Aquaculture and Restoration) model on Martha's Vineyard. With the help of TNC, local oyster growers and the Edgartown Shellfish Department, hundreds of thousands of cultured oysters, not worthy of the half shell market, have been planted within a town-designated oyster sanctuary area. Several restoration benchmarks have been reached, including wild sets of oyster spat which have not occurred in several years. This poster will discuss the wide-reaching benefits of these partnerships and how they have impacted the aquaculture community on Martha's Vineyard. Monitoring methods employed to continuously evaluate the efficacy of SOAR and other restoration efforts will be shared, as well as lessons learned in the process.

INTERACTIONS BETWEEN TOXIC DINOFLAGELLATE *ALEXANDRIUM PACIFICUM* EXPOSURE AND INCREASED WATER TEMPERATURE IN *PERNA CANALICULUS* SPAT

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The *Alexandrium* spp. is a globally distributed harmful algal bloom (HAB)-forming genus of dinoflagellate which can produce a range of biotoxins including paralytic shellfish toxins (PST) and other unelucidated bioactive extracellular compounds (BEC). Since 2011, blooms of *Alexandrium pacificum* have been occurring annually in the Marlborough Sounds of New Zealand, a significant farming location for the key aquaculture species, *Perna canaliculus* (= green-lipped mussels, GLM). In the years since blooms of *Alexandrium* spp. began in the Marlborough Sounds, there has also been a major reduction in wild spat fall of GLM (juvenile mussels) in this area. GLM are not only exposed to annual blooms of *A. pacificum,* but also to increasing ocean temperatures and marine heatwaves, further adding to a complex environment for GLM populations.

In this work, GLM spat were exposed to either typical (17°C) or warmer temperatures (22°C) and fed a lower or higher ration of paralytic shellfish toxin-producing *A. pacificum* cells. Spat exposed to a combination of high HAB exposure and warm temperatures had the highest mortality rate, with 39% mortality compared to 0-15% in other treatments. Exposure to the toxic dinoflagellate at 17°C had a more negative effect on growth than when combined with high temperatures. Byssal plaque production was significantly reduced with HAB exposure, indicating a potential impact on the ability of GLM spat to anchor themselves to a substrate. These results, combined with histological and transcriptomic analyses, will further enhance knowledge of how multiple stressors could impact GLM spat populations.

TELOMERIC REPEATS IN PENAEID SHRIMP AND BIVALVES – A REVIEW AND RESEARCH NEEDED FOR *PENAEUS VANNAMEI*

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Telomeric repeats, which are critical for chromosomal stability, are highly conserved. All vertebrates and some protozoans, slime molds and fungi share the same telomeric repeat of (TTAGGG)n. Green algae use (TTTTAGGG)n as telomeric repeats, and most higher plants have (TTTAGGG)n. Bivalve molluscs have the same telomeric repeat as vertebrates. The shrimp *Penaeus vannamei* shares the same telomeric pentanucleotide repeat (TTAGG)n with most insects. Telomeric repeats in the shrimp are not limited to telomeres or subtelomeric regions. They are widely distributed in the genome and sometimes associated with higher order repetitive elements and fossilized viral sequences. Three recently sequenced *P. vannamei* genomes confirms that the telomeric repeat (TTAGG)n is highly abundant and widely distributed in intron and intergenic regions of the genome. They are also the site of insertion of nimavirus *Nimav-1_LVa*. The wide interstitial distribution of telomeric repeats is intriguing and may have important implications for the shrimp genome that is also rich in other simple sequence repeats. The evolutionary origin of telomeric repeats is not fully understood, but it has been suggested that the invasion of circular chromosomes by telomeric repeats may have given rise to linear chromosomes of eukaryotes. The wide interstitial distribution of telomeric repeats in the shrimp genome may represent extensive, recent, or active invasion by the pentanucleotide repeat. Considering that the estimated genome size of SPF *P. vannamei* from the United States is 2.89 Gb, a new contiguous, whole reference genome for *P. vannamei* is needed to fully characterize telomeric repeats.

MULTIFACETED STUDY OF AN ONGOING RANGE EXPANSION OF BLUE CRABS (*CALLINECTES SAPIDUS*)

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Blue crabs (*Callinectes sapidus*) historically ranged from Cape Cod, Massachusetts (USA) to Uruguay, though in recent years have had an increased presence within the Gulf of Maine. Understanding this natural range expansion is crucial for getting a glimpse into how marine crustaceans may respond to the impacts of ongoing anthropogenic climate change, particularly regarding their complex, multi-step life cycles. Reports of blue crabs within the Gulf of Maine date back to the 1860s, primarily during warmer years, though from 2016 onward, their presence in southern Maine has been more consistent. This project seeks to understand the temporal dynamics and trophic impacts of blue crabs within this novel environment. To understand blue crab temporal dynamics, both environmental DNA (eDNA) and traditional survey methods were used in southern Maine. To understand trophic impacts, DNA-based gut content analyses were used to understand whether these crabs are likely to impact key shellfish species (e.g., softshell clams, lobsters), and stable isotopes to characterize their trophic niche. This presentation will demonstrate the methods used for understanding this ongoing range expansion, determine likely impacts of blue crabs on key Gulf of Maine shellfish, and what long-term outcomes could arise from a warming world for marine crustaceans.

PRODIGIOUS PEARLS: AN EXTREME INCIDENCE OF PEARL FORMATION IN THE RIBBED MUSSEL

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All calcareous molluscs are capable of producing pearls in response to an irritant, and the literature abounds with records of pearls in numerous taxa. Here, the first-known documented case of pearls in the ribbed mussel, *Geukensia demissa*, as well as the highest density (#/individual) of pearls reported in any bivalve will be discussed. At a single location in the Chesapeake Bay, pearls were incidentally discovered in ribbed mussels from samples collected in 2016. Numbers per individual ranged from 0 to 1,397, and ranged in size from 0.1 to > 2.0 mm, with a median diameter of ~0.5 mm. A targeted follow-up collection in 2022 found pearls in 23 of 40 mussels collected across the surface of the marsh. When present, counts ranged from 4 to 2361 pearls per mussel, with a median of 522 pearls. The median pearl diameter was 0.42 mm. A statistical analysis of pearl counts found that both distance into the marsh (m) and mussel density (individuals/m^2) were positively correlated with the number of pearls, while mussel length (proxy for age) did not have an additional directional effect. Histopathological analysis of the *in-situ* pearls suggested an organic irritant, likely a trematode parasite. The most likely candidate is *Proctoces maculatus*, but genetic analyses have yet to provide a positive identification.

PARALYTIC SHELLFISH TOXIN CONGENER PROFILES IN THREE SPECIES OF BIVALVE MOLLUSCS FROM RESURRECTION BAY, ALASKA, DURING THE SUMMER OF 2021 AND 2022

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Traditional subsistence food, such as shellfish, is integral in food security and culture for coastal Alaska Native and rural Alaskan communities. The presence of algal biotoxins in Alaska marine waters threatens food security, public health, and culture 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 cantanella,* have been associated with illness and death in Alaska for centuries, yet there is limited capacity for PST testing for subsistence and recreationally harvested shellfish. This project aims to understand toxicity and congener profiles of three different species, at a local recreation and subsistence shellfish beach, during the summers of 2021 and 2022. From April to September of 2021 and 2022, bi-weekly samples of three different bivalve species: blue mussels (*Mytilus edulis*) (n = 31), softshell clams (*Mya arenaria*) (n = 31), and cockles (*Clinocardium nuttallii*) (n = 24) were collected from Afognak Beach in Resurrection Bay. These samples were analyzed by the Department of Environmental Conservation using high-pressure liquid chromatography to identify PST congeners. Results showed measurable toxin levels in 16 of the 31 (51.6%) blue mussel samples, 3 of the 31 (9.7%) softshell clam samples, and 0 of the 24 (0%) cockle samples. All samples tested were below the FDA regulatory limit of 80 µg STX eq. $100g^{-1}$, with the highest toxin sample measuring at 9.63 µg STX eq. $100g^{-1}$.

GROWTH AND PLOIDY COMPARISON OF FOUR SELECTIVELY BRED TETRAPLOID LINES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Tetraploid oysters play a crucial role in oyster aquaculture, particularly in the production of triploid oysters. Tetraploid oysters can mate with normal diploids and produce 100% triploids that have three sets of chromosomes. Triploid oysters are favored by farmers due to their fast growth rate, better meat quality, and year-round harvest. In June 2022 four tetraploid lines were produced using one (WX1), two (WX2), three (WX3), and four (WX4) year-old tetraploid parents to determine if age plays a role in chromosome regression within the resulting progeny. Groups were deployed in three replicate bags on an intertidal flat for evaluation. All groups were sampled (50 per group) and measured over 18 months with the most recent sampling occurring in November 2023. While there is no significant difference between ploidy between lines, oysters produced from the oldest year class, WX4, had the lowest shell height and yield whole weight (64.8mm and 30.3g respectively) compared to the oysters produced from younger broodstock (WX1-WX3). Findings suggest that younger tetraploid oysters can effectively be utilized by hatcheries to produce triploid seed.

EFFECT OF $NANO_3$ SUPPLEMENTATION AS NITROGEN SOURCE TO TOTAL LIPID CONTENT OF MICROALGAE USED IN BIVALVE AQUACULTURE

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Accurate and quick evaluation of macro nutrients in microalgae is important to formulate a suitable feeding ration for the cultured animals. Flow cytometry is a technology to measure autofluorescence of single cells samples, providing a cost-effective, quick, and accurate method for analysis of microalgal samples. Microalgal lipids are known for its importance as source of energy and absolutely needed for broodstock sex maturity and larval growth and survival and its production could be enhanced with altering culturing conditions, such as limiting nitrogen supply, and others. This project aimed to evaluate the effects of $NaNO_3$ as nitrogen source on the total lipid production in three species of microalgae (*Tisochrysis lutea, Chaetoceros muelleri*, and *Tetraselmis suecica*). The objectives were to: 1) develop an effective methodology for total lipid measurement by use of fluorescent lipid probe (BODIPY 505/515) with flow cytometry, and 2) evaluate the total lipid production at different $NaNO_3$ supplementation from 0 to 200% of the normal amount. The effective BODIPY staining concentration and time were concluded as 2 mg/mL at 10 min for three microalgal species at room temperature respectively. Through manipulation of $NaNO_3$ level, evaluation of total lipid production indicated that total lipid production was significantly higher ($P < 0.05$) at 0% $NaNO_3$ supplementation for the three species of microalgae. This study proved that limited nitrogen supply can lead to different cellular biochemical pathways and impacting indirectly to lipid productivity.

GENETIC PARAMETERS FOR GROWTH TRAITS IN EASTERN OYSTER FAMILIES REARED IN HIGH AND LOW SALINITY ENVIRONMENTS IN THE GULF OF MEXICO

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The eastern oyster (*Crassostrea virginica*) supports large markets throughout the eastern United States. In recent decades, wild stocks have observed major declines across the species' range including in the Gulf of Mexico (Gulf). In 2019, the SALT consortium initiated a breeding program to support the developing industry in the Gulf with oysters bred for improved performance in different salinity environments. In September of 2020, the first generation was produced using 102 males and 102 females collected from 17 natural reefs between San Antonio Bay (Texas), and Cedar Key (Florida).

Families were bred according to a 2 x 2 factorial crossing design, pooled for common garden culture, and deployed at seven growout sites in April 2021. At the end of the growout period, four sites were selected that represented high (AH) and low (MB, USM, LSU) salinity environments based on salinity conditions recorded during the growout period. The 204 founders and 6,414 offspring were assayed at 192 Single Nucleotide Polymorphism markers and the obtained genotypes were used to assign offspring to parent pairs using a likelihood ratio approach. Genetic parameters were estimated using animal mixed models in ASREML v.4.2. Estimates of heritability at low salinity ranged between 0.63 ± 0.06 and 0.84 ± 0.05 and were significantly higher than the estimate obtained at the high-salinity site (0.38 ± 0.08). Estimates of dominance variance did not differ significantly from zero. Genotype x environment correlations for growth rate ranged from 0.62 to 0.99 and were highest between low salinity sites.

BIODEGRADABLE PLASTIC ALTERNATIVES FOR OYSTER SHELL BAGS IN LIVING SHORELINES FOR OYSTER HABITAT ENHANCEMENT IN THE DELAWARE BAY

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Partnership for the Delaware Estuary and Rutgers University developed the Delaware Estuary Living Shoreline Initiative in 2008 to help stabilize eroding shorelines using a combination of plants, natural structures, and intertidal shellfish. The design and subsequent monitoring of living shorelines differ by the target ecological goals of the installation. Plastic oyster shell bags are routinely used in living shorelines to provide structural stability and promote oyster reef development through oyster recruitment over time. Although plastic mesh is durable and effective for oyster reef development, the mesh contributes to plastic pollution. Biodegradable mesh products are available and may be an effective plastic alternative. Alternative materials must be durable and maintain shell bag structure for multiple years to be an effective solution. Three biodegradable candidates are cellulose, co-polyester, and biopolymer materials; the latter two are both certified compostable, synthesized materials.

This ongoing project explores how environmental factors influence the structural integrity of non-plastic shell bag materials in laboratory, storage, and field settings. Metrics collected include structural and material strength, fouling, and colonized shellfish population density. Observations occurred weekly for the first four weeks and continued monthly thereafter. Preliminary results indicate that cellulose material degrades within weeks and lacks the durability for oyster habitat enhancement; however, it may be useful as a method to deposit loose oyster shells or live shellfish for restoration purposes. The other three materials have remained intact. The final results from this multi-year study will inform recommendations for future living shoreline projects utilizing oyster shell bags.

A MISSING SEX: ENVIRONMENTAL INFLUENCES ON THE POPULATION SEX RATIO OF FARMED PACIFIC OYSTERS IN SOUTHEAST ALASKA

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Pacific oysters (*Crassostrea gigas*) are an important species for the growing Alaskan aquaculture industry; however, expansion is limited by access to oyster seed imported from out-of-state. A key component of a successful oyster hatchery is access to male and female oysters. Pacific oysters begin as males and change to females as they mature. Past studies found higher proportions of females in warm, phytoplankton-rich water, while ratios favored males in less ideal growing conditions. There are no studies on sex ratios of oysters on Alaska (AK) farms. To test the impact of environmental conditions on sex ratio, water samples were collected and 15-20 oysters (aged 2-3 years), from an oyster farm in Juneau, AK for eight weeks. Water samples were analyzed for temperature and phytoplankton abundance. Gonadal samples were viewed under a microscope to determine sex. Results showed a male bias, with hermaphrodites making up approximately 20% of samples; no females were observed. The percentage of hermaphroditic oysters was non-significantly correlated with water temperature and not with diatom abundance. The large proportion of hermaphrodites was surprising, as studies from other regions observed very low (<1%) proportions of hermaphrodites. Hermaphrodite presence could result from cold water inhibiting sex change or sampling highlighting sex transition. Future research should expand sampling throughout the year and investigate older age classes. An improved understanding of the drivers and timing of oyster sex changes will be critical if Alaska is to establish an in-state hatchery industry.

IMPACT OF TEMPERATURE AND FLUCTUATING PH ON PRODUCTION OF THE NORTHERN QUAHOG (= HARD CLAM), *MERCENARIA MERCENARIA*, POST-SET IN FLORIDA

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Results of a previous experiment determined that pH swings did not impact production of post-set *Mercenaria mercenaria*; however, the experiment was conducted at a single temperature. Florida represents the southernmost limit of this clam, with temperatures often exceeding optimal limits. To determine whether increased temperature would impact production under fluctuating pH conditions, a study was conducted that compared production under stable and fluctuating pH levels at two temperatures. Four-week-old clam post-set (825±80, 1350±12 µm) were added to one of four treatments: pH 8.0, 25°C; pH 8 30°C; fluctuating pH 25°C or fluctuating pH 30°C (N=5 replicates) and fed *Tisochrysis lutea* and *Chaetoceros neogracile* twice daily. Growth was evaluated bi-weekly, survival at 6 and 12 weeks, volumetric counts at 4, 8 and 12 weeks, and condition index, and bacterial analysis at experimental termination. Growth was significantly greater ($P < 0.05$) in the 30°C treatments at week 2 and 4, fluctuating pH, 25°C in week 8 and in both fluctuating pH treatments at week 12. Volumetric counts were significantly ($P < 0.05$) different at 4, 8 and 12 weeks and was driven by temperature rather than pH. No difference was seen in survival or condition index. Total bacterial and *Vibrio* colony forming units (CFU) were low and did not differ significantly between treatments. Total bacterial CFU were higher in water samples, while total *Vibrio* CFU were similar between clams and water. Results of this experiment suggest that exposure to fluctuating pH and temperatures up 30°C have no detrimental effect on clam post-set.

OYSTER METAPOPULATION MODELING: LINKING WATER QUALITY, HYDRODYNAMICS, SPATIAL CONNECTIVITY, INDIVIDUAL BIOENERGETICS, AND STRUCTURAL MECHANICS TO SUPPORT RESTORATION IN COASTAL BASINS OF LOUISIANA

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Despite awareness of the importance of maintaining healthy oyster populations, data-driven and process-based information are lacking to guide oyster restoration and management efforts. Part of the challenge lies in the fact that oyster reefs constitute metapopulations, which can be sustainable yet extremely dynamic at a local scale. This project aims to develop a metapopulation model coupling hydrodynamic/water quality modeling (Hydro) with larval transport modeling (Transport) and reef individual based modeling (Reef) to support decision-making in Louisiana estuaries. Environmental variables generated by the Hydro model force the Transport model, which simulates oyster larval settlement over space and time. The Reef model also uses environmental variables from the Hydro model to compute individual oyster bioenergetics on the reef, as well as larval settlement from the Transport model to fuel population dynamics. Finally, the Reef model provides larvae through spawning to the Transport model, which simulates their dispersal. This presentation provides an overview of this model and its application to a major Louisiana estuary for natural oyster reefs and oyster aquaculture. Model outputs include reef connectivity matrices, single reef spawning contribution and available settlement area, on-reef oyster density and individual oyster growth among other metrics. This study is designed to provide managers with a powerful and process-based tool that could be used in for decision-making under both current and projected future conditions.

TRACKING SEA SCALLOP PREDATOR ABUNDANCE FROM 2015-2023

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To effectively and holistically manage the sea scallop (*Placopecten magellanicus*) fishery, managers should consider all biotic and abiotic factors that impact scallop population dynamics. One of these ecological factors is the presence and role of scallop predators. The Virginia Institute of Marine Science has surveyed the sea scallop resource and collected spatio-temporal predator data since 2015 in the mid-Atlantic Bight. Using data from 2015-2023, the presence and intensity of two major starfish predators, *Astropecten americanus* and *Asterias* spp., were mapped and used a population hotspot analysis to identify areas of greater predator abundance. Using point estimates of predator abundance from the surveys, maps were generated across the survey domain to compare predator abundance across species and year. By tracking spatio-temporal shifts in predator abundance, fishery managers can identify potential trends related to ecological shifts such as climate change and anticipate potential impacts to the scallop population and fishery.

STUDIES ON THE YELLOW-GREEN FLESH ATTRIBUTE OF KUMAMOTO OYSTERS, *CRASSOSTREA SIKAMEA*, GROWING IN CHINA

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The Kumamoto oyster, *Crassostrea sikamea,* is a native species on the coasts of China between Jiangsu and Hainan Provinces. The Kumamoto oysters growing in some areas (e.g., the Xiangshan Bay in Zhejiang Province) exhibit a yellow-green color in mantle and gills and color intensity of the flesh is often treated as an indicator attribute for the oyster quality. In contrast, Portuguese oysters, *Crassostrea angulata*, another native oyster species on the southern coasts of China growing closely in the same environments, always show a white color in the flesh.

To investigate the substances that determine the flesh color attribute in *C. sikamea*, its copper contents in the oyster soft tissues were compared with that of the *C. angulata* from the same growing site. The measured results of both the whole flesh part and the mantle tissues showed that Portuguese oysters contained significantly more Cu than the Kumamoto oysters ($P<0.05$), indicating that the yellow-green flesh attribute was unlikely related to elevated Cu contents in tissues. Additionally, algal enrichment culture of oyster gill homogenates in f/2 medium did not observe algal growth in either oyster species, excluding the presence of algal symbionts. Interestingly, the chromogenic substances could be extracted from tissues with 10% SDS and 1% $NH_3 \cdot H_2O$; however, the substances were not detected to have any significant absorbance peak in the wavelength between 200 and 1000 nm. These results suggest that the substance basis for the flesh color attribute of Kumamoto oysters likely involves molecules yet to be investigated.

A RELIABLE NON-DESTRUCTIVE TISSUE SAMPLING METHOD FOR THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Non-destructive sampling of eastern oyster, *Crassostrea virginica*, tissue is important for physiology, pathology, and genetics research. It can be used to observe gonad development during broodstock conditioning, track pathogen load in disease-challenged animals, and genotype selected oysters for estimating breeding values. The USDA ARS NCWMAC developed a straight-forward anesthesia and biopsy protocol routinely used in experimental work which includes a 45–60-minute air exposure, overnight incubation in an aerated 5% (w/v) Epsom salt bath, and removal of ~ 5mm tissue from gaping oysters.

To test the limits of the protocol, two experiments were conducted. The first addressed how sampling frequency affects gaping success and survival. Oysters were divided into three groups: control, anesthesia + biopsy on Day 0, and anesthesia + biopsy on Days 0 and 7. Gaping success was high overall but reduced in oysters anesthetized on both Day 0 and Day 7. Survival of oysters experiencing the protocol twice (57%) was lower than those experiencing the protocol once (77%). The second experiment focused on survival in two-year classes exposed to anesthesia alone or anesthesia + biopsy on Day 16 of a 50-day experiment. Gaping success was high across treatments, but slightly lower in year class 1 compared to year class 2. Very little mortality in this experiment (< 5%) was seen and there was no meaningful difference in survival between treated groups and controls. Taken together, results suggest this is an effective single-use, non-destructive sampling protocol. More work is needed to assess its utility at higher frequencies.

COMMERCIAL FIELD PERFORMANCE TRIAL OF TWO CLAM CONGENERS IN COASTAL GEORGIA, USA

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The population of *Mercenaria campechiensis* ranges from the Chesapeake Bay to Florida and then west to the Yucatán Peninsula. This species co-occurs with the northern quahog throughout the southern range of *M. mercenaria* where hybridization between species occurs. In Georgia, there is commercial interest in the culture of southern quahogs within the state to reduce heat losses observed with northern quahog culture. Southern quahogs reportedly have higher growth and survival rates than northern quahogs at warmer water temperatures. This research evaluates the field performance of southern versus northern quahogs at three different sites on a commercial clam farm in Sapelo Sound, Georgia in an effort to determine if clam farmers can offset summer losses observed with farming northern quahogs in the south. Clam seed were deployed in separate plots at each site in multiple arrays of six ~1m^2 soft nylon mesh clam bags during October 2021. Survival, growth, and condition index data were collected quarterly from each site through October 2023. Temperature and salinity were collected continuously with HOBO loggers at each site over the course of the field deployment. Research was supported by NOAA award number: NA21NMF4270355. Results will be discussed herein.

RECONSTRUCTING BOTTOM WATER TEMPERATURES FROM BIVALVES ON THE CONTINENTAL SHELF: HOLOCENE HISTORY AS A WINDOW TO THE FUTURE IN THE MID-ATLANTIC

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The history of climate change recorded by the shells of long-lived bivalves can provide information on past climatic changes and the impact of these changes on ongoing and projected range shifts. This study uses oxygen isotopes and growth rates recorded in shells of the Atlantic surfclam (*Spisula solidissima*) and the ocean quahog (*Arctica islandica*) to reconstruct bottom water temperatures on the mid-Atlantic continental shelf, including the Cold Pool region over the last ~5,000 years. Additionally, this study aims to describe the range dynamics of the cold temperate Atlantic surfclam and boreal ocean quahog on the mid-Atlantic continental shelf. The study will determine the historical frequency and, where possible, rapidity of major climatic changes and corresponding range shifts since the beginning of the Neoglacial Period, the potential climate drivers of bottom-water temperatures associated with the range changes, and the effects of bottom water temperature changes on the timing of mortality events. Bottom-water temperature proxies are developed from clam growth rates paired with modern bottom-water temperature observations, and for earlier times, clam shell oxygen isotopes. These data are used to develop relationships between growth increment width and temperature using animals with birthdates over the last 5,000 years, that - together with spatial information from eddy-resolving ocean models - inform spatial-temporal reconstructions of bottom water temperatures.

A COMPARISON OF METHODS TO ESTIMATE SIZE-AT-MATURITY FOR CHANNELED WHELKS (*BUSYCOTYPUS CANALICULATUS*) FOUND IN MASSACHUSETTS

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The channeled whelk (*Busycotypus canaliculatus*) is a benthic marine gastropod that supports a niche fishery in Massachusetts and is regulated by the Massachusetts Division of Marine Fisheries (DMF). In 2019, the DMF biennially increased to the minimum landing size by 3.175 mm, after fishery independent surveys showed no mature females at the legal-size limit (76.2 mm) and an increase in landings in early 2010s. The schedule was revised in the fall 2022 to occur every three years until 2033. The terminal gauge size (92.08 mm) may result in the removal of mainly large reproductive females from the population. To estimate size-at-maturity, a collaboration between industry partners and independent whelk fishers enabled the School for Marine Science and Technology (SMAST) to weigh, measure, dissect, and sex approximately 1,949 (n=1,260 males, n=686 females, n=3 unknown sex) whelks from December 2021 until November 2023 from four survey areas in Massachusetts. Histology was processed on 337 (n=178 males, n=159 females) whelks from December 2021 until November 2022 from three survey areas in Massachusetts. Macroscopic assessment of the gonads was compared to histological assessment to determine size-at-maturity for males and females. Macroscopic results show males reached 50% sexual maturity at a smaller shell width size range (59.8 - 72.9 mm) than females (86.3 - 103.1 mm). Histology was used to verify size-at-maturity for both male and female whelks. Ocean temperatures affect reproduction in channeled whelks, and with rising ocean temperatures a new baseline study to assess data limited whelk stocks is essential.

RECRUITMENT PATTERNS OF OYSTERS AND RIBBED MUSSELS ON A NATURE-BASED LIVING SHORELINE IN DELAWARE BAY, USA

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Living shorelines are a nature-based tactic for enhancing ecosystem services and protecting coastal wetlands. This approach often utilizes materials resourcefully; living shorelines utilize bags of recycled oyster shell. Oyster shells provide habitat for native shellfish like oysters (*Crassostrea virginica*) and ribbed mussels (*Geukensia demissa*), which provide water quality benefits and habitat for other species. These installations are commonly referred to as shellfish-based living shorelines.

In 2014, Partnership for the Delaware Estuary (PDE) installed a shellfish-based living shoreline along the Mispillion River, a Delaware Bay tributary rich with shellfish recruitment activity. Oyster recruitment monitoring began in 2014, and five additional shell bags were installed in three zones within the 2014 installation for a complementary recruitment study in 2022. In fall 2023, a shell bag from each zone of the 2022 installation was deconstructed to evaluate shellfish recruitment to compare bag contents between installations and evaluate recruitment activity over time. Monitoring also included oyster counts from 30 random points in each zone within the 2014 installation. In the low zone of the 2022 installation, oyster shell lengths were larger (41 ± 17 mm) than those at the other installation points (28 ± 12 mm, 33 ± 12 mm) for mid and high regimes respectively. Random point monitoring data from 2023 was just collected; preliminary data indicate consistent but low recruitment in the high reef zone (i.e., exposed during low tide). Comparisons to earlier installations will contribute to improved understanding of shellfish recruitment and PDE-led development of shellfish-based living shorelines.

MONITORING SURFCLAMS AT OFFSHORE WIND ENERGY PROJECT SITES IN THE MID-ATLANTIC

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The Atlantic surfclam fishery is among the most susceptible 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 mid-Atlantic 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 offshore wind lease locations. Surveys of the wind lease area and control locations will continue annually through the construction and early operation of two wind farms, and a before-after-control-impact sampling design will allow changes in clam abundance due to the wind project to be evaluated. Experiments to calibrate the dredge by quantifying its size selectivity and sampling efficiency have been completed, allowing data from this sampling tool to be compared to, and potentially integrated with, long-term federal survey data.

Survey habitats 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) have been measured with carbonate chemistry observations at the sampling locations. Coordinated survey programs will enhance understanding of how important fisheries resources may be impacted by construction of offshore wind projects and future environmental conditions.

A NEUROPHYSIOLOGICAL FUNCTION FOR GLUTAMATE IN GANGLIA OF THE BIVALVE *CRASSOSTREA VIRGINICA*

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Glutamate neurons (GN) are excitatory neurons in mammals and various invertebrates. GN disfunctions are associated with Parkinson's and Alzheimer's diseases. GN have not been reported in *Crassostrea virginica;* however, NMDA glutamate receptors are reported involved in metamorphosis in some bivalves. GABA is synthesized from glutamate. In *C. virginica* and other studied bivalves, gill lateral cells (GLC) are innervated by cilio-excitatory serotonin and cilio-inhibitor dopamine nerves from their visceral ganglia (VG). GABA has been detected in *C. virginica*, having a neurophysiological function inhibiting serotonin neurons. To test the hypothesis GN function in VG of *C. virginica,* effects of glutamate application to VG on GLC cilia beating rates were studied. Applying glutamate to VG increased GLC cilia beating from 5 to 20 beats/sec. When repeated in the presence of dextromethorphan hydrobromide (DMT), a NMDA receptor antagonist. DMT reduced cilia beating to 0 beats/sec. Applying glutamate after DMT did not increase beating rates. The study revealed a neurophysiological role for glutamate as an excitatory neurotransmitter in VG, possibly exciting serotonin neurons. DMT results are inconclusive and need to be further investigated. DMT does have side effects, including decreasing reuptake of catecholamines. If DMT is decreasing reuptake of dopamine in VG, that could cause the deceased beating rates observed, as the cilio-inhibitory actions of dopamine, a catecholamine, would be increased. The work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0537231071 of the NYSDoE-CSTEP program, P120A210054 of the DoE-MSEIP Program and K12GM093854 of the NIH IRACDA Program of Rutgers University.

SHELL COLOR VARIATION IN SELECTED EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*

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The eastern oyster, *Crassostrea virginica*, is found along the east coast of North America, spanning from the Gulf of St. Lawrence to the Gulf of Mexico, where it plays a vital ecological and economical role. Shells of the eastern oyster display variation in color which may be influenced by genetic and environmental factors. How shell color affects the fitness and adaptation of *C. virginica* is not clear. This study compared the coloration of the top and bottom shells of selected and wild stocks of *C. virginica*. Juveniles from six hatchery-produced stocks (~96 per group) were analyzed for shell color pattern and pigment intensity. The six stocks included selected lines from Maine (ME), New York (NY), New Jersey (NJ), their hybrids, and a wild stock from Delaware Bay (DB). The top shell was classified into four patterns: dark, light, negative, and positive pen-stripe, and pigment of the bottom shell were scored from 1 – 4 with 4 being the darkest. Color pattern and intensity did not affect whole body weight. All selected stocks showed more dark top shells and intensely pigmented bottom shells than DB wild stock. The selected stock from NY had more dark top shell with no or negative stripes, while selected stocks from ME and NJ (NEH®) had more light top shells with positive stripes. Whether shell color is associated with thermos-adaption in the eastern oyster requires further investigation of wild stocks from wide geographic regions.

MONITORING GULF WEDGE CLAMS, *RANGIA CUNEATA*, TO ASSESS ECOLOGICAL RESPONSES TO CHANGES IN FRESHWATER INFLOWS IN THE UPPER CALOOSAHATCHEE RIVER ESTUARY IN SOUTHWEST FLORIDA

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Several monitoring and research efforts are conducted to evaluate collectively the current recommended Minimum Flow and Minimum Water Level (MFL) criteria for the Caloosahatchee River Estuary (CRE) in southwest Florida. Specifically, these efforts will document ecological responses of indicator species before and after operation of a newly constructed reservoir to determine benefits of future freshwater inflows. One of these species is the Gulf wedge clam (*Rangia cuneata*) which is a filter-feeding bivalve native to the Gulf of Mexico and commonly found in the brackish waters of the upper CRE. The clam has been selected as a benthic indicator for the mid-to-upper CRE due to its optimal salinity tolerance range of < 18 for adults and 2 to 10 for larvae. Sampling to assess clam density, size class distribution, and physiological condition was conducted at six stations within the upper and middle portions of the CRE in March and October 2023.

Initial results show that the greatest densities and largest clams were found at the upstream stations where salinities were consistently within the optimal range for larvae and adults. Very few live clams were found at the most downstream stations where salinities frequently exceeded the optimal salinity range. Findings from the first year of the study demonstrate that *R. cuneata* functions as an ideal indicator species for the oligohaline and mesohaline zones of the upper CRE and will provide invaluable guidance to water managers on improving the quantity and timing of freshwater inflows to the estuary.

BIVALVE ECOSYSTEM SERVICES IN THE GUANA RIVER ESTUARY, FLORIDA

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Motivated by shared concern among local stakeholders for the ecological well-being of the Guana River Estuary, a collaborative team of scientists from the University of Florida embarked on a comprehensive 3-year project in 2021. This initiative aimed to provide valuable insights into the nitrogen dynamics of the area and formulate effective management recommendations. The lab focused on conducting experiments involving local bivalves, specifically the eastern oyster (*Crassostrea virginica*) and the ribbed mussel (*Geukensia demissa*). The primary objective was to gain a nuanced understanding of various ecosystem services, such as filtration and ammonium excretion.

The study further sought to discern regional variations in these services and elucidate differences between the two bivalve species under investigation. To enhance the ecological significance, research was extended to encompass an in-situ study of bivalve filtration rates and other ecosystems services. This phase explored their interactions based on seston composition and phytoplankton community, contributing valuable real-world context to the findings from our laboratory experiments. Notably, the experiments to date have unveiled a remarkable degree of variability in filtration rates for the ribbed mussel (*Geukensia demissa*), contrasting with the more consistent patterns observed in the eastern oyster (*Crassostrea virginica*) population. This research also encompassed analysis of sediment biodeposition rates and nutrient assimilation rates, both intricately linked to water quality. The overarching goal is to identify management strategies for improving water quality and mitigating elevated nutrient concentrations.

PRESENCE OF GLUTAMATE NEURONS AND GLUTAMATE RECEPTORS IN GANGLIA OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Mammals and invertebrates have glutamate neurons in their nervous systems. Glutamate dysfunction is associated with Parkinson's and Alzheimer's diseases. Glutamate is synthesized into GABA. GABA neurons recently were found in *Crassostrea virginica* that inhibit serotonin neurons. To test the hypothesis that glutamate is a neurotransmitter in *C. virginica,* immunohistofluorescence (IHF) along with PAGE and Western Blotting (WB) were used to view glutamate neurons and the glutamate GluR-1 receptor in visceral ganglia (VG) and adductor muscle (PAM) of *C. virginica*. VG and PAM were dissected and prepared for IHF or PAGE and WB. For IHF, VG and PAM were frozen, cryostat sectioned, fixed with EDAC and incubated with GluR-1 FITC antibodies. Sections were viewed and photographed on a fluorescence microscope. VG and PAM also were prepared for PAGE and WB, incubated with GluR-1 HRP antibodies and viewed with an iBright Fl1500 image analyser. IHF showed the presence of glutamate nerves and GluR-1 receptors in the VG cortex and neuropile. PAGE and WB showed GluR-1 receptor bands in VG and to a lesser extent in PAM. The study shows glutamate neurons and GluR-1 type receptor present in VG of *C. virginica*. This study complements other lab work showing a neurophysiology function of glutamate as an excitatory neurotransmitter. The work was supported by grants 2R25GM06003 of the Bridge Program of NIGMS, 0537231071 of the CSTEP program of the NYSDOE, P120A210054 of the MSEIP Program of the DoEd, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

RESPONSE OF STRESS INDUCED GENES IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) EXPOSED TO PLASTIC LEACHATE

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An estimated 368 million tons of plastic is produced worldwide each year. As much as 10% of this plastic can end up in the oceans, causing many different hazards to a variety of marine organisms. This study focused on how eastern oysters (*Crassostrea virginica*) respond to plastic debris exposure by measuring differential expression of stress-related genes in juveniles exposed to plastic-polluted water compared to control conditions. One hundred oysters were randomly distributed to ten 1-liter beakers, each with ten oysters, for a four-week experiment. Five beakers contained clean saltwater with a salinity of 17, and the other five contained plastic leachate at 17ppt. To make the leachate, water with polyethylene terephthalate plastic pieces was exposed to warm temperatures and sunlight for two months. After two weeks of leachate exposure, the treatment oysters were moved to the same clean water as the control group and maintained for an additional two weeks of recovery time. Gill tissue samples were taken from two oysters from each beaker every week. RNA was extracted from the tissues samples and used to synthesize complementary DNA (cDNA). The cDNA was then used to measure relative expression of genes involved in stress responses using quantitative PCR (qPCR). Exposure to plastic leachate resulted in altered expression in the stress related genes in treatment oysters compared to control oysters. After being placed in clean water for recovery, expression levels in the treatment oysters returned to the control oyster baseline. Chemical leachate from plastic debris can initiate a reversible stress response in oysters.

INFLUENCE OF STOCKING DENSITY ON OYSTER AQUACULTURE PRODUCTIVITY AND MICROSCALE WATER QUALITY

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Eastern oysters (*Crassostrea virginica*) are an ecologically and economically important species in coastal Georgia. Due to their economic impact, there is interest in growing oyster aquaculture production in the State. As the industry grows, and to prepare the industry for future challenges, it is critical to understand issues that could impact productivity, especially low dissolved oxygen and pH conditions inside oyster bags. Water quality conditions around and within culture gear used by oyster growers may impact the quantity and quality of oysters produced, but how oyster density affects the water quality oysters experience within culture bags remains unclear. This study analyzed differences in microscale water quality changes via the continuous measurement of dissolved oxygen, pH, and temperature within oyster bags stocked at three different densities deployed at the UGA Shellfish Hatchery on Skidaway Island, in comparison to loggers deployed outside the bags. Oyster growth rates and water quality characteristics were tracked over time, and at the end of five months we also measured oyster condition. Oysters grown in higher stocking densities tended to be significantly smaller than oysters grown in lower stocking densities, with varying water qualities depending on stocking density. With a better understanding of the microscale influence, oyster growers can make informed decisions regarding the practices used in their aquaculture system, improving the production quality of their operation.

EXPLORING VARIATIONS IN THE PHENOTYPIC RESPONSE AND MORTALITY RATES OF THREE POPULATIONS OF EASTERN OYSTER LARVAE TO DIEL-CYCLING OF DISSOLVED OXYGEN AND pH

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To better inform oyster aquaculture practices and oyster reef restoration efforts, we examined variations in size and mortality rate differences between three populations of eastern oyster (*Crassostrea virginica*) larvae before and after exposure to diel-cycled coastal stressors. These stressors include low pH and low DO, mimicking coastal acidification and hypoxia conditions that have historically been observed in estuaries and shallow coastal waters. Oyster larvae are exposed to these stressors in an experimental aquarium setting for a period of 7-10 days, with density and genomic samples taken at initial and final time points. Variations in body size observed between initial and final time points and between populations combined with differences in mortality rate may serve as a proxy for the genetic underpinnings of traits that yield a survival advantage, especially in suboptimal conditions. This analysis will be used in conjunction with genomic analysis data in the future, with the implication that this knowledge may be used to identify and artificially select for specific traits that will enhance survivability in an aquacultural setting and in wild populations.

THE PRESENCE OF PFAS IN ATLANTIC BLUE CRABS FROM THE MARYLAND COASTAL BAYS

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Per- and Polyfluorinated substances (PFAS) are a group of synthetic chemicals that are prevalent in everyday consumer use. Widespread use of PFAS has led to PFAS becoming an environmental contaminant of concern. Known mostly for its widespread use in firefighting foams, and presence in soil, sediment, foods such as seafood, and produce. PFAS are a concern because they are a group of chemicals that are challenging to break down, hence "forever chemical" and has been shown to cause detrimental health effects in human populations. The objective of this study was to test surface water for PFAS at six sites the Maryland coastal bays and *Callinectes sapidus,* the Atlantic blue crab, at each site. *Callinectes sapidus* after collection were dissected, and claw tissue and hepatopancreases tissue were then tested for 35 different PFAS compounds. Results are to be determined. While the biological samples will require further investigation regarding their impacts on the ecosystem, this study will show the concentration of PFAS in the Maryland coastal bay blue crab and surface waters as preliminary data to then offers guidance for potential remediation techniques of affected areas and future sampling.

SCREENING AND SELECTION OF POTENTIAL PATHOGENIC AND PROBIOTIC BACTERIA FROM BIVALVE SHELLFISH HATCHERIES

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Disease control is critical for effective hatchery production of bivalve shellfish. Bacterial infections, particularly those associated with *Vibrio* and *Aeromonas*, cause rapid larval mortality with severe consequences for hatcheries and farmers who rely on them. This study aims to screen and identify potentially pathogenic and probiotic bacteria in bivalve shellfish facilities.

A total of 122 bacterial isolates from water, algae, and larval samples were identified using 16S rRNA sequencing and screened for their antimicrobial activity against shellfish pathogens, hemolytic activity, and biofilm formation. Among the 20 genera identified, *Vibrio* (34%), *Pseudoalteromonas* (23%), and *Alteromonas* (18%) are the most abundant. The pathogenicity of the selected potential pathogenic and probiotic isolates was tested with oysters and clam larvae, and adult oyster hemocytes. Results showed that potential probiotic isolates are generally safe while some potential pathogens showed host-specific pathogenicity to either clam or oyster larvae. Results from the high-throughput screening assay using oyster hemocytes were concordant with the results of the more labor-intensive larval assays. Further work is being done to optimize the high-throughput screening pipeline.

6-HYDROXYDOPAMINE TREATMENT CAUSES SUPERSENSITIVITY OF DOPAMINE D2R RECEPTORS IN GILL LATERAL CELLS OF *CRASSOSTREA VIRGINICA*

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Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by dopamine and serotonin nerves from their ganglia. Dopamine decreases while serotonin increases cilia beating. 6-Hydroxydopamine, a neurotoxin destroying dopamine neurons, induces Parkinson's Disease in animals. In *C. virginica,* 6-hydroxydopamine decreases the cilio-inhibitory actions of dopamine when applied to VG on GLC cilia beating. Denervation supersensitivity is a phenomenon observed after nerve cell damage. It is due to increased postsynaptic receptor sensitivity to the neurotransmitter. Manganese causes the neurodegenerative disease Manganism, which has similar symptoms as Parkinson's Disease but affects dopamine postsynaptic signal transduction (PST). Manganese decreases cilio-inhibitory actions of dopamine on GLC cilia beating in *C. virginica*. To test the hypothesis that treating *C. virginica* with 6-hydroxydopamine causes supersensitivity of dopamine on GLC cilia beating, 500 µg of 6-hydroxydopamine was injected into posterior adductor muscles. After 5 days dose responses of dopamine on GLC cilia beating were conducted. 6-hydroxydopamine treated animals demonstrated supersensitivity compared to controls. The dopamine dose response curve of 6-hydroxydopamine treated animals was shifted 1 log dose to the left. In contrast, earlier work with manganese treatments reduced dopamine potency, shifting the dose response curve to the right. The study shows 6-hydroxydopamine produces a supersensitive response to dopamine postsynaptic receptors present in GLC. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

TOWARD A BETTER UNDERSTANDING OF DISEASE AND MORTALITY DIFFERENCES BETWEEN OYSTER PLOIDY CONDITIONS IN COMMERCIAL LINES IN VIRGINIA, USA

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The eastern oyster, *Crassostrea virginica*, is the basis of an important and growing shellfish aquaculture industry from the Atlantic Provinces of Canada to the Gulf of Mexico. Aquaculturists increasingly report significant unexplained mortalities of near market-sized oysters, primarily in late spring and early summer. Few studies have examined the variation in stress response between diploid and triploid oysters, yet different responses, manifested for example in gene expression differences, may provide critical insights into the role of ploidy in host response to stressors, and its potential role in mortality. In the current study, diploid and triploid LOLA, DEBY, and XB oyster lines were produced and experimentally deployed at two collaborating commercial oyster farms in Virginia. Concurrent laboratory-based experiments were performed challenging the same lines with elevated temperature and food limitation stressors. Mortality and shell height were assessed monthly (March – October) in field-deployed oysters. In the laboratory experiment, mortality was assessed daily for 60 days, and shell height measured after 30 and 60 days. Tissue samples for histopathology and downstream molecular studies were collected from both field-deployed and laboratory held oysters. In the field study, differences in survival were observed between the lines and ploidies, with LOLA having the highest cumulative mortality. Future studies will involve RNA Sequencing (RNA-Seq) of archived gill samples and histopathology for perspective on underlying disease differences. Oyster transcriptomes will be mapped to the annotated *C. virginica* genome to identify and assess whether differential gene expression levels, relative to environmental conditions, are associated with ploidy.

POPULATION ECOLOGY OF EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*, IN GREAT BAY ESTUARY, NEW HAMPHIRE, USA

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Great Bay Estuary (GBE) in New Hampshire, USA, is a well-mixed, productive estuary situated along the Atlantic Ocean coast. One of the greatest industries within GBE is eastern oyster, *Crassostrea virginica*, aquaculture, which has 185 hectares of farms and accounted for $4.8 million in revenue in 2022. Due to factors including climate change, predation, and disease, oyster populations in GBE are declining. To inform restoration attempts, this research uses an integral projection model (IPM) to estimate potential restoration success in GBE based on known population data collected by NH Fish and Game and previous GBE eastern oyster research. Data for larval and adult population dynamics are incorporated to estimate whether there are sufficient larvae in the system to recruit to existing reefs. Results from this study provide survival and extinction trajectories for future populations under different restoration scenarios.

MOLECULAR EVOLUTION LEADS TO FUNCTIONAL DIVERGENCE OF INVERTEBRATE TYPE LYSOZYMES IN OYSTERS

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Lysozymes are antibacterial proteins playing a role in animal host defense. They also function in digestion in some species including bivalve molluscs. Lysozymes in oysters are variable in molecular characteristics. Three invertebrate type lysozymes, for example, are purified and characterized from eastern oysters, *Crassostrea virginica*. Among them are cv-lysozyme1 of 18 kDa and cv-lysozyme2 of 13 kDa. Sequence comparison reveals that cv-lysozyme1 contains about 50 more residues than cv-lysozyme2 at the N-terminus, which are predicted to constitute a peptidoglycan recognition protein (PGRP) domain; however, the functional significance of the added sequence fragment in cv-lysozyme1 remained to be understood.

Recently, a homolog of cv-lysozyme1, named cg-ly3, was identified from Pacific oysters, *Crassostrea gigas,* to consist of 169 amino acids. Structural modeling using Alphafold2 indicated that the 119 C-terminal amino acids formed a typical lysozyme conformation and the 50 N-terminal residues that cover the PGRP domain folded into an independent tertiary structure stabilized with 3 intra-domain disulfide bridges. The PGRP domain and the lysozyme domain were linked with a coil. Analysis using synthesized peptides showed that the PGRP domain selectively bound to cell surface of Gram-positive bacteria and the activity was affected by the molecular conformation as disulfide bridged peptides had significantly higher activity than unbridged peptides. Additionally, the recombinantly expressed lysozyme domain exhibited different enzyme activities than the complete cg-ly3 molecule. The results suggest that the appendage of a PGRP domain in cg-ly3 and its homologs may have added new molecular and functional properties in the evolved protein.

PROBIOTIC SUPPLEMENTATION EFFECTS ON SETTERS IN EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) LARVAE

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Off-bottom oyster aquaculture is a relatively new and growing industry in the northern Gulf of Mexico. As of 2021, all five Gulf States have established oyster farms. This industry primarily produces oysters for the premium half shell market which requires single-set animals; however, seed limitations resulting from variable survival in hatchery systems is a hurdle for continued expansion of the industry. Methods to improve survival and production consistency are needed for hatcheries to meet seed demand in this region.

Poor water quality and negative bacterial interactions can lead to mass mortality events in the larval stages of aquatic organisms. Use of probiotics in hatcheries has increased due to the ability of the beneficial bacteria to improve water quality and compete against potentially harmful bacteria. This study tested a commercial probiotic (ProFin), shown to increase survival and stress tolerance in larval fishes, for its effectiveness in oyster larval rearing. Two 21-day trials were completed in the summer of 2023, with the first supplementing probiotics to static rearing systems every other day and the second adding the beneficial bacteria daily. No significant differences were identified in survival, growth, or number of setters in trial 1. In trial 2, probiotic-supplemented systems had significantly more setters than controls, despite similar survival and growth. Future studies will investigate the mechanisms behind the increased set rate.

MODELING INDIVIDUAL GROWTH OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) IN MAINE ESTUARIES: ASSESSING PHENOTYPIC RESPONSES TO DIVERSE NUTRITIONAL SOURCES

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Culture of the eastern oysters (*Crassostrea virginica*) on the Atlantic and Gulf Coasts relies on the production of seed that perform well across a broad range of environmental gradients. Breeding programs have facilitated appropriate seed production by developing genetic stocks with improved growth and yield under these variable conditions; however, field trials testing these genetic lines have typically measured shell size or weight at discrete time points on oysters haphazardly sampled from replicate grow-out cages. Estimates of growth are then derived from the average sizes measured at each time point for each cage. Unfortunately, this approach masks the tremendous degree of variability in the growth of individuals over time, which can reflect underlying differences between individuals in their metabolic response to the environment or their capacity to utilize diverse nutritional sources.

Individual growth of oysters cultured in two Maine estuaries were monitored by taking bi-weekly measurement throughout one growing season. Concurrently, water quality parameters were tracked, including chlorophyll-*a* concentration, temperature, turbidity, and salinity to assess individual phenotypic responses. A variety of growth phenotypes were observed including oysters with fast initial growth that peaked during spring bloom conditions, and more slow and steady phenotypes where growth occurred during both bloom periods and when the nutrition available in these estuaries is more detrital in nature. In this presentation, approaches to modeling individual growth that were applied to the data will be explored and how the shape of the growth curves indicates oysters response to variation in water quality conditions will be discussed.

HOW DO MULTIPLE STRESSORS IMPACT OYSTER RECRUITMENT?

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This project analyzed the effects of a combined treatment of coastal hypoxia and acidification, in addition to sewage effluent on the larval stage of the eastern oyster (*Crassostrea virginica*). Coastal hypoxia is defined as dissolved oxygen (DO) levels less than 2 mg/L. Coastal acidification (CA) refers to the decrease in pH of water due to excess nutrient loading, or eutrophication. These two phenomena are linked due to community metabolism and are combined in treatment (CADO). Sewage Effluent (SE) is the by-product from wastewater treatment facilities. In Narragansett Bay, 768 million liters of sewage effluent are discharged daily into coastal waters. After 24-hour exposure to SE and CADO, this project aimed to gather size and mortality data. Preliminary results show that the SE treatment alone did not have a significant effect in mortality but resulted in significantly larger larvae when compared to larvae in ambient conditions (control). Results from an additional treatment, combining SE and CADO exposure will also be presented. Preliminary results indicate that although a 24-hour SE exposure alone did not induce significant larval mortality, it is still important to continue analyzing the effects of sewage effluent on the eastern oyster as negative effects may be exacerbated when other stressors, like CADO, are present.

UNDERSTANDING HOW COASTAL STRESSORS AFFECT SELECTIVELY BRED EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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This study aimed to measure how environmental stressors affect the survival and growth of larval oysters. While many studies have investigated the effects of single environmental stressors (i.e., acidification, temperature, nutrient loading, salinity changes) these stressors do not occur in isolation. There still needs to be a comprehensive, mechanistic understanding of how multiple stressor environments impact shellfish populations, particularly at the larval stage. To address this knowledge gap, our study included a cycled stress treatment to mimic a eutrophic estuary in which DO and pH cycle from 2.5-7 mg/L and 7.1-7.8, respectively, in 24 hours. Selectively bred oyster larvae were separated into control and stress groups and reared for 7 days. Density samples were taken before and after treatments. These samples were later counted to measure the survival rate per treatment. In addition, 30 larvae/samples were imaged for size measurements. There was no significant difference between the control and stress treatment average survival. These findings may be a result of oyster sensitivity, the selected larval population, or the treatment level. Although these results were unexpected, they opened new doors for future research which may include larval size comparison, genomic sampling, and additional populations.

PRODUCTION AND FIELD EVALUATION OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) SELECTED FOR DERMO TOLERANCE

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The DARPA Biological Technologies Office Reefense Program was designed to "develop self-healing, hybrid biological and engineered reef-mimicking structures for coastal protection of civilian and Department of Defense infrastructure and personnel." An adaptive biology component investigates using genomic selection to enhance oyster tolerance to Dermo disease and increase growth rates by 20% and 15%, respectively. Broodstock oysters were sourced from wild populations at the proposed reef site in St. Andrew Bay, Florida (FL) and from an existing aquaculture line of oysters created from oysters spanning the northern Gulf of Mexico. Broodstocks were lab-challenged with Dermo for phenotypic and genomic selection. Genomic estimated breeding values (GEBV) were generated based on associations between single nucleotide polymorphisms (SNP) and Dermo survival. Growth was only selected in the aquaculture line of known-age oysters. Four F1 generation groups were produced consisting of two genomically selected groups (FL and aquaculture lines), one phenotypically selected group (FL), and one genomic control group (FL). F1 oysters were deployed in Alabama, Louisiana, and Florida for field testing. Survival and growth were assessed monthly, while Dermo body burden and condition index were determined quarterly. F1 oysters were lab-challenged with Dermo to assess their tolerance and to generate, in conjunction with whole wet weight, new GEBV for genomic and phenotypic selection used for production of the F2 generations. The FL genomically selected oysters were more tolerant to Dermo infection than the genomic controls while the aquaculture genomically selected oysters used for reference exhibited the highest growth rate but lowest tolerance to Dermo.

COMPARISON OF THE NEUROTOXIC ACTIONS OF MANGANESE AND 6-HYDROXYDOPAMINE ON GILL LATERAL CELL DOPAMINE D2R RECEPTORS OF *CRASSOSTREA VIRGINICA*

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Parkinson's Disease (PD) and Manganism are human neurodegenerative diseases with similar symptoms but different neurophysiological causes. PD degenerates dopamine neurons in the substantia nigra. Manganism, caused by elevated manganese levels in the brain, does not degenerate dopamine neurons, rather postsynaptic signal transduction (PST) is impaired. Neuronal degradation can cause denervation supersensitivity at the innervated cells. PST impairment causes decreased response to stimulation. 6-Hydroxydopamine, a neurotoxin selectively destroying dopamine neurons, induces PD in animal models. In *Crassostrea virginica,* 6-hydroxydopamine and manganese reduce dopamine neurons ability to slow down gill lateral cell (GLC) cilia beating. The present study contrasts neurotoxic actions of 6-hydroxydopamine vs. manganese on GLC dopamine D2R receptors using immunohistofluorescence. To test the hypothesis, animals treated with 6-hydroxydopamine will have increased D2R fluorescence intensity, while manganese will decrease fluorescence intensity, animals were treated 5 days with 500 µg of 6-hydroxydopamine or manganese, then gills were processed for immunohistofluorescence with D2R/FITC conjugated antibodies. Photomicrographs were taken and fluorescence intensity measured using ImageJ from NIH. 6-Hydroxydopamine increased D2R fluorescence by 40%, while manganese decreased it by 35%, compared to the controls. These results are consistent with physiological data observed measuring GLC cilia beating rates in similar experiments. The study shows the two neurotoxins have different mechanisms of action. This can be helpful in differentiating the cause and designing the appropriate potential therapeutic treatments for these neurological disorders. The work was supported by grants 2R25GM06003 of NIGMS-Bridge, 0537231071 of NYSDoE-CSTEP, P120A210054 of DoEd-MSEIP, and K12GM093854 of the NIH IRACDA Program of Rutgers University.

DO MICROBIOMES CREATE INDICATOR SPECIES?

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The microbiomes of marine invertebrates have attracted increasing attention in recent years for their potential in revealing how anthropogenic stressors alter their environment. For example, it was found that multiple species of *Perkinsus* with extremely low genetic diversity have been identified in novel geographic areas. This suggests a significant role for marine transport in spreading parasites, showing how monitoring macroinvertebrates can help track threats.

Organisms in estuaries face rapid changes of salinity, water temperature, and dissolved oxygen levels in the summer months. A study was conducted to evaluate how microbiomes within marine invertebrates from Chesapeake Bay respond to multiple stressors. To do this, three species with distinct migration patterns: a sessile species (the eastern oyster, *Crassostrea virginica*), a horizontally migratory species (the American blue crab, *Callinectes sapidus*), and a vertical + horizontal migratory species (the Atlantic brief squid, *Lolliguncula brevis*) were used. Each of these species will have their gill microbiomes undergo genetic sequencing to characterize microbiome composition. In addition, a portion of squid samples from hypoxic and oxic waters have undergone shotgun metagenomics to determine what functional genes are present within the gills; to potentially confirm the presence of genes associated with endosymbionts. Gill microbial communities extracted from different species were evaluated to see whether they are similar when the samples are taken close to each other. Additionally, it is anticipated that dissolved oxygen to be a major factor that contributes to gill microbiome changes seen between samples extracted from the same species but in separate locations.

LONG-TERM VALVE OPENING BEHAVIOR OF *CRASSOSTREA VIRGINICA* IN A LOW SALINITY ESTUARY

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Unlike motile organisms, oysters are unable to escape changes in environmental conditions. Only by closing their shell valves can they seclude their body from the surrounding water, and either adjust to new the conditions or wait until more tolerable conditions occur. Understanding how oyster behavior links with environmental variables and identifying any potential behavioral warning signs could be used to guide more efficient site selection for aquaculture efforts and determine under which conditions intervention by oyster fishers may be needed. In this study, magnetic sensors were used to record oyster valve opening behavior in a natural system to quantify their response to concomitant changes in abiotic conditions. Sixteen oysters were deployed at Louisiana Universities Marine Consortium (LUMCON) in Cocodrie, LA between July and September 2023. Mean percent of maximum opening, percent of time open (> 80% maximum opening), percent-time closed (< 10% maximum opening) were calculated from continuous recording. Oyster behavior data were then compared to the LUMCON continuous environmental data to characterize the relationships between oyster behavior and abiotic conditions including temperature, salinity, dissolved oxygen, chlorophyll-*a*, and depth. Linking oyster behavior to environmental stressors could help better identifying thresholds in the physiological tolerance range of organisms. This knowledge could inform predictive tools used by resource managers and aquaculture professionals.

USING GENETICS TO MONITOR AND ADVANCE WILD FISHERY STOCK RESTORATION OF BAY SCALLOPS (*ARGOPECTEN IRRADIANS*) IN VIRGINIA

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Bay scallops, *Argopecten irradians*, (Lamarck, 1819) were once abundantly harvested in the coastal bays on the Eastern Shore of Virginia, but in the early 1930s the fishery collapsed and never recovered. Bay scallop restoration was initiated in 2009 when scallops from North Carolina were brough to the VIMS Eastern Shore Lab (ESL) and used to develop an ESL scallop line. This ESL line has been used to create larvae, juveniles, and adults that have been released into restored seagrass beds since 2009. Concerns about limited genetic diversity of bay scallops in Virginia prompted the acquisition of new broodstock scallops in 2018-2019 from New York (NY), North Carolina (NC), and Florida (FL). These three new lines have been used to create and deploy juvenile bay scallops into restored seagrass beds since 2019. The annual summer scallop survey, started in 2013, has shown that after fluctuating and declining scallop numbers up to 2018, the population has experienced 5 years of consistent increases coincident with the introduction of new genetic lines in 2019. Whether these four different genetic lines experience different survival rates or are interbreeding to contribute new combinations of alleles to the population is not known. Understanding the genetic contribution of each line to the wild population and if the scallop population is reproducing *in situ* will help estimate the length to which stock augmentation will be needed. High throughput genotyping-by-sequencing was used to determine how the genetic profile of the restored Virginia bay scallop population has changed from 2016-2023.

AN ESTIMATE OF CARBON STORAGE CAPABILITIES OF WILD AND CULTURED SHELLFISH IN THE NORTHWEST ATLANTIC AND THEIR POTENTIAL INCLUSION IN A CARBON ECONOMY

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Production of bivalve molluscs has been proposed as a method to reduce carbon emissions as: 1) a low-emission protein source, and 2) via carbon stored within their shells. To address the fate of shell carbon for the northwest Atlantic, stored oceanic carbon equivalents (Eq), released CO_2 via calcification, and hypothetical carbon credit value ($24 tCO_2), for both cultured and wild-captured bivalves for New England and Canadian Provinces on the Atlantic between 2016 and 2020 were estimated. Bivalve shells do not sequester atmospheric CO_2, instead storing oceanic CO_2 Eq and cannot be included directly in a carbon sequestration scheme. Total annual estimates of stored oceanic CO_2 Eq were approximately 202,253 and 363,243 tons, with concurrent releases of approximately 121,255 and 217,771 tons of CO_2 to the atmosphere. Even if bivalve shells sequestered atmospheric CO_2, current shellfish production levels are inconsequential with regard to current anthropogenic greenhouse gas (GHG) emissions. Stored oceanic carbon Eq for bivalve aquaculture is equivalent to 0.001% and 0.0005% of Canadian and US annual anthropogenic CO_2 emissions, whereas wild-capture would store 0.028% and 0.005% of Canadian and US emission, respectively. Bivalve shell will not solve climate change, but the expansion of bivalve production provides a protein source with the lowest GHG emissions, which provides a multitude of environmental services.

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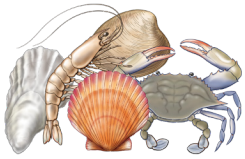

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