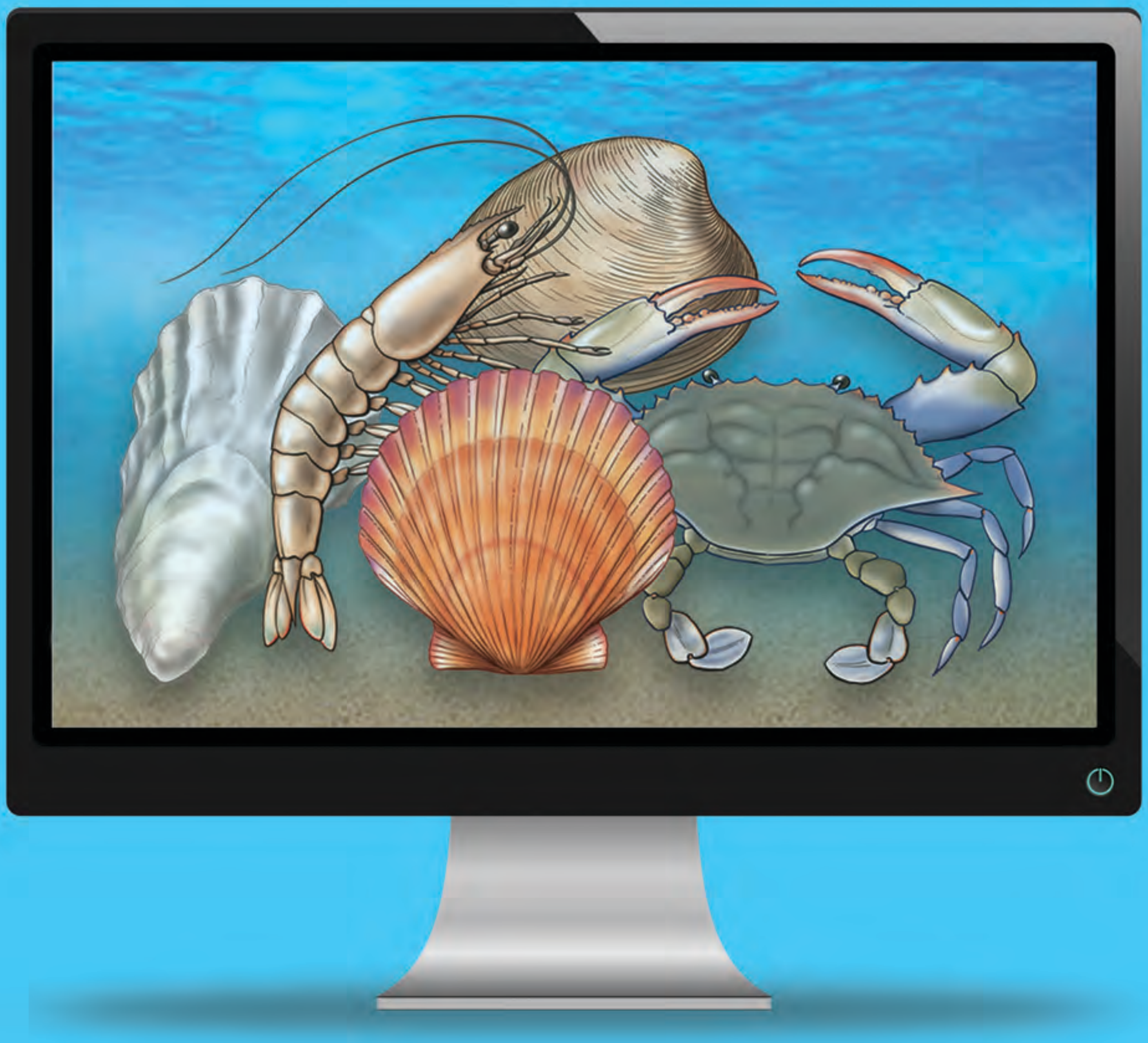
NATIONAL SHELLFISHERIES ASSOCIATION

Program and Abstracts
of the
113th Annual Meeting



March 22 − 25, 2021
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NSA 113th ANNUAL MEETING (virtual)
National Shellfisheries Association
March 22—March 25, 2021

MONDAY, MARCH 22, 2021

8:00 AM	DAILY MEETING UPDATE (LIVE) Gulf of Maine				
	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay	Monterey Bay
8:30-10:30 AM	SHELLFISH AQUACULTURE BUSINESS & ECONOMICS	CEPHALOPODS	OYSTER I	SHELLFISH RESTORATION & CONSERVATION	ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP
10:30-10:45 AM	MORNING BREAK				
10:45-1:00 PM	THE SEA GRANT COVID-19 RESPONSE TO THE NEEDS OF THE SHELLFISH INDUSTRY	GENERAL CONTRIBUTED I	OYSTER I	SHELLFISH RESTORATION & CONSERVATION	ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP
1:00-1:30 PM	LUNCH BREAK WITH SPONSOR & TRADESHOW PRESENTATIONS				
1:30-2:30 PM	PLENARY LECTURE: Roger Mann (Virginia Institute of Marine Science, USA) (LIVE) Chesapeake Bay				
2:30-3:45 PM	EASTERN OYSTER GENOME CONSORTIUM WORKSHOP	BLUE CRABS	*VIBRIO*	SHELLFISH RESTORATION & CONSERVATION	ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP
3:45–5:45 PM	EASTERN OYSTER GENOME CONSORTIUM WORKSHOP	BLUE CRAB GENOMICS & TRANSCRIPTOMICS: THE PROGRAM OF THE BLUE CRAB GENOME PROJECT	*VIBRIO*	SHELLFISH RESTORATION & CONSERVATION	ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP

TUESDAY, MARCH 23, 2021

8:00 AM	**DAILY MEETING UPDATE (LIVE)** **Gulf of Maine**			
	Gulf of Maine	**Gulf of Mexico**	**Puget Sound**	**Chesapeake Bay**
8:30-10:30 AM	**OYSTER II**	**SEAGRASS BIVALVE INTERACTIONS**	**HATCHERIES**	**OFFSHORE WIND ENERGY DEVELOPMENT & COMMERCIAL FISHERIES**
10:30-10:45 AM	**MORNING BREAK**			
10:45-11:30 AM	**OYSTER II**	**SEAGRASS BIVALVE INTERACTIONS**	**HATCHERIES**	**BIVALVES, MODELING, & CLIMATE CHANGE**
11:30-1:00 PM	**OYSTER II**	**AQUACULTURE & THE PRESS: A NEW WAY FORWARD**	**HATCHERIES**	**BIVALVES, MODELING, & CLIMATE CHANGE**
1:00-1:30 PM	**LUNCH BREAK WITH SPONSOR & TRADESHOW PRESENTATIONS**			
1:30-2:30 PM	**PLENARY LECTURE: João Ferreira (University of Lisbon, Portugal) (LIVE)** **Chesapeake Bay**			
2:30-4:00 PM	**DIVERSITY AND INCLUSIVE EXCELLENCE LECTURE AND DISCUSSION (LIVE)** **Randy Williams (Elon University, USA)** ***How might a shellfisheries society operate with a DEI lens*** **Moderator: Aswani Volety** **Monterey Bay**			
4:00-6:00 PM	**POSTER SESSION, TRADE SHOW, AND HAPPY HOUR (BYOBeverage) (LIVE)** **Gulf of Mexico**			
5:00-6:00 PM	**RECRUITS JOB PANEL (LIVE)** **Monterey Bay**			

WEDNESDAY, MARCH 24, 2021

8:00 AM	DAILY MEETING UPDATE (LIVE) Gulf of Maine				
	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay	Monterey Bay
8:30-10:30 AM	SHRIMP GENOME AND EPIGENOME (SHRIMPENCODE) PROJECT	DISEASE	CLAMS	COMMERCIAL SHELLFISHERIES	NAEMO WORKSHOP: DEFINING BARRIERS AND IDENTIFYING SOLUTIONS FOR MUSSEL AQUACULTURE EXPANSION
10:30-10:45 AM	MORNING BREAK				
10:45AM-1:00 PM	SHRIMP GENOME AND EPIGENOME (SHRIMPENCODE) PROJECT	DISEASE	CLAMS	COMMERCIAL SHELLFISHERIES	NAEMO WORKSHOP: DEFINING BARRIERS AND IDENTIFYING SOLUTIONS FOR MUSSEL AQUACULTURE EXPANSION
1:00-1:30 PM	LUNCH BREAK WITH SPONSOR & TRADESHOW PRESENTATIONS				
1:30-2:30 PM	PLENARY LECTURE: J. Evan Ward (University of Connecticut, USA) (LIVE) Chesapeake Bay				
2:30-3:45 PM	SHRIMP GENOME AND EPIGENOME (SHRIMPENCODE) PROJECT	DISEASE	UNDERGRADUATE RESEARCH COLLOQUIUM	COMMERICAL SHELLFISHERIES	
4:00-4:30 PM	NSA AWARD PRESENTATIONS (LIVE) Monterey Bay				
4:30-6:00 PM	POSTER SESSION, TRADE SHOW, AND HAPPY HOUR (BYOBeverage) (LIVE) Gulf of Mexico				
5:00-6:00 PM	RECRUITS SETTLEMENT SUITE-CHAT ROOM (LIVE) Gulf of Maine				

THURSDAY, MARCH 25, 2021

8:00 AM	**DAILY MEETING UPDATE (LIVE)** **Gulf of Maine**				
	Gulf of Maine	**Gulf of Mexico**	**Puget Sound**	**Chesapeake Bay**	**Monterey Bay**
8:30-10:45 AM	**SHELLFISH GENETICS & GENOMICS**	**CONTAMINANTS OF EMERGING CONCERN**	**DOWN ON THE FARM**	**SCALLOPS**	**MANGROVE EPIGENOME (MANGROVEENCODE) PROJECT: A ONE HEALTH APPROACH (LIVE POSTER SESSION)**
10:45-11:00 AM	**MORNING BREAK**				
11:00-1:00 PM	**SHELLFISH GENETICS & GENOMICS**	**COASTAL ACIDIFICATION**	**BIVALVE ECOSYSTEM SERVICES**	**SCALLOPS**	**MANGROVE EPIGENOME (MANGROVEENCODE) PROJECT: A ONE HEALTH APPROACH (LIVE POSTER SESSION)**
1:00-1:30 PM	**LUNCH BREAK WITH SPONSOR & TRADESHOW PRESENTATIONS**				
1:30-2:30 PM	**PLENARY LECTURE: M. Luz Pérez-Parallé (University of Santiago de Compostela, Spain) (LIVE)** **Chesapeake Bay**				
2:30-4:00 PM	**FUNCTIONAL GENOMICS**	**SUMMER MORTALITY**	**GENERAL CONTRIBUTED II**	**ECHINOIDS**	
4:00-6:00 PM	**CLOSING HAPPY HOUR & SILENT AUCTION RESULTS (LIVE)** **Gulf of Mexico**				

NOTES:

There will be a Live Q&A session at the end of each plenary lecture as well as at the end of each session.

All times are Eastern Daylight Savings Time (EDT).

In addition to the scheduled Poster Sessions, posters will be available for viewing throughout the conference. Check the meeting website for location.

Silent Auction—bidding will be open throughout the meeting. Winners will be announced at the closing Happy Hour. Check the meeting website for items and bidding instructions.

All presentations will be available for viewing until April 9th, 2021.

For the best virtual experience, be sure to download the Zoom Client for Meetings to your computer. A personal device is recommended if your institution or agency will not allow the download of the Zoom app.

MONDAY
March 22, 2021

ROOM	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay	Monterey Bay
SESSION TITLE	**(#1) SHELLFISH AQUACULTURE BUSINESS & ECONOMICS** **Matt Parker & Jonathan van Senten**	**(#3) CEPHALOPODS** **Camino Gestal, Jeffrey Taylor Good & Maria Prado**	**(#5) OYSTER I** **Bill Fisher**	**(#6) SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**(#7) ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren & Kathy Tang**
8:30 AM	Sustainable oyster aquaculture, water quality improvement, and ecosystem service value potential in Maryland, Chesapeake Bay, USA **Parker, Bricker**	Rickettsia-like organisms (RLO) in *Octopus bimaculatus* Verill 1883 from Baja California, Mexico **Castellanos-Martinez, Sánchez-Serrano**	Spatial and temporal variation in growth rates of wild eastern oysters (*Crassostrea virginica*) from Delaware Bay, New Jersey, USA **Gius, Morson, Munroe, Kraeuter**	Large-scale oyster restoration in the Chesapeake Bay, Maryland, USA **Westby**	
8:45 AM	Building Maine aquaculture businesses: strategic planning, resiliency, and distribution **Brayden, Belle**	Investigating the life history of the Atlantic brief squid, *Lolliguncula brevis*, from the Charleston Harbor estuary, South Carolina, USA **Good*, Kendrick, Kingsley-Smith**	Climate and estuarine gradient influence Pacific oyster condition, spawning, and perhaps mortality events in a U.S. west coast estuary **Dumbauld, Ruesink, Trimble, Forster, Hasegawa, Bolm, Durland, McIntyre**	Repurposing of bridge materials for oyster reef creations **Klein III, Leonard**	Recognition of winners of 2021 "Johnny Alcivar-Arteaga Research and Travel Awards" and "Johnnie Castro Montealegre Travel Awards" for 71 international students from eleven countries, and twelve "2020-2021 Outstanding ONE HEALTH Researchers in Aquaculture" by the FUCOBI Foundation of Ecuador **Alcivar-Arteaga, Romero-Arteaga, Figueroa, Aveiga, Hernandez, Espinoza, Alarcon, Asuncion, Zuniga**
9:00 AM	The effects of permitting delays on return on investment for Pacific coast shellfish aquaculture **Senten, Engle**	Handbook of pathogens and diseases in cephalopods **Gestal, Pascual, Guerra, Fiorito, Vieites**	Responses of juvenile *Crassostrea virginica* to flood-associated water quality stressors **Pruett, Barnett, Keylon, Willett, Otts, Gochfeld**	Sediment, sounds, and settlement: the three S's of oyster restoration success **Caretti*, Eggleston, Bohnenstiehl**	
9:15 AM	Effects of different financing scenarios on Maryland oyster farm profitability and success **Parker**	Diversity and gene expression analysis of thioester-containing proteins (TEP) in the squid *Euprymna scolopes*, a molluscan model **Thuraisamy*, Castillo**	Hurricane impacts on oyster reefs of North Carolina, USA: is this the new paradigm? **Bowling*, Caretti, Eggleston**	Does boat noise delay oyster larvae metamorphosis? **Gilmore*, Munroe, Nowacek, Piniak, Wilson**	Reverse transcriptase-related genes and their possible role in the host cell response to transition metal pollution **Yushenova, Rodriguez, Maffa, Metzger, Barnard-Pratt, Arkhipova**
9:30 AM	Economics of subtidal oyster culture in Delaware Bay, USA **Sullivan, Bushek, Calvo, Bochenek, Harman, Hollinger**	The Hawaiian bobtail squid, *Euprymna scolopes*, as a model host for understanding the role of beneficial bacteria in egg defense and development in cephalopods **Nyholm**	Effect of environmental history on the physiology and acute stress response of the eastern oyster (*Crassostrea virginica*) **Ashey*, Rivest**	Water quality benefits of a shellfish-based living shoreline in Milford, Delaware, USA **Moody, Bouboulis, Kreeger, Haaf, Rothermel**	
9:45 AM	The economic impact of shellfish aquaculture in Maryland, USA **van Senten, Engle, Parker, Webster**	Effect of an enriched diet on the global performance and transcriptomic response in *Octopus vulgaris* **Prado-Alvarez, Garcia-Fernández, Tur, Domingues, Dios, Varó, Gestal**	The unconventional findings of Herbert Prytherch on oyster setting and metamorphosis **Fisher**	Maximizing shellfish recruitment in living shorelines for restoration and habitat conservation efforts **Bouboulis, Moody, Gentry, Kreeger**	Inhibitory effect of marine microalgae on *Vibrio parahaemolyticus* strain causing acute hepatopancreatic necrosis disease **Soto-Rodriguez, Soto, Servin, Vela**
10:00 AM	Economic trade-offs between traditional bottom and container culture of oysters on Maryland farms **Parker, Engle, van Senten, Webster**	Question and Answer (LIVE Chat Session)	A potential role for amebocytes in oyster shell deposition **Fisher**	Comparative analysis of habitat provisioning by shellfish-based living shoreline projects in the Delaware Estuary **Shinn, Bushek, Zito-Livingston**	Abiotic and biotic factors related to the proliferation of *Vibrio* spp. that cause AHPND in the white shrimp, *Penaeus vannamei* (Boone, 1931) **Galaviz^P, Magallon-Servin, Gomez-Gil, Soto-Rodriguez, Hou**
10:15 AM	Question and Answer (LIVE Chat Session)		Oyster shell production and reef accretion rates: a first comparison of extant and fossil shell data **Mann, Southworth, Lockwood**	Optimizing remote setting on different cultch types for small-scale oyster restoration in Barnegat Bay, New Jersey, USA **Thompson, Parsons, Evert, Ambrose**	
10:30-10:45 AM			**MORNING BREAK**		
SESSION TITLE	**(#2) THE SEA GRANT COVID-19 RESPONSE TO THE NEEDS OF THE SHELLFISH INDUSTRY** **LaDonn Swan, Kola Garber, Charles Weirich, & Mark Rath**	**(#4) GENERAL CONTRIBUTED I** **Shirley Baker & Tyler Griffin**	**(#5) OYSTER I** **Bill Fisher**	**(#6) SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**(#7) ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren & Kathy Tang**
10:45 AM	The Connecticut response to the shellfish market collapse of 2020 **Getchis, Carey, De Guise, DeRosia-Banick**	Juvenile sea cucumber (*Apostichopus californicus*) feeding trials at Washington State nurseries and home offices **Suhrbier, Crim, Platten, Horkan, Houle**	Optimizing mabé pearl culture in the Kingdom of Tonga using the winged pearl oyster, *Pteria penguin* **Gordon*, Wingfield, Smallhorn-West, Malimali, Halafihi, Schoeman, Southgate**	Creating living shorelines to support habitat resiliency and ecosystem services in the urbanized watershed of Charleston County, South Carolina, USA **Kingsley-Smith, Sundin, Hodges, Bell, Morganello**	Development of a contingency plan for shrimp acute hepatopancreatic necrosis disease (AHPND) **Tang, Bondad-Reantaso, Arthur**
11:00 AM	Taking public outreach into home kitchens: Stuck at home? #ShuckatHome! **Tossey, Hood**	Flow cytometric and microscopic characterization of hemocytes of sea hares *Aplysia kurodai* (Baba, 1937), *Aplysia juliana* (Quoy & Gaimard, 1832), *Aplysia parvula* (Mörch, 1863), and *Aplysia oculifera* (A. Adams & Reeve, 1850) from tidal pools in Jeju Island of the south coast of Korea **Kajino*, Hong, Choi**	Pacific oyster microbiomes in a southern California bay, USA: linking microbial ecology to environmental conditions and human pathogen accumulation **Diner, Zimmer-Faust, Cooksey, Allen, Gilbert**	Unoccupied aerial vehicles (UAV): a new tool to improve the restoration and management of intertidal oysters (*Crassostrea virginica*) in South Carolina, USA **Sundin, Kingsley-Smith, Cook, Dyar**	
11:15 AM	Virginia Sea Grant COVID-19 rapid response to local aquaculture and seafood businesses **Hudson, King, Lawrence, van Senten, Lane, Villalba, Yusuf, Andrews, Schwarz, Rudders, Hartley**	Impact of spawning stress on hemocyte parameters of blood cockle *Tegillarca granosa* (Linnaeus, 1758) on the south coast of Korea **Kim*, Hong, Lee, Cho, Shin, Choi**	Unique microbiomes of oyster gill tissue and pallial fluid are specific to site and season **Guidry*, Reigel, Johnson, Kelly**	Using a multi-year, statewide demographic assessment of eastern oysters (*Crassostrea virginica*) in South Carolina as a tool to support restoration and management **Wagner, Sundin, Dyar, Kingsley-Smith**	Horizontal plasmid transfer between *Vibrio parahaemolyticus* provides a novel mechanism for genetic exchange and environmental adaptation mediated by the insertion sequence *ISVal1* **Fu, Wei, Yang, Xie, Huang, Feng, Liu**
11:30 AM	Identifying consumer preferences for delivery and pick up of aquaculture farm products in Virginia, Maryland, and New York in response to the COVID-19 pandemic **van Senten, Parker, Ciaramella**	Words matter: Standardizing nonnative species terminology **Baker, Iannone III, Bell, Carnevale, Hill, McConnell, Main, Enloe, Johnson, Cuda, Andreu**	"What is eating you?": A comparison of faunal communities and trophic structure on harvested and unharvested oyster reefs **Outhwaite*, Pollack**	Reactive to proactive: a goal for improved shellfish resource conservation and management **Dyar, Taylor, Wagner, Sundin, Kingsley-Smith**	Bulk segregation method with transcriptomics is an innovative method for identifying true SNP and functional genes in a breeding line of specific pathogen resistant (SPR) WSSV-resistant Madagascar–Malaysia *Penaeus monodon* **Bhassu, Ghani**
11:45 AM	Evaluating alternative marketing opportunities to strengthen the South Carolina mariculture industry **Gaines, Gorstein, Nath, Swain, Giebelhausen, Weathers**	Comparison of the pearl quality of mabé *Pteria penguin* cultured in bay and strait in the province of Southeast Sulawesi, Indonesia **Yusnaini, Nur, Indrayani, Nerliano**	Red mangroves (*Rhizophora mangle*) positively influence the eastern oyster (*Crassostrea virginica*) along an intertidal gradient **Chacin, Bell, Stallings**	Oyster metapopulation dynamics **Theuerkauf, Eggleston^P, Puckett**	The *NonLTR-1_LVa* non-LTR retrotransposon from the original specific pathogen-free (SPF) *Penaeus* (*Litopenaeus*) *vannamei* produced by the United States is similar to the NLRS retrotransposon associated with abdominal segment deformity disease (ASDD) of farmed *P. vannamei* from Thailand **Espinoza^P, Karoonuthaisiri, Uengwetwanit, Sittikankaew, Alcivar-Arteaga, Hernandez, Alcivar-Warren**
12:00 NOON	Concerned oystermen restoring estuaries program **Grice, Swann, Walton**	Occurrence variation in pedunculate barnacle *Octolasmis* sp. and gill tissue damage of mangrove crabs (*Scylla* sp.) in Southeast Sulawesi, Indonesia **Nur, Yusnaini, Abidin, Santi, Ayuningtyas**	Effect of tidal resuspension with oyster biodeposits on nutrient and oxygen dynamics **Porter, Blickenstaff, Cornwell, Jackson, Tolbert**	A GIS-based approach for shellfish restoration planning in Connecticut, USA **Getchis, Carey, Yamalis, Barrett, Carta,DeRosia-Banick, Chadwick, Zuber**	
12:15 PM	Discussion (LIVE)	A method to perturb the gut microbiome of the blue mussel (*Mytilus edulis*) experimentally with antibiotics **Griffin*, Holohan, Nigro, Ward**	Shellfish poisoning and poisoning shellfish: effects of *Alexandrium catenella* and *Dinophysis acuminata* on larval eastern oysters **Pease*, Brosnahan, Smith**	Engaging stakeholders and partners for the successful implementation of a community-based oyster restoration program over the past 20 years in South Carolina, USA **Hodges, Dyar, Hillman, Kight-Somers, Kingsley-Smith**	Transcriptomic response during compensatory growth of the Pacific white shrimp, *Litopenaeus vannamei* **Peña-Rodriguez, Cota-Quintero, Elizondo-González, Gamboa-Delgado, Escobedo-Fregoso**
12:30 PM		Assessing contribution of shellfish aquaculture to global food security **Azra, Tatabaei, Lam, Hassan, Karim, Waiho, Fazhan, Kasan, Liew, Norainy, Abol-Munafi, Ikhwanuddin**	Question and Answer (LIVE Chat Session)	Short-term economic impacts of ecological restoration in estuarine and coastal environments: a case study of Lone Cabbage Reef **Botta*, Borsum, Camp, Court, Frederick**	A novel RNA virus, crustacean hepe-like virus 1 (CHEV1), from farmed giant freshwater prawn *Macrobrachium rosenbergii* **Dong, Hu, Liu, Li, Sun, Wang, Shi, Zhao, Huang**
12:45 PM		Marketplace shrimp mislabeling in North Carolina, USA **Bruno, Korzik*, Steinwand, Fodrie**			Thermal stress response genes regulated by methylation in the Pacific oyster, *Crassostrea gigas* **Arredondo^P, Escobedo-Fregoso, Sicard-Gonzales, Peña-Rodriguez, Roberts, Ibarra**
1:00-1:30 PM			**LUNCH BREAK WITH SPONSOR & TRADE SHOW PRESENTATIONS**		

* denotes student presenter

^{P} denotes non first-author presenter

MONDAY
March 22, 2021

1:30-2:30 PM	**PLENARY: Roger Mann** – ***Managing fisheries in the mid-Atlantic and New England regions in the coming decades – moving resource footprints, competing societal needs, and facilitating the discussion*** **(LIVE with Q&A to follow)** **Chesapeake Bay**				
ROOM	**Gulf of Maine**	**Gulf of Mexico**	**Puget Sound**	**Chesapeake Bay**	**Monterey Bay**
SESSION TITLE	**(#8) EASTERN OYSTER GENOME CONSORTIUM WORKSHOP** **Marta Gomez-Chiarri & Erin Roberts**	**(#9) BLUE CRABS** **Daphne Munroe & Joseph Caracappa**	**(#11) *VIBRIO*** **Steve Jones & Cheryl Whistler**	**(#6) SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**(#7) ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren & Kathy Tang**
2:30 PM	Training on the use of **NCBI** resources for exploring genomes and annotation tools (LIVE)	Patterns and drivers of female blue crab (*Callinectes sapidus*) size at maturity in South Carolina, USA **Thienes*, Kendrick**	Phage-host interactions shaped the native ST36 population succession in the Pacific and governed successful invasions into the North Atlantic **Whistler, Means, Foxall, Hartwick, Jones**	Increases in populations of the northern quahog (= hard clam) *Mercenaria mercenaria* following the creation of spawner sanctuaries in Shinnecock Bay, New York, USA **Doall, Cottrell, Peterson, Gobler**	
2:45 PM		Influences of brood-dependent behavioral variation on blue crab (*Callinectes sapidus*) larval transport in a wind-driven estuarine plume **Caracappa, Munroe, Chant, Fuchs**	Application of multiple methods for the detection and enumeration of pathogenic *Vibrio* sp. in mid-Atlantic seawater and oysters **Parveen, Jacobs, Ozbay, Chintapenta, Almuhaideb, Mereditth, Ossai, Grant, Abbott, Chigbu, Brohawn, Richards**	Assessing oyster restoration as a remediation strategy in Georgica Pond, Southampton, New York, USA **Morrell, Doall, Gobler**	
3:00 PM		Assessing the role of blue crab predation in driving top-down regulation of a salt marsh trophic cascade **Small*, Johnson**	Improving quantification of *Vibrio vulnificus* and *Vibrio parahaemolyticus* to support the shellfish industry of North Carolina, USA **Noble, Blackwood, Clerkin, Stoops, Foster, Froelich**	Mass die-off of adult bay scallops in New York following successful restoration: the looming specter of climate change **Tettelbach, Allam, Hughes, Peterson, Smith**	
3:15 PM		Association of climate and season with the prevalence and distribution of a pathogenic virus affecting the Atlantic blue crab across its trans-hemispheric range **Zhao*, Behringer, Bojko, Kough, Plough, Schott**	Estimating illness risk associated with *Vibrio parahaemolyticus* from Pacific oysters harvested in southern California using a quantitative microbial risk assessment framework **Cooksey*, Hamilton, Zimmer-Faust, Reynolds, Burgess, Verhougstraete**	The effects of tidal location on the boring sponge-oyster interaction: implications for management **Carroll, Dieudonne**	
3:30 PM		Question and Answer (LIVE Chat Session)	A case-control analysis of traceback investigations for vibriosis and pre-harvest environmental conditions in Washington State, 2013-2018 **Davis, Corrigan, Sun, Atherly, DePaola, Curriero**	*In situ* clearance rates of Olympia oyster, *Ostrea lurida*, habitat and Pacific oyster, *Crassostrea gigas*, aquaculture in California, USA **Marks*, Zacherl**	
SESSION TITLE	**(#8) EASTERN OYSTER GENOME CONSORTIUM WORKSHOP** **Marta Gomez-Chiarri & Erin Roberts**	**(#10) BLUE CRAB GENOMICS & TRANSCRIPTOMICS: THE PROGRAM OF THE BLUE CRAB GENOME PROJECT** **J. Sook Chung**	**(#11) *VIBRIO*** **Steve Jones & Cheryl Whistler**	**(#6) SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**(#7) ONE HEALTH: EPIGENOMES & MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren & Kathy Tang**
3:45 PM	Training on the use of **NCBI** resources for exploring genomes and annotation tools (LIVE)	Cracking the genome of the blue crab, *Callinectes sapidus* **Bachvaroff, Plough, Chung**	Management of *Vibrio* risk from oysters **Jones, Miller, Marchant, Jaillet-Neil, Pruente, Walton**	Can you eat them to save them? Farming the west coast native oyster, *Ostrea lurida*, for food and restoration in Tomales Bay, CA, USA **Fleener, Cortez, Grosholz**	
4:00 PM			Experimental study of total and potentially pathogenic *Vibrio parahaemolyticus* in temperature-abused and resubmerged oysters at sub-tidal and inter-tidal aquaculture sites **Petitpas, Lundgren, Boehler, Shanks, Regan**	Only time will tell: Successes and failures of restoring native oyster populations in habitat-limited systems **Barber, McArdle, Grossman, Hunter, Greiner, Cook, Nelson**	
4:15 PM		Population genomic analysis of the blue crab, *Callinectes sapidus*, across its range: insights into gene flow, local adaptation, and the potential for geographic source tracking **Plough, Lee, Schott, Kough, Behringer, Boijko, Bachvaroff, Chung**	The seasonal ecology of Vibrio parahaemolyticus in a New England estuary **Hartwick*, Berenson, Whistler, Naumova, Jones**	Abalone mariculture in Baja California: a conservation aquaculture project **Bauer*, Lorda, Beas-Luna, Malpica-Cruz, Rogers-Bennett, Micheli, Lafarga-De la Cruz, Searcy-Bernal**	
4:30 PM		Mitochondrial haplotypes suggest genetic component for habitat preference in blue crabs **Moran, Schulz, Rittschof**	Cool waters run deep - phylogenetic characterization of *Vibrio vulnificus* from the Great Bay Estuary of New Hampshire reveals unique environmental sequence types **Launen, Foxall, Early, Moore, Kiley, Sanders, Jones, Whistler**	Question and Answer (LIVE Chat Session)	
4:45 PM		Transcriptomic and expression analysis of the genes involved in ecdysteroidogenesis and cholesterol uptake in the Y-organ of the blue crab, *Callinectes sapidus* **Legrand, Bachvaroff, Schock, Chung^{P}**	Endemic populations of pathogenic *Vibrio* sp. in natural reservoirs from an eastern Florida estuary **Jayakumar, Grant, Lopez-Perez, Almagro-Moreno^{P}**		
5:00 PM		Understanding eyestalk neuropeptides influencing vitellogenesis of the red deep-sea crab, *Chaceon quinquedens* **Green*, Bachvaroff, Chung**	*Vibrio parahaemolyticus* strain-level diversity in sediment, water, and oysters in an aquaculture embayment **Santamaria, Lyons, Tlusty, Hamad-Shcifferli, Shiaris**		
5:15 PM		Is there a relationship between sexual maturity and expression levels of crustacean male hormone, insulin-like androgenic gland hormone (IAG)? **Lawrence*, Green, Wang, Bachvaroff, Chung**	Question and Answer (LIVE Chat Session)		
5:30 PM		Question and Answer (LIVE Chat Session)			

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

TUESDAY
March 23, 2021

ROOM	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay
SESSION TITLE	**(#12) OYSTER II** **Bill Fisher**	**(#13) SEAGRASS BIVALVE INTERACTIONS** **Kay McGraw & Brett Dumbauld**	**(#15) HATCHERIES** **Don Webster**	**(#16) OFFSHORE WIND ENERGY DEVELOPMENT & COMMERCIAL FISHERIES** **Daphne Munroe, Jennifer Beckensteiner, & Andrew Scheld**
8:30 AM	Overcoming the Tragedy of the Oyster: a global review on production and governance **Borsum*, Camp, Botta, Asche**	Meta-analysis and review of reciprocal interactions between bivalves and seagrass **Fales, Boardman, Ruesink[P]**	Hard clam hatchery development: in the beginning **Kraeuter**	Interactions and impacts of offshore wind development on East Coast shellfish fisheries **Munroe, Powell, Hofmann, Klinck, Scheld, Beckensteiner**
8:45 AM	Continuous water quality monitoring at sites of oyster farms and artificial oyster reefs in Rehoboth Bay, Delaware, USA **Bland, Ozbay**	Obligate and facultative facilitation of seagrasses by chemosymbiotic bivalves **Chin, de Fouw, van der Heide, Cahill, Katcher, Paul, Campbell, Peterson**	The production of seed shellfish does not need to be rocket science: the case for small hatcheries using simple technologies **Karney**	Assessing economic impacts to the US commercial surfclam fishing industry from offshore wind energy development **Scheld, Beckensteiner, Munroe, Powell, Solinger, Hofmann, Klinck, González-Díaz**
9:00 AM	Lone Cabbage Reef restoration and monitoring progress **Ennis, Pine, Frederick, Sturmer, Allen**	Identification of chemosynthetic symbionts in the lucinid clam, *Pillucina pisidium*, inhabiting a lagoonal seagrass bed in Jeju Island on the south coast of Korea **Shin*, Kang, Choi**	Hatcheries don't have to be complicated: the Cedar Key Seed model **Sturmer**	Spatial and temporal variations of Atlantic surfclam (*Spisula solidissima*) population demographic characteristics along the Mid-Atlantic Bight **González-Díaz*, Hofmann, Klinck, Munroe, Powell, Scheld**
9:15 AM	Supporting oyster aquaculture and restoration, program progress, and future directions **Hancock, Jones, Kornbluth, Rheault, Pilaro**	The effects of temperature on Pacific oyster filtration as a sink and potential source of an eelgrass pathogen, *Labyrinthula zosterae* **Agnew*, Burge, Groner, Eisenlord, Friedman**	Soft shell clam and Arctic surfclam hatchery development in Maine, USA **Beal, Pepperman**	northeast continental shelf of North America **Stokesbury**
9:30 AM	Effects of intertidal culture practices on the levels of *Vibrio parahaemolyticus* in farmed oysters (*Crassostrea gigas*) from the Pacific Northwest **Kelly*, Walton, Jones**	A shellfish industry perspective on shellfish-eelgrass interactions – a picture is worth a thousand words and a video worth a million **Dewey**	Hatchery operations for genetic improvement of shellfish **Allen, Jr.**	Industry Panel Discussion – live
9:45 AM	Characterizing eastern oysters, *Crassostrea virginica*, bred from native Louisiana broodstock under different salinity regimes: effect of stock and cohort **Bodenstein*, Tiersch, Callam, Walton, LaPeyre**	Assessment of ecological function and interactions of oyster culture and eelgrass **Hudson, Ruesink, Boardman, Houle, Dumbauld, Bloch, Lummis, Kroeker**	Nurturing the industry-academia collaboration: experiences and perspective from a private hatchery with an eye toward R&D **Congrove**	
10:00 AM	Breeding eastern oysters (*Crassostrea virginica*) for high-salinity environments **Guo, Whiteside, Wang, Ratcliff, Woodruff, Zeng, Haggard, Munroe, Calvo, Bushek, De Luca**	Habitat use by nekton in structurally complex oyster aquaculture and seagrass habitats **Boardman*, Ruesink, Hudson, Houle, Suhbrier, Lummis, Kroecker**	A hatchery certification program for the interstate transfer of shellfish seed **Hudson, Calvo, Bushek, Carnegie, Gustafson, Rheault, Marxen**	
10:15 AM	Stress tolerance in diverse lines of eastern oyster (*Crassostrea virginica*) **Haggard, Guo**	Small invertebrates in bivalve-cultivated and unmodified habitats of nearshore ecosystems **Munsch, Barber, Cordell, Kiffney, Sanderson, Toft**	Sea urchin hatchery technology **Pearce**	
10:30-10:45 AM	**MORNING BREAK**			
SESSION TITLE	**(#12) OYSTER II** **Bill Fisher**	**(#13) SEAGRASS BIVALVE INTERACTIONS** **Kay McGraw & Brett Dumbauld**	**(#15) HATCHERIES** **Don Webster**	**(#17) BIVALVES, MODELING, & CLIMATE CHANGE** **Tom Soniat & Eric Powell**
10:45 AM	Effects of inbreeding and outcrossing on early performance of the eastern oyster (*Crassostrea virginica*) **Wang*, Zeng, Guo**	Effects of seagrass and culture method on the growth of juvenile oyster seed along a gradient in two US west coast estuaries **Dumbauld, McIntyre[P], Durland, Bolm**	Queen conch aquaculture in Puerto Rico: hatchery and nursery phases **Davis, Espinoza, Cassar**	Coupling oyster stock assessments and shell-budget modeling to determine sustainable harvests for the northern Gulf of Mexico **Soniat, Powell, Cooper, Pace**
11:00 AM	Development of a cost effective and portable aeration freezing system for high-throughput sperm cryopreservation in the eastern oyster, *Crassostrea virginica* **Huo, Yee, Yang**	Is a precautionary approach to permitting too conservative? Quantifying the impacts of oyster aquaculture on submerged aquatic vegetation (SAV) **Kellogg, Shields, Dreyer, Luckenbach, Orth, Wilcox**	Heterotrophically conditioned recirculation system for bivalve larval culture **Bentley, Snyder[P], Ovissipour, Schwarz, Shiroodi, Urick, van Senten, Congrove, Bond**	Environmental controls on Withering Syndrome in abalone: a modeling study **Hofmann, Friedman, Powell, Klinck, Neuman, Moore, Taniguchi, Kushner, Miner, Hemeon, Poussard, Solinger**
11:15 AM	The use of selective breeding to understand the genetic underpinnings of resiliency to ocean acidification in the Pacific oyster (*Crassostrea gigas*) **Wright-LaGreca*, Mackenzie, Green**	On the co-existence of submerged aquatic vegetation and cage-based oyster aquaculture in Virginia, USA **Southworth, Wesson, Berman, Rudnicky, Mann**	Use of citizen scientists to monitor harmful algal blooms, changes in environmental conditions, and its utilization in aquaculture **Morton, Maucher-Fuquay**	Influences of environmental factors on temporal and spatial variation in Atlantic surfclam, *Spisula solidissima solidissima*, recruitment in New York State waters **Czaja, Jr.*, Hennen, Cerrato, Lwiza, Espinosa, O'Dwyer, Allam**
SESSION TITLE	**OYSTER II** **Bill Fisher**	**(#14) AQUACULTURE & THE PRESS: A NEW WAY FORWARD** **Rona Kobell, Tim Wheeler, & Louise Schaivone**	**(#15) HATCHERIES** **Don Webster**	**(#17) BIVALVES, MODELING, & CLIMATE CHANGE** **Tom Soniat & Eric Powell**
11:30 AM	A new 200K high-density SNP array specifically designed for Canadian eastern oyster (*Crassostrea virginica*) aquaculture **Laporte, Normandeau, Xuereb, Yáñez, Mallet, Bernatchez**	Panel Discussion (live)	Observations on the use of a McDonald fish hatching jar for oyster seed culture and improvements in bottle silo design **Supan, Truesdale**	The potential to model future range shifts of commercial species and their fisheries: a possible new approach **Powell, Mann, Munroe, Hofmann, Klinck**
11:45 AM	Developing technologies to induce reproductive sterility in eastern oysters without chromosome set manipulation **Xu*, Peng, Zohar, Wong**		Question and Answer (LIVE Chat Session)	Forecasting future range of sea scallops using a trophically-linked species distribution model: will climate change constrain scallop distribution in the Mid-Atlantic Bight? **Chang, Bart, Munroe, Curchitser, Rudders**
12:00 NOON	Question and Answer (LIVE Chat Session)			The confusion of complexity versus dynamics: habitat management and surfclams off Nantucket, Massachusetts, USA **Powell, Mann**
12:15 PM				Aids for the identification of larval and post-larval *Donax fossor* Say (Bivalvia: Donacidae) **Lutz**
12:30 PM				Spatial distribution of *Geukensia demissa* in salt marshes of Georgia, USA **Annis*, Carroll**
12:45 PM				Question and Answer (LIVE Chat Session)
1:00-1:30 PM	**LUNCH BREAK WITH SPONSOR & TRADESHOW PRESENTATIONS**			

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

	TUESDAY **March 23, 2021**
1:30-2:30 PM	**PLENARY: João Ferreira –** ***The coming of age precision aquaculture – how sensors and models are changing the way we grow shellfish*** **(LIVE with Q&A to follow)** **Chesapeake Bay**
ROOM	**Gulf of Maine**
SESSION TITLE	**(#18) DIVERSITY & INCLUSIVE EXCELLENCE LECTURE AND DISCUSSION (LIVE)** **Randy Williams –** ***How might a shellfisheries society operate with a DEI lens*** **Moderator: Aswani Volety**
2:30 PM	**The 2020 events of racial injustice in the United States spawned a widespread reaction across the globe and in various sectors of society.** **Many organizations have increased or started their efforts to create more diverse and inclusive settings for members,** **even those spaces where social identity issues are not part of the routine lexicon.** **This presentation will provide an introductory exploration of how human diversity, equity, and inclusion issues have a place in the sciences.**
2:45 PM	
3:00 PM	
3:15PM	
3:30 PM	
3:45 PM	
4:00 – 6:00 PM	**POSTER SESSION, TRADE SHOW, AND HAPPY HOUR (BYOBeverage) (LIVE)** **Gulf of Mexico**
5:00 – 6:00 PM	**RECRUITS JOB PANEL (LIVE)** **Monterey Bay**

WEDNESDAY
March 24, 2021

ROOM	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay	Monterey Bay
SESSION TITLE	**(#19) SHRIMP GENOME AND EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia-Alcivar Warren & Kathy Tang**	**(#20) DISEASE** **Roxanna Smolowitz & Ryan Carnegie**	**(#21) CLAMS** **Brian Beal**	**(#22) COMMERCIAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**	**(#23) NAEMO WORKSHOP: DEFINING BARRIERS AND IDENTIFYING SOLUTIONS FOR MUSSEL AQUACULTURE EXPANSION** **Asa Strand, Julie Webb, & Alessandro Laudicella**
8:30 AM	The Shrimp Genome and Epigenome (ShrimpENCODE) Project session: reviewing new whole genome sequencing (WGS) projects for Penaeoidea, transcriptomes and epigenomes of *Penaeus vannamei* and *P. monodon*, epigenetic components of penaeids, transposable elements in specific pathogen-free (SPF) *P. vannamei* produced by the United States, sex-determining genes of shrimp, and transgenerational epigenetic inheritance **Alcivar-Warren, Tang**	Taking the "X" out of QPX: completion of the life cycle and erection of a new genus and species, *Mucochytrium quahogii*, for the northern quahog (= hard clam) pathogen **Geraci-Yee*, Brianik, Rubin, Collier, Allam**	Commercial clams and fisheries of Maryland, Chesapeake Bay, USA **Dungan**	Examining spatial heterogeneity trends in ocean quahog growth and recruitment **Sower*, Powell, Mann, Hemeon, Pace**	**THE WORKSHOP WILL INCLUDE I) SHORT PRESENTATIONS ABOUT THE STATUS AND PRACTICES OF THE MUSSEL INDUSTRY IN DIFFERENT GEOGRAPHICAL REGIONS, II) BREAKOUT GROUPS WHERE SPECIFIC QUESTIONS WILL BE ADDRESSED, AND III) AN INTERACTIVE PLENARY SESSION TO SUMMARIZE THE MAIN FINDINGS. (LIVE)**
8:45 AM	Non-canonical epigenetic system of bacterial origin in aquatic micro-invertebrates **Rodriguez, Yushenova, Arkhipova**	An update concerning the ongoing research and occurrence of Neoplasia and QPX in the northern quahog (= hard clam) in Massachusetts, USA **Smolowitz, Sero, Gourlay, Gast, Reitsma, Murphy**	Historical range shifts and the influence of global warming on ocean quahogs (*Arctica islandica*) **LeClaire*, Powell, Mann**	Using a sclerochronological approach to determine a climate-growth relationship for waved whelk, *Buccinum undatum*, in the U.S. mid-Atlantic **Borsetti*, Hollyman, Munroe**	
9:00 AM		Perspective on disseminated neoplasia in the eastern oyster, *Crassostrea virginica*, based on analyses in Virginia from 1999-2020 **Safi, Crockett, Carnegie**	Temporal and spatial variation in growth in the surfclam, *Spisula solidissima* **Hollander*, Mann**	Modeling growth of two co-occurring Dungeness crab cohorts in the inland waters of Washington State **Cook, Grossman, Barber**	
9:15 AM	The Shrimp Genome and Epigenome: a review of genome sizes, transposable elements, simple sequence repeats, integrated viruses, and epigenetic components of Penaeids **Alcivar-Warren**	Diseases and parasites of commercially exploited *Mya arenaria* clams in Chesapeake Bay, Maryland, USA **Dungan**	Breeding farmed Atlantic surfclams (*Spisula solidissima*) for greater heat tolerance **Acquafredda, Guo, Munroe**	Comparing growth rates of banded tulips (*Cinctura hunteria*) using three methods **Geiger, Levine**	
9:30 AM	Exposing the secrets of the nephrocomplex I ("antennal gland"): a major portal of entry for pathogens in *Penaeus vannamei* shrimp **De Gryse, Thuong, Descamps, Van Den Broeck, Vanhove, Cornillie, Sorgeloos, Bossier, Nauwynck^{P}**	Ecological and environmental determinants for the pathobiome of bay scallops, *Argopecten irradians*, in the northern Gulf of Mexico **Sero*, Behringer, Bojko**	Effects of green crab, *Carcinus maenas*, predation on soft shell clam, *Mya arenaria*, populations in Maine during a warming ocean environment **Beal, Coffin, Randall**	Refining reproductive assessment protocols to better inform management of the South Carolina white shrimp (*Penaeus setiferus*) fishery **Brunson, Wagner, Gooding, Kendrick, Kingsley-Smith**	
9:45 AM		Comparison of histological and molecular methods in the diagnosis of *Merocystis kathae* infection in Georges Bank Atlantic sea scallops **Felson, Sero, Gourlay, Smolowitz, Siemann, Garcia**	A novel social-ecological clam garden site selection process **Greiner, Barber^{P}, Donatuto, Poe, McArdle, Hunter, Heidt, Campbell, Loomis**	The effect of density on reproductive effort in the Atlantic sea scallop, *Placopecten magellanicus* **Clark*, Roman, Mann, Rudders**	
10:00 AM	Screening of major shrimp pathogens in imported whiteleg shrimp (*Penaeus vannamei*) to Korea **Kim, Han**	Revisiting the role of copper and zinc in antimicrobial defenses of eastern oysters **Fisher**	Comparative transcriptomics of *Mercenaria mercenaria* and *Mercenaria campechiensis* in response to heat stress **Song, Yang**	Using baseline data from a before-after-control-impact (BACI) survey of American lobster (*Homarus americanus*) and Jonah crab (*Cancer borealis*) to explain relative abundance and size structure in offshore southern New England (SNE) **Zygmunt*, Stokesbury**	
10:15 AM		The role of mitochondrial and lysosomal permeabilization in the eastern oyster apoptotic response to *Perkinsus marinus* **Roberts*, Wikfors, Proestou, Lundgren, Sullivan, Gomez-Chiarri**	Evaluating environmental tolerance of the northern quahog (=hard clam) *Mercenaria mercenaria* to assess adaptive potential with applications to aquaculture **Himes*, Rivest, McDowell, Reece, Snyder**	Ocean quahogs: a glimpse into the population structure of the longest-lived, non-colonial animal on Earth using one of the largest age datasets in the world **Hemeon*, Powell, Mann, Redmond, Pace**	
10:30-10:45 AM	**MORNING BREAK**				
10:45 AM	First report of acute hepatopancreatic necrosis disease (AHPND) outbreak in *Penaeus vannamei* cultured in Korea **Jeon*, Han**	The disease diagnostic dilemma: the use of a novel testing method for determining disease prevalence and intensity in *Crassostrea virginica* **Gourlay, Sero, Smolowitz**	Effects of microalgal diets on growth, development, and survival of northern quahog (=hard clam) *Mercenaria mercenaria* larvae **Hassan, Park, Laramore**	Pacific Northwest Crab Research Group: closing critical Dungeness crab data gaps in Washington State waters **Buckner, Cook, Tobin, Barber, Bosley, Nelson, Harrington, Grossman**	
11:00 AM	Conjugative transfer of the pVA1 plasmid resulted in the formation of AHPND-causing *Vibrio* bacteria **Tang, Dong, Song, Chen, Bi, Wang, Wang, Ren, Guo, Wang, Huang**	Tidal and seasonal abundance of environmental *Perkinsus marinus* in the York River, Virginia, USA **Bienlien*, Carnegie**	Aquaculture potential of the angelwing clam: the southern geoduck? **Sturmer, Simon, Markham**	Shifting phenology of commercial white shrimp landings in South Carolina, USA: the roles of shrimp migration and climate **Kendrick, Brunson, Dukes, Whitaker, Kingsley-Smith**	
11:15 AM	The complete genome of an endogenous nimavirus (Nimav-1_LVa) from the Pacific whiteleg shrimp *Penaeus (Litopenaeus) vannamei* **Bao, Tang, Alcivar-Warren**	Prevalence and intensity of three oyster parasites (*Perkinsus marinus*, *Haplosporidium nelsoni*, and *Bonamia* sp.) in wild and cultured oysters (*Crassostrea virginica*) on an oyster farm in southeastern North Carolina, USA **Varney, Wilbur**	Pismo clams in California: growth and reproduction of an iconic species **Marquardt*, Park, Clark, Maietta, Ruttenberg**	Surveying fisheries in the wake of COVID-19 **Cassidy, Stokesbury**	
11:30 AM	Characteristics of the crustacean hyperglycemic hormone (CHH) genes and their functions in the processes of molting and male sexual differentiation in *Litopenaeus vannamei* **Xiang**	Surveillance of *Perkinsus olseni* infection in the Manila clam, *Ruditapes philippinarum*, in Korean waters **Cho*, Lee, Kim, Shin, Jang, Hwang, Choi**	Arctic surfclam, *Mactromeris polynyma*, field growout trials using cultured juveniles in eastern Maine, USA **Beal, Pepperman, Ellis**	Piloting the fuel efficient, low bycatch, and habitat friendly N-Viro dredge in the southern New England sea scallop fishery **Long, Marchetti, Roebuck, Sheehan, Bethoney**	
11:45 AM	Characterization and expression patterns of a new crustacean hyperglycemic hormone (CHH) gene from the Pacific white shrimp, *Penaeus vannamei* **Ventura-López, Gómez-Anduro, Arcos, Llera-Herrera, Racotta, Ibarra**	Down regulation of T6SS gene expression in the bivalve pathogen, *Vibrio coralliilyticus*, during competition with the probiont, *Phaeobacter inhibens* **Coppersmith*, Camm, Schuttert, Nelson, Rowley, Gomez-Chiarri**	Improved fishery-independent surveys of gaper clam (*Tresus capax*) populations in Oregon estuaries using an adaptive cluster sampling design **D'Andrea, Bancroft**	Selectivity of two commercial dredges fished in the northwest Atlantic sea scallop fishery **Roman, Rudders**	
12:00 NOON	The *fem-1* gene and its antisense transcript may have a function in sexual development of the Pacific whiteleg shrimp, *Penaeus vannamei* **Galindo-Torres*, Ventura-López, Llera-Herrera, Ibarra**	Using probiotic bacteria to reduce larval mortality and improve metamorphosis of *Crassostrea gigas* due to the bacterial pathogen, *Vibrio coralliilyticus* **Madison, Schubiger, Mueller, Landa, Langdon**	Seasonal production of atretic oocytes in the Manila clam, *Ruditapes philippinarum*, in northern Japan **Sugiura**	An investigation of the harvest practice of salting razor clams in the intertidal fishery **Reitsma, Archer, Burch, Curran, Booth, Smolowitz**	
12:15 PM	A chromosome-level assembly of the black tiger shrimp (*Penaeus monodon*) genome **Uengwetwanit, Pootakham, Nookaew, Sonthirod, Angthong, Sittikankaew, Rungrassamee, Arayamethakorn, Wongsurawat, Jenjaroenpun, Sangsrakru, Leelatanawit, Khudet, Koehorst, Schaap, dos Santos, Tangy, Karoonuthaisiri^{P}**		QUESTION AND ANSWER (LIVE CHAT SESSION)	Management strategy evaluation suggests Atlantic surfclam may be resistant to current fishing pressure despite uncertainties **Solinger*, Powell, Hennen, Cadrin**	
12:30 PM				Integration of different data sources for management of offshore bivalve aquaculture at Sagres, Portugal **Icely, Blount, Cristina, Danshenko, Fragoso, Freita, Goela, Moore**	
12:45 PM				QUESTION AND ANSWER (LIVE CHAT SESSION)	
1:00-1:30 PM	**LUNCH BREAK WITH SPONSOR & TRADE SHOW PRESENTATIONS**				

* denotes student presenter

^{P} denotes non first-author presenter

WEDNESDAY
March 24, 2021

1:30-2:30 PM	PLENARY: J. Evan Ward – *Looking down the barrel of an endoscope: insights from thirty years of in vivo investigations of suspension-feeding molluscs* (LIVE with Q&A to follow) Chesapeake Bay			
ROOM	**Gulf of Maine**	**Gulf of Mexico**	**Puget Sound**	**Chesapeake Bay**
SESSION TITLE	**(#19) SHRIMP GENOME AND EPIGENOME (ShrimpENCODE) PROJECT** **Acacia-Alcivar Warren & Kathy Tang**	**(#20) DISEASE** **Roxanna Smolowitz & Ryan Carnegie**	**(#24) UNDERGRADUATE RESEARCH COLLOQUIUM** **Edward Catapane & Margaret Carroll**	**(#22) COMMERICAL SHELLFISHERIES** **Kevin Stokesbury & David Rudders**
2:30 PM	Simple sequence repeats drive genome plasticity and promote adaptive evolution in penaeid shrimp **Yuan*, Zhang, Li, Xiang**	Probiotics for eastern oyster hatcheries: commercial formulations and effect on microbial communities **Takyi*, Roberts, Gregg, Chesler-Poole, Small, Rowley, Nelson, Hashman, Giray, Gomez-Chiarri**	Dopamine receptors: a genomic study of the bivalve mollusc *Crassostrea virginica* **Small*, Eid, Hinkley, Carroll, Catapane**	Discussion (live)
2:45 PM		Lobster shell disease in the NOAA Northeast Groundfish Surveys 2018 - 2019 **Kunkel, Galbraith, Kireun, Wilson, Reardon**	Manganese toxicity, mitochondrial dysfunction, and the potential therapeutic value of p-aminosalicylic acid, taurine, and carnosine **Bowman*, Wallach, Carroll, Catapane**	
3:00 PM	Transposable elements (TE) from specific pathogen-free (SPF) shrimp *Penaeus (Litopenaeus) vannamei* produced by the United States **Bao, Tang, Alcivar-Warren**	Identification of a new Reovirus in *Callinectes danae*: what does it mean for soft-shell crab production in Brazil? **Tavares*, Zhao, Vogt, Model, Vinagre, da Silva, Ostrensky, Schott**	Genomic study of GABA receptors in the bivalve *Crassostrea virginica* **Foster*, Eid, Hinkley, Carroll, Catapane**	
3:15 PM	Discussion (live)	Question and Answer (LIVE Chat Session)	Histamine receptors: a genomic study of the bivalve *Crassostrea virginica* **Larios*, Mansfield, Eid, Hinkley, Carroll, Catapane**	
3:30 PM			Question and Answer (LIVE Chat Session)	
4:00-4:30 PM	**NSA AWARD PRESENTATIONS (LIVE)** **Monterey Bay**			
4:30-6:00 PM	**POSTER SESSION, TRADE SHOW, AND HAPPY HOUR (BYOBeverage) (LIVE)** **Gulf of Mexico**			
5:00-6:00 PM	**RECRUITS SETTLEMENT SUITE-CHAT ROOM (LIVE)** **Gulf of Maine**			

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ᵖ denotes non first-author presenter

THURSDAY
March 25, 2021

ROOM	Gulf of Maine	Gulf of Mexico	Puget Sound	Chesapeake Bay	Monterey Bay
SESSION TITLE	**(#25) SHELLFISH GENETICS & GENOMICS** **Louis Plough & Jon Puritz**	**(#26) CONTAMINANTS OF EMERGING CONCERN** **J. Evan Ward & Kayla Mladinich**	**(#28) DOWN ON THE FARM** **Leslie Sturmer**	**(#30) SCALLOPS** **Richard Snyder & Michael Acquafredda**	**(#31) MANGROVE EPIGENOME (MangroveENCODE) PROJECT: A ONE HEALTH APPROACH** **Iris Hernandez, Alfredo Quarto, Jim Tang, & Acacia Alcivar-Warren**
8:30 AM	An assembled genome reference for the eastern oyster: a resource for discovery and innovation **Puritz, Zhao, Weedop, Modak, Roberts, Allen, Jr., Hare^{P}, Lotterhos, Rawson, Schwartz, Proestou, Guo, Warren, Gomez-Chiarri**	Selective ingestion and egestion of microplastics in the blue mussel, *Mytilus edulis*, and eastern oyster, *Crassostrea virginica* **Mladinich*, Holohan, Shumway, Ward**	Decreasing mortalities of triploid eastern oysters (*Crassostrea virginica*) in the estuaries of the northern Gulf of Mexico: field evaluation in coastal Alabama, USA **Eastburn*, Walton, LaPeyre**	Holding mirrors up to nature: the structure and function of the eyes of scallops **Speiser**	LIVE POSTER SESSION & DISCUSSION
8:45 AM	Whole-genome resequencing reveals genetic variations and selection signatures in eastern oyster populations from the Atlantic coast and Gulf of Mexico **Liu, Guo, Yang, Wilbur, Varney, Casas-Liste, La Peyre, Ashton-Alcox**	Physiological effects of microfiber ingestion by oyster larvae (*Crassostrea virginica*) **Knauss*, McFarland**	Assessing the effectiveness of desiccation in controlling biofouling in water column cultured oysters, *Crassostrea virginica*, in the Choptank River, Maryland, USA **Hood***	Panoramic spatial vision in the bay scallop, *Argopecten irradians* **Chappell*, Speiser**	
9:00 AM	Genomic signatures of selection on oysters within a single estuary **Zhao*, Simon, Hartung, Howlader, Manuel, Munroe, North, Hare**	Effects of microfibers on the gut microbiome and gut tissues of the blue mussel, *Mytilus edulis* **Collins*, Holohan, Griffin, Ward**	The role of characterizing the physical environment in oyster aquaculture to better predict production outcomes **Campbell*, Gray**	Optimizing batch-culture conditions for larvae of the lion's paw scallop, *Nodipecten subnodosus* **Garcia-Esquivel, Angel-Dapa, Nava-Gómez, Cordero-Esquivel, Bricelj**	
9:15 AM	Genetic basis of extreme low salinity survival in the eastern oyster (*Crassostrea virginica*) **McCarty*, Allen, Plough**	The impacts of microplastics on a largely overlooked marine invertebrate – the sea urchin **Suckling**	Effects of co-culture of urchins, *Lytechinus variegatus*, with eastern oysters, *Crassostrea virginica* **Walton, Robitaille, Wilson, Chehade, Wasden, Michaelis, Watts**	Strategies to enhance bay scallop populations on Martha's Vineyard, Massachusetts, USA **Karney**	
9:30 AM	From sequence to consequence: genomic selection to expand and improve selective breeding for the eastern oyster **Guo, Allen, Jr., Proestou, Allam, Gomez-Chiarri, Hare, Liu, Lotterhos, Kube, Plough, Puritz, Rawson, Small, Varney, Verbyla, Wikfors, Wilbur**	Ingestion, bioaccumulation, and depuration of micro- and nanoplastics by oysters (*Crassostrea virginica*) and mussels (*Mytilus edulis*) **Ward, Haynes, Mladinich, Griffin, Holohan**	Video documentation of the marine community utilizing an oyster farm **Shinn, Munroe, Ambrose, Calvo**	Survival and growth of selected bay scallops (*Argopecten irradians*) in Barnegat Bay, New Jersey, USA **Whiteside*, Acquafredda, Woodruff, Deck, Munroe, Calvo, De Luca, Gao**	
9:45 AM	Temperature-associated selection linked to putative chromosomal inversions in king scallop (*Pecten maximus*) **Hollenbeck, Portnoy, de la Serrana, Magnesen, Matejusova, Johnston**	Microplastics in sandy environments in the Florida Keys and the Florida panhandle, and the ingestion by sea cucumbers (Echinodermata: Holothuroidea) and sand dollars (Echinodermata: Echinoidea) **Plee*, Pomory**	Automating oyster aquaculture with the sun **Rice, Pattison, Summers^{P}, Borgert, Hines, Frost**	Bay scallop, *Argopecten irradians*, culture in Wachapreague, Virginia, USA **Turner-Smith, Kelley, Turner, Orlando, Smith, Snyder^{P}**	
10:00 AM	Atlantic surfclam harvest management: How many species? How many management units? **Hartung*, Hare**	The interactive effects of titanium dioxide nanoparticles and light on fertilization and embryogenesis on the Pacific oyster (*Crassostrea gigas*) **Haynes, Tallec, Paul-Pont, Soudant, Ward**	Shellfish farming and cultural services, the other ecosystem service **Michaelis, Walton, Webster, Shaffer**	Farm production of sea scallops (*Placopecten magellanicus*) in Maine, USA **Morse, Cowperthwaite**	
10:15 AM	Characterizations of the immune-regulatory function of CSDE-1 in *Crassostrea virginica* hemocytes **Ricigliano*, Kuldell, Gorson, Krause**	Question and Answer (LIVE Chat Session)	International shipping (export) of live molluscs and crustaceans **Marston**	Assessing the effects of culture method and environment on sea scallop (*Placopecten magellanicus*) growth and mortality in the northwest Atlantic **Kiffney*, Coleman, Tanaka, Morse, Brady**	
10:30 AM	Eastern oyster transcriptomic response to different *Perkinsus marinus* exposure methods and infection intensities **Proestou, Sullivan**		Question and Answer (LIVE Chat Session)	A pilot study evaluating gonad ripening and spawning cycles in sea scallops (*Placopecten magellanicus*): potential gear and site effects and comparisons to wild populations **Jekielek, Batchelder, Maier, Huntsberger, Arno**	
10:45-11:00 AM	**MORNING BREAK**				
SESSION TITLE	**(#25) SHELLFISH GENETICS & GENOMICS** **Louis Plough & Jon Puritz**	**(#27) COASTAL ACIDIFICATION** **Shannon Meseck**	**(#29) BIVALVE ECOSYSTEM SERVICES** **Daniel Taylor**	**(#30) SCALLOPS** **Richard Snyder & Michael Acquafredda**	
11:00 AM	Epigenetic effects of ocean acidification in the eastern oyster **Lotterhos, Downey-Wall, Venkataraman, McNally, Titmuss, Ries, Roberts**	Multi-stressor extremes found on tropical coral reefs impair performance **Lucey, Haskett, Collin**	Quantifying farm-scale ecosystem services associated with eastern oyster aquaculture in the Northeast **Barr*, Munroe, Calvo, Kreeger, Cheng, Rose, Bayer**	Sea scallop, *Placopecten magellanicus*, filtration and feeding relative to seston quantity and quality in the Damariscotta River, Maine, USA **Dixon, Mizuta, Meseck, Morse, Bayer, Wikfors**	LIVE POSTER SESSION & DISCUSSION
11:15 AM	Assessing the evolutionary response of eastern oyster larvae to exposure to coastal acidification and sewage effluent: a case study **Puritz, Harvey, Lotterhos**	Effects of ocean acidification and climate change on the growth and development of Oregon pink shrimp (*Pandalus jordani*) larvae **Nguyen*, Johnson, Myers, Otenburg, Kela-Pacheco, Zirbel, Waldbusser**	Nitrogen filtration by freshwater and saltwater bivalves: importance of seston composition **Kreeger, Cheng, Moody, Gentry**	Spillover of sea scallops from rotational closures in the Mid-Atlantic Bight (USA) **Hart, Munroe, Caracappa, Haidvogel, Shank, Rudders, Klinck, Hofmann, Powell**	
11:30 AM	Investigating the effects of coastal stressors on the genomic variation of oyster populations in Narragansett Bay, Rhode Island, USA **Zyck*, Stevick, Gallagher, Padro, Gomez-Chiarri, Puritz**	Identifying molecular markers associated with resilience to ocean acidification in the eastern oyster **Schwaner*, Farhat, Tanguy, Boutet, Barbosa, Espionsa, Allam**	Phytoplankton depletion in and around mussel farms in eutrophic Baltic coastal seas and fjords **Taylor, Saurel, Petersen, Maar, Larsen, Jakobsen, Darecki**	Transmission of the sea scallop nematode: temporal variation and thermal tolerance **McGurk, Bushek, Munroe, Bochenek, Borsetti, Rudders, Roman**	
11:45 AM	The enzyme defense mechanism encountered in marine green mussel, *Perna viridis*, in response to hydrocarbon (ethyl-naphthalene) pollution **Dinesh*, Amutha**	Glider-based observations reveal seasonal pH and aragonite saturation state variability in coastal U.S. Mid-Atlantic shellfishery management zones **Wright-Fairbanks*, Saba, Chen, Cai, Miles**	Nutrient ecosystem services derived from bivalves on engineered structures **Cornwell, Owens, Gray, Nardin, Colden, Poskaitis**	A newly-discovered didymozoid trematode infecting the gill of its first intermediate host, the bay scallop **Buck, Thompson, Crook, Smith, Priester, Varney, Wilbur**	
12:00 NOON	Intraspecific comparison of oyster gene expression response to low oxygen **Davis*, Plough, McFarland, Paynter**	Projected effect of future coastal acidification conditions upon the physiology of the eastern oyster (*Crassostrea virginica*) and the Atlantic surfclam (*Spisula solidissima*) through DEB modeling **Pousse, Redman, Sennefelder, Krisak, Li, Dixon, Poach, Veilleux, Milke, Wikfors, Hofmann, Klinck, Munroe, Meseck**	Comparing the impact of artificial oyster reefs and oyster farms on wild oyster restoration, aquatic species diversity, and water quality in Delaware inland bays **Nakazwe*, Gadde, Bland, Ozbay**	Is an apicomplexan parasite responsible for the collapse of the bay scallop (*Argopecten irradians irradians*) population in New York? **Muchl*, Espinosa, Tettelbach, Geraci-Yee, Farhat, Kristmundsson, Allam**	
12:15 PM	Unlocking the exome: exploring *de novo* assembly options for capture sequencing **Green*, Puritz**	Ocean acidification effect on eastern oyster, surfclams, and sea scallops: commonalities and differences **Pousse, Redman, Sennefelder, Krisak, Li, Dixon, Poach, Veilleux, Milke, Wikfors, Hart, Hennen, Gaughan, Gerrior, Hubard, Osborne, Munroe, Meseck^{P}**	Nitrogen bioextraction by juvenile alewife floaters, *Utterbackiana implicata*, during pond rearing in the Delaware River Basin **Gentry, Kreeger, Cheng, Gray**	Question and Answer (LIVE Chat Session)	
12:30 PM	Modeling genetic risks of native shellfish aquaculture **Lowell*, Vadopalas, Ward, Hauser**	A slow growing perspective on multi-generational responses to future change **Suckling**	Question and Answer (LIVE Chat Session)		
12:45 PM	East coast northern quahog (= hard clam) selective breeding collaborative **Allam, Farhat, Espinosa, Tanguy, Reece, Yang, Rivara, Reitsma, Clemetson, Guo**	Question and Answer (LIVE Chat Session)			
1:00-1:30 PM	**LUNCH BREAK WITH SPONSOR & TRADE SHOW PRESENTATIONS**				

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

	THURSDAY March 25, 2021			
1:30-2:30 PM	**PLENARY: M. Luz Pérez-Parallé – *'Omic' technologies applied to aquaculture* (LIVE with Q&A to follow)** **Chesapeake Bay**			
ROOM	**Gulf of Maine**	**Gulf of Mexico**	**Puget Sound**	**Chesapeake Bay**
SESSION TITLE	**(#32) FUNCTIONAL GENOMICS** **Tim Bean**	**(#33) SUMMER MORTALITY** **Tim Green**	**(#34) GENERAL CONTRIBUTED II** **Gulnihal Ozbay**	**(#35) ECHINOIDS** **Chris Pearce & Stephan Watts**
2:30 PM	Chromosome-level assemblies of the northern quahog (= hard clam) and its harmful parasite QPX **Farhat, Espinosa, Tanguy, Boutet, Allam**	The first detection of a novel OsHV-1 microvariant in San Diego, California, USA **Burge, Friedmam, Kachmar, Humphrey, Moore, Elston**	Analysis of carbon and nitrogen isotopes to assess nutrient loading and its effects on oyster activities in Rehoboth Bay, Delaware, USA **Gadde*, Nakazwe, Bland, Ozbay**	Effects of feed ration on growth and gonad production in small sea urchins, *Lytechinus variegatus* **Gibbs, Heflin, Taylor, Lawrence, Watts**
2:45PM	Harnessing the power of single-cell RNA sequencing to control reproductive development in bivalves **Gavery, Saunders, Vadopalas, Luckenbach, Trapnell, Roberts**	Varying responses of different oyster species during field trials and injection challenges with OsHV-1 variants **Friedman, Reece, Wippel, Agnew, Dégremont, Dhar, Kirkland, MacIntyre, Morga, Robison, Burge**	Reestablishment of a population of adult queen conch, *Aliger gigas*, population in a marine protected area in The Bahamas **Norton, Booker, Ajemian, Davis**	Effect of transport method on subsequent survivorship and gonad yield and quality in the red sea urchin (*Mesocentrotus franciscanus*) **Pearce, Warren**
3:00 PM	Question and Answer (LIVE Chat Session)	Initiation of a sentinel program to monitor herpes virus in juvenile Pacific oysters (*Crassostrea gigas*) at commercial farms along the US west coast **Evans, Dumbauld, Burge, Langdon, Schoolfield, Dayal, Schoeneck, McIntyre, Divilov**	The guishe of *Agave lechuguilla* as source of nutritional biomolecules to promote shrimp productivity **Peña-Rodriguez, Pelletier-Morreeuw, García-Luján, Rodríguez-Jaramillo, Guzmán-Villanueva, Escobedo-Fregoso, Tovar-Ramírez, Reyes[P]**	Expanding production method information for sea urchins **Suckling**
3:15 PM		2018 summer mortality event of Pacific oysters in Baynes Sound is linked to a seawater temperature spike and infection with *Vibrio* sp. **Green, Cowan, Pearce, Meyer**	Exploring mechanisms underlying the range limits of a marine crab in a warming hotspot **Barley*, Cheng**	Effect of diet and temperature on gonad enhancement of green (*Strongylocentrotus droebachiensis*) and red (*Mesocentrotus franciscanus*) sea urchins **Warren*, Flaherty, Cross, Pearce**
3:30 PM		Impacts of seawater pH buffering on larval stage Pacific oysters and repercussions for susceptibility of spat to summer mortality stressors **Mackenzie, Green, Leduc, Roth, Pearce**	Responses of ribbed mussels to environmental stressors **Chester*, Volkenborn**	Question and Answer (LIVE Chat Session)
3:45 PM		Question and Answer (LIVE Chat Session)	Question and Answer (LIVE Chat Session)	
4:00 – 6:00 PM	**CLOSING HAPPY HOUR & SILENT AUCTION RESULTS (LIVE)** **Gulf of Mexico**			

* denotes student presenter

[P] denotes non first-author presenter

CONTENTS

ORAL PRESENTATIONS

POSTER PRESENTATIONS

BREEDING FARMED ATLANTIC SURFCLAMS (*SPISULA SOLIDISSIMA*) FOR GREATER HEAT TOLERANCE

Michael P. Acquafredda*, Ximing Guo, and Daphne Munroe

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The Atlantic surfclam (*Spisula solidissima*) is emerging as an attractive alternate species grown by aquaculturists across the northeast, USA. This species is native, grows rapidly, and complements the region's established farming framework; however, the surfclam is vulnerable to high temperature conditions, an issue that will be exacerbated by rising ocean temperatures and one that will be problematic on shallow coastal farms. This study explored the feasibility of selectively breeding farmed Atlantic surfclams fo r greater heat tolerance. It was found that when juvenile surfclams were exposed to prolonged lethal temperatures, the adult survivors withstood subsequent heat stress for significantly longer than individuals not exposed to lethal temperatures as juveniles. It was also found that selective breeding enhanced heat tolerance in first-generation surfclam progeny. Moreover, growth of the heat-selected progeny was not significantly different from that of control clams when they were reared under ambient conditions. It also examined the transcriptomic response of heat-selected and control surfclams to heat stress. Naïve (control) surfclams had a more intense transcriptomic response to a heat challenge, differentially expressing more genes compared to clams that had previously survived lethal temperatures; however, the heat-selected clams exhibited stronger heat-shock protein and anti-apoptosis responses than the control clams during heat stress. Together, this work provides insights into how surfclams adapt to heat stress and should inform future attempts to breed surfclam for greater heat tolerance.

THE EFFECTS OF TEMPERATURE ON PACIFIC OYSTER FILTRATION AS A SINK AND POTENTIAL SOURCE OF AN EELGRASS PATHOGEN, *LABYRINTHULA ZOSTERAE*

M. Victoria Agnew*[1], Colleen A. Burge[1], Maya L. Groner[2], Morgan E. Eisenlord[3], and Carolyn S. Friedman[4]

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Global seagrass declines are hypothesized to be the result of a variety of factors including eutrophication, sedimentation, increases in sea surface temperature, and diseases such as eelgrass wasting disease (EGWD). Additionally, there is concern regarding the negative impacts from bivalve aquaculture on seagrass population growth and density, which results from the physical structures and harvesting methods associated with aquaculture. Oyster aquaculture and seagrasses often overlap within the intertidal zone, which leads to restrictions on oyster farming due to protections on seagrass habitat; however, as filter feeders, oysters offer a potential mitigation strategy to one of the threats against seagrasses: EGWD. Pacific oysters, *Crassostrea gigas*, are known to filter the causative agent of EGWD, *Labyrinthula zosterae* (*Lz*), out of the water, even though the accumulation and reintroduction of *Lz* from oysters into the water may act as a source of infection. To investigate whether oysters act as a sink or source of *Lz*, laboratory experiments were conducted in the San Juan Islands, WA. Oysters and eelgrass were co-cultured in tanks and exposed to an infectious isolate of *Lz* for 24 hours. A total of five treatments were run in triplicate at 11°C and 18°C to investigate how temperature affects this relationship. After 13 days, ImageJ and qPCR analysis were run to determine the severity and prevalence of EGWD and *Lz* in the presence and absence of oysters. Results from this experiment will provide important insight on the potential for synergism between oysters and eelgrass.

THE SHRIMP GENOME AND EPIGENOME: A REVIEW OF GENOME SIZES, TRANSPOSABLE ELEMENTS, SIMPLE SEQUENCE REPEATS, INTEGRATED VIRUSES, AND EPIGENETIC COMPONENTS OF PENAEIDS

Acacia Alcivar-Warren

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The goal of ShrimpENCODE is to understand the epigenetic mechanisms associated with susceptibility and tolerance of Pacific whiteleg shrimp, *Penaeus* (*Litopenaeus*) *vannamei*, to bacterial [acute hepatopancreatic necrosis disease (AHPND)] and viral [white spot syndrome virus (WSSV), infectious hypodermal and hematopoietic necrosis virus (IHHNV), Taura syndrome virus (TSV)] diseases. It was proposed that transposition of mobile genetic elements [transposable elements (TEs)], among AHPND-causing *Vibrio* spp. occurs via horizontal gene transfer (HGT), horizontal transfer of plasmids (HTP) and transposons (HTT), and transgenerational epigenetic inheritance (TGEI). To test the hypothesis, a contiguous, fully-assembled whole genome sequence (WGS) for *P. vannamei* is needed. To date, six WGS assemblies are available: two for *P. vannamei* farmed in China [Breed: Kehai No. 1 (ASM378908v1, ~1.6 Gb) and Breed: F1 (ASM373033v1], one *P. japonicus* (~1.4 Gb), and three *P. monodon* from China (~1.6 Gb), Vietnam (~1.6 Gb) and Thailand (~2.37 Gb). Expected size of SPF *P. vannamei* is ~2.87 Gb. In ASM378908v1, large number (23.93%) of simple sequence repeats, 25,572 protein-coding genes, and noncoding RNA [1,458 tRNA, 464 rRNA, 296 snRNA, 255 snoRNA, 90 ribozymes, 59 cis-regulatory elements, 214 microRNA] were found. Three hundred twelve repetitive sequences were characterized in a pilot WGS (~470 Mb) from SPF *P. vannamei* of Kona Line domesticated by the USMSFP, including 105 DNA transposons, 119 long terminal repeat (LTR) retrotransposons, 76 non-LTR retrotransposons, a few unclassified, and one endogenous virus, *Nimav-1_LVa*, integrated into telomeric repeats (TAACC/GGTTAn) of SPF *P. vannamei*, but not in *P. monodon*. Epigenetic components of Penaeids will be presented.

THE SHRIMP GENOME AND EPIGENOME (SHRIMPENCODE) PROJECT SESSION: REVIEWING NEW WHOLE GENOME SEQUENCING (WGS) PROJECTS FOR PENAEOIDEA, TRANSCRIPTOMES AND EPIGENOMES OF *PENAEUS VANNAMEI* AND *P. MONODON*, EPIGENETIC COMPONENTS OF PENAEIDS, TRANSPOSABLE ELEMENTS IN SPECIFIC PATHOGEN-FREE (SPF) *P. VANNAMEI* PRODUCED BY THE UNITED STATES, SEX-DETERMINING GENES OF SHRIMP, AND TRANSGENERATIONAL EPIGENETIC INHERITANCE

Acacia Alcivar-Warren*[1,2] and Kathy Tang[3]

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The speakers of the ShrimpENCODE session will address the following topics: non-canonical epigenetic system of bacterial origin in aquatic micro-invertebrates, the shrimp genome and epigenome: a review of genome sizes, transposable elements, simple sequence repeats (SSR), integrated viruses and epigenetic components of Penaeids, six whole reference genomes (WGS for Penaeoidea, a chromosome-level assembly of black tiger shrimp genome (*Penaeus monodon*) from Thailand, simple sequence repeats (SSR) drive genome plasticity and promote adaptive evolution in penaeid shrimp, screening of major shrimp pathogens in imported whiteleg shrimp (*P. vannamei*) to Korea, transcriptomes of *P. vannamei* and *P. monodon,* epigenetic components of penaeids (DNA methylation, histone methylation-acetylation, non-coding RNA) in WGS assembly (~1.6 Gb) of *P. vannamei* farmed in China, transposable elements of specific pathogen-free (SPF) *P. vannamei* domesticated by the US Marine Shrimp Farming Program (USMSFP) consortium, genome size (~2.87 Gb) of 'SPF' *P. vannamei* from a commercial hatchery in USA, transgenerational epigenetic inheritance, conjugative transfer of the pVA1 plasmid resulted in the formation of AHPND-causing *Vibrio* sp. bacteria, horizontal transfer of plasmids and transposons, shrimp endogenous viral elements (EVE) of infectious hypodermal and hematopoietic necrosis virus (IHHNV)- their implications for shrimp diagnosis and the OIE international trade certification, the *fem-1* gene and its antisense transcript may have a function in sexual development of *P. vannamei*, the complete genome of an endogenous nimavirus (*Nimav-1_LVa*) from *P. vannamei*, 'Shrimp Scampi: A Citizens Science Project' of high school students from the USA, and crustacean hyperglycemic hormone (CHH) genes and their functions in the processes of molting and male sexual differentiation in *P. vannamei,* among others.

RECOGNITION OF WINNERS OF 2021 'JOHNNY ALCIVAR-ARTEAGA RESEARCH AND TRAVEL AWARDS' AND 'JOHNNIE CASTRO MONTEALEGRE TRAVEL AWARDS' FOR 71 INTERNATIONAL STUDENTS FROM ELEVEN COUNTRIES, AND TWELVE '2020-2021 OUTSTANDING ONE HEALTH RESEARCHERS IN AQUACULTURE' BY THE FUCOBI FOUNDATION OF ECUADOR

Miriam Alcivar-Arteaga*, Jorge Romero-Arteaga, Sofia Figueroa, Andrés Aveiga, Iris Hernandez, Daniela Espinoza, Karol Alarcon, Gober Asuncion, and Liliana Zuniga

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Members of the FUCOBI Foundation of Ecuador will read the award certificates for 71 international students representing eleven countries from three continents (Brazil, Colombia, Ecuador, Indonesia, Mexico, Nigeria, Peru, Spain, Thailand, Singapore, United States), who are winners of the FUCOBI 2021 'Johnny Alcivar-Arteaga Research and Travel Awards' and 'Johnnie Castro Montealegre Travel Awards'.

Twelve certificates of awards will be read by members of the FUCOBI Foundation Board for 12 scientists nominated for '2020-2021 Outstanding ONE HEALTH Researchers in Aquaculture' (Ana Ibarra, Ana Soto, Irina Arkhipova, Jianhai Xiang, Jurgenne Primavera, Kathy F.J. Tang, Nitsara Karoonuthaisiri, Sandra Shumway, Suhua Shi, Tim Flegel, Weidong Bao, Ximing Guo) representing five countries (China, Mexico, Philippines, Thailand and United States).

The board of the FUCOBI Foundation of Ecuador would like to thank Dr. Sandra Shumway and the National Shellfisheries Association (NSA) for helping train the next generation of ONE HEALTH aquaculture and fishery researchers.

EAST COAST NORTHERN QUAHOG (= HARD CLAM) SELECTIVE BREEDING COLLABORATIVE

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

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The northern quahog (= hard clam), *Mercenaria mercenaria*, is extensively cultured along the Atlantic seaboard of the U.S. and represents the most important marine resource in several states including New York, Virginia, and Florida. Maintenance and growth of this aquaculture industry relies on hatchery production of seed, and billions of seed clams are produced annually to fulfill aquaculture and restoration needs. Several states regularly suffer losses in aquacultured and wild hard clam stocks due to disease (e.g. QPX in the northeast) and environmental stress (e.g. heat waves in Florida). Therefore, the production of quality seed able to survive under harsh biological and environmental conditions represents a priority for the aquaculture community.

This collaborative initiative builds on ongoing cooperation and new partnerships among Sea Grant programs, scientists and extension teams in five Atlantic states to develop a hard clam selective breeding program using state of the art genomic tools, for the benefit of clam farmers throughout the region. The team has just completed the sequencing and assembly of the hard clam genome and is currently re-sequencing clams collected from Maine to Florida. Generated genomic data will be used to develop an efficient and cost-effective genotyping platform (SNP array) for *M. mercenaria*. This genotyping platform will then be used to enable genome-assisted selection for traits relevant to various regions supporting the growth of the hard clam aquaculture industry. These activities will serve as a basis to establish clam breeding programs linking scientists, extension networks and the industry to provide growers with superior clam stocks.

HATCHERY OPERATIONS FOR GENETIC IMPROVEMENT OF SHELLFISH

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Research hatcheries, of which a breeding program would avail, have several key elements that distinguish them from commercial space. The principal needs for research or breeding are tank replication, "table" space, and plastic ware, including microscope(s) and (especially) labelling tape. All other supporting functions of a hatchery are more or less equivalent to a commercial operation.

Research (breeding) hatcheries are characterized by many small tanks rather than smaller numbers of very large ones. This derives from the need for replication to accommodate experimental design in the case of research hatcheries or multiple crosses for progeny tests in the case of breeding. In the example of the VIMS breeding program, 200-300 crosses might be executed per year, often with >70 running simultaneously. That number of crosses, also spawned at the same time, militates the separation of gametes to effect precise pedigrees. Therefore, whether gametes are strip spawned or naturally spawned, they need to be contained until use, necessitating lots of plastic ware for eggs and sperm and the 2D space to place them.

Finally, because of the maxim that requires separation of breeding from routine commercial activity, the ideal is to have a dedicated set-aside in the hatchery for R&D work. While this set-aside can easily share common features, such as water filtration and algae feed, the 2D space, plastic ware, screen sets and other toys of R&D, and especially the gametes and larvae should be inviolately separate.

SPATIAL DISTRIBUTION OF *GEUKENSIA DEMISSA* IN SALT MARSHES OF GEORGIA, USA

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The ribbed mussel, *Geukensia demissa,* is an ecologically important bivalve species found in salt marshes along the Atlantic coast and has been found to increase *Spartina alterniflora* (cordgrass) growth in marsh restoration projects. Byssal threads from *G. demissa* stabilize marsh sediments and nitrogenous waste fertilizes *S. alterniflora*. Despite the potential application of *G. demissa* in marsh restoration, little is known about their spatial distribution in Georgia. This study seeks (1) to examine both landscape and marsh scale factors that may contribute to the distribution of *G. demissa* in Georgia and (2) to determine how growth rate, survival, and recruitment of *G. demissa* vary at different locations in the marsh. These objectives were addressed through a GIS analysis and field experiments. Preliminary data from two sites shows that on the marsh scale, *G. demissa* densities are affected by elevation, slope, and distance to creek heads. Highest *G. demissa* densities were found on the lower marsh platform, close to creek heads. Lowest *G. demissa* densities were found on levees along subtidal creeks. In these low elevation areas close to creek heads, *G. demissa* growth rates and recruitment were the highest. It is hoped that findings from this study can be used to optimize the placement of *G. demissa* for the greatest growth and survival in future salt marsh restoration projects.

THERMAL STRESS RESPONSE GENES REGULATED BY METHYLATION IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*

Roberto E. Arredondo[1]*, Cristina Escobedo-Fregoso[2], M. Teresa Sicard-Gonzales[1], Alberto Peña-Rodriguez[2], Steven Roberts[3], and Ana María Ibarra[1]

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Thermal stress is one of the factors that affects production through aquaculture of the Pacific oyster, *Crassostrea gigas,* in Mexico. Increases in temperature up to 34°C or more in shallow waters had been associated with high mortalities. Selective breeding of thermal-resistant oysters represents an alternative to improve survival. Research aimed to understand if genetic differences exist for resistance among families within a breeding program being developed in CIBNOR since 2013 will be presented. After an induced acute thermal challenge, three families were phenotypically characterized as thermal-resistant and three as thermal-susceptible. Unexposed oysters from the same six families were subjected to a chronic thermal stress for 30 d using daily oscillating temperatures between 26°C and 34°C. At day 30 gill tissue was sampled and processed for RNA-seq and Whole Genome Bisulfite Sequencing (WGBS) with the objective of identifying differentially expressed (DE) genes and transcripts and differentially methylated regions (DMR) between phenotypes in response to thermal stress. Gene ontologies for DE genes were assigned to energy production, metal ion binding, DNA and transcription regulations. The result in DMR analysis, suggested that DE between phenotypes is related to DMR in promoters, exons, and introns. In this presentation will summarize how families were selected, the differences between thermal phenotypes at the transcriptomic level and in methylation of gene regions, and on the relationship between DMR and phenotypes differential gene expression. This research will serve as the bases for further basic research needed to understand the impact of climate change stress on oyster genomes.

EFFECT OF ENVIRONMENTAL HISTORY ON THE PHYSIOLOGY AND ACUTE STRESS RESPONSE OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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Environmental history may influence how the physiology of eastern oysters (*Crassostrea virginica*) responds to future environmental conditions caused by climate change; however, previous research has only examined environmental history in a one-dimensional framework, which fails to fully capture environmental history complexity through space and time. In this study, environmental history was examined as a multi-faceted parameter, incorporating abiotic water quality components that differ among locations. Additionally, the effects of different lengths of environmental histories, defined as proximal and distal environmental history, on oyster physiology and stress response were assessed. Finally, the relative influence of abiotic components of environmental history on oyster physiology was compared. Oyster physiology and stress response are differentially affected by proximal and distal environmental history, demonstrating the importance of examining environmental history as a multi-faceted and dynamic parameter. Specifically, distal environmental history primarily influenced condition index and total antioxidant potential, while proximal environmental history primarily influenced glycogen. Salinity was identified as the component of distal environmental history that significantly shaped condition index, establishing salinity as a principal factor when considering acclimatization to variable environmental conditions; however, no water quality components were identified as significant influences on glycogen and total antioxidant potential, which provides opportunities for future research on other abiotic and biotic components of environmental history. Identifying the temporal portion of the environmental history of oysters that influences physiological parameters supports future efforts to predict population tolerance to climate change. Additionally, examining multiple abiotic and biotic components of environmental history can elucidate means of acclimatization to future environmental change.

ASSESSING CONTRIBUTION OF SHELLFISH AQUACULTURE TO GLOBAL FOOD SECURITY

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Aquaculture is considered as the fastest growing food industry production sector, and is recognised worldwide as among the most sustainable options for improving food security. Food is always a timely issue since we all have to eat, and also a basic human need. Shellfish seafood is among one of the most important sources of protein in the world. Sustainable production of food from the shellfish has an important role in future food supply and food security.

An adequate amount of food, reduced production cost, reduced food waste and sustainable resources are the four pillars of future food which support sustainable aquaculture production. Seafood also contributes substantially to the overall protein, as well as micronutrients and essential fatty acids that are not easily found in land-based foods. Trends in seafood research have been studied extensively owing to its important implications for human health, economy, social, food security and the environment.

The future contribution of seafood from the shellfish aquaculture to global food supply will depend on i) available of biological and technical knowledge, ii) a range of biotic and abiotic stress response and tolerance, iii) short life cycles, iv) high demand species, v) health benefit, vi) nutritive value, vii) consumer safety and viii) household budget with good market price. The paper concludes that shellfish aquaculture will have to produce more food with less cost, sustainably with less food waste, more efficient use of natural resources and with minimal impact on the environment in order to meet growing population.

CRACKING THE GENOME OF THE BLUE CRAB, *CALLINECTES SAPIDUS*

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The blue crab, *Callinectes sapidus,* has major cultural and economic importance to the Chesapeake Bay region. The genome sequence was determined using multiple different approaches including short and long read sequencing as well as scaffolding using HiC. After initial assembly of scaffolds with MASurCA the genome length was ~1.1 billion bases with two peaks of coverage at 100 and 200 fold, suggesting high levels of heterozygosity. Further scaffolding using HiC reads using Juicebox assembly tools led to an 810 Mb assembly of 50 chromosome sized scaffolds with a median length of 14.5 Mb. Annotation revealed these scaffolds were 36% repeats, with ~100 million bases of simple repeats. Approximately 25 thousand predicted protein coding genes were determined from ~880 million RNAseq reads using the MAKER pipeline of which 9,423 were predicted orthologs with *Portunus trituberculatus*. In addition, 41 of the 50 largest chromosome scale scaffolds were likely homologous between *P. trituberculatus* and *C. sapidus* in nucleotide and protein coding analyses. The genome resource for gene discovery, population level analysis, and further study of the biology of this resilient species.

WORDS MATTER: STANDARDIZING NONNATIVE SPECIES TERMINOLOGY

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Invasive species pose environmental and economic threats, including to shellfish aquaculture and fisheries; however, many nonnative shellfish species are cultured outside their native range and provide great benefit to the industry. Variability in terminology and incorrect use of terms associated with these species may hinder communication between stakeholders (scientists, Extension professionals, growers, fishers, regulators, and the public) and lead to misunderstanding of the threats of invasive species vs. the benefits provided by the many nonnative species used in the industry. Members of the University of Florida (UF) Invasive Species Council (ISC) compiled a standardized set of seven terms (native, nonnative, introduced, established, invasive, nuisance, and range change) that are applicable across taxa, understandable, typically interpreted correctly, and useful for describing most situations regarding nonnative species. The terms and their suggested uses were developed by consensus over a yearlong discussion among members of the UF ISC which consists of 36 scientists and Extension professionals who work closely with a wide range of stakeholders. The UF ISC also listed six terms to avoid (native invasive, invasive exotic, invasive weed, alien, foreign, and nonindigenous) that create confusion via their misuse and misinterpretation. The UF ISC encourages colleagues in other states to review the terminology used in communicating with stakeholders. Effective communication strategies, using consistent and proper terminology, will advance efforts to expand awareness and understanding of invasive and nonnative shellfish species.

THE COMPLETE GENOME OF AN ENDOGENOUS NIMAVIRUS (*NIMAV-1_LVA*) FROM THE PACIFIC WHITELEG SHRIMP *PENAEUS* (*LITOPENAEUS*) *VANNAMEI*

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White spot syndrome virus (WSSV), the lone virus of the genus Whispovirus under the family Nimaviridae, is one of the most devastating viruses affecting the shrimp farming industry. Knowledge about this virus, in particular its evolution history, has been limited, partly due to its large genome and the lack of other closely related free-living viruses for comparative studies. In this study, a full-length endogenous nimavirus consensus genome, *Nimav-1_LVa* (279,905 bp), was reconstructed in the genome sequence of *Penaeus vannamei* breed Kehai No. 1 (ASM378908v1), in which ~12 copies of *Nimav-1_LVa* exist. *Nimav-1_LVa* fragment sequences are also found in some genomes from *Penaeus monodon* (GCA_002291185.1) and *Penaeus* (*Marsupenaeus*) *japonicus* (GCA_002291165.1), but are not in the full-genome assembly of *P. monodon* (GCA_015228065.1) from Thailand. This endogenous virus seems to insert exclusively into the telomeric pentanucleotide microsatellite (TAACC/GGTTA) n. It encodes 117 putative genes, with some containing introns, such as g012 (IAP), g046 (CHH), g155 (innexin), g158 (BI-1-like). More than a dozen *Nimav-1_LVa* genes are involved in the pathogen-host interactions. We hypothesize that g046, g155, g158 and g227 (semaphorin 1A like) are recruited host genes for their roles in immune regulation. The data indicates that a total of 43 WSSV genes are core/ancestor nimavirus genes, including four genes reported in this study: wsv112 (dUTPase), wsv206, wsv226 and wsv308 (nucleocapsid protein). Availability of *Nimav-1_LVa* sequence will help understand the genetic diversity, epidemiology, evolution and virulence of WSSV.

TRANSPOSABLE ELEMENTS (TE) FROM SPECIFIC PATHOGEN-FREE (SPF) SHRIMP *PENAEUS* (*LITOPENAEUS*) *VANNAMEI* PRODUCED BY THE UNITED STATES

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A total of 312 transposable elements (TE) were identified in a partial genome sequence (~470 Mb) of Kona Line SPF *Penaeus vannamei* domesticated by the U.S. Marine Shrimp Farming Program (USMSFP). These included 105 DNA transposons, 119 long terminal repeat (LTR) retrotransposons, 76 non-LTR retrotransposons, and 1 integrated Nimavirus, *Nimav-1_LVa*, and 11 unclassified. A Type-A endogenous hypodermal and hematopoietic necrosis virus (IHHNV) related sequence (DQ228358, 4,655bp), previously identified in the genome of *P. monodon* from Africa, is demonstrated integrated into an RTE-like non-LTR retrotransposon. The 3'-flanking sequence of the integrated IHHNV, 3,262-4,655 of DQ228358, shows 98% nucleotide identity to 1,531-2,924 of a *P. monodon* repeat family *RTE-2_PMon* (3,656-bp) which share 85% sequence along the whole length with the *RTE-3_LVa* (3,654-bp) from *P. vannamei*. *RTE-2_PMon* is a relatively young family, members of this family showing only 0.5-2% sequence divergency, suggesting DQ228358 represents a relatively young integration of IHHNV, and probably only present in some genomes of *P. monodon* across the world. Indeed, such integration (DQ228358) is absent in the *P. monodon* assembly (GCA_015228065.1) from Thailand. These results illustrate the genome diversity due to viruses and transposons. Considering that the remarkable smaller genome sizes shown by the current assemblies for *P. vannamei* from China (～1.6 Gb) vs the *P. monodon* from Thailand (～2.37 Gb), and the ～2.87 Gb estimated for SPF *P. vannamei* from the USMSFP, a new whole reference genome of SPF *P. vannamei* from the founders of the USMSFP breeding program is highly worthwhile for shrimp genome study and breeding.

ONLY TIME WILL TELL: SUCCESSES AND FAILURES OF RESTORING NATIVE OYSTER POPULATIONS IN HABITAT-LIMITED SYSTEMS

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Historically, Olympia oysters (*Ostrea lurida*) played an important economic, ecological, and cultural role as Washington's only native oyster. Yet, due to overexploitation, loss of habitat, and other human-related factors, only ~5 % of the once-known beds remain in Puget Sound. In 2012, the Swinomish Tribe began an Olympia oyster restoration effort with the intent of eventually establishing self-sustaining populations that could act as larval sources for additional sites. During the onset of the project, we initiated a monitoring plan to track survival and growth of outplanted seed by site. Initially encouraging results lead to the expansion of our restoration project and research objectives. Preceding work addressed the following goals: (1) determine when our oysters were brooding, (2) investigate larval supply and distribution to better target habitat enhancement efforts, (3) monitor oyster growth, survival, and recruitment, and (4) quantify parameters of ecological change before and after restoration. These oyster populations successfully brood at low temperatures and late-stage larvae were documented in areas surrounding restoration sites. Despite the presence of larvae, we have not yet found evidence of successful recruitment. Specifically, we last seeded our sites in 2017, yet we did not record signs of new cohorts in 2018 - 2020. Quantifying ecological change due to restoration efforts is more difficult when the population does not expand naturally. Our combined results highlight the importance of consistent monitoring and analysis, as we were able to identify the lack of recruitment and respond by developing innovative approaches to enhance methods for successful future restoration.

EXPLORING MECHANISMS UNDERLYING THE RANGE LIMITS OF A MARINE CRAB IN A WARMING HOTSPOT

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Ocean warming and species range shifts have the capacity to widely change biodiversity and ecosystem structure. The Gulf of Maine (GOM) is experiencing particularly rapid warming compared to the global ocean and there are at least two documented range shifts in this system, *Minuca pugnax* and *Callinectes sapidus*. Because temperature is often a driving factor for development of ectotherms, it is thought that a species' thermal threshold plays an important role in setting range limits. The effects of warming on purple marsh crabs (*Sesarma reticulatum*) were tested by identifying the temperature threshold needed for the larval development sourced from one range edge and one interior population on Cape Cod. It is important to document thermal physiology from two populations because of the potential for local adaption to play a role in this trait. Salt marsh presence/absence surveys were conducted to identify the current population range edge of *S. reticulatum*. The surveys suggest a small range expansion from YEAR. Surprisingly, it was found that *S. reticulatum* has the same thermal threshold for development as *M. pugnax* and that the interior population develops faster than the edge population, suggesting an inability to expand its range currently. Therefore, it is likely that the range expansion of *S. reticulatum* is not constrained by temperature in the larval phase. More research is planned through experiments focusing on the role of larval behavior in the dispersal potential of *S. reticulatum*. Taken together, larval behavior and temperature experiments can elucidate species specific drivers that set range limits.

QUANTIFYING FARM-SCALE ECOSYSTEM SERVICES ASSOCIATED WITH EASTERN OYSTER AQUACULTURE IN THE NORTHEAST

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The eastern oyster (*Crassostrea virginica*) is a commercially important aquaculture species and food resource along the Atlantic and Gulf coasts of the United States (U.S.). Oyster aquaculture is the most common form of molluscan farming in the world and U.S. oyster production is valued at $192 million annually. In addition to its economic value, oyster aquaculture provides ecological value such as water quality improvement; however, the east coast of the U.S. is projected to experience increases in the frequency and intensity of freshwater events (*i.e.,* storms and precipitation) with climate change. These climate change stressors may alter oysters' ability to provide these water quality benefits. The purpose of this research is to provide a scientifically rigorous account of an ecosystem service provided by oyster farms in the northeast. Specifically, this project aims to (1) estimate farm-level year-round filtration and nitrogen removal occurring at three oyster farms in the Delaware Bay region to quantify local farm contributions to improved water quality and (2) estimate impacts of low-salinity events to oyster farm filtration. Experiments to estimate individual oyster *in-situ* filtration and nitrogen removal are being conducted using a flow-through filtration chamber, from which, oyster biodeposits are collected for analysis. These methods capture variations in seasonal temperature, food quality and quantity, oyster size and energetic demands, among other conditions to accurately characterize annual filtration. These results may support the development of nutrient management programs in the Delaware Bay region similar to those in the Chesapeake Bay and elsewhere in the world.

ABALONE MARICULTURE IN BAJA CALIFORNIA: A CONSERVATION AQUACULTURE PROJECT

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Landings of fished abalone have significantly decreased in the last decades and global production has drastically changed from fishing to farming. In particular, multiple stressors related to climate change and overfishing are threatening these resources in California, USA, and Baja California, Mexico. Aquaculture and subsequent restocking efforts may support sustainable harvesting of abalone. To test, inform and promote innovative sustainable seafood production strategies in the northeastern Pacific, an experimental mariculture system was designed at San Jeronimo Island, Baja California in collaboration with the local fishing cooperative. Specifically, this pilot experiment aimed to explore the feasibility of rearing red abalone, *Haliotis rufescens,* during its early stages to larger size for a future local restocking program. The effects of two different depths, surface and bottom (6 m) and three different macroalgae diets on the survival and growth of juvenile red abalone (30 ± 8 mm), using a long line system was also tested. Results show a 7.22 ± 0.27 mm mean increase in shell length after four months of experiment, which appears to be greater than for abalone raised in the lab. Any effect of depth or macroalgae diet treatments were found. High growth rates suggest mariculture might allow abalone to attain size refuge and increase its survival when restocked in its natural habitat. If scaled successfully, these conservation aquaculture strategies could contribute to sustainable abalone populations and landings in North America.

SOFT SHELL CLAM AND ARCTIC SURFCLAM HATCHERY DEVELOPMENT IN MAINE, USA

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The Downeast Institute (DEI) is a 501(c)(3) nonprofit corporation located on Great Wass Island in the town of Beals, Maine that operates a 10,000 ft^2 shellfish production, research and development center. Historically, DEI evolved from its predecessor the Beals Island Regional Shellfish Hatchery (BIRSH) that was created in 1987 by renovating a clam shucking shack located on a 100-ft wharf overlooking Moosabec Reach, the body of water separating the island community of Beals from the mainland community of Jonesport in eastern Maine. BIRSH was the first-ever shellfish hatchery dedicated to the production of cultured soft-shell clam, *Mya arenaria*, juveniles ($<$ 12 mm SL) that were distributed to local shellfish management committees for stock enhancement purposes. Today, DEI continues to be the only producer of cultured soft-shell clams in Maine, and continues working with clammers and coastal communities to enhance wild stocks. Soft-shell clam broodstock are conditioned using traditional techniques that involve regulating seawater temperature from 1-15°C and microalgae over a two-month interval. Thermal shock (to 24°C) is used to stimulate spawning. Larvae are reared at 20°C in 400-l conical tanks for 18-22 days, and settle at sizes of 200-225 microns. Arctic surfclams, *Mactromeris polynyma*, are deep-water, shallow-burrowers that are harvested commercially only in Maritime Canada, but populations exist in the Gulf of Maine south to offshore Rhode Island. Surfclam broodstock are spawned by conditioning using techniques similar to those used for soft-shell clams, but over temperatures that range from 1-10°C. Spawning and larval rearing occurs at 12°C.

EFFECTS OF GREEN CRAB, *CARCINUS MAENAS*, PREDATION ON SOFT SHELL CLAM, *MYA ARENARIA*, POPULATIONS IN MAINE DURING A WARMING OCEAN ENVIRONMENT

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Green crabs purportedly invaded the shores of North America somewhere near Long Island, NY during 1815-1820. The first reports of green crabs in Maine were made by Rathbun in 1905 from Casco Bay, near Portland. The north and eastward progression of *Carcinus* reached Washington County, the easternmost coastal county in Maine, when it was observed in a variety of intertidal habitats in 1951. The northeastward progression along the Maine coast was not constant, but punctuated by fluctuations in populations due, apparently, to winter temperatures. Cold winters coincided with population declines, while the opposite was true when seawater temperatures were mild. An especially noticeable increase in seawater temperature occurred during the five-year period from 1945-1949 when winter (Jan-Mar) seasurface temperatures at Boothbay Harbor, ME averaged 1.9 ± 0.12°C vs. 1950-1954 when temperatures averaged 4.81 ± 0.11°C. The approximate 150% increase in temperatures coincided with a population explosion of green crabs along the Maine coast, and, at that time, with the largest decline in soft-shell clam populations that averaged 40.3 million pounds (1945-1949) vs. 9.7 million (1955-1959), the five-year period after the warming period. Today, seasurface temperatures in the Gulf of Maine are warming faster than most other areas of the global oceans, green crab populations are, once again, exploding, and, once again, soft-shell clam populations are at/near all-time lows measured by both fisheries dependent and independent sources. Clam losses due to green crab attack are disproportionately associated with 0-year class individuals where post-settlement mortality has been estimated to be $>$ 99%.

ARCTIC SURFCLAM, *MACTROMERIS POLYNYMA*, FIELD GROWOUT TRIALS USING CULTURED JUVENILES IN EASTERN MAINE, USA

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Arctic surfclams are shallow-burrowing, deep-water bivalves (Family Mactridae) with a circumboreal distribution. In the northwest Atlantic, this species is harvested commercially in Atlantic Canada and Quebec (10-15 cm SL) for its naturally-occurring purple foot that turns bright red upon cooking, and is served as hokkigai, a sushi and sashimi delicacy. In 2017, Canadian surfclam sales topped $100 million. This species populates the Gulf of Maine and south to offshore Rhode Island; however, no extensive beds have been located in U.S. waters. An attempt to create a new culture candidate and live product (4-5 cm SL) for domestic markets began in 2009 at the Downeast Institute to learn about the hatchery, nursery, and growout phases of this species. Since 2013, field trials using cultured juveniles (4-15 mm SL) have been conducted in the soft-bottom lower intertidal in eastern Maine where large tides exposed hundreds of acres of mudflats that are relatively depauperate in the native soft-shell clam, *Mya arenaria*. Small-scale trials over five years in Maine's two easternmost counties demonstrated that traditional techniques to deter predators with plastic mesh netting applied directly to flats (similar to those used to protect *Mya*) repeatedly resulted in short-term (6 mo.) survival rates $< 5\%$. Netting did not deter predators, mostly green crabs, *Carcinus maenas*, that ripped, cut, and/or burrowed beneath the edges of the netting to consume the surfclam seed. A new growout method was recently discovered that resulted in survival rates $> 90\%$ over 166-days (April to October) with growth rates of 175%.

HETEROTROPHICALLY CONDITIONED RECIRCULATION SYSTEM FOR BIVALVE LARVAL CULTURE

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Standard bivalve hatchery practices rely on ambient water quality for production, however ambient water quality can cause impaired hatchery performance. The development a recirculating aquaculture system (RAS) would allow bivalve hatcheries to reuse production water and minimize impact from fluctuating ambient water quality. Two pilot scale systems were developed for testing. The system design consisted of a 600 L traditional moving bed bioreactor with K1 Kaldnes carrier elements (AnoxKaldnes, Lund, Sweden). Media were conditioned for ammonia reduction and enriched heterotrophic microbial community to reduce organic waste and remove bacteria from larval production waters. A conventional foam fractionator was also used to assist with removal of dissolved organics. A standardized a heterotrophic conditioning protocol was developed.

Trials were conducted in 600 L bioreactors to test biofilm development procedure and survival of bivalve larvae in system water. Standard bacteriological media as an organic source was used to dose the system at a level expected in a worst-case scenario for larval culture failure. Organics were absorbed and treated by the system with very little perturbation of the biomass in the reactor. Cultured *Vibrio* spp. were loaded to the system and eliminated from the planktonic phase. Bay scallop and eastern oyster larvae were used to test reactor water quality. A pilot scale system was then installed in a commercial oyster hatchery to test in parallel with normal practices. Future includes scale up to full commercial volumes, assimilation capacity analysis, and economic analysis of implementing of the system.

BULK SEGREGATION METHOD WITH TRANSCRIPTOMICS IS AN INNOVATIVE METHOD FOR IDENTIFYING TRUE SNP AND FUNCTIONAL GENES IN A BREEDING LINE OF SPECIFIC PATHOGEN RESISTANT (SPR) WSSV-RESISTANT MADAGASCAR-MALAYSIA *PENAEUS MONODON*

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Industry-driven aquaculture shapes the high productivity for economic growth; however, shrimp are susceptible to infection by many pathogens, which then shapes the question of why and how the population could shape resistance. Therefore, a selection program, which is linked with the shrimp industry to be the major driver in the genetic improvement program as they have base population from countries, ultimately focused on the Madagascar-Malaysia *Penaeus monodon* breeding line. The stocks were 13th generation Madagascar and 5th generation Malaysian line. This project investigated: 1) can this selected WSSV-SPR line, and (2) what causes this line to be resistant. Considering selection was based on Madagascar which was selected for fast growth and Malaysian line for disease resistance criteria, we performed gene expression and functional gene profiling on this line at 100 days old line to investigate whether the population biomarkers HMCB, Lectins, and few other genes and and SNP associated with resistance traits can be identified. The strategy incorporated bulk segregant analysis method, which was developed to find QTL, in addition to transcriptomics approach to aid the selection process in innovative way. Results indicate that linking the gene expression and SNP biomarkers are crucial for further genetic improvement studies and also possibility to cross reference the utility of this markers in other genetic lines in different geographical regions.

TIDAL AND SEASONAL ABUNDANCE OF ENVIRONMENTAL *PERKINSUS MARINUS* IN THE YORK RIVER, VIRGINIA, USA

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The oyster pathogen *Perkinsus marinus* causes substantial oyster mortality along the Atlantic and Gulf Coasts of the U.S. There have been numerous investigations of this protozoan parasite within the context of its oyster host, yet much remains unknown in terms of its environmental ecology. While transmission may be primarily through released dead and decaying tissues of infected oysters into the water column in the late summer and fall, transmission can occur year-round even through periods of low oyster mortality.

To better understand the environmental ecology of *P. marinus*, we investigated the relationship of tidal cycle and season with the abundance of *P. marinus* in the benthos and surface water. Sediment and water samples were collected at three adjacent sites on the lower York River, Virginia, over a three-day tidal cycle in August 2019 when infection levels in oysters near their seasonal peak. Samples were also collected monthly, from October 2019 to September 2020. Samples were filtered, DNA was extracted, and qPCR was applied to quantify *P. marinus* in surface water and sediment. The pathogen was detectable across the tidal cycle, with levels generally highest at low tide, highlighting *P. marinus* environmental variability on short time scales. Seasonally, *P. marinus* levels generally followed temperature, as expected. Interestingly, while parasite levels fell below the level of detection in surface water, *P. marinus* was detectable year-round in sediment samples, indicating that the benthos may be an underappreciated reservoir of *P. marinus* contributing to the transmission of this parasite in marine systems.

CONTINUOUS WATER QUALITY MONITORING AT SITES OF OYSTER FARMS AND ARTIFICIAL OYSTER REEFS IN REHOBOTH BAY, DELAWARE, USA

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Oyster aquaculture returned to the Delaware inland bays with the issuing of shellfish leasing areas in 2018, bolstering local economies, improving water quality, and providing structured habitat for fish and invertebrates. Additionally, the Delaware Center for Inland Bays established three pilot artificial oyster reefs beginning in 2019 to restore the native oyster population and further improve the inland bay environment. Successful management of oyster farming and restoration efforts depends on continuous monitoring of oyster growing conditions.

A pilot water quality monitoring program was established in Rehoboth Bay, Delaware, which included multiparameter continuous water quality instruments (sondes) deployed at sites of oyster aquaculture (Salley's Cove) and artificial oyster reefs (Camp Arrowhead and Big Bacon Island) from summer through late fall this year. Trends in water temperature, salinity, dissolved oxygen, pH, and turbidity were examined with respect to oyster growing conditions. In the summer, sites differed in their daily temperature ranges; in the fall, Camp Arrowhead was consistently cooler than other sites. Sustained warmer temperatures likely promote oyster growth and survival. Arrowhead and to a lesser extent Salley's Cove had greater month to month variability in salinity, potentially indicating greater influence of freshwater input. Turbidity readings were compromised by biofouling, but were high in general; large quantities of suspended matter dilute organic matter available for oyster consumption, reducing their growth potential. Sonde monitoring challenges included biofouling and equipment failures. These preliminary findings are expected inform the management of Delaware oyster aquaculture and restoration efforts and shape the direction of future monitoring efforts.

HABITAT USE BY NEKTON IN STRUCTURALLY COMPLEX OYSTER AQUACULTURE AND SEAGRASS HABITATS

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Complex three-dimensional structure associated with oyster aquaculture is expected to increase nekton diversity similarly to foundation species such as eelgrass. Previous work documents seagrass-specific nekton communities that are distinct from neighboring unvegetated habitats. Funded by PSMFC, a consortium of scientists in Washington, Oregon and California has been assembled to study the habitat value of oyster aquaculture. During Year 1, three regions were sampled in Willapa Bay, Washington (WA) and two regions were sampled in Hood Canal, WA in spring and late summer of 2020. Seines and cameras were used to investigate whether different methods of oyster aquaculture (*Crassostrea gigas*) support distinct nekton communities compared to nekton communities found in eelgrass (*Zostera marina*) and unvegetated habitats. A gradient of habitat types were sampled, with three levels of eelgrass (absent, sparse, dense) and three levels of oyster aquaculture (absent, bottom culture, off-bottom culture) for a combined total of nine habitat types. The sampling design enables a test of nekton community response to the two structured habitats, eelgrass and oyster aquaculture, as well as a comparison of the community responses in the spring versus summer, which are expected to differ due to seasonal changes in estuarine nekton assemblages. These data on habitat use will underpin decisions regarding the best practices to grow oysters while supporting other species. Ultimately, this design will span multiple estuaries across three states.

CHARACTERIZING EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*, BRED FROM NATIVE LOUISIANA BROODSTOCK UNDER DIFFERENT SALINITY REGIMES: EFFECT OF STOCK AND COHORT

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Louisiana has a long history of oyster farming; however, many farmers in the region are now experiencing high oyster mortality from prolonged low salinity events due to increased use of freshwater spillways. To address the challenges of low salinity events, wild Louisiana oyster germplasm could be stored in genetic repositories. Measuring the responses of different native oyster stocks to salinity stress would facilitate repository development in conjunction with gamete cryopreservation.

This study characterized the salinity tolerances of oysters bred at two hatcheries (the Auburn University Shellfish Lab and the Louisiana Sea Grant Oyster Research Lab) making up the two cohorts of the study. Within each cohort, three Louisiana broodstock populations (Calcasieu Lake, Vermillion Bay, and Sister Lake) were spawned to create diploid and triploid stocks from each population. Stocks from both cohorts were deployed at a high and a low salinity field site. Monthly growth and mortality measurements were taken for one year, and growth and survival rates among stocks and between cohorts at each site were compared. Preliminary results suggest that at the low salinity site, cohort affected triploid mortality and diploid and triploid growth. Oysters from the Auburn hatchery had lower cumulative mortality and faster growth. At the high salinity site, triploid oysters from the Auburn hatchery again had the fastest growth but had similar cumulative mortality to the Louisiana cohort. Furthermore, diploids in the Auburn cohort no longer had faster growth than diploids in the Louisiana cohort.

USING A SCLEROCHRONOLOGICAL APPROACH TO DETERMINE A CLIMATE-GROWTH RELATIONSHIP FOR WAVED WHELK, *BUCCINUM UNDATUM*, IN THE U.S. MID-ATLANTIC

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Using growth rings observed in statoliths, the size-at-age relationship was modeled for waved whelk (*Buccinum undatum*) populations within the Mid-Atlantic Bight. A total of 45 sites in the mid-Atlantic were sampled between 2016-2019 using a scallop dredge, and a subset of the whelk collected were aged ($n=318$). Lab-reared individuals and back-calculation methods were used to fill missing juvenile observations. The Mid-Atlantic Bight population appears to differ in the fit of growth curves, compared to other assessed populations, due to a timing difference in hatching. Growth curves for whelk from this region show that maturity is reached between 4 and 6 years of age. A statolith chronology spanning a 10-year period was developed using a mixed-effects modeling approach. The chronology was used to explore the influence of temperature variation on growth during ecologically relevant periods. Growth increased with higher annual temperatures however specific seasonal bottom temperature had varying effects on growth. Increasing bottom temperature during summer, the anticipated egg-development and hatching period, resulted in an age-dependent decline in growth with a positive effect on younger whelk and a negative effect on older whelk growth. Higher summer temperatures provide larger time-windows for growth, facilitating increased growth in early life stages. It appears that whelk in this region possess sufficient growth plasticity to adapt to warmer conditions throughout the year, but increased warming during specific seasons may depress growth in older individuals, potentially affecting fitness and population persistence. Understanding these temperature-growth dynamics are critical for disentangling the effects of climate change on whelk growth, allowing for population predictions in the future.

OVERCOMING THE TRAGEDY OF THE OYSTER: A GLOBAL REVIEW ON PRODUCTION AND GOVERNANCE

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Oysters have provided humans a valuable food resource since ancient times. Current understanding suggests that oyster reef area has declined substantially around the globe (Beck et al 2013). Relative to many other marine species, the decline has been well-documented. The literature provides a number of relatively similar development patterns after humans start harvesting oyster that are associated with indicators of increased scarcity of oysters. To highlight these patterns, a conceptual model of human responses to oyster scarcity was developed, and is applied to specific oyster harvest regions from around the globe. The model provides a framework for comparing and contrasting the development of oyster production industries and associated governance response to perceived scarcity overtime. The apparent similarity of ancient and very modern trends in oyster production creates a seeming paradox. Seen in concert, the modern declining wild oyster fisheries concomitant to growing aquaculture paints a picture of widespread failure of modern governance to protect wild oyster resources. At the same time, the ancient historical records would suggest the possibility that oysters have been exploited and even overexploited for literally millennia. Yet oysters remain today, so past approaches to sustaining them must not have wholly failed. A retrospective look provides insight to help inform future management developments particularly given modern challenge of recovering oyster reefs for their ecosystem services value in addition to retaining historic consumptive value.

SHORT-TERM ECONOMIC IMPACTS OF ECOLOGICAL RESTORATION IN ESTUARINE AND COASTAL ENVIRONMENTS: A CASE STUDY OF LONE CABBAGE REEF

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Increasing demand for ecological restoration in the United States have resulted in the development of a “restoration economy” in attempt to ensure long-term persistence of resource benefits, which has provided opportunity for business growth in the sustainability sector; however, nearly all the restoration monitoring and evaluation efforts focus on the ecological outcomes of restoration, while the social and economic outcomes have received far less attention. One type of economic outcome that is often overlooked includes short-term economic impacts, which measure the market activity associated with the pre-planning, planning, and construction stages of an ecological restoration project. This presentation will provide an overview of how the IMPLAN© regional economic modeling software can be used to perform input-output analysis as a method to quantify the economic impacts of ecological restoration projects. Using the Lone Cabbage Reef Restoration Project in Florida as a case study, it was found that the construction phase of the projected supported 44 full-time and part-time jobs earning $1.01 million in labor income, supported $3.02 million in gross regional development, and generated $5.08 million in total industry output within the regional economy. These findings support the notion that short-term economic impacts are a useful component when evaluating ecological restoration projects and can provide stakeholders with immediate and tangible results.

MAXIMIZING SHELLFISH RECRUITMENT IN LIVING SHORELINES FOR RESTORATION AND HABITAT CONSERVATION EFFORTS

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Living shorelines represent a suite of methods aimed at stemming the erosion of coastal habitats while providing ecological uplift. Inclusion of bivalve shellfish in living shoreline designs can help achieve these goals due to the variety of important ecosystem services shellfish can provide. Their filter feeding facilitates particle removal and nutrient cycling between the water column and benthos. The physical structure and binding created by aggregates of shellfish can also promote habitat complexity and stability, both within and behind the living shoreline. In the Delaware Estuary, both ribbed mussels (*Guekensia demissa*), and to a lesser extent oysters (*Crassostrea virginica*), are the dominant shellfish providing these services. The Partnership for the Delaware Estuary has tracked shellfish population changes on a variety of living shorelines for several years. On a hybrid living shoreline installed in 2014 results showed that shellfish mediated water quality services take time to develop, and are dependent on growth and survivorship. Oyster population development was more consistent over time compared to the more spatially and temporally variable ribbed mussel populations. Additional studies showed that shellfish recruitment and persistence are affected by substrate type, available interstitial space, and protection from predators. These research findings informed the design of new living shoreline projects to test subtle variations in the above factors and their effects on shellfish-based restoration efforts. If variations of these factors can facilitate colonization and persistence during early stages of living shoreline maturation, then they can potentially enhance water quality and habitat conservation benefits.

HURRICANE IMPACTS ON OYSTER REEFS OF NORTH CAROLINA, USA: IS THIS THE NEW PARADIGM?

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North Carolina is second only to Florida on the United States east coast for most impacted by hurricane tracks since 1850. These storms can bring widespread flooding, coastal storm surge, and devastating winds, but opportunistic studies and field observations suggest that their impact may have further reaching ecological consequences. The impacts of a series of hurricanes from 2016-2019 were documented on a set of subtidal oyster reefs in Pamlico Sound, North Carolina. These observations included changes in water quality, reef habitat characteristics, and oyster density and demographics. Widespread sedimentation, prolonged hypoxic conditions (DO $<$ 2 mg/L), low salinity environments, strong water column stratification, and turbulent displacement of reef material occurred on deep, natural reefs in the southwest and northern Pamlico Sound following Hurricane Florence (2018) and Dorian (2019), respectively. The resulting conditions at these sites correlated with increased oyster mortality. Comparatively, oyster populations at restored cultch reefs in shallow bays in the western Pamlico Sound experienced minimal impacts from Hurricane Matthew (2016) and Florence (2018). The oyster reefs of North Carolina support a multimillion-dollar commercial fishery, and they provide invaluable ecological services such as water filtration, bottom and shoreline stabilization, and vital nursery habitats. These findings highlight potential management implications for coastal oyster growing states that face increased threats from frequent hurricanes. Additional evaluation of oyster habitat, consideration of higher reef profiles and larger reef footprints, improved reef siting methods, and rotational harvest systems are encouraged as they may provide practical solutions to mitigate mortality in the face of increasing storm frequency.

MANGANESE TOXICITY, MITOCHONDRIAL DYSFUNCTION, AND THE POTENTIAL THERAPEUTIC VALUE OF P-AMINOSALICYLIC ACID, TAURINE, AND CARNOSINE

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Manganese is an essential metal. Toxic exposure causes accumulation in human brain and Manganism, which is similar to Parkinson's disease. Manganese disrupts dopamine neurotransmission. The neurotoxic mechanism is not fully understood. Proposed mechanisms include elevated oxidative stress and mitochondria dysfunction. Studies using the oyster, *Crassostrea virginica* showed manganese interferes with dopamine's cilio-inhibitory effect in gill cells, and reduces gill mitochondria O_2 consumption and membrane potential. P-aminosalicylic acid, taurine and carnosine reduced the toxic effects. To test the hypothesis p-aminosalicylic acid, taurine and carnosine protect against manganese induced mitochondria dysfunction in other animals, published data of other labs on manganese induced mitochondria dysfunction and the effectiveness of p-aminosalicylic acid, taurine and carnosine's in alleviating the damage were reviewed. Manganese caused mitochondria dysfunction in other animals, including: inhibition of electron transport, decreased O_2 consumption, interference of ATP synthase, altered mitochondria permeability, decreased membrane potential, disruption of Ca^{2+} homeostasis and swelling. Less was available on p-aminosalicylic acid, taurine and carnosine. P-aminosalicylic acid reduced neuro-inflammation, oxidative stress and intracellular reactive O_2 species generation, prevented loss of mitochondria membrane potential and protected O_2 consumption. Taurine preserved mitochondria ATP and membrane potential, and prevented swelling. Carnosine regulated mitochondria matrix pH, preserved membrane potential, increased respiratory chain activity and enhanced energy production. These findings concur with studies on oyster mitochondria, and support the hypothesis. They generate new information to assist in designing future experiments, the results of which should be of interest to those exploring possible agents in the prevention or therapeutic treatment of Manganism.

BUILDING MAINE AQUACULTURE BUSINESSES: STRATEGIC PLANNING, RESILIENCY, AND DISTRIBUTION

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Growers become growers to focus on production—not business plans, sales, and distribution. The Maine Aquaculture Association, working in partnership with several parties, has launched a drive to help strengthen aquaculture businesses across Maine. This work, which is built atop several recently completed projects, begins with the Maine Aquaculture Association (MAA) meeting individually with farmers of all scales, species raised, and years of experience to discuss strategic business planning, financial analysis, and risk management. The first meeting with each grower discusses business goals, and arms growers with a bundle including a Maine and species-specific production plan and business plan, tools to perform a benchmark analysis, COVID-19 and risk management strategies and resources, as well as webinars. Growers continue to meet with MAA as they develop their business plans, COVID-19 strategies, and approaches to risk management.

Meanwhile, COVID-19 has structurally and fundamentally changed seafood distribution channels, and the supply of live shellfish begins to approach demand (The Hale Group, 2016). Maine growers must react, but currently make decisions based on limited information. MAA is working to map the distribution system of aquaculture products in Maine, including the identification of new potential pathways for sales, and providing economic analysis on each option (total volume, cost, and ROI). This work will then feed into a future project that will allow Maine growers to expand beyond local markets by exploring consumer preferences for Maine shellfish products in inland and nontraditional markets.

MARKETPLACE SHRIMP MISLABELING IN NORTH CAROLINA, USA

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Seafood mislabeling occurs in a wide range of seafood products worldwide, resulting in public distrust, economic fraud, and health risks for consumers. In 2018, the extent of shrimp mislabeling in coastal and inland North Carolina was quantified. Standard DNA barcoding procedures were used to determine the species identity of 106 shrimp sold as 'local' by 60 vendors across North Carolina. Thirty-four percent of the purchased shrimp was mislabeled, and surprisingly the percentage did not differ significantly between coastal and inland counties. One third of product incorrectly marketed as 'local' was in fact whiteleg shrimp: an imported and globally farmed species native to the eastern Pacific, not found in North Carolina waters. In addition to the negative ecosystem consequences of shrimp farming (e.g., the loss of mangroves forests and the coastal buffering they provide), North Carolina fishers—as with local fishers elsewhere—are negatively impacted when vendors label farmed, frozen, and imported shrimp as local, fresh, and wild-caught.

REFINING REPRODUCTIVE ASSESSMENT PROTOCOLS TO BETTER INFORM MANAGEMENT OF THE SOUTH CAROLINA WHITE SHRIMP (*PENAEUS SETIFERUS*) FISHERY

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The Atlantic white shrimp, *Penaeus setiferus* (Linnaeus, 1767), supports the highest valued commercial fishery in South Carolina, with recent landings valued at $5-8 million annually. While recent landings in the historically-important fall season have trended downwards, the harvest of larger, high-value shrimp in the spring and early summer, when white shrimp spawning activity is at its peak, has been increasing. The SCDNR has statutory authority to open and close the commercial shrimp season, with the spring season opening date considering factors such as winter water temperatures, the abundance of overwintering white shrimp, and adult female reproductive status. Assessments of reproductive status in the field are currently based on long-standing and commonly accepted macroscopic characterizations of ovarian development. Since female white shrimp are iteroparous, macroscopic techniques should have the ability to identify females that have previously spawned.

This presentation will describe efforts to increase confidence in this approach by comparing macroscopic determinations of shrimp reproductive status conducted in the field with histological assessments of white shrimp ovarian tissues conducted at the MRRI. For white shrimp sampled across coastal South Carolina, both macroscopic and histological techniques found evidence of repeated spawning by individual females in early April and extensive spawning activity within the population by early May. Evidence of previous spawning was found in nearly all specimens where the ovaries were translucent. Monitoring the reproductive status of white shrimp throughout the spring is necessary to understand the phenology of spawning activity and to provide improved information to fisheries managers.

A NEWLY-DISCOVERED DIDYMOZOID TREMATODE INFECTING THE GILL OF ITS FIRST INTERMEDIATE HOST, THE BAY SCALLOP

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Starting in 2012, bay scallops (*Argopecten irradians*) in North Carolina were observed to be infected by an unidentified macroparasite, and the same parasite has recently been observed infecting bay scallops on the west coast of Florida. Phylogenetic analysis of DNA sequence data from a nuclear 28S rDNA fragment indicates that the parasite is a trematode (fluke) in the family Didymozoidae (superfamily Hemiuroidea) and that it forms a well-supported clade with another didymozoid from Australia. Dissection and histopathological examination confirm that the trematode is using the scallop as a first intermediate host, infecting and greatly distorting the afferent vessels of the host's gill filaments. Condition analysis reveals that in infected individuals, a higher proportion of body mass is found in the viscera (including parasitized gills) and a lower proportion of body mass is found in the muscle and gonad. Although the full life cycle of the parasite is unknown, most didymozoids use copepods as second intermediate hosts, small fish as third intermediate hosts, and predatory fish as final hosts. The parasite infects (at prevalences as high as 15%) a commercially important bivalve (wild and cultured) and yet has never been described, suggesting that it might be recently introduced or has recently jumped into the scallop host. Regardless of its origins, however, the newly-discovered trematode represents a novel threat to an already-imperiled fishery, and as such, merits further investigation.

PACIFIC NORTHWEST CRAB RESEARCH GROUP: CLOSING CRITICAL DUNGENESS CRAB DATA GAPS IN WASHINGTON STATE WATERS

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Dungeness crab (*Metacarcinus magister*) is one of the most highly-valued marine species in Washington state. This decapod crustacean forms the foundation of local fishing communities and holds economic, recreational, and cultural significance in the region. Despite its importance, very little is known about Dungeness crab recruitment patterns, population structure, and life history in waters of Washington State, particularly in the Salish Sea. Currently, the fishery is co-managed based on fishery-dependent data and harvest drives decisions setting annual quotas. The lack of fishery-independent information limits the ability of fishery managers to generate stock assessments and react to changing environmental conditions that could impact Dungeness crab populations. In order to address these limitations and improve our ability to make data-driven, sustainable management decisions, the Pacific Northwest Crab Research Group (PCRG) was formed in December 2018. The PCRG is a unique cooperative research group of representatives from Washington tribes, state and federal agencies, nonprofit organizations, and universities. This presentation will provide some background to the formation and research objectives of the group, as—a statewide monitoring effort of Dungeness crab megalopae via light trap deployment. Data from the 2019 and 2020 field seasons indicate that postlarval Dungeness crab abundance can vary dramatically across time and space, with some evidence of synchronous pulses in delivery. Captured megalopae showed a decrease in carapace width over the sampling season, supporting the hypothesis of distinct recruitment cohorts in the Salish Sea.

THE FIRST DETECTION OF A NOVEL OSHV-1 MICROVARIANT IN SAN DIEGO, CALIFORNIA, USA

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The spread, emergence, and adaptation of pathogens causing marine disease has been problematic to fisheries and aquaculture industries for the last several decades creating the need for strategic management and biosecurity practices. The Pacific oyster (*Crassostrea gigas*), a highly productive species globally, has been a target of disease and mortality caused by a viral pathogen, the Ostreid herpesvirus 1 (OsHV-1) and its microvariants (OsHV-1 µvars). During routine surveillance to establish health history at a shellfish aquaculture nursery system in San Diego, California, the presence of OsHV-1 in Pacific oyster juveniles was detected. Quantification of OsHV-1 in tissues of oysters revealed OsHV-1 viral loads > 106 copies/mg. The OsHV-1 variant was characterized and identified by sequencing of ORFs 4 (C2/C6) and 43 (IA1/IA2), which demonstrated that this variant is a novel OsHV-1 microvariant: OsHV-1 µvar SD. A pilot transmission study indicates that OsHV-1 µvar SD is infectious with high viral loads ~7.57 x 10^6 copies/mg detected in dead individuals. The detection of OsHV-1 µvar SD in a large port mirrors previous studies conducted in Australia where aquaculture farms and feral populations near port locations may be at a higher risk of OsHV-1 emergence. Further research is needed to understand the impacts of OsHV-1 µvar SD, such as transmission studies focusing on potential vectors and characterization of virulence as compared to other OsHV-1 µvars. To increase biosecurity of the global aquaculture industry, active and passive surveillance may be necessary to reduce spread of pathogens and make appropriate management decisions.

THE ROLE OF CHARACTERIZING THE PHYSICAL ENVIRONMENT IN OYSTER AQUACULTURE TO BETTER PREDICT PRODUCTION OUTCOMES

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To facilitate growth in the oyster aquaculture industry, it is crucial to explore the role that hydrodynamic forces play in the production of oysters inside cages. Water flow through culture gear to maximize food accessibility is undoubtedly a driver in the growth and quality of cultured oysters however, water flow and wave forcing inside culture gear has not be rigorously studied and rarely quantified. As a result, there remains a lot of uncertainty about how best to manage animals and gear to optimize crop growth. New tools are needed to better characterize the internal physical conditions within aquaculture gear to draw clear relationships between grower management strategies, physical forcing, and oyster production.

This research aimed to validate the use of low-cost, hydrodynamic sampling tools to characterize the changing physical environment within aquaculture cages when exposed to a range of management strategies. Management strategies include biofouling mitigation, stocking density, and culture method. We then looked to understand the effects that changes in the environment (i.e. water flow, cage jostling) had on oyster growth and condition.

The use of clod cards (integrated water motion) and accelerometers (jostling) were capable of characterizing small-scale changes in the physical environment in response to various grower management practices (biofouling mitigation, stocking density, and culture method), which have been correlated with changes in the growth and condition of cultured oysters. These results can provide strong insight to growers looking to optimize their production by giving the capability of making more informed decisions regarding management strategies.

INFLUENCES OF BROOD-DEPENDENT BEHAVIORAL VARIATION ON BLUE CRAB (*CALLINECTES SAPIDUS*) LARVAL TRANSPORT IN A WIND-DRIVEN ESTUARINE PLUME

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Blue crabs (*Callinectes sapidus*) support valuable fisheries in the US mid-Atlantic, and their unpredictable and variable recruitment suggests that a better understanding of larval development and dispersal is still needed. Blue crab larval dispersal involves export to the continental shelf followed by a re-entry of estuaries. In the mid-Atlantic Bight, transport is facilitated by wind and buoyancy-driven surface currents, and zoeae generally maintain a near-surface distribution throughout their development. Though several studies have investigated *C. sapidus* larval dispersal, none have evaluated the effects of individual behavior. This study used observed brood-dependent larval behavior and an idealized wind-driven estuarine plume to simulate larval transport and better understand the biophysical interactions involved during *C. sapidus* dispersal. Model results showed that larval transport was predominantly influenced by wind speed, but behavioral and brood-level influences also significantly altered trajectories. Faster swimming larvae were able to maintain a near-surface position in the presence of turbulence better, and in all model scenarios, larvae travelled farther and had different vertical distributions than passive particles. Model results also showed that larval transport varied by a factor of 1.7 among broods and by a factor of 4.9 overall. These results indicate that blue crab larval swimming behavior and variability in behavioral traits may be an important factor in larval dispersal. The inclusion of variable behavior should be carefully considered when developing future models.

SEDIMENT, SOUNDS, AND SETTLEMENT: THE THREE S'S OF OYSTER RESTORATION SUCCESS

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Restored oyster reefs contribute to enhancing ecosystem services in coastal environments. Spatial and temporal changes in habitat availability can affect reef persistence and restoration benefits, and understanding these changes is crucial for optimizing restoration efforts. A set of six subtidal restored oyster reefs in Pamlico Sound, North Carolina (NC) were studied by repeated mapping using high-resolution bathymetric and side scanning sonar data, and by collecting a two-year time series of oyster demographic and passive acoustic data that monitored changes in the local soundscape. The data were used to examine how the construction and location of a restored habitat affects its persistence and function over time. All six reefs provided habitat for the settlement and growth of oyster populations, but this role changed as reefs underwent varying degrees of sedimentation. Reefs constructed in relatively low energy environments lost ~18–35% of their substrate area, primarily by deposition of sediment along their margins. Reefs having greater sediment supply and greater exposure to hydrodynamic processes were most susceptible to burial and became heavily fragmented with ~50–65% of the restored habitat lost. Declines in habitat availability greatly reduced oyster recruitment and survival. High frequency signals were lost from the soundscape on reefs with greater habitat loss and declines in oyster densities, indicating a decrease in habitat quality, change in community composition, and overall loss in ecosystem function. These results underscore the importance of site selection and design in determining oyster restoration success, and sites in high-energy environments may have limited long-term economic and ecosystem benefits.

THE EFFECTS OF TIDAL LOCATION ON THE BORING SPONGE-OYSTER INTERACTION: IMPLICATIONS FOR MANAGEMENT

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Eastern oysters are commercially valuable resources that provide numerous ecosystem services throughout their range. Due to their declines, oysters are the target of many restoration efforts. It is therefore critical to explore factors that might limit their recovery. In particular, oysters are negatively affected by species like boring sponges, which can reduce individual growth and condition while destroying critical reef substrate. Biotic stressors may further interact with abiotic stressors (i.e., water quality, exposure) to impact oysters. This study explored the distribution pattern of boring sponges and examined potential trade-offs in oysters between abiotic variables and boring sponge infestation. Boring sponges were most common in the lower intertidal zones of oyster reefs, and decreased with increasing aerial exposure. Boring sponges also had the largest negative effect on oyster condition in the lower zone. In a follow-up experiment, the potential three-way interaction between site, tidal exposure and sponge presence on oyster growth and condition was explored. All factors had statistically significant effects on oyster growth rate and condition index. Several interesting patterns emerged. Site had the largest effect on growth—oysters at the site with the lowest salinity exhibited the fastest growth and greatest tissue condition. Interestingly, even sponge-infested oysters at this site exhibited higher growth rates than 'healthy' oysters from the other two sites. High intertidal oysters also grew the fastest. This study highlights the importance of considering site and location within the tidal prism for oyster restoration in Georgia.

SURVEYING FISHERIES IN THE WAKE OF COVID-19

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At sea monitoring and research are vital components for assessing fishery stocks and ecosystems. Data gaps in the survey time series can have detrimental effects particularly for tracking aggregations. For the 2020 survey season the Covid-19 pandemic disrupted many of these times series. To avoid these breaks for the Atlantic sea scallops, Northeast groundfish species, and American lobster research, it was essential to develop survey protocols that would safely allow scientists to conduct the proposed research, upholding policies set in place by project sponsors and the University, and overcome technical challenges. An approved survey plan was developed in collaboration with the fishing industries, the University, the port of New Bedford, Vineyard Wind, and other research partners. Research activities were slowly phase in as the year progressed: 1) a 100% industry conducted groundfish fishery independent survey, 2) daily lobster research trips with limited personnel, 3) multiday sea scallop optical surveys with limited crew and scientific personnel, and finally 4) a multiday groundfish survey with full crew and limited scientific personnel.

In addition to facilitating the field research component of each project there were several technical advancements made which allowed researchers to analyze these data collected remotely. The processes for image analysis, daily workflow, and data uploading were altered to accommodate remote work without sacrificing data quality or processing speed. Through these highly-coordinated efforts, the Marine Fisheries Field Research Group was able to successfully conduct all proposed research in 2020 and meet all essential data deadlines, maintaining a consistent survey timeline.

RICKETTSIA-LIKE ORGANISMS (RLO) IN *OCTOPUS BIMACULATUS* VERILL 1883 FROM BAJA CALIFORNIA, MEXICO

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Rickettsia-like organisms (RLO) are intracellular, obligate, parasites that have been recorded in a wide variety of invertebrate hosts. To date, the infection by a marine leech is the only record of parasites/symbionts known to be harbored by *Octopus bimaculatus* in such locality. With the economic importance of *O. bimaculatus* to the octopus' fishery in Baja California (B.C.), Mexico and its potential for aquaculture, there is a need to find out the pathogens that naturally infect this octopus. Therefore, the present study describes a pathogen found in *O. bimaculatus* from B.C. using the histopathological technique. A total of 20 *O. bimaculatus* were collected from the commercial fishery developed in Bahía de Los Ángeles, B.C. The specimens were reviewed for clinical signs of pathology. A sample of gills, cecum, and gut was removed and fixed in buffered formalin 10% for 24 h. The tissue was embedded in paraffin wax, sliced in 5 mm, and stained with hematoxylin-eosin. Only the epithelial gill cells of 10% of octopuses were found infected by RLO, characterized by basophilic inclusions, causative of the destruction of the gill filaments in some octopuses. The RLO are recorded for the first time in *O. bimaculatus*. The effect of the RLO on the host health is not yet clear, however, and the destruction of the gill filaments will surely affect the proper performance of the organ.

RED MANGROVES (*RHIZOPHORA MANGLE*) POSITIVELY INFLUENCE THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) ALONG AN INTERTIDAL GRADIENT

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Desiccation stress tends to be higher in upper intertidal zones compared to lower ones; however, adjacent macrophytes may provide shade ameliorating stressful conditions thus positively influencing associated organisms. The eastern oyster can form reefs and clusters on red mangrove prop roots and although oyster demographic rates across intertidal zones have been examined in reefs at higher latitudes, far less is known about them at subtropical locations where desiccation stress is expected to be greater due to higher temperatures. Furthermore, little is known about whether shade from mangrove canopies can reduce desiccation stress on oysters. This study addressed (a) how the density and survival of oysters varied along intertidal zones (bottom, middle, and top) on prop roots and reefs and (b) whether the association of oysters with mangroves positively affected oysters at higher intertidal zones. Experimental and observational approaches were used in Tampa Bay, Florida and water loss (a proxy for desiccation stress) was measured on both habitats. Compared to reefs, oysters on prop roots were at significantly higher densities, had higher survival, and were exposed to fewer predator species. In addition, water loss was significantly lower on the prop roots compared to reefs. The results of this study suggest that oysters may benefit from its association to Red mangroves via decreased exposure to predators and reduced desiccation stress. As temperature increases due to climate change, mangroves may provide a desiccation refuge for associated oysters, thus Red mangroves should be considered in oyster restoration efforts.

FORECASTING FUTURE RANGE OF SEA SCALLOPS USING A TROPHICALLY-LINKED SPECIES DISTRIBUTION MODEL: WILL CLIMATE CHANGE CONSTRAIN SCALLOP DISTRIBUTION IN THE MID-ATLANTIC BIGHT?

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In the Mid-Atlantic Bight (MAB), the southern and inshore distribution of sea scallops is limited by summer maximum bottom temperatures. The offshore extent is probably limited by prohibitively high pre-recruit predation by *Astropecten americanus* sea stars that dominate benthic assemblages at greater depths in the MAB. The inshore and northern extent of this predator, in turn, is limited by winter minimum bottom temperatures. Under this scenario, increased water temperatures would induce summer maxima isotherms to move offshore and winter minima isotherms to move inshore, resulting in a contracting distribution of sea scallops and a concomitant loss of fishery landings. The abiotic factors (e.g., thermal parameters) and biotic interactions (predation) that determine the distribution of sea scallops in the MAB were modeled. It was found that the theoretical niche (i.e., locations within the thermal tolerance of scallops and outside preferred predator habitat) decrease slightly over time, whereas realized niche based on survey data decreased more abruptly from 1987 to 2000. Simulations were conducted using forecast oceanographic conditions (2070-2099) along with our thermal/predator habitat distribution model to examine changes in scallop and *Astropecten* distributions under three climate scenarios. If the current greenhouse gas emission continues, scallop habitat could drop between 23%-55%.

PANORAMIC SPATIAL VISION IN THE BAY SCALLOP, *ARGOPECTEN IRRADIANS*

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Scallops have a distributed visual system that consists of dozens of eyes spread across both margins of mantle tissue. Scallops have been studied for their unique mirror-based eyes and light-influenced behaviors, but it is still largely unknown how their sensory-motor circuits integrate and process visual information to guide behaviors. It has been suggested that scallops and other animals with distributed visual systems consolidate visual information early in their sensory-motor pathways, resulting in them being able to detect visual cues (i.e. spatial resolution) without being able to locate them (i.e. spatial vision). To explore how scallops process visual information, bay scallops (*Argopecten irradians*) were filmed extending their sensory tentacles in response to lateral visual stimuli in different locations and of different sizes. Bay scallops distinguished between visual stimuli in different locations by directing their sensory tentacle towards them. They distinguished between visual stimuli of different sizes by directing tentacles more often towards larger ones. Scallops are known to have spatial resolution, but these results show for the first time that scallops have spatial vision, indicating their sensory-motor circuits include neural representations of their visual surroundings. Exploring the visual processing of scallops and other animals with distributed visual systems will help uncover the different ways through which non-cephalized animals convert sensory input into behavioral output.

RESPONSES OF RIBBED MUSSELS TO ENVIRONMENTAL STRESSORS

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Ribbed mussels, *Geukensia demissa*, serve as a keystone species in salt marsh ecosystems. These mussels face large daily changes in environmental conditions, which can place stress on the mussels. This stress can come from several factors such as temperature, air exposure, hypoxia, and salinity. To better understand this stress, high frequency sensors were utilized to detect ribbed mussel heartbeat *in situ* over the course of a one-month field deployment in Flax Pond, New York. These mussels were deployed in conjunction with environmental loggers to gain a profile the nearby environment. Using high frequency sensors, separate laboratory studies were also conducted observing the impacts of temperature, salinity, hypoxia, and pH stress on ribbed mussels. Hall effect sensors were also used during these laboratory experiments to assess valve gaping behavior. These studies were designed to mimic the conditions observed during the Flax Pond field deployment, while isolating individual stressors. The field deployment showed changes in mussel heartrate throughout the day; however, the results were inconsistent, and due to the coupling of environmental factors, the cause of these changes cannot be ascertained. The laboratory tests supported a strong temperature dependance on heartrate, regardless of mussel exposure to air or water. In addition, the laboratory tests supported that the ribbed mussels partially closed when subjected to low salinity conditions, and some mussels showed changes in valve gaping behavior when exposed to higher temperatures. These laboratory results help to understand some of the changes in heartrate which were observed during the field deployment.

OBLIGATE AND FACULTATIVE FACILITATION OF SEAGRASSES BY CHEMOSYMBIOTIC BIVALVES

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Facilitations involving foundation species are critical to ecosystem function. Lucinid clams, which are physiologically dependent on symbiotic sulfur-oxidizing gill bacteria, are thought to facilitate seagrasses worldwide by decreasing potentially phytotoxic sulfide concentrations in sediment porewater; however, little is known regarding how the strength of this facilitation changes with environmental context. Two factorial mesocosm experiments were conducted using lucinid-seagrass species pairs from south Florida and Mediterranean France to determine if the presence of lucinids increased the resistance of seagrass to multiple environmental stressors. In these experiments, condition, growth, and survival of seagrass with and without lucinids was compared when ambient light was reduced by ~65% and/or sediment porewater sulfide concentrations were increased by ≥250%. Over a six-week experiment in Florida, growth rates of seagrass tissues were significantly lower than those in controls when light availability was decreased and/or porewater sulfide was increased in the absence of lucinids. In the presence of lucinids, seagrass growth was similar to controls regardless of which stressors were applied. By contrast, ambient sulfide production in the sediment collected from France was so high that seagrass did not survive over the nine-week experiment without lucinids to decrease porewater sulfide levels. Neither shading nor sulfide addition was necessary to produce this effect. These two studies provide experimental evidence of both facultative and obligate facilitation of seagrasses by lucinids: one case in which lucinids allowed seagrass to maintain growth under multiple environmental stressors, and one case in which the presence of lucinids was required for seagrass survival.

SURVEILLANCE OF *PERKINSUS OLSENI* INFECTION IN THE MANILA CLAM, *RUDITAPES PHILIPPINARUM*, IN KOREAN WATERS

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Several surveys carried out in Korean waters reported that Manila clams *Ruditapes philippinarum* in tidal flats on the west and south coast are heavily infected by *Perkinsus olseni*. In this study, *P. olseni* infection intensity and prevalence were surveyed in clams using RFTM and histology. Clams were collected from 24 tidal flats on the west and south coast in May and September 2019. Histology indicated that clams collected in May were reproductively in developing and ripe, while most of the clams collected in September were in partially spawning or spent stages. The gill RFTM assay revealed that clams from the south coast were 100% infected by *P. olseni*, whereas the prevalence ranged from 70 to 100% on the west coast. The population mean infection intensity varied temporally and spatially. Out of 24 sampling sites, the mean infection intensity determined from 16 sites was significantly higher in September (2.7×10^6 cells/g gills) than May (1.7×10^6 cells/g gills). The elevated infection levels recorded in September is believed to be linked to combined effects of the higher water temperature and depressed clam fitness due to spawning stresses. Infection intensities of *P. olseni* recorded from the south coast (3.2×10^6 cells/g gill tissue) were higher than the levels determined from the west coast (2.0×10^6 cells). The observed higher infection prevalence and intensity was believed to be associated with the warmer water temperature on the south coast, where the winter lowest water temperature is 3-5 degrees higher than the west coast.

THE EFFECT OF DENSITY ON REPRODUCTIVE EFFORT IN THE ATLANTIC SEA SCALLOP, *PLACOPECTEN MAGELLANICUS*

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The Atlantic sea scallop fishery employs a rotational area management strategy designed to increase future yield-per-recruit and spawning potential due to fast growth observed by scallops afforded protection from fishing pressure; however, it is unclear how well the analytical models that underpin this strategy hold under conditions that deviate from long-term averages, such as the high-density recruitment events observed in 2012 in the Nantucket Lightship and 2013 in the Elephant Trunk. The scallops at these sites have persisted at high densities and appear to be exhibiting varying degrees of impacted performance. The effect of scallop density on growth, yield, and reproduction was investigated through quarterly sampling trips in 2018 and 2019 with sampling at 21 sites divided among high, medium, and low-density scallop beds. In addition to total catch and length data, 30 scallops were retained at each site to determine meat, viscera, and gonad weights along with sex and reproductive stage. Reproductive effort was quantified as the ratio of gamete production estimated as gonad weight to total production in meat weight and viscera weight to determine how this metric differs across population density. Responses varied between sampling locations. In the Nantucket Lightship, scallops at high densities exhibited lower reproductive effort than those at medium or low densities, which is consistent with a density-dependent effect as resources become limiting. In the Elephant Trunk, the response of reproductive effort to population density was more mixed, suggesting that other factors such as food availability may be operating between these two regions.

EFFECTS OF MICROFIBERS ON THE GUT MICROBIOME AND GUT TISSUES OF THE BLUE MUSSEL, *MYTILUS EDULIS*

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Microplastics are a ubiquitous emerging contaminant across marine compartments. As a result of their small size and global distribution, ingestion of microplastics could pose a threat to suspension-feeders. Microplastics can act as a vector for foreign or pathogenic microbial species, potentially affecting the gut microbiome of the host. In many species the microbial community of the gut aids in digestion, mediates abiotic stressors, and affects host immunity, and may perform similar functions in bivalves. Thus, changes in the gut microbiome may have indirect effects on organismal health. Additionally, there are questions as to whether or not microplastics act as a mechanical obstruction and cause gut tissue alteration. To test whether or not microplastics affect the gut microbiome or tissues of the blue mussel, *Mytilus edulis*, animals were exposed to aged nylon microfibers (length = 500 mm, diameter = 30 mm), aged *Spartina* sp. particles, or no particle, for 21 days. Particles of *Spartina* sp. were of comparable size and aspect ratio to nylon fibers and were used to control for the presence of indigestible particles. Genomic DNA was extracted from half of the gut tissue samples and sequenced using 16S high throughput techniques to determine community taxonomic composition. The remaining gut tissues were sectioned, stained, and examined using microscopy. Preliminary molecular data indicate that gut microbial communities of mussels exposed to microfibers did not differ significantly from control and *Spartina* exposed mussels. Therefore, nylon microfibers 500 mm in length appear to have little effect on the gut microbiome of blue mussels.

NURTURING THE INDUSTRY-ACADEMIA COLLABORATION: EXPERIENCES AND PERSPECTIVE FROM A PRIVATE HATCHERY WITH AN EYE TOWARD R&D

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Industry-academia research collaboration is not new, particularly in the shellfish community, where R&D is at the heart of both the economy and ecology. Never has demand for this type of collaboration been higher with the recent emphasis from grantors that industry-academia collaborations are mandatory. This ratchets up the expectations for deliverables on both parties and can be quite challenging for small or even medium sized businesses.

This session will explore the nature of these collaborations from the perspective of the Oyster Seed Holdings, Inc. oyster hatchery in Virginia, which has participated in numerous such collaborations to date, and is involved in several recent submissions of increasing involvement and complexity. Presented material will include perspectives on the critical need for industry driven collaboration, the onus on parties involved, potential pitfalls, administrative support for industry, and a proposed recipe for success.

MODELING GROWTH OF TWO CO-OCCURRING DUNGENESS CRAB COHORTS IN THE INLAND WATERS OF WASHINGTON STATE

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The carapace dimensions of Dungeness crab (*Metacarcinus magister*) at a given molt stage vary greatly throughout their range. Although growth models have been developed for various coastal Dungeness crab populations, the patterns of growth for juvenile Dungeness crab in the inland waters of Washington State remain largely unknown. Larval Dungeness crab within the Salish Sea waters of Washington are believed to be sourced from at least two different cohorts, distinguished by timing of arrival to the region and differences in carapace dimensions. The co-occurrence of multiple cohorts complicates efforts to understand the population dynamics of this critically important species. Thus, in 2019 larvae from two phenotypically-distinct cohorts were reared in the laboratory to evaluate differences in carapace dimension, intermolt period, and molt increment over the period of one year. Simultaneously, wild juvenile crabs were surveyed and measured bi-weekly in the intertidal to compare sizes with that of laboratory-reared individuals. The resulting growth models allow researchers to elucidate the source cohort, molt stage, and relative age of juvenile Dungeness crab found in these inland waters. Improved understanding of cohort composition of juvenile crab at the beach or basin level offers important insight into the stock supply of the region, and can be used to address questions of differential impacts to cohorts and potential effects on the fishery.

ESTIMATING ILLNESS RISK ASSOCIATED WITH *VIBRIO PARAHAEMOLYTICUS* FROM PACIFIC OYSTERS HARVESTED IN SOUTHERN CALIFORNIA USING A QUANTITATIVE MICROBIAL RISK ASSESSMENT FRAMEWORK

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Oyster-related *Vibrio parahaemolyticus* illness causes approximately 34,000 infections a year with associated costs of $168 million per year in medical, lost wages, and premature death in the USA. Furthermore, cases have an increasing trend over the last decade. This study integrated environmental sampling with quantitative microbial risk assessment (QMRA), a mathematical approach to estimate health risks, to approximate *V. parahaemolyticus* illness risks from consuming recreationally harvested Pacific oysters in Southern California. Culture-based methods followed by PCR confirmation were used to enumerate *V. parahaemolyticus* in oysters harvested throughout Newport Bay, California. A QMRA model was used to estimate *V. parahaemolyticus* illness rates from consumption of harvested oysters following a simulated "sea-to-fork" pathway. Estimated illness risk varied across sites in Newport Bay. Additional analyses were used to identify potential interventions to reduce health risk from oyster consumption. Temperature abuse during the "sea-to-fork" pathway elevated illness risks. This QMRA model coupled with further studies can be used to inform decisions regarding harvest, post-harvest practices, and transportation time or temperatures to reduce risk of *V. parahaemolyticus* illness.

DOWN REGULATION OF T6SS GENE EXPRESSION IN THE BIVALVE PATHOGEN, *VIBRIO CORALLIILYTICUS*, DURING COMPETITION WITH THE PROBIONT, *PHAEOBACTER INHIBENS*

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Oyster aquaculture is a growing industry, though it carries large risks due to disease outbreaks that decimate larval and juvenile stocks. The addition of the probiotic bacterium, *Phaeobacter inhibens* (S4), to aquaculture systems has been demonstrated to protect oyster larvae against bacterial pathogens such as *Vibrio coralliilyticus* (RE22). Gene deletion mutants of S4 were previously used to identify the importance of antibiotic production, biofilm formation, and quorum sensing in the probiotic activity against RE22. Here a transcriptomic approach was used to gain a more comprehensive understanding of this complex bacteria-bacteria interaction and identify novel pathways involved in probiont activity. RE22 and S4 were co-cultured in exponential growth phase for five hours after which biofilm and planktonic samples were collected and subjected to transcriptomic analysis. Results of differential gene expression in the pathogen RE22 revealed down regulation of genes involved in virulence (e.g. Type 6 secretion system) and up regulation of genes involved in detoxification and bacterial immune response. The results further confirmed the role of quorum quenching and antibiotic production as probiotic mechanisms of S4 against RE22. This pilot study indicates the modulation of unexpected biochemical pathways during direct competition between S4 and RE22 and may provide future targets to increase the effectiveness of probiotic bacteria in mitigating diseases in aquaculture systems.

NUTRIENT ECOSYSTEM SERVICES DERIVED FROM BIVALVES ON ENGINEERED STRUCTURES

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The nutrient removal value of bivalves, particularly oysters, has attracted considerable scientific and management consideration in the last two decades. Increased oyster and other bivalve populations can remove phosphorus and nitrogen through nutrient assimilation and harvest. In the case of nitrogen, increased microbial denitrification has been of particular interest. While much effort has been devoted to on-bottom oyster restoration and various aquaculture practices, the intentional seeding of hard structures such as reef balls and oyster castles has not previously been evaluated for nutrient removal.

To determine rates of denitrification and nutrient exchange, *ex-situ* incubations of reef balls and oyster castles from the mesohaline Choptank River (Chesapeake Bay) were carried out. Reef balls were deployed primarily for habitat purposes and the oyster castles were deployed for shoreline protection. These structures had variable numbers of eastern oysters—*Crassostrea virginica*. Time courses of changes in dissolved nutrient and gas concentrations were used to determine rates of nutrient and oxygen exchange, with changes in the ratio of N2 to Ar used to estimate denitrification rates. High rates of oxygen uptake and denitrification were observed in reef balls and oyster castles that had high oyster biomass. Denitrification was also observed in the absence of oysters, with high densities of filtering bryozoans and barnacles of potential importance. The observed rates of denitrification are of sufficient magnitude to merit consideration as a quantifiable nutrient reduction benefit in nutrient-impacted coastal ecosystems.

INFLUENCES OF ENVIRONMENTAL FACTORS ON TEMPORAL AND SPATIAL VARIATION IN ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA SOLIDISSIMA*, RECRUITMENT IN NEW YORK STATE WATERS

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Supporting a multimillion-dollar fishery in New York State (NYS) waters, the Atlantic surfclam, *Spisula solidissima solidissima*, has experienced a local population decline of 72% from 2002 to 2012 and record low juvenile abundances. Laboratory experiments and field surveys suggest that increased sea surface temperatures (SST) cause physiological stress and limit abundances in warmer waters; however, no analyses exist to link environmental factors (e.g. SST and wind patterns) to surfclam recruitment. This study uses regression analyses (e.g. LASSO and GLMs) to link environmental factors to a developed Cohort Strength Index (CSI) from 1987 to 2004. CSI values serve as relative estimates of recruitment strength and are calculated from adult surfclam age structure matrices. Three east to west regions in NYS waters yielded distinct spatial and temporal recruitment patterns, with the population in western waters experiencing recent sharp decreasing recruitment and the population in eastern waters experiencing increasing recruitment. Results showed a negative relationship between SST and CSI values in western waters but a positive relationship in eastern waters. Furthermore, CSI values in eastern waters showed negative relationships with northward spring wind intensity, during gonad maturation, and eastward summer wind intensity, during larval transport and settlement. These results suggest that thermal stress may be more prominent in western, warmer waters and that hydrodynamic processes (e.g. wind-induced changes in larval transport) may have greater influence in eastern waters. Unraveling such recruitment-environment relationships may aid in fisheries management, help predict future recruitment and provide insight regarding surfclam fishery responses to climate change.

IMPROVED FISHERY-INDEPENDENT SURVEYS OF GAPER CLAM (*TRESUS CAPAX*) POPULATIONS IN OREGON ESTUARIES USING AN ADAPTIVE CLUSTER SAMPLING DESIGN

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The gaper clam (*Tresus capax*) are a common bivalve species in Oregon estuaries which supports a thriving intertidal recreational fishery and a subtidal commercial dive fishery. Management of these fisheries is dependent on the extensive fisheries-independent surveys of gaper clam and other bay clam populations conducted by the Oregon Department of Fish and Wildlife (ODFW). Gaper clams occur in highly aggregated populations and tend to be undersampled in the stratified-random sampling (SRS) design currently used. This can lead to inaccurate estimates of gaper clam populations and a misrepresentation of the spatial distribution of this species. To address these issues, a field study was conducted in Yaquina Bay, Oregon comparing SRS to two adaptive sampling approaches: Two-Stage Sampling (2S) and Adaptive Cluster Sampling (ACS). The gaper clam populations at the study sites were highly aggregated and spatially discrete. The SRS and 2S sampling methods undersampled the gaper populations relative to the ACS approach. The ACS method also had lower variability and provided the best population estimates. The trade-offs for using the ACS approach are sampling uncertainties and in general larger sample size that creates logistical challenges for large sampling programs. In summary, ACS decreases variability in population density and biomass estimates that can be used to improve management of gaper clam fisheries. The higher sampling intensity of ACS limits its incorporation into the extensive fisheries-independent sampling used by ODFW but can complement the standard methods with focused ACS sampling on regions of the estuary with known gaper populations and/or fishing effort.

INTRASPECIFIC COMPARISON OF OYSTER GENE EXPRESSION RESPONSE TO LOW OXYGEN

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Hypoxia, defined as oxygen concentrations below 2.0 mg L^{-1}, is an increasing threat both to coastal waters and their inhabitants worldwide. There is great interest in understanding the mechanisms that organisms employ to tolerate current extremes in environmental stressors, such as hypoxia, as these can provide insights into their capacity to tolerate projected changes. Intraspecific comparisons of gene expression in response to hypoxic exposure provide a useful tool to elucidate tolerance differences and the genetic underpinnings to tolerance. The eastern oyster, *Crassostrea virginica*, is an ecologically and economically important sessile bivalve that resides in coastal environments prone to hypoxic events. While much is known about hypoxia tolerance in oysters generally, less is known about intraspecific differences in molecular response to hypoxia that might give rise to different tolerances. To better understand this knowledge gap, oysters from six different sites—three that experience seasonal hypoxia and three that experience annual normoxic conditions—throughout the Maryland portion of the Chesapeake Bay were collected. After six months of common garden acclimation, oysters were brought into the laboratory and exposed to either a hypoxic or normoxic treatment for 96 hours. RNA was extracted from dissected gill tissue from each oyster, sequenced, and differential gene expression analysis was conducted on the resulting reads. Preliminary results showed significant differences in gene expression between oysters in normoxic and hypoxic treatments and an indication of site-specific intraspecific patterns of gene expression. Results are expected to provide novel insights into the gene expression response of *C. virginica* to hypoxia.

A CASE-CONTROL ANALYSIS OF TRACEBACK INVESTIGATIONS FOR VIBRIOSIS AND PRE-HARVEST ENVIRONMENTAL CONDITIONS IN WASHINGTON STATE, 2013-2018

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The pathogen, *Vibrio parahaemolyticus*, is a major cause of seafood-borne illness and accumulates in shellfish. Vibriosis cases are rising globally. The goal of this research was to evaluate associations between vibriosis traceback investigations in Washington State and pre-harvest measurements sampled from shellfish (*Crassostrea gigas*). Successful tracebacks were spatiotemporally matched to routine sampling events, which included measurements of temperature, salinity, and genetic targets (*tlh*, *tdh*, *trh*). Unmatched events were treated as controls. Associations were evaluated using logistic regression.

Systematic differences were observed across harvesting zones. These included positive associations between vibriosis and all three genetic targets in South Puget Sound, with a large odds ratio for an increase in *tdh* when total bacterium abundance was low (*tlh* <1 log10 MPN/g). A positive association also occurred for tissue temperature while a negative association simultaneously occurred for water temperature. The coastal bays displayed positive associations for water temperature and for an increase in the *tdh*:*trh* ratio. Hood Canal had no statistically significant associations.

The zonal variation in associations indicates unique pathogenic strain prominence, suggesting *tdh*+/*trh*+ strains in South Puget Sound, such as the O4:K12 serotype, and *tdh*+/*trh*− strains in the coastal bays. The temperature discrepancy between water and oyster tissue suggests that South Puget Sound pathogenic strains flourish with exposure to relatively warm air during low tide. These findings identify new ecological risk factors for vibriosis in Washington State that can be used in future prevention efforts.

QUEEN CONCH AQUACULTURE IN PUERTO RICO: HATCHERY AND NURSERY PHASES

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The queen conch, *Aliger gigas*, formally known as *Strombus gigas*, is the most important molluscan fishery in the Caribbean and is in a state of steady decline due to overfishing and habitat degradation across its geographic range—the Caribbean Sea, The Bahamas, Gulf of Mexico, Florida and Bermuda. The heritage of conch, a species of subsistence and economic importance, is deeply rooted in the island nations. As a response to population declines, queen conch aquaculture began in many laboratories the 1970s and a commercial farm operated in the Turks and Caicos between 1984 to the mid-2010s. Female conch lay nine egg masses during the summer breeding season, with each containing about 500,000 eggs. After three to four days, eggs hatch and planktonic veligers (larvae) develop for three weeks before metamorphosis into benthic juveniles.

As the plight of the conch persists, the need for solutions has become urgent. Conch aquaculture for restoration and sustainable seafood production has received high interest as one of the solutions, along with improved fishery regulations, to help conserve populations. A fishers-operated queen conch hatchery and nursery in Puerto Rico, located at the Naguabo Fishing Association and supported by a Saltonstall-Kennedy NOAA grant, was initiated in 2019. To assist with training, a comprehensive user manual for conch aquaculture was completed in English and is being translated to Spanish. This aquaculture project will serve as a model, which can be implemented by other fishing communities in Puerto Rico and across the Caribbean.

EXPOSING THE SECRETS OF THE NEPHROCOMPLEX 1 (‘ANTENNAL GLAND’): A MAJOR PORTAL OF ENTRY FOR PATHOGENS IN *PENAEUS VANNAMEI* SHRIMP

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Viruses, such as white spot syndrome virus, and bacteria, such as *Vibrio* species, wreak havoc in shrimp aquaculture. As the main portal of entry for various pathogens in shrimp remain unclear, infectious diseases are difficult to prevent and control. Because the cuticle is a strong pathogen barrier, regions that lack cuticular lining, such as the excretory organ of the shrimp, or the ‘the antennal gland’, are major candidate entry-portals. The antennal gland, up until now was morphologically underexplored, was studied using several imaging techniques. Using histology based 3D-technology, it was demonstrated that the antennal gland resembles a kidney, connected to a urinary bladder with a nephropore (exit opening) and a complex of diverticula, spread throughout the cephalothorax. Micro Magnetic Resonance Imaging of live shrimp not only confirmed the histology-based model, but also indicated that the filling of the diverticula is linked to the molting cycle and possibly involved therein. Based on the hemolymph filtration function and attached diverticle complex, it has been proposed to rename the antennal gland as the “nephrocomplex”. By an intrabladder inoculation, data showed high susceptibility of this nephrocomplex to both white spot syndrome virus and *Vibrio* infection compared to peroral inoculation. An induced drop in salinity allowed the virus to enter the nephrocomplex in a natural way and caused a general infection followed by death; fluorescent beads were used to demonstrate that particles may indeed enter through the nephropore. These findings pave the way for an oriented disease control in shrimp.

A SHELLFISH INDUSTRY PERSPECTIVE ON SHELLFISH-EELGRASS INTERACTIONS—A PICTURE IS WORTH A THOUSAND WORDS AND A VIDEO WORTH A MILLION

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Eelgrass is recognized and protected as a critical marine habitat by many federal, state and local resource management agencies. To the frustration of many shellfish growers, resource managers often fail to recognize that shellfish crops and gear also provide ecosystem services of comparable value to eelgrass and that the two can and do often co-exist synergistically. In many regions’ regulations prohibit shellfish culture in or around eelgrass; however, there are countless examples of shellfish growers observing eelgrass becoming established and thriving in their shellfish farms likely due to the synergistic effect (improved water clarity, nutrient coupling etc.)

Moreover, beyond fostering conditions for eelgrass to thrive, shellfish crops and gear provide habitat, refuge and foraging opportunities for a variety of marine organisms. While not identical to eelgrass it is evident to growers witnessing it every day on their farms that these are most definitely functioning healthy ecosystems.

Recently with the advent of GoPro cameras growers have taken to capturing video footage of eelgrass shellfish mosaics and the flora and fauna using their crops and gear. These videos have inspired scientists, ENGO and resource managers to do the same, partnering with growers to access their farms and using the videos to attempt to quantify the comparative value of these ecosystems. The videos and research are improving our understanding of the ecological value of habitats created by eelgrass, shellfish crops and gear and informing policy and regulatory decisions around them.

THE ENZYME DEFENSE MECHANISM ENCOUNTERED IN MARINE GREEN MUSSEL, *PERNA VIRIDIS*, IN RESPONSE TO HYDROCARBON (ETHYL-NAPHTHALENE) POLLUTION

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The green-lipped mussel, *Perna viridis*, is normally found in estuaries and coastal marine beds, which are the portal entry for land-based pollutants. In order to overcome the pollution risks, the animals defense mechanisms and show elevated levels of alkaline phosphatase (ALP), GOT and GPT activity. The determination of tissue (digestive gland, liver, mantle, and gill) ALP, GOT, and GPT activities help predict the impairment in the organs and the possibility for survival in the polluted water. The activity of ALP, GOT, and GPT are likely to reflect the metabolic state of fish/shellfish sample from the different regions. In the present study, *Perna viridis* were exposed to polyaromatic benzoic hydrocarbon-naphthalene (PAH) and showed elevated levels of ALP, GOT, and GPT that indicated cellular damage in the vital tissues of the animal. Therefore, this study demonstrated that the PAH pollution induced levels of ALP, GOT and GPT in *Perna viridis* will serve as bioindicator to monitor certain types of organic pollution contained in the water.

PACIFIC OYSTER MICROBIOMES IN A SOUTHERN CALIFORNIA BAY, USA: LINKING MICROBIAL ECOLOGY TO ENVIRONMENTAL CONDITIONS AND HUMAN PATHOGEN ACCUMULATION

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Pacific oysters (*Crassostrea gigas*) naturally thrive along the southern California coastline. While they are locally invasive, they nonetheless harbor great potential as a prolific aquaculture species. Bivalve-associated microbes are influenced by variable environmental conditions in other geographic regions, which may impact host health, however, this has not been studied in southern California. Furthermore, their microbiomes are poorly understood in the context of human pathogen accumulation, which is important for maintaining food safety.

To address these research gaps, Pacific oysters were deployed at 12 sites in Newport Bay, CA following a two-week depuration period, then collected water and oyster tissue samples (whole oyster meats, gills, and digestive glands) over six weeks. It was quantified human pathogens in these samples and also characterized microbial community dynamics using 16S amplicon sequencing. Oyster tissues harbored distinct microbial communities which diverged greatly from the water samples. Oysters collected from sites farthest from the estuary mouth, with higher temperatures and lower salinities, had a lower rate of pathogenic bacteria accumulation compared to sites nearest the coastal ocean and also had different dominant microbial taxa. It was observed that *Vibrio* spp. bacteria, which are typically abundant members of shellfish microbiomes, were scarce in our samples and coincided with low levels of human pathogenic *Vibrio* species in shellfish tissues.

By characterizing microbial taxa associated with Pacific oysters in southern California at different sites and timepoints, we aim to better understand what environmental conditions alter host-microbe dynamics and potentially prevent or facilitate human pathogen accumulation.

SEA SCALLOP, *PLACOPECTEN MAGELLANICUS*, FILTRATION AND FEEDING RELATIVE TO SESTON QUANTITY AND QUALITY IN THE DAMARISCOTTA RIVER, MAINE, USA

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The sea scallop, *Placopecten magellanicus*, is a highly valuable fishery resource, consistently ranking at the top of dollar-value landings. Accordingly, a great deal of biological, ecological, and fisheries science data are available concerning wild-harvested populations. There is a growing interest, with some success already exhibited, in cultivating sea scallops in coastal Maine. Potential farm sites are outside of the typical sea scallop habitat, and few data exist to assess how sea scallops may perform in these alternative habitats with aquaculture potential.

A group of researchers from the NOAA Fisheries laboratory in Milford CT conducted biodeposition trials in the Damariscotta River, currently a pilot-scale sea scallop aquaculture site, in June and September of 2019. Preliminary data show that sea scallop absorption efficiency in the Damariscotta River is variable and largely dependent upon seston quality. Under favorable conditions, absorption efficiency was above 0.9—more efficient than other commonly-cultured shellfish tested to date. Sea scallop clearance rates, 0.7 to 1.5 liters per hour, and absorption rates were comparable to other cultured shellfish; whereas, sea scallop filtration rates, 4.75 to 6.75 milligrams per hour, were lower than other cultured shellfish. These results, coupled with growth rates reported by academic and industry partners, indicate that sea scallops have strong potential as an aquaculture species on farms sited where trophic resources are sufficient in terms of both quantity and quality.

INCREASES IN POPULATIONS OF THE NORTHERN QUAHOG (= HARD CLAM) *MERCENARIA MERCENARIA* FOLLOWING THE CREATION OF SPAWNER SANCTUARIES IN SHINNECOCK BAY, NEW YORK, USA

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Shinnecock Bay (SB) is a shallow-water, barrier island estuary in Long Island, NY that has experienced sharp declines in the commercially important clam, *Mercenaria mercenaria*, since the 1970s, and the reoccurrence and intensification of harmful algal blooms (HAB) know as brown tides since the 1980s that have had devastating ecological consequences. To help reverse these negative trends the Shinnecock Bay Restoration Program (ShiRP) initiated bay-wide hard clam restoration efforts in 2012 through the establishment of spawner sanctuaries with the goal of increasing the total biotic filtration of the bay. To date the ShiRP has planted over three million adult clams into spawner sanctuaries and has conducted a suite of monitoring efforts to measure success. Since 2015, commercial landings of hard clams from SB have increased sharply and steadily. In 2019 landings were up 933% from when restoration began in 2012, and at the highest level in 33 years. A disproportionate increase in smaller clams (littlenecks) suggests that landings increases have been due to recent population increases rather than solely increased fishing pressure. This has been supported by fishery independent stock assessments that have found increases in hard clam recruitment in recent years. The timing and location of population increases suggest that larvae originated from the spawner sanctuaries, but additional research is needed to directly connect population increases to restoration efforts. Nonetheless, the results provide the first documentation of system-wide increases in hard clam abundance following the implementation of spawner sanctuaries in over forty years of efforts in Long Island estuaries.

A NOVEL RNA VIRUS, CRUSTACEAN HEPE-LIKE VIRUS 1 (CHEV1), FROM FARMED GIANT FRESHWATER PRAWN *MACROBRACHIUM ROSENBERGII*

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The family Hepeviridae includes several positive-stranded RNA viruses and infects a wide range of mammalian species, birds, and trout; however, to our knowledge, few viruses from the family Hepeviridae have been characterized from invertebrates, of which none have been fully-sequenced or well-identified from crustaceans. In this study, diseased *Macrobrachium rosenbergii* with growth retardation were sampled and none of ten known shrimp pathogens were detected. Meta-transcriptomic sequencing results of viral crude extracts from the pooled samples showed that a novel virus of Hepeviridae was identified. The complete genome with 7750 nucleotides in length was successfully obtained using Sanger sequencing and 5'/3' RACE. Similar to other recognized HEV, the sequenced genome had a similar structure to known hepatitis E virus genomes including a 5' untranslated region (UTR), followed by two major ORF and a hypothetical ORF3, and a 3' UTR. Based on the RNA-dependent RNA polymerase (RdRp) and capsid protein sequences, phylogenetic analyses suggested it might be a novel hepe-like virus within the family Hepeviridae. It was proposed that the novel viral isolate belongs to the Hepeviridae family and provisionally name this virus crustacean hepe-like virus 1 (CHEV1). To our knowledge, this is the first hepe-like virus identified from crustaceans and our study highlighted the expanding host range and the increasing species diversity of the family Hepeviridae.

EFFECTS OF SEAGRASS AND CULTURE METHOD ON THE GROWTH OF JUVENILE OYSTER SEED ALONG A GRADIENT IN TWO US WEST COAST ESTUARIES

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Negative effects of acidic seawater on oyster larval survival and growth are well-documented, particularly along the US west coast where the shellfish industry has developed strategies to reduce these impacts in hatcheries where these effects can be controlled to produce viable seed. Once seed is planted in estuaries; however, juvenile oysters experience a suite of environmental factors and potential stressors, including unfavorable carbonate chemistry that vary across the estuary and might affect their continued survival and growth. The presence of seagrass has been suggested as one factor that alters water chemistry and could reduce this stress creating more favorable growing conditions at least at local scales. This study was implemented to investigate the effects of seagrass (here eelgrass, *Zostera marina*) on juvenile oyster growth at several locations at sites in two estuaries where the carbonate chemistry gradient was expected to differ. Oysters were deployed inside and outside eelgrass and at two heights above the seafloor representing on- and off-bottom culture conditions. Shell growth was documented monthly from June—September, 2019 and condition index measured in September. Discrete water samples were collected to measure pCO2 and chl-a, and paired YSI sondes were deployed for 24-hour periods to collect continuous temperature, salinity, pH, turbidity, and chl-a inside and outside eelgrass habitat at two out plant locations per estuary. Preliminary results suggest that culture method affected juvenile oyster growth across sites, but the effect of eelgrass on water carbonate chemistry and juvenile oyster growth was site specific.

CLIMATE AND ESTUARINE GRADIENT INFLUENCE PACIFIC OYSTER CONDITION, SPAWNING, AND PERHAPS MORTALITY EVENTS IN A U.S. WEST COAST ESTUARY

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Pacific oysters, *Crassostrea gigas*, were introduced to, and became 'naturalized' in, several estuaries along the US West Coast including Willapa Bay, Washington where conditions allowed for adult oysters to condition and spawn and larvae to be retained, settle and survive. The oyster industry relied on "natural" set at some of these locations and/or continued to import seed from Japan until the late 1970s advent of hatchery production of oyster larvae. The industry continued to take advantage of natural sets in Willapa Bay where it remains an important feature of management on state established oyster reserves. An analysis of the monthly condition index data for this naturalized Pacific oyster population which has been collected since 1955, indicates that teleconnections affecting the nearshore coastal ocean environment may also influence seasonal timing and location of spawning in this estuary. A new study designed to compare this seasonal gametogenic cycle with that in Japan where these oysters were originally sourced in order to discover links to mortality events in both locations was fortuitously implemented in 2019 when a large mortality event was observed in many locations along the US west coast. Preliminary results suggest that seasonal timing and magnitude of such spawning events could be linked to mortality, but other variables should be measured in order to understand and potentially mitigate for the effects of anthropogenic changes to these estuaries and an uncertain future climate.

COMMERCIAL CLAMS AND FISHERIES OF MARYLAND, CHESAPEAKE BAY, USA

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Clams of two species are harvested by hydraulic escalator dredges from benthic habitats in mesohaline Maryland waters of Chesapeake Bay. As adults, clams of both species occupy stable burrows within benthic sediments, which allow their relatively quick withdrawals from threats by surface predators, including rays, fishes, and crabs. Since 1951, hydraulic escalator dredges have harvested clams from relatively shallow bottoms, using jets of pressurized water to excavate benthic trenches, and to wash excavated clams onto a mesh escalator belt for collection on deck.

Those novel dredges enabled harvests of abundant and previously inaccessible populations of benthic soft shell clams, *Mya arenaria*. For 35 early years, those previously unexploited populations supported a rapidly capitalized fishery during 1955-1970, followed by reduced harvests through 1990. During 30 recent years since 1990; however, annual harvests of Maryland soft shell clams have plummeted to average only 3% of the peak harvests of 1964, reflecting a severe population decline. With persistently scarce *M. arenaria* harvests, clam dredge vessels now predominantly target razor clams, *Tagelus plebeius*, which are primarily marketed as crab bait.

Despite fishery histories and the drastic modern decline in soft shell clam harvests, no formal Fishery Management Plan exists to guide management and conservation of either *M. arenaria* or *T. plebeius* clam resources of Maryland, Chesapeake Bay waters. Although documented negative impacts on benthic habitats and living resources have prohibited the use of hydraulic escalator dredges in waters of Virginia and of Maryland coastal bays, that destructive harvest technology remains active in Maryland waters of Chesapeake Bay.

DISEASES AND PARASITES OF COMMERCIALLY EXPLOITED *MYA ARENARIA* CLAMS IN CHESAPEAKE BAY, MARYLAND, USA

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Several diseases and parasites may have augmented clam mortalities from marginally regulated harvests, to decimate formerly abundant benthic populations of subtidal *Mya arenaria* in Maryland waters of the Chesapeake Bay. Epidemiological and other metrics for those diseases and parasites were particularly well-documented by extended annual surveys during 2000-2009.

Lethal disseminated neoplasias (DN) are documented since 1983, at sample prevalences of 0-100% and at mean annual prevalences of 3-43%. In advanced cases, abundant, proliferating DN cells largely displace circulating hemocytes and their critical functions. Since 1990, previously absent and potentially lethal protist infections by *Perkinsus chesapeaki* have been consistently detected, at individual sample prevalences of 0-100% and at mean annual prevalences of 25-83%. Focal lesions may compromise gill functions locally; while proliferative and necrotic systemic infections appear lethal.

Prevalent and abundant virus infections cause extreme hyperplasia among the nuclei of infected gill epithelial cells. Since 2000, such (GENHV) infections are reported at sample prevalences of 0-100%, and at mean annual prevalences of 18-90%. The identity of the virus remains uncertain and its pathological consequences are unknown, but critical gill functions may be compromised in common cases where lesions are abundant. Additional, common parasites with low apparent impacts include rickettsia-like microcolonies that consistently proliferate among or within cells of digestive gland epithelia at sample prevalences of 40-100%. Several types of ciliates commonly infest external epithelia of gills and mantle in approximately 65% of all clams. Other parasites occasionally include apparent copepods and plerocercoid cestode larvae colonizing the lumens of clam digestive systems.

REACTIVE TO PROACTIVE: A GOAL FOR IMPROVED SHELLFISH RESOURCE CONSERVATION AND MANAGEMENT

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In South Carolina oysters are an ecologically, culturally, and economically valuable resource, resulting in the fourth largest commercial fishery in the state, and supporting hundreds of industry members as well as a presumably significant recreational fishery. In 1986 nearly half of the privately-managed oyster leases of South Carolina were converted to open-access, state-managed grounds to allow for greater opportunities and easier entry into the fishery. Inadequate management tools and regulatory mechanisms that only allow for opening and closing of grounds have limited state managers to a reactionary management approach, which has created a cyclical boom and bust commercial fishery on state managed common grounds, and a largely unmanaged and unknown recreational fishery. This is compounded by limitations in funding to adequately return enough oyster shells back onto state managed grounds for use as substrate in population recruitment.

This presentation will cover limitations to current management practices, challenges faced, and the proactive strategies that are required to maintain sustainable oyster populations on state-managed grounds. These strategies will focus on sustainable harvesting practices, sufficient regulatory mechanisms, and improved management tools. These strategic goals, along with other currently gathered data, will utilize a better understanding of the drivers for the natural oyster population demographics in South Carolina in their approach. A proactive management plan will provide a healthier, sustainable oyster resource and a more consistent economic benefit to the commercial oyster industry in South Carolina.

DECREASING MORTALITIES OF TRIPLOID EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) IN THE ESTUARIES OF THE NORTHERN GULF OF MEXICO: FIELD EVALUATION IN COASTAL ALABAMA, USA

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With the establishment of off-bottom oyster farming in the Gulf of Mexico, oyster farmers in the region have widely adopted triploid oysters as the mainstay of their production, due to their faster growth and better summer meat condition. Wadsworth et al. (2018) found that triploids grew larger and faster than diploids, but also had higher mortality rates across farm sites. Salinity changes were suggested as a possible driver of this pattern. To determine the effect of salinity on growth and survival of triploid and diploid oysters at different salinity regimes, a comparative field study was conducted at three coastal Alabama sites: Grand Bay, Mobile Bay, and Dauphin Island. Six groups of half-sibling oysters were spawned from wild broodstock collected from areas with different salinity regime histories: Calcasieu Lake, Sister Lake, and Vermillion Bay in Louisiana. At each site, 12 replicates of each experimental treatment (2 ploidy x 3 broodstock origin, or 6 total experimental treatments) were deployed in November 2019 and sampled every other month. Data collection was completed in November 2020, and growth and mortality records will provide a comparison among groups under different salinity gradients. The goal of this study is to test whether use of broodstock selected from areas with different salinities can decrease triploid mortalities in the region.

LONE CABBAGE REEF RESTORATION AND MONITORING PROGRESS

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In less than 30 years, 3,000-year-old oyster reefs off the Florida Big Bend coastline have declined by 88 percent. This project included a broad collaboration between local oystermen, community volunteers and the National Fish and Wildlife Foundation to restore approximately five linear kilometers of oyster reef along the historic Lone Cabbage Reef tract. This restoration effort was done on the footprint of the historic Lone Cabbage Reef based on surveys conducted in the 1800s. Located at the mouth of the Suwannee River, Florida, the reef construction was completed in 2018 and consisted of 21 separate reef elements, each composed of locally sourced limestone. It was hypothesized that building the reef structure would retain freshwater in the estuary and make oysters on the reef and associated estuary less vulnerable to mortality events following drought events.

Following construction of the reef, research efforts were continued expanding on pre-construction data to i) assess how the addition of rock substrate promoted oyster reef recovery and resilience and ii) evaluate if the newly constructed reef is influencing the detention of freshwater in the Suwannee Sound promoting inshore oyster growth and habitat suitability. To address these primary project goals, a water quality monitoring network using stationary dataloggers was created in the Suwannee sound and a randomized oyster sampling protocol was established to determine changes in oyster counts between harvestable and non-harvestable areas.

THE *NONLTR-1_LVA* NON-LTR RETROTRANSPOSON FROM THE ORIGINAL SPECIFIC PATHOGEN-FREE (SPF) PENAEUS (*LITOPENAEUS*) *VANNAMEI* PRODUCED BY THE UNITED STATES IS SIMILAR TO THE NLRS RETROTRANSPOSON ASSOCIATED WITH ABDOMINAL SEGMENT DEFORMITY DISEASE (ASDD) OF FARMED *P. VANNAMEI* FROM THAILAND

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Abdominal Segment Deformity Disease (ASDD) of farmed *Penaeus vannamei* from Thailand was previously associated with a host genetic element non-LTR retrotransposon (KC179708, 4,101bp), which is potentially related to either inbreeding or long-term use of eyestalk-ablated females used in commercial hatcheries, as they increased the intensity of the diagnostic amplicons and the prevalence of ASDD in mysis 3 stage offspring of those broodstock. A search of the Rebpase database (www.girinst.org) revealed that nucleotides 3-4,101 of KC179708 are similar to nucleotides 1,974-6,062 of *NonLTR-1_LVa* non-LTR retrotransposon (6,180bp) characterized from the first specific pathogen-free (SPF) *L. vannamei* produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP). The translated protein of *NonLTR-1_LVa* contains six conserved domains: RT_nLTR_like [non-LTR retrotransposon and non-LTR retrovirus reverse transcriptase (RT); Rnase_HI_RT_non_LTR; group_II_RT_mat [group II intron RT/maturase]; RVT_1 [RT (RNA-dependent DNA polymerase)]; group_II_RT_mat; RNase_H; and R1-I-EN.

The *NonLTR-1_LVa* is 97% identical to a genome sequence in P vannamei farmed in China (breed Kehai No. 1 (ASM378908v1, ~1.6 Gb), LVANscaffold_231 (QCYY01000231) in which 7 copies of *NonLTR-1_LVa* exist. Fragment sequences are also found in some genomes from *P. monodon* from China (GCA_002291185, ~1.6 Gb), P. japonicus from China (GCA_002291165, ~1.4 Gb), and *P. monodon* from Thailand (GCA_015228065.1, ~2.37 Gb), where about 67% of *NonLTR-1_LVa* has about 76% similarity to the *P. monodon* genome sequence. Transcriptome homologs to *NonLTR-1_LVa* were found in several locations in different *P. monodon* chromosomes. *NonLTR-1_LVa* is expressed in *P. vannamei* transcriptomes from various developmental stages (nauplii, mysis, postlarvae) and adult tissues (testis, ovaries). Basic research is needed to confirm if ASDD expression is related to (a) inbreeding, (b) long-term use of eyestalk-ablated females used in commercial hatcheries, (c) increased ASDD prevalence in mysis 3 stage.

INITIATION OF A SENTINEL PROGRAM TO MONITOR HERPES VIRUS IN JUVENILE PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) AT COMMERCIAL FARMS ALONG THE US WEST COAST

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Ostreid herpesvirus 1 (OsHV-1) has impacted Pacific oyster (*Crassostrea gigas*) production globally. Within the United States, OsHV-1 was first detected in 1995 in Tomales Bay, California, and has subsequently been found in neighboring bays. In 2018 a microvariant of OsHV-1 was detected in San Diego Bay, California. Recognizing the risk of regional spread, a multi-state sentinel program was initiated to monitor the prevalence and pathogenesis of OsHV-1 in juvenile Pacific oysters planted at commercial farms in California (CA), Oregon (OR), and Washington (WA).

In Spring 2020, two sentinel oyster families were created, one susceptible and one tolerant to OsHV-1. In June/July 2020, OsHV-1 susceptible spat were planted in San Diego Bay (CA), Tomales Bay (CA), Tillamook Bay (OR), Willapa Bay (WA), and Totten Inlet (WA). OsHV-1 tolerant spat were planted in San Diego Bay and Tomales Bay. Industry partners determined spat survivorship every two weeks through early fall and sent samples for lab analysis to determine OsHV-1 viral load and variant type.

Sentinel spat at sites in Oregon and Washington demonstrated high survival and tested negative for OsHV-1. Sentinel spat from both crosses planted in San Diego Bay experienced nearly 100% mortality over a four-week period with high OsHV-1 viral loads. OsHV-1 was detected in Tomales Bay where spat survival was higher for the OsHV-1 tolerant family than for the OsHV-1 susceptible family and spat planted in June had higher survival than spat planted in July. Lessons learned from the first year of the project will be discussed.

META-ANALYSIS AND REVIEW OF RECIPROCAL INTERACTIONS BETWEEN BIVALVES AND SEAGRASS

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Bivalves and seagrasses may interact through a wide variety of potential mechanisms involving their structural and metabolic traits. Pathways mediated by biogenic structure could be facilitative through protection from predation or bioturbators, or by harboring beneficial interactors, or alternatively could result in competition for space or reduced food supply. Other pathways mediated by biological activity could positively link autotrophic roles of seagrass and heterotrophic roles of bivalves, but excessive organic matter production or nutrient release could be damaging. Published studies were compiled for a meta-analysis of field experiments testing bivalve response to seagrass (25 studies) and vice versa (11 studies), as well as for surveys of bivalves in and out of seagrass (39 studies). In experiments, seagrass improved bivalve survival, and bivalves at high cover reduced seagrass density, but seven other response metrics showed no consistent change. In surveys of particular bivalve species, densities were 1.6 times higher in seagrass than out of seagrass. This augmentation did not differ by body size but was especially pronounced in some functional groups. Generally weak effects, as well as facilitation, enable coexistence of bivalves and seagrasses under many conditions, yet some strong negative effects among the cases in this review indicate the importance of identifying key pathways of interaction in further work, as well as of expanding this type of research to larger spatio-temporal scales.

CHROMOSOME-LEVEL ASSEMBLIES OF THE NORTHERN QUAHOG (= HARD CLAM) AND ITS HARMFUL PARASITE QPX

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There is a growing interest in the use of high-throughput genotyping methods for unraveling the genomic bases of animal resilience to environmental stress or infectious diseases, particularly in non-model species. The decrease in sequencing costs made these technologies within reach, leading to an increase in the number of genomes assembled at a chromosome level, making comparative analyses between species more accurate. The complete genomes of the northern quahog (= hard clam), *Mercenaria mercenaria*, were sequenced and its parasite QPX (Quahog Parasite Unknown) which is responsible for epizootic losses in Northeastern states of the USA. Short and long read sequencing methods were combined with the Hi-C technology, allowing for the complete chromosomes for each species to be covered. As a result, 19 chromosomes of *M. mercenaria* were assembled for a total genome length of 1.85Gb. Around 29,000 coding genes were predicted, with the help of additional RNAseq data (92% of the genes having an assigned functional annotation). The QPX genome is 42.3Mb in length assembled into 42 scaffolds with a N50 of 1.9Mb. These findings are in line with those obtained in other members of the *Labyrinthulomycota* family, which are known to have a large number of chromosomes. Having high quality genomes for both the clam and its parasite allows the identification of specific genomic features in each species, but may also facilitate the identification of pathways involved in the host-parasite interactions that takes place during infection.

COMPARISON OF HISTOLOGICAL AND MOLECULAR METHODS IN THE DIAGNOSIS OF *MEROCYSTIS KATHAE* INFECTION IN GEORGES BANK ATLANTIC SEA SCALLOPS

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The increasing incidence of grey meats in Atlantic sea scallops (*Placopecten magellanicus*) and their subsequent toll on fisheries landings has caused concern since the early 2000s. Recently, this “grey meat disease” has been attributed to infection by the apicomplexan parasite *Merocysitis kathae*, which was previously identified as responsible for disease and mortality in populations of the Icelandic scallop (*Chlamys islandica*). A correlation between meat color and infection severity has not been observed in our analyses, necessitating the development of specific molecular methods for diagnosis. This study utilizes scallops collected by the Coonamessett Farm Foundation Seasonal Bycatch Survey of Georges Bank (funded by the NOAA Sea Scallop Research Set-Aside Program). Here, an update will be provided on the data collected using a diagnostic PCR to identify *M. kathae* infection and on the development of a quantitative (qPCR) assay to diagnose severity of infection. Molecular data is correlated with histological diagnoses from the same individuals.

THE COMING OF AGE OF PRECISION AQUACULTURE —HOW SENSORS AND MODELS ARE CHANGING THE WAY WE GROW SHELLFISH

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Over the last fifty years, aquaculture has grown very rapidly worldwide in response to (i) the stagnation and decline of capture fisheries; (ii) increased consumer demand; and (iii) the natural evolution of production systems from hunting and gathering to cultivation, mirroring the emergence of agriculture in the Neolithic period, four hundred generations ago.

This led to improvements in husbandry and genetics of aquatic organisms, and to other developments such as tools for production and zoning of aquaculture systems. Because social license and sustainability are major concerns of present-day societies, the growth of aquaculture in the West faces regulatory challenges that were never an issue for agriculture, perhaps because it developed over thousands of years. The human perspective on the marine environment as a common wealth introduced further concerns, particularly in coastal communities.

This review focuses on the ways in which environmental sensors, mathematical models, and management platforms have changed our understanding of shellfish farming and explores the ways in which precision aquaculture can contribute to a better world for both farmers and consumers. We are at a stage now where it is feasible to model individual animals as part of a farmed population and predict a wide range of aspects related to growth, food depletion, environmental effects, and pathogen spread. Tools are becoming available to help industry forecast the consequences of climate change for their crops, and Big Data and Deep Learning hold substantial promise in helping interpret how environmental changes affect bivalve production and how farmers can leverage this to optimize harvest.

A POTENTIAL ROLE FOR AMEBOCYTES IN OYSTER SHELL DEPOSITION

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It has been generally accepted that mantle tissue is responsible for constructing and repairing oyster shell; however, past and recent evidence indicates a role for oyster amebocytes, which are locomotory blood cells capable of migrating inside and outside of tissues. It was noted as early as 1901 that ‘migratory cells’ participated in pearl formation in oysters and by the mid-20th century ‘migrating epithelial cells’ were observed to participate in shell formation of the garden snail, another mollusc. A separate line of evidence for amebocyte participation has emerged from research showing that amebocytes are capable of bioaccumulating terrestrial metals, particularly copper and zinc, into intracellular vesicles. As part of the inflammatory response to a wound, these metals are released from amebocytes into extracellular spaces to precipitate hemolymph proteins, thereby forming a protective, antimicrobial ‘blood clot’. A similar process may be at play in shell deposition. At the very least, amebocytes are hypothesized to release metals into the conchiolin matrix to precipitate protein and crystallize the shell. Such a process would explain the higher concentration of metals in adult shell relative to larval shell which is formed before amebocytes are released into the bloodstream. Adult shell concentrations of many metals are orders of magnitude higher than surrounding seawater, indicating a bioconcentration capacity that is unique to amebocytes and lacking for mantle epithelial cells. This physiological role for terrestrial metals may also explain the distribution of oysters at locations near freshwater runoff.

REVISITING THE ROLE OF COPPER AND ZINC IN ANTIMICROBIAL DEFENSES OF EASTERN OYSTERS

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Eastern oyster amebocytes accumulate both copper and zinc against concentration gradients to extraordinarily high concentrations. The physiological purpose for this bioaccumulation was unexplained for many years. Several authors anticipated a microbicidal function for copper because they noted green coloration at the site of wounds, ostensibly transported to the site by amebocytes during the inflammatory response. In 1961 Frederick Bang described how bacteria were immobilized in an extracellular gel (clot) that formed around aggregates of responding amebocytes. He hypothesized that the gel was initiated by material extruded from granular amebocytes (degranulation). These observations were corroborated in 1971 by Craig Ruddell who not only demonstrated the high accumulation of copper and zinc in amebocyte granules but also showed that both metals were present extracellularly at the site of wounds. In 1975 Robert Brown completed an unpublished dissertation that experimentally confirmed oyster amebocytes as the source of clot-promoting substances and, moreover, that copper and zinc were released from amebocyte granules to initiate clot formation through precipitation of hemolymph proteins. He proposed that the metals may also play a role in intracellular microbial killing: When phagosomes fuse with cytoplasmic granules during phagocytosis, captured microorganisms are exposed to very high, and likely toxic, concentrations of metals and hydrolytic enzymes. The relationship of copper and zinc with higher microbial killing has since been demonstrated in field studies, thus supporting at least one physiological purpose for their high bioaccumulation.

THE UNCONVENTIONAL FINDINGS OF HERBERT PRYTHERCH ON OYSTER SETTING AND METAMORPHOSIS

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The location and distribution of natural reefs establish that eastern oysters are found primarily in coastal areas where salt water of the ocean is considerably diluted with fresh water from rivers or streams. Attachment of oyster larvae at metamorphosis is therefore not a haphazard process, but one that in some aspect requires fresh water. Working at the Bureau of Fisheries Field Station in Milford, Connecticut, Herbert F. Prytherch investigated the role of fresh water in larval setting and metamorphosis. He found in laboratory studies that setting, contrary to conventional wisdom, was not induced simply by decreased salinity. Setting was induced only if seawater was diluted with river water and was not induced by dilution with distilled water. This indicated that setting required some additional component of river water. By process of elimination, he identified copper as that component and demonstrated a dose response between copper and frequency of setting. Copper is a terrestrial element delivered to the coastal zone through freshwater efflux; and copper is also found to be highly concentrated in granules of oyster amebocytes. In corollary studies, Prytherch described the role of the pigment spots—aggregates of amebocytes often incorrectly called ‘eyespots’—in setting and metamorphosis. He observed that a few copper-rich amebocytes would break away from the aggregates to initiate setting and then the entire aggregate would dissipate into the hemolymph to initiate other morphological processes. These extraordinary studies, published in 1934, have been obscured by their complete absence from a subsequent and highly prestigious compendium.

CAN YOU EAT THEM TO SAVE THEM? FARMING THE WEST COAST NATIVE OYSTER, *OSTREA LURIDA,* FOR FOOD AND RESTORATION IN TOMALES BAY, CA, USA

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

While a handful of shellfish growers in the Salish Sea region continue to grow Olympia oysters for market and restoration purposes, in California the commercial farming of *O. lurida* has all but disappeared. In 2018 Hog Island Oyster Co. began experimenting with the culture of native oysters for Bay Area oyster bars and in support of local restoration efforts. This presentation will give an overview of the Hog Island project, discuss commercial opportunities and challenges, and explore the potential of native oyster farming to enrich larval abundance and recruitment in nearby wild populations. The session may also provide an opportunity to discuss the development of 'best practices' that unify sustainable seafood production and the conservation of a diminished native species.

GENOMIC STUDY OF GABA RECEPTORS IN THE BIVALVE *CRASSOSTREA VIRGINICA*

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GABA, an inhibitory neurotransmitter in molluscs and other animals, has not been well studied in bivalves. GABA neurotransmission impairment in humans causes epilepsy. In the bivalve *Crassostrea virginica* serotonin is an excitatory neurotransmitter accelerating gill lateral cell (GLC) cilia beating. This serotonin innervation originates in the cerebral and visceral ganglia. Previous studies demonstrated applying GABA to visceral or cerebral ganglia blocked serotonin's action on accelerating *C. virginica* GLC cilia beating. Additionally, the GABAa receptor antagonist bicuculline methchloride blocked the action of GABA. HPLC detected GABA in ng amounts in *C. virginica* ganglia. Immunofluorescence histochemistry showed GABA neurons present in the ganglia and that some serotonin neurons had GABA receptors on their soma. The *C. virginica* genome has begun to be mapped. To test the hypothesis *C. virginica* contains GABA receptor genes and these receptors are similar to those of other animals, BLAST searches of the NCBI database were conducted using DNA and protein sequences from *C. virginica* for GABAa and GABAb receptor genes. Matches for GABAa and GABAb receptor genes were found on *C. virginica* chromosomes 3 and 5, respectively. BLASTS of other animals found matches with similarities to GABAa and GABAb receptors of *C. virginica*. This study complements the studies demonstrating the presence and function for GABA in *C. virginica*. It shows *C. virginica* genome contains genes for GABA receptors similar to other animals. This information is valuable as it shows the simple nervous system of *C. virginica* can be used to conduct studies on GABA neurotransmission.

VARYING RESPONSES OF DIFFERENT OYSTER SPECIES DURING FIELD TRIALS AND INJECTION CHALLENGES WITH OSHV-1 VARIANTS

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Ostreid herpesvirus 1 (OsHV-1) variants, particularly the microvariants (μvars), are virulent and economically devastating viruses of oysters. Although all life stages of oysters are affected, usually larvae and juveniles experience the highest mortality. OsHV-1 μvars have spread rapidly since 2008 damaging aquaculture industries around the world, particularly in Europe, Australia and New Zealand. In Tomales Bay, Califorinia, where a non-μvar OsHV-1 variant is established, three stocks of Pacific oysters and the Kumamoto stock were deployed. The Pacific oysters experienced higher mortality (64-99%) than the Kumamotos (∼25%). Injection trials with the French and Australian μvars, compared effects in stocks of Pacific oyster (n=3), *Crassostrea gigas*, eastern oyster (n=2), *C. virginica*, stocks and a Kumamoto oyster (n=1), *C. sikamea* stock. Each 'exposed' oyster was injected with ~106 virus particles and control oysters were injected with artificial seawater. No mortality was observed in control oysters. One *C. virginica* stock suffered ∼10% mortality with both μvars, while two *C. gigas* stocks suffered 75-90% mortality. One *C. gigas* stock had relatively low mortality when challenged with the Australian μvar (∼22%) and much higher mortality with the French μvar (∼72%). Conversely, for *C. sikamea* there was lower mortality when exposed to the French μvar (∼22%) as compared to the Australian μvar (∼~44%). Dead oysters had ~1,000X higher viral loads than survivors. Field mortality correlated with laboratory mortality of the French μvar (69%), but not the Australian. These variations have important implications for selective breeding strategies for OsHV-1 resistance with different species and in different regions.

HORIZONTAL PLASMID TRANSFER BETWEEN *VIBRIO PARAHAEMOLYTICUS* PROVIDES A NOVEL MECHANISM FOR GENETIC EXCHANGE AND ENVIRONMENTAL ADAPTATION MEDIATED BY THE INSERTION SEQUENCE IS*VAL1*

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The foodborne pathogen, *Vibrio parahaemolyticus*, has recently gained particular notoriety because it causes acute hepatopancreatic necrosis disease (AHPND) in shrimp, which has caused significant economic losses in shrimp industry. Previous studies have shown that the specific AHPND-causing *V. parahaemolyticus* strains acquired a 63- to 73-kb plasmid, which harbored binary toxin PirAB^{vp}. These toxins have been determined to be the primary virulence factors causing AHPND. In our study, a consecutive monitoring in a shrimp farm was conducted to observe the horizontal plasmid transfer. Results showed that *pirAB*-negative (avirulent) strains were present in the environment until the introduction of *pirAB*-positive strain. Afterwards, horizontal plasmid transfer occurred between different genotypes of *V. parahaemolyticus*. Thereafter, an insertion sequence IS*val1* excised from the *pirAB*-positive plasmid, resulting in several insertion and deletion events in the chromosome of *V. parahaemolyticus*, including an 11 kb deletion regulating cell mobility and the production of capsular polysaccharides. Phenotype assays confirmed that this deletion enhanced biofilm formation, providing a novel mechanism for environmental adaptation. To confirm the transferability of IS*Val1* from plasmid to chromosome, a co-culture experiment of *V. parahaemolyticus* with IS*Val1*-containing plasmids was conducted. The results confirmed that IS*Val1* was transferred from the constructed plasmid in 6.9% of *V. parahaemolyticus* colonies. In conclusion, the introduction of the AHPND-associated plasmid offers a novel mechanism of genetic exchange mediated by insertion sequences and improved the fitness of *V. parahaemolyticus* in a harsh environment.

ANALYSIS OF CARBON AND NITROGEN ISOTOPES TO ASSESS NUTRIENT LOADING AND ITS EFFECTS ON OYSTER ACTIVITIES IN REHOBOTH BAY, DELAWARE, USA

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Since the 1950s, losses in the Delaware Inland Bays (DIB) oyster population have weakened the Bays' ability to tolerate nutrient pollution. Newly-established oyster aquaculture sites and artificial oyster reefs will aid in bay restoration but require monitoring to identify nutrient pollution sources. Thus, this research focuses on comparing nitrogen and carbon isotope data from terrestrial, estuarine, and biological sources within Rehoboth Bay, Delware to identify possible nonpoint pollution sources through nutrient tracking.

The primary objective is to identify non-point pollution sources through monitoring of field sites. It is hypothesized that the sites near the wastewater plant and *marina* near the agricultural area will have high nutrient loading; these sites may have higher isotopic values and poorer water quality than other sites. Samples of soil, submerged sediment, water, and oyster tissues were collected across the bays and analyzed for stable nitrogen and carbon isotopes. Water quality parameters were monitored weekly at aquaculture sites, artificial oyster reefs, and non-reef locations, and nutrient tests identified concentrations of nitrogen, nitrate, ammonia, calcium carbonate hardness, alkalinity, and orthophosphate. Total suspended solids, stable isotopes, and biological analyses were conducted following the standard protocols previously published.

Preliminary results showed improved water quality at aquaculture sites and highlighted oyster effectiveness on ecosystem restoration; however, nutrient test analyses indicated a necessity for increased monitoring and data analysis at sites for clearer identification of non-point pollution sources. Results will aid in the creation of best management practices for oyster aquaculture and bay health restoration.

EVALUATING ALTERNATIVE MARKETING OPPORTUNITIES TO STRENGTHEN THE SOUTH CAROLINA MARICULTURE INDUSTRY

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The South Carolina Sea Grant Consortium has implemented a direct marketing support project for South Carolina mariculture industry, to explore both immediate and long-term solutions to the impacts of COVID-19. Recent data and interviews with seafood producers have revealed a need for alternative marketing options to build resiliency and to capitalize on shifting consumer trends. Alternative supply chains would allow new opportunities to sell an increasing supply of single-shell oysters and other regional seafood products important to the coastal economy of South Carolina. The market potential—along with obstacles to such an operational shift —will first be characterized. Findings will then help guide producers in their decision of whether to invest more into direct-marketing operations. The following three-pronged approach is used:

1. *Understand consumer preferences for direct-to-consumer (DTC)*: a team of marketing researchers are investigating the potential for DTC cultured (and feasibly cultured) seafood products, including oysters, clams, blue crabs, and shrimp. Interviews and consumer surveys will assess demand, consumer preferences, and willingness-to-pay for DTC seafood.
2. *Help seafood producers to navigate direct marketing regulatory considerations:* Researchers will compile regulatory considerations into a direct marketing guide for seafood producers, with guidance on obtaining licenses to sell directly (e.g. roadside sales, food trucks, and online sales).
3. *Direct support of online marketing tools and methods:* A committee of seafood stakeholders are developing direct marketing tools that support on-line sales, standards and best practices for delivery-based packaging materials, and considerations for logistical needs.

ABIOTIC AND BIOTIC FACTORS RELATED TO THE PROLIFERATION OF VIBRIO SPP. THAT CAUSE AHPND IN THE WHITE SHRIMP, *PENAEUS VANNAMEI* (BOONE, 1931)

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Acute hepatopancreatic necrosis disease (AHPND) causes a high mortality in white shrimp and the principal causal agent is *Vibrio parahaemolyticus*. Several works have described abiotic factors that influence the disease to cause toxicity and mortality in shrimp, as well as the dynamics, evolution and ecology of the *Vibrio* genus, as well as biotic factors, such as microbial community management in order to obtained a mature microbial community (K strategist); however, the relationship, type and amount of nutrients involved in the proliferation of *Vibrio* spp., as well as the structure of the microbiological community during a mortality event, are still unknown. The objective of this work was to determine the principal abiotic and biotic factors causing the proliferation of *Vibrionaceae* (AHPND$^+$). This was determined by nutritional and environmental gradients with growth kinetics, where it was obtained as a result that the optimal pH was 7.5 to 8, and temperature 30°C, for nutritional factors organic nitrogen hydrolysate casein, for carbon malt extract and monoammonic phosphate and some microelements such as Iron (Fe^{2+}) are key in the proliferation of these genus of bacteria, and causes a massive proliferation.

THE *FEM-1* GENE AND ITS ANTISENSE TRANSCRIPT MAY HAVE A FUNCTION IN SEXUAL DEVELOPMENT OF THE PACIFIC WHITELEG SHRIMP, *PENAEUS VANNAMEI*

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The *fem-1* gene in Caenorhabditis elegans is involved in sex differentiation and it is specifically required for all aspects of male sexual development. A *fem-1* transcript (Genbank accession # KF573432, 3778 bp) was found in transcriptomic libraries of the Pacific whiteleg shrimp *Penaeus vannamei*. In this study, the full-length cDNA of the *fem-1* (*Pvfem-1*) gene was isolated from *P. vannamei*, and the translated protein (AHA90856) shows a significant structural similarity with the C. elegans *Fem-1* protein. *Pvfem-1* expression was evaluated by means of quantitative polymerase chain reaction (qPCR) and *in situ* hybridization during embryogenesis, larval development, multiple tissues of juveniles, subadults, and adult males and females, and gonads of both genders in subadult and adult life stages. When quantified by qPCR, *Pvfem-1* was found expressed in juveniles, subadults and adults in brain, intestine, hepatopancreas, and in the gonads of both genders in subadults and adults. *In situ* hybridization allowed for an interesting discovery: a natural antisense transcript (NAT) of the *Pvfem-1* that was found highly expressed in the oocyte nucleus of subadult female shrimp gonads. No NAT was seen within oocytes of adult females, although it was detected in follicular cells, suggesting a possible post-transcriptional regulation of the sense *Pvfem-1* in female gonads. Conversely, in males, no NAT was observed, and the sense *Pvfem-1* was found expressed in spermatogonia of both, subadult and adult shrimps, indicating a function of PvFEM-1 protein in male sexual differentiation and gamete generation.

OPTIMIZING BATCH-CULTURE CONDITIONS FOR LARVAE OF THE LION'S PAW SCALLOP, *NODIPECTEN SUBNUDOSUS*

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Mariculture of the large subtropical scallop, *Nodipecten subnodosus*, has experienced increased interest due to overexploitation of wild populations and the lack of a reliable hatchery production technology. The combined effects of larval density (LD = 5, 10, and 15 mL^{-1}) and food concentration (FC = 15, 30, 45, and 60 cells µL^{-1} of *Tisochrysis lutea* and *Pavlova pinguis*) on survival (S), growth and ingestion rates (IR) were assessed in small vessels ($\leq$ 1L). Three additional cohorts were batch-reared in 500-L tanks at 26oC. Lowest S (19 - 22%) was observed at 15 cells µL^{-1}, while S $>$ 50% prevailed at ³ 30 cells µL^{-1}. Both LD and FC significantly affected gross growth rate (GGR). Mean GGRs of 6.1 to 6.9 µm d-1 were obtained at 10 - 15 larvae mL-1 and 45 to 60 cells µL^{-1}. Larval IR increased with increasing FC, reaching asymptotic values (9.7 to 11.5 cells larva^{-1} h^{-1}) at 45 and 60 cells µL^{-1}. Development lasted 12 to 15 days in 500-L trials, but half of this time corresponded to the D-stage, indicating slow development of this first-feeding stage. Maximal S to pediveliger was 22-27%, while GGR (7.8 to 8.8 µ d^{-1}) did not differ significantly among cohorts. The combined experiments produced consistent growth results and actual food requirements were assessed for the first time throughout larval development, thus contributing to the optimization of future hatchery protocols.

HARNESSING THE POWER OF SINGLE-CELL RNA SEQUENCING TO CONTROL REPRODUCTIVE DEVELOPMENT IN BIVALVES

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Sterile or non-reproductive shellfish are both a market driven need and an ecologically sustainable approach to increasing food production via aquaculture. Current methods for inducing sterility in bivalve shellfish focus on ploidy manipulation. An alternative approach is the induction of sterility by inactivation of genes essential for germ cell formation and development. The power of this biotechnological approach has been realized recently in some finfish species, where suppression of a critical germ-cell specific gene, *dead end* (*dnd*), results in fish with no detectable gametes. Given the recent advances in finfishes, the shellfish industry is now poised to adopt these technological advances. Unfortunately, the use of this technology in shellfish is hampered by a lack of knowledge of the genes essential for primordial germ cell (PGC) specification in bivalves. To overcome this challenge, single-cell RNA-Seq (scRNA-seq) was used to identify genes involved in PGC specification. This cutting-edge approach uses high-throughput sequencing to identify genes expressed in individual cells; scRNA-seq is particularly suited to identify PGC markers in bivalves, as germ cell precursors represent a very small number of cells at these early developmental stages. To date, more than 25,000 cells in early Pacific oyster embryos have been transcriptionally profiled. Cells associated with PGC formation were tracked using the germ cell marker gene, vasa, and candidate genes, uniquely expressed in the germ cell lineage, were identified. These candidate genes will be used in experiments designed to temporarily block their expression in embryos and evaluate their efficacy in disrupting reproductive development in shellfish.

COMPARING GROWTH RATES OF BANDED TULIPS (*CINCTURA HUNTERIA*) USING THREE METHODS

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Banded tulips can be found in marine waters of the United States from North Carolina to Texas. The taxonomy remains fluid and includes recent descriptions from shallow and deeper waters that are at minimum forms but are currently described as unique species. Biological studies that focus on any of the species are limited.

Growth rates of the most frequently encountered estuarine species *Cinctura hunteria* (G. Perry, 1811) have been measured in Tampa Bay, Florida using three methods. Monthly mark-recapture and length-frequency analysis were attempted in three habitats: seagrass, oyster reef, and open sand. Samples were also collected to analyze reproductive activity and size at maturity. Growth of individuals in a laboratory was recorded weekly.

Preliminarily, observations of length frequencies in the field suggest the highest growth rates, followed by growth rates of marked and recaptured snails, with growth in the lab being slowest. Gender could be differentiated in the smallest samples collected, 25-30 mm, but mature specimens may not occur until sizes exceeding 40mm. Reproduction appears to peak in December through February. All of the analyses are ongoing.

NITROGEN BIOEXTRACTION BY JUVENILE ALEWIFE FLOATERS, *UTTERBACKIANA IMPLICATA*, DURING POND REARING IN THE DELAWARE RIVER BASIN

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Freshwater mussels are filter-feeding bivalves that occupy diverse freshwater environments. Nationwide, mussel assemblages are declining in range, abundance, and species richness. Restoration can involve reintroduction of mussels to historical ranges. Reintroduction success (i.e. survival, persistence) depends on both habitat suitability and size of animals used. Juvenile mussel survival in nature is thought to be low but advances in hatchery spawning and pond rearing have significantly increased survival. Pond rearing can raise hatchery-spawned mussels to sizes appropriate for release, presenting an opportunity for transient ecosystem services in eutrophic ponds. Hatchery-spawned Alewife Floater mussels (*Utterbackiana implicata*), 1-3 years in age, were pond-reared in New Castle County, Delaware beginning in 2017. The filtration of particulate nitrogen (PN), and its partial assimilation into biomass, by over 8,000 of these mussels that remain in the rearing pond as of December 2020 was calculated to quantify one aspect of PN removal as an ecosystem service. Final nitrogen contents of *U. implicata* tissues and shells averaged 6.90% w/w and 0.65% w/w of dry biomass, respectively, and estimated yearly averaged clearance rates were 0.88 L/hr per gram dry tissue. This cohort of mussels had an average shell length of 44.19 mm, 262 g of nitrogen accrued in biomass, and filtered 735 g of PN per year. With mussel relocation for restoration projects, the sequestered nitrogen is permanently removed from rearing ponds. These data suggest that tangible water quality benefits could be realized in rearing ponds depending on scale and duration of mussel residency.

TAKING THE “X” OUT OF QPX: COMPLETION OF THE LIFE CYCLE AND ERECTION OF A NEW GENUS AND SPECIES, *MUCOCHYTRIUM QUAHOGII*, FOR THE NORTHERN QUAHOG (= HARD CLAM) PATHOGEN

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Quahog Parasite Unknown (QPX) is a facultative parasite of the northern quahog (= hard clam), *Mercenaria mercenaria*. Although it has been observed in clams since the 1960s and cultivated since the 1990s, conflicting reports on important aspects of its biology have prevented its formal description. 18S rRNA gene sequences identify QPX as a thraustochytrid (Labyrinthulomycetes), but its production of copious mucus is atypical for this group. There are also conflicting reports about whether QPX shares common features of thraustochytrids, such as the production of an ectoplasmic net and zoospores.

Through culture manipulation demucusing and washing of thalli (vegetative cells) and sporangia, zoospores were successfully and reliably produced in multiple strains from several geographic locations, including strains that were isolated over 20 years ago, as well as newly isolated strains. Zoospores demonstrated no attraction to or preference to settle on pine pollen, clam tissue, or sand. The need for complete demucusing to trigger zoosporulation in cultured cells raises new questions about mucus production and its influence on QPX disease in clams and the QPX organism in the environment.

Further, this study describes new aspects of the life cycle not previously observed, including a secondary replication pathway, production of both non-motile spores and motile zoospores, cyst and protoplast stages. As the mechanism of QPX disease transmission in hard clams remains unknown, this research opens new avenues into understanding disease pathogenesis and dynamics. Finally, this study provides a formal species description and erection of *Mucochytrium quahogii* gen. nov. sp. nov. to accommodate this unusual thraustochytrid.

HANDBOOK OF PATHOGENS AND DISEASES IN CEPHALOPODS

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Cephalopods are valuable seafood for human consumption, good candidates for aquaculture and interesting models for research. The recent inclusion of cephalopods in the Directive 2010/EU regulates the use of animals for scientific purposes and obliges researchers to promote the best health and welfare practices during aquarium maintenance. The identification of pathogens and produced diseases are consequently of major interest to improve the cephalopod welfare and husbandry.

Despite the increased interest in cephalopods as sea food, and the recommendations of FSA on parasite risk in fishery products, currently only fragmentary information on pathogens and diseases in cephalopods exists. This book has been designed as a short, easy to follow “handbook” with the aim of facilitate the identification and description of the different organs as well as pathogens and diseases affecting the most representative species of cephalopods focused on *Octopus vulgaris*, *Sepia officinalis*, and *Loligo vulgaris*. The study is based on photographs at macroscopic and histological level in order to illustrate the role of the most important pathogens and related diseases. The reader is able to familiarize with functional anatomy, necropsy and general histology of adults and paralarvae, as well as with the identification of different pathogens and pathologies. This work is thus a guide for the diagnosis of cephalopod diseases. Besides including pathogens for non-European cephalopod species, it also provides a useful contribution encouraging marine pathologists, parasitologists, veterinarians and those involved in fishery sanitary assessments, aquarium maintenance and aquaculture practices aiming to increase their knowledge about the pathology of cephalopods.

THE CONNECTICUT RESPONSE TO THE SHELLFISH MARKET COLLAPSE OF 2020

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When the COVID-19 pandemic struck and public health mitigations measures resulted in the closing of restaurants, shellfish aquaculture sales were essentially brought to a halt nationwide. In Connecticut, a major shellfish producing state, sales revenue was down an average of 93% from the same period in the previous year. Greater than 70% of the workforce lost their jobs. Shellfish product was returned or destroyed following delivery to market which represented an additional loss to operations. By the late spring, a large percentage of the cultured oysters reached a size beyond market acceptability. The accumulation of product threatened a loss of space for new crops, and with excess inventory, there was concern about market flooding and subsequent price drops.

A plan was implemented to assist the industry by providing short-term work and income and simultaneously improved the condition of the state's extensive natural shellfish beds. The objectives were to: 1) provide immediate cash flow opportunities, 2) offer alternative marketing strategies for farmed product, 3) minimize product flooding in shellfish markets, and 4) improve the condition of the state's natural beds by employing industry to remove silt, add clean shell and plant oversized market oysters. The overall goal of this effort was to retain Connecticut aquaculture jobs, businesses and revenue, ensuring the long-term economic viability of the industry.

The effort was successful in retaining jobs, providing income and helping to divert a portion of shellfish product into direct-to-consumer markets. It also resulted in the rehabilitation of a significant natural shellfish bed acreage.

A GIS-BASED APPROACH FOR SHELLFISH RESTORATION PLANNING IN CONNECTICUT, USA

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Bivalve shellfish are part of a healthy Long Island Sound and play a role in improving impaired estuarine environments. Natural shellfish reefs and cultivated shellfish beds provide numerous ecosystem services including habitat and food provision for marine organisms, water filtration and erosion control; however, not all of these habitats are in an optimal condition to support the provision of ecosystem services, fisheries or aquaculture production, or their status is simply unknown. Given their ecological and economic importance, environmental managers are developing a plan to conserve, manage and restore Connecticut's shellfish habitats using a GIS-based approach.

GIS-based analyses have proven useful in site selection and prioritization for shellfish restoration efforts in other locales. The process in Connecticut involves an exclusionary or buffer analysis using environmental and human use data to eliminate sites that are unsuitable for restoration, and a site suitability ranking process using shellfish biological factors to identify sites suitable and optimal for shellfish production. The result will be a planning tool that helps regulators identify locations where there may be a higher likelihood of restoration success.

EFFECTS OF FEED RATION ON GROWTH AND GONAD PRODUCTION IN SMALL SEA URCHINS, *LYTECHINUS VARIEGATUS*

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Proper feed management in the culture of aquatic organisms reduces feed waste and cost, preserves water quality, and supports maximal growth of the species. A cost-effective practice provides the lowest ration size that still supports adequate growth of the organism. In this study, two daily rations of a nutrient dense, formulated diet were evaluated for optimal growth and gonad production in small sea urchins of the species, *Lytechinus variegatus*.

Small sea urchins (ca. 23 mm diameter and 5.6 g wet weight) were maintained in recirculating seawater systems and were fed a formulated diet (28.5% protein, 26.8% carbohydrate, 7.7% crude lipid). Individuals were provided a daily ration of either sub-satiation (1.5% body weight day-1 set at Week 0) or *ad libitum* (~3.8% body weight day-1). Individuals were weighed every two weeks, and sea urchins were sacrificed at the end of 8 wk to quantify gonad production.

Overall wet weight gain after 8 wk was higher for individuals fed *ad libitum* (338 ± 48% vs. 228 ± 37% for sub-satiation; mean ± SD, $p < 0.0001$). Estimated production efficiency based on feed proffered was higher for individuals fed a sub-satiation ration (68.2 ± 5.8% vs. 31.0 ± 5.1% for *ad libitum*). Gonad index was higher for individuals fed *ad libitum* (14.5 ± 4% vs. 9.26 ± 2% for sub-satiation) and was higher for females regardless of ration size (13.9 ± 4% female and 9.85 ± 3% male). Overall, the sub-satiation ration minimized feed waste and supported efficient growth and gonad production.

DOES BOAT NOISE DELAY OYSTER LARVAE METAMORPHOSIS?

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A multitude of marine organisms rely on underwater sounds for communication and survival. Previous studies indicate that eastern oyster larvae (*Crassostrea virginica*) attuned to the soundscape of oyster reefs. It is well documented that eastern oyster larvae can wait for preferred environmental conditions before settling, attaching to surfaces, then metamorphosing into spat. Oyster settlement cues include chemical cues, substrate textures, microbial films, light levels and oyster reef soundscapes. Recreational boat noise can mask the oyster reef soundscape, potentially interfering with one of the settlement cues.

In a laboratory experiment, eyed pediveliger oyster larvae were exposed to one of two pre-recorded soundscapes played on repeat through underwater speakers: an oyster reef and an oyster reef masked by recreational boat noise, as well as an ambient noise control. Competent larvae were exposed to the soundscape, in the presence of settlement habitat, for 39 to 49 hours. Afterwards, the number of attached spat and unsettled larvae were counted. It was hypothesized that more larvae would metamorphose into spat in the oyster reef soundscape and less would metamorphose in the boat noise treatment. If larvae exposed to boat noise tend to delay metamorphosis, that could impede recruitment on reefs near highly trafficked boat-ways. Given the millions of dollars invested in oyster reef restoration and living shoreline projects, successful recruitment is imperative. Noise pollution may be an important consideration for project siting.

SPATIAL AND TEMPORAL VARIATION IN GROWTH RATES OF WILD EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) FROM DELAWARE BAY, NEW JERSEY, USA

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Trends in length frequency from an annual stock assessment survey, as well as anecdotal reports from the fishery, suggest growth rates of wild oysters (*Crassostrea virginica*) in Delaware Bay, New Jersey may be increasing. Growth rates are utilized in managing the fishery by providing an estimate of how many oysters are likely to grow to a marketable size in a given season. Growth racks were first deployed on oyster beds in Delaware Bay in 2001, and then again in 2018 and 2019. Deployment sites spanned the salinity gradient. Oysters were initially collected and measured in April or May of each year, tethered to a metal frame, and redeployed on their bed of origin. Racks were recovered and redeployed monthly allowing height to be measured on each individual oyster through the growing season (to November). Mean total growth was calculated for each of three initial size classes (50-57 mm, 57-63 mm, and 63-70 mm). Preliminary results indicate that growth rates have increased since 2001 across all sites. In 2018 and 2019, respectively, oysters from the southernmost site increased in height by 16-30% and 23-37% over the duration of the experiment, while in 2001 oysters increased in height by only 15-24%. Additionally, in all years, growth rates were higher in the lower Delaware Bay, where salinity is higher. Having up-to-date and accurate growth rate estimates is important for managing the oyster resource in Delaware Bay and for informing our understanding of how environmental changes may be influencing the dynamics of the population.

EASTERN OYSTER GENOME CONSORTIUM WORKSHOP

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A recent project by the Eastern Oyster Genome (EOG) led to the development of a reference genome and set of transcriptomes critical to the discovery and analysis of the genetic basis for traits that are important for improving the culture of this species for food and restoration purposes (private and public aquaculture). These traits include, for example, disease resistance, resistance or tolerance to environmental stress, fast growth, and desired shell characteristics. Development of an extensive, genome-wide catalog of functional elements for the EOG would facilitate further application of genomic resources to basic and applied research in eastern oysters, such as genomically-informed approaches in selective breeding and consideration of epigenetic priming approaches to improve the precision and efficacy of breeding. This functional annotation of the EOG will also facilitate understanding of the mechanisms involved in adaptation to a changing environment in this keystone species. The proposed EOG annotation efforts will have synergistic pay-offs by performing informative comparisons with the Pacific oyster genome and the genomes of other commercially important bivalve molluscs, such as mussels and scallops.

Direct involvement of the bivalve research community in tool development and implementation is key to the successful application of these resources. The objectives of this workshop are to: 1) provide training on how to use genomics resources already available in NCBI for the eastern oyster, *Crassostrea virginica*; 2) discuss with representatives from NCBI the needs for improved annotation of the EOG; and 3) coordinate community efforts in the functional annotation of the EOG.

SPATIAL AND TEMPORAL VARIATIONS OF ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*) POPULATION DEMOGRAPHIC CHARACTERISTICS ALONG THE MID-ATLANTIC BIGHT

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The distribution of Atlantic surfclams (*Spisula solidissima*) along the continental shelf of the Mid-Atlantic Bight (MAB) has been routinely surveyed since the 1980s by the National Marine Fisheries Service. The surfclam length and age data obtained from the surveys were binned by decade and survey location and then used to estimate latitudinal variability in growth rate, asymptotic length, and mortality rate. These parameter estimates show north-south differences since the 1980s, with the largest change associated with the surfclam mortality rate in the southern portion of the distribution. The asymptotic length of surfclams and growth rate estimated for the 2010s increased towards the northern end of the distribution. These demographic parameters were input to a surfclam population dynamics model to assess trends in surfclam biomass distribution along the MAB continental shelf from 1980s to the end of 2010s. Simulations indicate that an increase in mortality of about 7%, with no change in growth rate, results in a 16% reduction in surfclam reproductive biomass. This mortality increase is supported by the trends obtained from the stock survey analysis. This level of mortality requires unrealistic increases in growth rates to maintain surfclam densities observed in the historical survey data. This has important consequences for surfclam populations because larger (older) surfclams with slower growth rates contribute to the major fraction of the reproductive biomass. An implication of these results is that environmental conditions that affect surfclam mortality rates, such as warming bottom temperatures, have a disproportionate effect on larger surfclams.

INVESTIGATING THE LIFE HISTORY OF THE ATLANTIC BRIEF SQUID, *LOLLIGUNCULA BREVIS*, FROM THE CHARLESTON HARBOR ESTUARY, SOUTH CAROLINA, USA

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The Atlantic brief squid, *Lolliguncula brevis*, is a euryhaline cephalopod which inhabits estuaries ranging from the Chesapeake Bay to Argentina. In the southeastern U.S., *L. brevis* can comprise a considerable portion of the estuarine animal biomass. Further, historical data collected by the SCDNR Estuarine Trawl Survey indicate that *L. brevis* exhibits spatially-variable size frequency distributions within the Charleston Harbor estuary.

This project seeks to investigate the life history of *L. brevis* collected at four stations along a salinity gradient within the Charleston Harbor. Specimens of *L. brevis* collected in fall of 2020 were assessed to determine size, sex, and maturity. Statoliths were removed to count daily growth increments and determine individual squid ages. These ages were used to calculate the timing of statolith formation during early development which, for the purposes of this study, is currently considered as the time of recruitment. Additionally, buccal tissue samples were analyzed to generate stable isotope ratio values for $\delta^{13}C$ and $\delta^{15}N$ to investigate ontogenetic changes in dietary sources and trophic position, respectively. Male and female squid from these samples ranged in gladius lengths from 2.8 cm to 5.4 cm and 2.5 cm to 8.4 cm, respectively. Statolith-based age determinations revealed ages ranging from 40 to 126 days, corresponding to recruitment in April through August 2020, suggesting highly asynchronous reproduction within the population. Stable isotope analyses are intended to improve our understanding of the influences of an ontogenetic habitat shift from the benthos to the nekton on trophic interactions within the estuarine food web.

OPTIMIZING MABÉ PEARL CULTURE IN THE KINGDOM OF TONGA USING THE WINGED PEARL OYSTER, *PTERIA PENGUIN*

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The winged pearl oyster, *Pteria penguin*, is widely-cultured for the production of high-quality mabé pearls (half-pearls), which provide a sustainable, culturally appropriate income source to many remote coastal communities throughout the Kingdom of Tonga and the Pacific region. However, optimal environmental conditions for *P. penguin* growth and mabé pearl production in Tonga are currently unknown, which limits sector potential and profitability.

This study examines spatio-temporal variation in growth and nacre deposition by *P. penguin* between island groups in Tonga, and its impacts on mabé pearl farm profitability. Growth and nacre deposition of *P. penguin* varied significantly between island groups and was most strongly related to latitudinal variation in water temperature. These results suggest that in oligotrophic marine environments with minimal terrestrial inputs, such as Tonga, water temperature may be the primary environmental condition influencing the growth performance and nacre deposition by *P. penguin*. Culture of *P. penguin* at warmer sites enables pearl production to begin up to 34.2 % (6.5 months) sooner and may reduce mabé pearl production time by 11 - 26 % (1-3 months), thereby increasing annual mabé pearl farm profitability by up to 45 % relative to cooler sites in Tonga. Results of this study inform sector planning, policy development and research prioritization by donors and government bodies to help maximise profitability and livelihood benefits offered by the Tongan mabé pearl sector.

THE DISEASE DIAGNOSTIC DILEMMA: THE USE OF A NOVEL TESTING METHOD FOR DETERMINING DISEASE PREVALENCE AND INTENSITY IN *CRASSOSTREA VIRGINICA*

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Diseases plague every species. Detecting and quantifying the disease causing pathogens in infected tissues is both important and necessary to maintain both natural stocks and a profitable aquaculture industry. The eastern oyster, *Crassostrea virginica*, is one bivalve species that has been infected with many diseases, most notably *Perkinsus marinus* (Dermo). In order to determine infection levels in oysters, the two most common methods are through histological examination of tissue and through Ray's Fluid Thioglycollate Medium (RFTM) assay. Both of these methods are time consuming, and unfortunately can be interpreted differently based on the person reading the results. The lab at Roger Williams University has developed, and are currently using, a technique of extracting the DNA from specific tissue where these pathogens reside, and determining prevalence and intensity using quantitative PCR (qPCR). Plasmid controls of known copy numbers of the pathogen have been developed, which can be used to equate back to the Mackin rating and allow for detection of pathogens down to 10 copies. All diagnostic methods have some flaws, therefore there are limitations to qPCR just as with other stated methods; however, this qPCR method can quickly and accurately determine the abundance of this disease, allowing for a greater amount of monitoring data to be generated for both aquaculturists and regulators, as the environment changes and pathogen ranges grow.

UNLOCKING THE EXOME: EXPLORING *DE NOVO* ASSEMBLY OPTIONS FOR CAPTURE SEQUENCING

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Sequencing the genomes and transcriptomes of non-model organisms has transformed the way ecologists and evolutionary biologists study the marine environment. A major challenge in bioinformatic studies is building robust reduced representation assemblies in the absence of complete, well-annotated genomes. High rates of genetic polymorphism and genomic rearrangements within shellfish populations pose difficult challenges in sequencing. New sequencing methods, such as Expressed Exome Capture (EecSeq), present a unique approach to these challenges. EecSeq has the potential to be applied to any organism, if loci can be efficiently assembled directly from capture reads. This study sought to test a *de novo* assembly and assessment pipeline for EecSeq studies using sample reads from the eastern oyster (*Crassostrea virginica*) to build an exome assembly. Four transcriptome assembly programs (Oases, rnaSPAdes, Trans-ABySS, and Trinity) and one genome assembly program (SPAdes) were utilized to build oyster exomes. To categorize these exome assemblies the number of transcripts, N50 values, annotation rates, BUSCO, and read mapping were used. No single assembly outperformed all others across assessment parameters. The Oases assembly had the highest N50 values (2147 bp) but exhibited an elevated annotation (169,198 genes); while Trans-ABySS annotation (40,964 genes) was closest to the predicted number of oyster genes (55,531 genes) and showed the most complete BUSCO percentages. All EecSeq *de novo* assembly reads mapped reflected the proportional abundance of genes identified in the eastern oyster genome. This study presents compelling evidence that EecSeq can provide a cost and time effective solution for building complete *de novo* assemblies.

UNDERSTANDING EYESTALK NEUROPEPTIDES INFLUENCING VITELLOGENESIS OF THE RED DEEP-SEA CRAB, *CHACEON QUINQUEDENS*

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The eyestalk neuropeptides, including the crustacean hyperglycemic hormone (CHH) neuropeptide family, regulate the vitellogenesis of decapod crustaceans. The red deep-sea crab, Chaceon quinquedens, a data-poor, deep- (>500 m), cold-water species, has supported a small male-driven fishery in the eastern US for over 40 years. Regardless, the reproductive cycle, including vitellogenesis and spawning of the females, is unknown.

This study aimed to determine if molt-inhibiting hormone (MIH) and CHH function in the reproduction of the females with a long-period of a molt cycle. There are two forms of CHH: ChqCHH1 and 2, and an MIH are present in the sinus gland and their cDNA sequences are isolated in the eyestalk ganglia. The amounts of CHH2, the major form, are stored in the sinus gland four times greater than CHH1. MIH transcripts are significantly higher in the eyestalk ganglia of females at stage 3 than 5. The *de novo*, eyestalk transcriptome assembly (159,079 contigs) at ovarian stages 1 and 3 was generated to identify if additional neuropeptides may function in female reproduction. Seven (a total of 34 are identified) candidates are found: MIH, insulin-like peptide-binding protein, CHH, crustacean female sex hormone, and three Allostatins (A, B, and C). The mandibular organ-inhibiting hormone is absent in the assembly.

This study provides an insight into which MIH and other neuropeptides present in the eyestalk ganglia play a crucial role in the reproduction of the female red deep-sea crab, *C. quinquedens*, and possibly those of species with an extended molt cycle.

2018 SUMMER MORTALITY EVENT OF PACIFIC OYSTERS IN BAYNES SOUND IS LINKED TO A SEAWATER TEMPERATURE SPIKE AND INFECTION WITH *VIBRIO* SP.

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The Pacific oyster, *Crassostrea gigas* is cultivated in many regions of the world. In cultivation, adult *C. gigas* are prone to mass mortality events during the summer months. A complex combination of environmental and biological parameters has been suggested as the cause of this disease. In recent years, summer mortality has had a significant economic impact on oyster farms in British Columbia, Canada. From late July 2018 to August 2018, mass mortalities were reported in adult Pacific oysters cultivated in Baynes Sound, British Columbia. Up to 95% mortality was reported in diploid and triploid *C. gigas*. Farmers in Baynes Sound first observed mortalities of adult oysters on the 24th of July, which coincided with a spike in sea surface temperatures (SST) in the Sound above the 90th percentile for three days (SST = 20.9 oC, 2.7 oC above climatology). Histological examination of moribund *C. gigas* collected during the mortality event displayed early stage tissue necrosis combined with systemic bacterial infections comprised of bacteria with uniform short rod-shape morphology. Microbiological characterization, combining 16S rRNA amplicon sequencing with bacterial culture, revealed the microbiome of moribund oysters were dominated by *Vibrio* mediterranei. These observations build upon previous studies that identified summer mortality of *C. gigas* is caused by temperature stress and opportunistic *Vibrio* pathogens.

A NOVEL SOCIAL-ECOLOGICAL CLAM GARDEN SITE SELECTION PROCESS

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Clam gardens are intertidal features modified by Northwest Coastal Indigenous people to enhance clam habitat for optimal shellfish production. The Swinomish Indian Tribal Community (SITC) recently initiated a clam garden project to address declining clam populations and community concerns regarding climate change and ocean acidification. This effort will integrate traditional ecological knowledge into contemporary resource management and climate adaptation strategies, encourage local food security and sovereignty, and promote sustainable seafood production. The SITC Fisheries Department and Community Environmental Health Program have co-designed a social-ecological site selection process focused on community participation to promote the long-term success of the project. This presentation will discuss clam gardening and the SITC work to revive the ancient practice into modern day use.

CONCERNED OYSTERMEN RESTORING ESTUARIES PROGRAM

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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 efforts, oyster reproduction has varied wildly over the last five years from Florida to Texas causing nearly catastrophic consequences to the Gulf oyster community. The goal is to determine the ecosystem service benefits provided using large, single oysters, obtained from private commercial aquaculturists.

The objectives are to: 1. Partner with the Alabama Marine Resources Division and the Mississippi Department of Marine Resources to identify appropriate sites to place oysters. 2. Purchase oysters from farmers in Alabama and Mississippi to provide up to 450,000 3-plus inch farm-raised oysters for enhancement. 3. Monitor the farmed oysters' growth and survival and the ecosystem services they provide. 4. Conduct stakeholder engagement about the program. Participating oyster farmers are providing oysters to the appropriate state agencies (AL MRD and MS DMR) for deployment at designated sites.

In addition to the direct support to oyster farmers during the pandemic by paying a net price of $0.33 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. Thus far, five Alabama have deployed 42,000 oysters worth $13,860.00 and two Mississippi farmers have deployed 18,000 oysters worth $5940.00.

A METHOD TO PERTURB THE GUT MICROBIOME OF THE BLUE MUSSEL (*MYTILUS EDULIS*) EXPERIMENTALLY WITH ANTIBIOTICS

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Over the last decade, it has become evident that animal-associated microbiomes often contribute significantly to host physiological processes. The interactions between bivalve molluscs and their gut microbiota are not well-understood. The contribution of gut microbiota to host physiology can be assessed experimentally using model animals with perturbed microbial communities. Previous methods to manipulate the microbiome of bivalves lack standardization and, often, verification of successful disturbance. The goal of this study was to evaluate antibiotic administration as a method for perturbing the gut microbiome of bivalves by delivering an antibiotic mixture to blue mussels for 21 days and probing effects on microbial abundance, diversity, and taxonomic composition. Mussels were administered antibiotics in isolation, and stringent sterilization methods were employed, which included sterilized seawater and microalgal food. The perturbation period was successful; antibiotics significantly lowered microbial abundance and species richness, and significantly altered community composition. Future research that aims to experimentally perturb the microbiomes of suspension-feeding animals should incorporate aspects similar to this protocol. Namely, antibiotic administration should include multiple broad-spectrum antibiotics, be conducted on isolated animals, and take place in conditions of enhanced sterility. Additionally, future studies must include high-throughput DNA sequencing verification that the antibiotic perturbation was successful. This protocol for disturbing the gut microbiome will likely work on other groups of suspension-feeders, and the resulting animals are eligible for use in subsequent experiments. This method will serve as a powerful tool in future endeavors to investigate the symbiosis between bivalves and their gut microbiome.

UNIQUE MICROBIOMES OF OYSTER GILL TISSUE AND PALLIAL FLUID ARE SPECIFIC TO SITE AND SEASON

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Eastern oysters, *Crassostrea virginica,* are ecologically and economically valuable organisms in coastal Louisiana. This study analyzed the interaction of local environmental conditions and *Perkinsus marinus* infection intensities on the microbiomes of oyster gill tissue and pallial fluid. Wild oyster broodstock were collected from Lake Calcasieu and spawned at the Louisiana Sea Grant Grand Isle Hatchery. Offspring were reared in common garden at both a high salinity and a low salinity site for 14 months. Following that growth period, oyster gill tissue and pallial fluid samples were collected in July and again in October of 2018. Microbial DNA was extracted from gill tissue and pallial fluid samples and sequenced using Illumina HiSeq2000. The progression of *Perkinsus marinus* infection (hypnospores g^{-1} wet tissue) was measured for each individual sampled. By comparing microbiomes from gill tissue and pallial fluid between different outplant locations, across seasons, and a range of infection intensities, we were able to gain an initial understanding of the abundance and diversity of the oyster gill and pallial fluid microbiomes in the northern Gulf of Mexico. The diversity data identified unique microbial communities for gill tissue and pallial fluid, location specific microbial community structure, and distinct microbiomes for the two sampling months. From the diversity analyses, there is no evidence that *Perkinsus* infection influences the microbiome of either gill tissue or pallial fluid; however, a Weighted Network Analysis (WGCNA) of these data identified minor correlations between infection intensity, site, month, and sample type with KO metagenome functional groups.

BREEDING EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) FOR HIGH-SALINITY ENVIRONMENTS

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Eastern oyster breeding at Rutgers University has focused on disease resistance in mesohaline (18-23) environments of Delaware Bay. As oyster farming in coastal bays increases, there is a need to develop varieties that perform well in high-salinity environments. In 2019, diverse genetic lines representing northern, southern and New Jersey populations and their hybrids were produced using wild high-salinity eastern oysters collected from Maine to South Carolina. A Rutgers disease-resistant strain, its hybrids with the New Jersey line and triploid crosses were included for comparisons. Replicates from seven diploid and three triploid crosses were deployed at three high-salinity sites (Middle Island, Barnegat Light and Rose Cove) in Barnegat Bay and a moderate-salinity site (Cape Shore) in Delaware Bay. At 17 months old, oysters varied significantly ($p<0.001$) in size among sites and groups. Middle Island and Barnegat Light provided faster growth than Rose Cove and Cape Shore. All triploid crosses were significantly ($p<0.001$) larger than diploids by an average of 24% in shell height and 83% in whole body weight. Among diploid crosses, the New Jersey line, the Rutgers disease-resistant strain and their hybrids generally grew better. Mortality was lower at high-salinity sites in Barnegat Bay than at Cape Shore (22.4%) in Delaware Bay with the lowest observed at Rose Cove (4.9%). Mortality differences among most groups were not significant. While full evaluation to market size is yet to be conducted, these preliminary results suggest that triploids will outperform diploids at all four sites and some diploid crosses will outperform others.

FROM SEQUENCE TO CONSEQUENCE: GENOMIC SELECTION TO EXPAND AND IMPROVE SELECTIVE BREEDING FOR THE EASTERN OYSTER

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The sustainable development of the Eastern oyster aquaculture industry depends on continued improvement of cultured stocks through advanced breeding technologies. The Eastern Oyster Breeding Consortium (EOBC) was formed to advance genetics and breeding of the eastern oyster for the aquaculture industry. Members of the EOBC have developed oyster strains with improved disease resistance through selective breeding and sequenced the Eastern oyster genome. In this project funded by the Atlantic States Marine Fisheries Commission, the consortium seeks to accelerate and expand eastern oyster breeding for all growing regions on the east coast by developing, testing, and verifying genome-based breeding. One objective is to develop high-density single-nucleotide polymorphism (SNP) arrays for efficient genotyping. Oysters from diverse populations have been resequenced for SNP discovery, and a 600k SNP array have been designed. The 600k array is being used to characterize wild and selected populations and for the designing of a smaller breeding array. These genotyping platforms will be used to implement genomic selection at several breeding programs and to establish genotype-phenotype association for key production traits such as resistance/tolerance of diseases, low salinity, ocean acidification and hypoxia. Lines produced by genomic selection and traditional breeding will be evaluated in seven states along the Atlantic coast to identify best performing stocks for each region. The development and implementation of these tools are expected to accelerate genetic improvement of the eastern oyster, by streamlining the breeding process, increasing selection precision, lowering long-term costs and enabling advanced breeding across the region.

STRESS TOLERANCE IN DIVERSE LINES OF EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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Stress tolerance is an important production trait of cultured oysters that have to cope with large fluctuations in temperature and salinity. Stress tolerance was studied in ten diverse lines of eastern oyster (*Crassostrea virginica*) that were produced as part of a breeding program and reared in three locations. The lines consisted of mass-spawned groups from Rutgers disease-resistant oysters (RR), wild New Jersey oysters (JJ), wild oysters from Maine and Massachusetts (NN), from South Carolina, North Carolina, and Virginia (SS), three hybrid (JN, JR, JS) and three triploid crosses (3GR, 3JR, 3RR). Oysters were spawned in 2019 and cultured on farms at Middle Island, Rose Cove, and Cape Shore for 12 months before being collected from the field for this study. Twelve oysters from each group and location were challenged with a low salinity of 5 and a warm temperature of 30°C in separate raceways for 23 days with a total of 360 oysters per treatment. Dead oysters were removed daily and number of alive oysters were recorded for each group. Kaplan-Meier survivability and log-rank tests were performed for each treatment using group and location as factors. For both low salinity and heat stress, survival probability was significantly affected by locations ($p<0.0001$). Group has a significant effect on survival probability under heat stress ($p<0.002$), but not under low salinity($p=0.063$). These results indicated that culture environment has a major effect on the fitness or stress tolerance of Eastern oysters, and genetic differences may also play a role in heat tolerance.

SUPPORTING OYSTER AQUACULTURE AND RESTORATION, PROGRAM PROGRESS, AND FUTURE DIRECTIONS

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By April 2020, it had become obvious that Covid-19 would have severe market impacts for shellfish growers. 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, 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 enormous cooperation and support from all participants.

Approximately $2 million was secured for the oyster purchase program across seven states, Maine, New Hampshire, Massachusetts, New York, New Jersey, Maryland, and Washington, with each state having unique considerations. To minimize biosecurity risks, transport distance was minimized, and strict pathology testing, biofouling mitigation and screening implemented where necessary. Biosecurity was the main constraint on grower eligibility, limiting access to the program. The constraints and program rollout by state will be described with progress toward targets of 5 million oysters purchased, from 100 companies, impacting 224 jobs and restoring 27 acres of reef.

The Shellfish Growers Resiliency Fund currently has $1 million and a Request for Proposals will be announced in March 2021. Funded projects will help build industry resilience. It is anticipated proposals may include developing product diversification, market diversification and payment for ecosystem services such as nutrient mitigation.

SPILLOVER OF SEA SCALLOPS FROM ROTATIONAL CLOSURES IN THE MID-ATLANTIC BIGHT (USA)

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Evidence for larval spillover (increased recruitment outside the closures) of Atlantic sea scallops (*Placopecten magellanicus*) from rotational closures in the Mid-Atlantic Bight were examined using a 40 year fisheries survey time series and a larval transport model. Since the first closure of the Hudson Canyon South area in 1998, mean recruitment in the two areas directly down-current from this closure, Elephant Trunk and Delmarva, increased significantly by factors of about seven and two, respectively. Stock-recruit plots indicate that low biomasses in Hudson Canyon South were associated with reduced mean recruitment in Elephant Trunk and Delmarva. Simulations indicate that larvae spawned in Hudson Canyon South often settle in the two down-current areas, and that model-estimated settlement (based on gonad biomass in Hudson Canyon South and year-specific larval transport between the areas) are correlated with observed recruitment. This study gives strong evidence that the rotational closure of Hudson Canyon South has induced increased recruitment in down-current areas.

ATLANTIC SURFCLAM HARVEST MANAGEMENT: HOW MANY SPECIES? HOW MANY MANAGEMENT UNITS?

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For commercially harvested organisms, understanding population structure and connectivity is key for metapopulation management to maintain sustainable harvest protocols. Additionally, differentiating cryptic marine species is crucial for proper harvest and conservation management. High-throughput genomic DNA sequencing offers a powerful tool for studying metapopulation structure and gene flow among marine populations. Similarly, genomic data can unambiguously identify cryptic species and their hybrids, as well as estimate the relative roles of genetic drift and selection generating divergence. Commercially valuable offshore populations of *Spisula solidissima solidissima* surfclams are broadly distributed from New Brunswick to the Mid-Atlantic Bight. They also occur inshore where they grow to more modest size, similar to the maximum size of its sister taxon, *Spisula solidissima* similis, which is restricted to nearshore waters. Recent genetic analyses indicate these two taxa are sympatric in the nearshore waters of southern New England and New York. Little is known about gene flow connectivity among populations of either taxon, nor do we know id hybridization occurs in sympatry. Small-scale studies to date have had limited population and genomic sampling to address these questions. This presentation will constitute a progress report on sample collections and genomic analyses of surf clams to address the above questions, funded by the Mid-Atlantic Fisheries Management Council. Primary focus will be on development of markers to test for hybridization and a comparison of the transcriptomes from these two taxa.

THE SEASONAL ECOLOGY OF *VIBRIO PARAHAEMOLYTICUS* IN A NEW ENGLAND ESTUARY

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The emergence and establishment of *Vibrio parahaemolyticus* as a causative agent of shellfish-borne illnesses in the northeast United States has stimulated keen interest in understanding the environmental conditions that associate with this human health risk. The application of environmental indicators such as water temperature and salinity have not been completely successful for preventing shellfish consumers from becoming sick from pathogenic *V. parahaemolyticus*. A wide range of ecosystem variables have been reported to affect *V. parahaemolyticus* dynamics and little is known about the significance of zoo- and phytoplankton in the northeastern US. Concentrations of *V. parahaemolyticus* in the Great Bay Estuary (GBE) are highly seasonal and modeling approaches like harmonic regression provide the structure to untangle the complexity of the variables contributing to *V. parahaemolyticus* dynamics in the GBE. Recently published forecasting approaches with time series analysis were further developed to produce a holistic evaluation of the seasonal ecology of *V. parahaemolyticus* concentration in the GBE. Three years of plankton community analysis, water quality, and *V. parahaemolyticus* concentrations in water, sediment, and plankton were evaluated for seasonality using harmonic regression, photoperiod models and multivariate clustering methods to provide insight into the variables that relate to *V. parahaemolyticus* dynamics in oysters. Changing climate conditions are a major factor affecting the ability of *V. parahaemolyticus* to persist in new locations, especially in temperate regions. Analytic approaches like those presented produce standardized outcomes that are transferable to new locations and improve our understanding of the seasonal dynamics that contribute to risk for *V. parahaemolyticus* disease.

EFFECTS OF MICROALGAL DIETS ON GROWTH, DEVELOPMENT, AND SURVIVAL OF NORTHERN QUAHOG (=HARD CLAM) *MERCENARIA MERCENARIA* LARVAE

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Although culture of the northern quahog (= hard clam), *Mercenaria mercenaria*, larvae is almost entirely dependent on live microalgae, limited research has been conducted with regard to increasing larval production through optimization of microalgal diets, and current hatchery practices are primarily anecdotal.

Larval growth, development, and survival were evaluated in this study using six dietary treatments consisting of various combinations of *Isochrysis galbana* (clone T. Iso), *Chaetoceros gracilis* and Chaetoceros muelleri at 2-14-days post fertilization. Significantly higher growth, development, and survival were achieved by feeding larvae equal proportions of T. Iso and *C. gracilis*. About 15% higher growth and 10% higher survival of larvae were achieved using bi-species T. Iso and *C. gracilis* diet compared to mono-species T. Iso. In a bi-algal diet, *C. gracilis* performed better than *C. muelleri* when either of them was combined with T. Iso. An initial diet of T. Iso alone, followed by gradual step-wise addition of diatoms did not enhance performance compared to equal proportions of T. Iso and *C. gracilis* diet for the entire duration of larval period. This study indicated that feeding T. Iso and *C. gracilis* in combination increased hard clam larval production compared to feeding T. Iso alone or in combination with *C. muelleri*.

THE INTERACTIVE EFFECTS OF TITANIUM DIOXIDE NANOPARTICLES AND LIGHT ON FERTILIZATION AND EMBRYOGENESIS ON THE PACIFIC OYSTER (*CRASSOSTREA GIGAS*)

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Titanium dioxide nanoparticles (n-TiO_2) found in paints, sunscreens, and skin-care products are highly photoreactive, and generate reactive oxygen species when exposed to ultraviolet radiation. Upon entering the marine environment through product usage and industrial wastewater, n-TiO_2 quickly agglomerate and settle to the bottom, exposing benthic organisms. In nearshore waters, particles are continually re-suspended by tidal cycling and storm events, and therefore, planktonic organisms are also vulnerable to exposure of irradiated n-TiO_2. The Pacific oyster (*Crassostrea gigas*) is of high economic importance and provides crucial ecosystem services, including maintaining water quality in the Bay of Brest by filtering ca. 30% of the total volume daily. Previous studies have shown that irradiated n-TiO_2 can arrest development in mussel larvae, and exposure to other emerging contaminants affects the fertilization and embryogenesis of *C. gigas*. This study assessed the effects of n-TiO_2 and natural levels of light on fertilization yield and larval development in *C. gigas*. Adult gonads were stripped and gametes were collected for fertilization and embryo-larvae assays carried out in light and dark conditions with exposure to bulk- and n-TiO_2. There was a dose-dependent response of n-TiO_2 on the fertilization success of oyster oocytes. Additionally, n-TiO_2 reduced the number of normal D-larvae compared to bulk TiO_2 and control treatments. There was no effect of n-TiO_2 in the dark exposures. These results suggest that n-TiO_2 have the potential to limit reproductive success in oysters under natural levels of light.

OCEAN QUAHOGS: A GLIMPSE INTO THE POPULATION STRUCTURE OF THE LONGEST-LIVED, NON-COLONIAL ANIMAL ON EARTH USING ONE OF THE LARGEST AGE DATASETS IN THE WORLD

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The ocean quahog (*Arctica islandica*) is the longest-lived bivalve on Earth, with individuals often exceeding 200 years of age along the eastern United States' continental shelf. Ocean quahog landings in the United States represents a $24 million industry, yet very little is known about the resiliency of the ocean quahog stock to fishing activity, and ocean quahog recruitment patterns over time. Results by Pace et al. (2017) indicate that age at length data are extremely variable for this species and a robust age-length key cannot be created from a sparse data set (i.e. ~20 animals per 5-mm size class). Furthermore, the longevity of this animal ensures that an individual will encounter centuries of changing bottom water conditions over a single lifespan. Environmental changes are then manifested as growth signatures within the shell itself and a clear acceleration of growth rate over time is documented. Unfortunately, aging ocean quahogs is an extremely time-intensive process which limits the number of ages commonly used to generate an age-length key, an essential component to understanding the population dynamics of a species. Approximately 960 animals from Long Island and 650 animals from Georges Bank were aged to produce the first data-rich, sex-specific age-length keys and age-frequency distributions for the ocean quahog. Early evidence suggests that male and female quahogs exhibit different age and length class dominances at different life stages. Age structures found at both sites suggest regular recruitment to the population despite historic presumptions of prolonged lapses in recruitment.

EVALUATING ENVIRONMENTAL TOLERANCE OF THE NORTHERN QUAHOG (=HARD CLAM) *MERCENARIA MERCENARIA* TO ASSESS ADAPTIVE POTENTIAL WITH APPLICATIONS TO AQUACULTURE

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With climate change causing increasing water temperatures and altered precipitation rates in coastal systems, there is an increasing need to understand the environmental tolerances of coastal species that are commercially important. It is also necessary to understand the variation in environmental tolerance across a species' geographic range in order to predict the broader impacts of continuing climate change. In this study, the physiological effects of elevated temperature and lower salinity were assessed for juvenile northern quahogs (=hard clam), *Mercenaria mercenaria*, sampled from six populations ranging from Massachusetts to North Carolina. For each population, metabolic rate was measured using respirometry across four elevated temperature (27.5°C, 30°C, 32.5°C, and 35°C) and three lower salinity conditions (20, 15 and 10). The treatment levels selected are representative of current and future conditions projected for Chesapeake Bay, Virginia. To further understand potential differences among populations, mortality was assessed at an environmentally relevant, elevated temperature (36°C). Results showed differences among the six populations in temperature-related mortality rate as well as differences in oxygen consumption rates under low salinity conditions. The variations among these populations illustrate that the effects of climate change on hard clams will not be uniform and that some populations are more susceptible to environmental change than others. This characterization of environmental tolerance of juvenile hard clams can help predict the future success of this species and its commercially important stocks, as well as provide insight for the aquaculture industry about the potential for breeding more resilient broodstock lines.

ENGAGING STAKEHOLDERS AND PARTNERS FOR THE SUCCESSFUL IMPLEMENTATION OF A COMMUNITY-BASED OYSTER RESTORATION PROGRAM OVER THE PAST 20 YEARS IN SOUTH CAROLINA, USA

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Community-based restoration programs are a great way to engage not only volunteers, but also stakeholder groups and partner organizations. It is important to develop and maintain partnerships so that groups can be involved in key roles and decisions related to direct project implementation. The SCDNR South Carolina Oyster Recycling and Enhancement (SCORE) Program has been working with numerous entities, over the past 20 years, to continue its mission and involve groups in projects focused on coastal ecosystems. Since its inception, the SCORE Program has been included in many different facets of grant development and project implementation. This presentation will provide information on how this SCDNR program has continued to collaborate on projects and to facilitate programmatic growth.

ENVIRONMENTAL CONTROLS ON WITHERING SYNDROME IN ABALONE: A MODELING STUDY

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Abalone populations along the California coast have been severely impacted by Withering Syndrome, which is caused by a rickettsia-like organism (RLO), *Candidatus Xenohaliotis californiensis*. A model that includes abalone growth, host susceptibility to RLO, RLO body burden, and temperature and food availability was developed to assess biological and environmental controls on Withering Syndrome. The model implementation is based on experimental and field observations made for red abalone (*Haliotis rufescens*). Initial simulations reproduced the disease progression observed in red abalone that were held in laboratory tanks at constant temperature for more than one year. These simulations showed that after the initial infection, disease progression is determined by RLO growth in the host and that continued RLO exposure has little effect on the disease intensity. Simulations of RLO disease progression for red abalone exposed to warm events of days to weeks and events that persisted for months showed that long-term sustained warm water temperatures, as occurs during El Niño conditions, encourage RLO proliferation in the host and enhanced disease progression. The model was also parameterized for black abalone (*Haliotis cracherodii*) that are infected by RLO and by RLO with a phage (hyperparasite) that reduces the growth of the pathogen. These simulations show that the occurrence of the phage significantly reduces RLO body burden and infection intensity. This abalone model provides a tool to forecast population response to environmental variations, to guide plans for conservation and restoration of wild populations, and to inform best management practices for abalone aquaculture.

TEMPORAL AND SPATIAL VARIATION IN GROWTH IN THE SURFCLAM, *SPISULA SOLIDISSIMA*

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The surfclam, *Spisula solidissima*, is a benthic dominant in the shallower waters of the mid-Atlantic through Georges Bank region. Surfclams also support a substantial fishery with landings approximating 57 million pounds annually. The moving footprint of the range of exploited surfclams in these regions over the past four decades is now well documented in both the NEFSC stock assessment surveys and the gradual northeasterly movement of harvest activity. This moving footprint is related to warming of the US eastern continental shelf. This project is developing a 33-year retrospective, spatially explicit time series of growth rates in surfclams over the surveyed range to both document the aforementioned moving footprint in terms of population productivity and provide an explicit forward projection of future productivity. The research material is an archive of surfclams collected in the NEFSC surveys over the survey range. This archive has previously been used to estimate a growth curve for the entire fishery. This research extends this examination to estimate growth rate in a spatially explicit manner at smaller scales of space and time. Forward projections in the surfclam fishery are particularly challenging given the absence of a stock-recruit relationship and a life history strategy adapted to sedentary life on the rapidly changing continental shelf. These population traits drive observations that may be incorrectly interpreted as overfishing requiring precautionary management (e.g., decline of density in southern section of surveyed range) when the signal is, in fact, driven by warming waters.

TEMPERATURE-ASSOCIATED SELECTION LINKED TO PUTATIVE CHROMOSOMAL INVERSIONS IN KING SCALLOP (*PECTEN MAXIMUS*)

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King scallop (*Pecten maximus*) is a high-value molluscan species that supports a large fishery in the northeast Atlantic Ocean, and for which attempts to describe genetic population structure span decades. One unresolved question in king scallop genetics is the observation from transplant studies that have observed apparent genetic differences in the timing of reproductive maturity and spawning despite low levels of neutral genetic divergence. Utilizing a recent chromosome level genome assembly, a population genomic survey was conducted to describe the genomic landscape of divergence in king scallops sampled from Galicia, Spain to North-central Norway. Using a variety of genome scan and environmental association approaches, we assessed population structure and genetic diversity at both neutral and putatively adaptive loci across the genome, and report evidence of selective sweeps and genetic association with sea temperature that stands in contrast to neutral population structure and is localized specifically to at least three large, putative chromosomal inversions located on separate chromosomes.

ASSESSING THE EFFECTIVENESS OF DESICCATION IN CONTROLLING BIOFOULING IN WATER COLUMN CULTURED OYSTERS, *CRASSOSTREA VIRGINICA*, IN THE CHOPTANK RIVER, MARYLAND, USA

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Oysters and the equipment associated with water column oyster aquaculture serve as habitat for a host of other organisms. These marine plants and animals, collectively referred to as biofouling, may detract from the growing conditions available to the oysters and place added strain on culture equipment. Effects of these organisms range from reducing flow and food available to the oysters, to unsightly blemishes on the shell, to oyster mortality in extreme cases. Desiccation, or periodic air drying, of oysters and cages has been used to control colonization by biofouling organisms; however, the specific duration of desiccation time periods has yet to be thoroughly assessed. This project researched the effectiveness of different temporal desiccation regimes in controlling biofouling, with attention paid to species-specific effectiveness of the various desiccation regimes. Relevant impacts to oyster performance and physiology were also assessed. Monitoring took place at the University of Maryland Center for Environmental Science Horn Point Laboratory, adjacent to the Choptank River over a seven-month period between May–December 2019. Oysters were deployed to cages and replicate cages received one of four treatments - control (no desiccation), 4 hours of desiccation per week, 8 hours of desiccation per week, and 24 hours of desiccation per week. Percent valve coverage by individual biofouling species, bioexcavator infestation, oyster growth and oyster mortality were each monitored monthly.

ASSESSMENT OF ECOLOGICAL FUNCTION AND INTERACTIONS OF OYSTER CULTURE AND EELGRASS

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Preliminary results from the first year of a multi-year assessment of eelgrass response to shellfish culture practices will be presented. The overarching goal of the research is to better understand the value of habitats for managed fish and invertebrate species, including juvenile salmonids (*Oncorhynchus* spp.), Dungeness crab (*Metacarcinus magister*) and English sole (*Parophrys vetulus*). This research is funded by the Pacific States Marine Fisheries Commission and is designed to assess the interaction of eelgrass with various oyster culture systems, along with the ecological functions of these habitats.

In collaboration with shellfish farms, beginning in April 2020 research teams completed benthic and nekton sampling within a habitat mosaic design at three regions in Willapa Bay, WA, two regions in Hood Canal, WA, and two regions in Tomales Bay, CA. Three nekton sampling methods were used: modified seine net, minnow traps and underwater video. Teams also assessed eelgrass density, biomass, Pacific oyster (*Crassostrea gigas*) production, sediment condition, and fish were collected for gut content and stable isotope analysis. Oyster seed was out-planted in June 2020 at both Willapa Bay and Hood Canal farm sites, and subsampled in September for initial growth, survival and condition metrics. Bi-weekly bird camera surveys were completed in Grays Harbor, WA, during spring and fall migration periods. Aerial photography surveys and ground-truthing was also conducted at intertidal locations to measure eelgrass (both *Zostera marina* and *Z. japonica*) in Grays Harbor, WA. Finally, high-resolution drone imagery of target locations in Samish Bay and Willapa Bay, WA was collected.

A HATCHERY CERTIFICATION PROGRAM FOR THE INTERSTATE TRANSFER OF SHELLFISH SEED

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Policies for importation of shellfish seed vary by state, but all states require an importation permit that involves a health examination of the stock prior to transfer. Such examinations are costly and require specialized expertise and time. Subsequent regulatory review adds additional time, delaying commerce and imposing additional costs on industry. Because many transfers pose little to no risk, a better protocol that streamlines management of these transfers has been desired by industry and regulators alike.

For several years, shellfish pathologists, state regulators, and shellfish aquaculturists have worked to develop a program for certifying the biosecurity of hatcheries as a means to improve the permitting process for interstate transfer of shellfish seed. The Hatchery Certification Program arising from this effort relies on the young age of seed, a high level of water filtration or sterilization, and a history of clean pathology tests to ensure small seed do not transfer pathogens when sold. The voluntary program has three key requirements: 1) the hatchery must follow a set of Best Management Practices that are audited annually, 2) the hatchery must have and maintain a history of three years of acceptable pathology reports, and 3) the qualifying seed must have never been exposed to raw, unfiltered seawater. States and hatcheries that choose not to participate will continue to follow existing importation rules. This presentation will cover the experience in piloting the program at several hatcheries during 2020 and early 2021.

VIRGINIA SEA GRANT COVID-19 RAPID RESPONSE TO LOCAL AQUACULTURE AND SEAFOOD BUSINESSES

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As a result of COVID-19, restaurants and nonessential businesses throughout the United States were shut down in 2020 causing a monumental challenge for aquaculture and seafood businesses across the country. With the majority of seafood products consumed in restaurants (NOAA 2018), the result was an unparalleled shock to U.S. aquaculture producers. Many shellfish aquaculture businesses in Virginia responded to the loss of revenue from traditional marketing channels by establishing direct sales to consumer channels or enhancing their existing efforts.

With the aid of National Sea Grant funding, Virginia Sea Grant partners collaborated to support these new and enhanced direct marketing efforts of local aquaculture and seafood businesses. This presentation will cover the results of this collaborative effort which centers on creating direct marketing campaigns; delivering Ecommerce education; supplying regulatory and safe handling fact sheets to ensure commerce is achieved safely, and advising on consumer preferences for seafood products via a Qualtrics survey.

DEVELOPMENT OF A COST EFFECTIVE AND PORTABLE AERATION FREEZING SYSTEM FOR HIGH-THROUGHPUT SPERM CRYOPRESERVATION IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Cryopreservation is an important technology for germplasm preservation for animals and plants. Cooling rate is one of critical factors in the process of cryopreservation and usually can be achieved by using a programmable freezer; however, programmable freezers are usually too heavy and expensive to use in field experiments. The goal of this study was to develop a cost effective and portable cooling system using a Styrofoam box for sperm cryopreservation in the eastern oyster, *Crassostrea virginica*. The objectives were to: 1) determine the cooling rates by adjusting the height of samples above liquid nitrogen (LN) surface and the temperature of nitrogen vapor in the Styrofoam box (by aeration of liquid nitrogen); 2) evaluate and compare the post-thaw sperm viability of oyster sperm cooled by the designed aeration freezing system and a programmable freezer. A Styrofoam box (40.64 cm × 22.86 cm × 33.02 cm), which can hold a freezing rack for 40 straws (0.5-ml), was used as container for the freezing system. Cooling rates from 1.5°C/min to 29.8 °C/min were achieved by floating sample rack at 2-5 cm above LN surface with the LN amount at a 10-cm depth in the Styrofoam box. No difference in post-thaw sperm viability was found between the samples cooled by the designed aeration freezing system and a programmable freezer. The aeration freezing system developed in this study can efficiently freeze hundreds to thousands of sample straws per day, and the concept for designation can be used for users to develop their own systems.

INTEGRATION OF DIFFERENT DATA SOURCES FOR MANAGEMENT OF OFFSHORE BIVALVE AQUACULTURE AT SAGRES, PORTUGAL

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There is an increasing effort to integrate environmental data obtained from diverse sources to improve management systems for aquaculture. In the case of offshore longlines for mussel aquaculture at Sagres, SW Portugal, the data are supplied from a solar powered data logger with sensors installed on a signal buoy for offshore mussel aquaculture to estimate sub-surface temperature, salinity, fluorescence, turbidity and optical conditions. Data from these sensors are transmitted every two hours to a cloud-based platform, or downloaded manually and subsequently transferred to the platform. Classical oceanographic sampling has also been implemented to calibrate and validate the data from the sensor, with the deployment of: a CTD for conductivity and temperature profiles; a Secchi disc for water clarity; and a Niskin flask for water samples to estimate chlorophyll, total suspended matter, nutrients, as well as pigment and microscopical analysis to determine the microplankton community. This *in situ* data has also been complemented with satellite data, again from different sources such as the Copernicus Marine Service (EU) and the National Oceanic and Atmospheric Administration environmental data access programme (USA). With this approach, it has been possible to compare the quality of data obtained from different sources. For example, how does chlorophyll obtained from near real time fluorescence measurements compare with chlorophyll products from satellite images, and chlorophyll estimates with spectrophotometric and high pressure liquid chromatographic techniques for *in situ* water samples. These data are now available to reduce uncertainties associated with models that are available for farmers to improve their farming practices.

ENDEMIC POPULATIONS OF PATHOGENIC *VIBRIO* SP. IN NATURAL RESERVOIRS FROM AN EASTERN FLORIDA ESTUARY

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The Vibrionaceae is a highly diverse family of aquatic bacteria. Members of this ubiquitous family can colonize numerous niches within its natural habitat such as crustaceans, fish, cyanobacteria or oysters. The Vibrionaceae encompass several species that are also pathogenic to humans. These include *Vibrio cholerae*, the etiological agent of cholera, or *Vibrio vulnificus*, cause of a deadly septicemia. The preferential niche colonization dynamics of these pathogens in their natural environments remain to be further addressed. A large estuary in eastern Florida, the Indian River Lagoon (IRL) was surveyed where outbreaks of some of these diseases frequently occur and the presence of *Vibrio* sp. in this diverse environment was investigated. Endemic populations of *V. cholerae* and *V. vulnificus* were identified and sampling locations were establishd to study the environmental dynamics of these bacteria in several natural reservoirs such as water, sediment, cyanobacteria, and oysters from a nearby reef. It was found that most of the *V. cholerae* strains were isolated in the water body followed by cyanobacteria. Nonetheless, *V. cholerae* was no identified in oysters. Conversely, *V. vulnificus* was rarely isolated from cyanobacterial blooms but was frequently isolated from oysters (~20%). Strikingly, the *V. vulnificus* oyster isolates belong to a phylogenomic cluster typically associated with clinical-outcomes. These strains exhibit several pathogenic traits such as resistance to antibiotics and human bactericidal compounds. Overall, this study highlights the differential colonization dynamics of two bacterial pathogens in their natural environment and stresses the public health risk they pose in some endemic areas.

A PILOT STUDY EVALUATING GONAD RIPENING AND SPAWNING CYCLES IN SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*): POTENTIAL GEAR AND SITE EFFECTS AND COMPARISONS TO WILD POPULATIONS

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The sea scallop (*Placopecten magellanicus*) fishery is the third most lucrative marine fishery in the U.S., found in offshore populations and highly productive inshore aggregations supporting a state-managed fishery along the Maine coast. Recent declines in catch, compared to peak harvests in the 1980s, and projections forecasting demand for sea scallops to outstrip supply from fisheries has supported the rise in scallop aquaculture; however, biological and ecological effects of aquaculture on sea scallops is not well-understood and there is currently no hatchery production of scallop for culture. This study compares gonad ripening of sea scallops grown in aquaculture to those of wild scallop populations in Penobscot Bay, Maine. The hypothesis is that there will be a difference in gonad ripening both between gear types, sites, and between farmed and wild populations. Farmed scallops (n = 240) were sampled from lantern nets at Hurricane Island, ME, July 2019 to mid-October 2019. In 2020, scallops were sampled from two additional partner aquaculture sites and the wild population. Gonadosomatic indices (GSI) were analyzed to identify gonad ripening and spawning events and temperature was monitored continuously at each site. Differences in spawn magnitude and timing were seen between gear types, sites, and between cultured and wild populations. Differences in gonad ripening and spawning in farmed vs wild populations could influence recruitment and growth assumptions with the potential to impact management, aquaculture, and wild fisheries dynamics.

FIRST REPORT OF ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) OUTBREAK IN *PENAEUS VANNAMEI* CULTURED IN KOREA

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The occurrence of acute hepatopancreatic necrosis disease (AHPND) in Korean shrimp farms was reported internally by the National Institute of Fisheries Science of the Korean government in 2016, but to date, the detailed characteristics of the Korean AHPND isolates have not been reported. In this study, histopathological observations in the hepatopancreas of the field samples of two shrimp farms in Korea in 2019 showed symptoms of AHPND, including sloughing of undifferentiated cells in the hepatopancreatic tubule epithelium. By PCR, two toxin genes (*pir*A and *pir*B) associated with AHPND were detected in the samples, and the copy number of the AHPND plasmid ranged between 4.1×10^5 and 1.1×10^6 copies/mg in the hepatopancreas samples and between 1.1×10^5 and 1.4×10^5 copies/mL in the pond water samples by qPCR. Two *Vibrio* sp. strains were isolated from the pond water and diseased shrimp respectively, and those were confirmed to harbor AHPND plasmid by sequencing analysis. Furthermore, laboratory shrimp bioassays were performed to determine the pathogenicity of the AHPND strains and verified that those isolates were highly pathogenic to *P. vannamei*, causing high cumulative mortality within three days.

MANAGEMENT OF *VIBRIO* RISK FROM OYSTERS

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The leading causes of seafood-associated morbidity and mortality are caused by *Vibrio parahaemolyticus* and *Vibrio vulnificus* respectively, in the United States. Infections most commonly result from the consumption of raw molluscan shellfish. Risk management of vibriosis in shellfish has a multi-directional approach: understanding the ecology of the organisms in the estuarine environment, understanding the relative virulence of different strains, and understanding how harvest and handling practices in the shellfish industry affect the *Vibrio* levels in shellfish. The latter two topics, strain virulence and shellfish handling practices, will be the focus of this presentation. The geographical specificity and clinical predominance of certain *V. parahaemolyticus* strains, as identified by whole genome sequencing, will be discussed, along with the distribution of potential virulence markers across clinical and shellfish isolates. Additionally, an overview of recent studies on the effects of handling practices on *V. parahaemolyticus* and *V. vulnificus* levels in cultured oysters will be presented. The presentation will be concluded with a look forward to ongoing and upcoming research and discussion on how data from multiple areas of study can contribute to more accurate risk modeling.

FLOW CYTOMETRIC AND MICROSCOPIC CHARACTERIZATION OF HEMOCYTES OF SEA HARES *APLYSIA KURODAI* (BABA, 1937), *APLYSIA JULIANA* (QUOY & GAIMARD, 1832), *APLYSIA PARVULA* (MÖRCH, 1863), AND *APLYSIA OCULIFERA* (A. ADAMS & REEVE, 1850) FROM TIDAL POOLS IN JEJU ISLAND OF THE SOUTH COAST OF KOREA

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The members in the family Aplysidae known as sea hares play a crucial role as a grazer in small tidal pools or shallow subtidal hard bottoms. Like other marine gastropods, hemocyte types and their functions of sea hares are poorly understood. In this study, we identified and characterized the hemocytes of four *Aplysia* species including *Aplysia kurodai*, *A. juliana*, *A. parvula*, and *A. oculifera* using flow cytometry and light and electron microscopy. Flow cytometry identified three types of circulating hemocytes in the hemolymphs of the four sea hare species; granulocytes, hyalinocytes and blast-like cells. The hyalinocytes were the most abundant cells accounting for 89.6-92.8% of the total hemocytes. Flow cytometry indicated that the granulocytes and blast-like cells were less than 5.6% and 5.3% of the total hemocyte populations. The granulocytes of sea hares exhibited pseudopodia on the cell surface and granules in the cytoplasm. Morphology of the hyalinocyte was similar to that of the granulocytes, while they lack cytoplasmic granules. The blast-like cells were small and round, with very thin cytoplasm. Flow cytometry also revealed that the hemocytes are engaged in the cellular defensive activities such as intra-cellular lysosomal content, phagocytosis and ROS production. The mean lysosomal contents of the granulocytes ($3.2 \times$x $10^4 - 1.2 \times 10^5$ A.U.) was about twice higher than that of hyalinocytes (1.6 x $10^4 - 5.9 \times 10^4$ A.U.). The granulocytes showed comparatively higher phagocytosis capacity (33.8-59.1%) than that of the hyalinocytes (13.1-24.5%). Of the four species of sea hares, the ROS production of the granulocytes ($4.7 \times 10^5 - 2.9 \times 10^6$ A.U.) was 1.6-2.1 times higher than that of the hyalinocytes ($4.4 \times 10^5 - 1.4$ x 10^6 A.U.), except in *A. kurodia*. Flow cytometry and microscopy indicated that the hemocyte types and their functions were identical, regardless of the species.

STRATEGIES TO ENHANCE BAY SCALLOP POPULATIONS ON MARTHA'S VINEYARD, MASSACHUSETTS, USA

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Bay scallop populations are generally in decline throughout their range due to a number of factors including pollution, loss of habitat and harmful algal blooms. Due in large part to the short life span of the species, bay scallop populations, even under good conditions, are notoriously unstable in both time and space. The valuable fishery, dependent on the harvest of a single year class, likewise fluctuates annually. Failure of a single year class can eliminate the broodstock of a local population. In such cases without management interventions, restoration of a local population depends upon chance inputs of larvae from a distant part of the metapopulation. Widespread recruitment failures within the metapopulation can eventually extirpate the species from a region.

Hatchery and field methods to enhance and stabilize local bay scallop populations on Martha's Vineyard are discussed including the use of spat bags for both nursery culture of hatchery seed and wild spat collection, and the use of floating 'spawning sanctuary' cages to increase wild spawning success.

THE PRODUCTION OF SEED SHELLFISH DOES NOT NEED TO BE ROCKET SCIENCE: THE CASE FOR SMALL HATCHERIES USING SIMPLE TECHNOLOGIES

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Although all bivalve hatchery systems need to address the basic, common requirements for successful algal, larval and juvenile culture, the systems employed to meet those needs vary. While most new hatcheries seek to incorporate the latest complex technologies, a case can be made for keeping it simple. Surely, new technologies are impressive and their application in large operations provide levels of efficiency necessary for mass production. But the truth of the matter is that seed shellfish can be reliably produced in small scale operations using simple basic methods. Adding levels of complexity when they are not necessary increases costs and creates a greater chance for technical glitches.

The Martha's Vineyard Shellfish Group has successfully produced shellfish seed for over 40 years using a simple technology grounded in methods used at the VIMS Eastern Shore Laboratory in the 1970s. This basic technology is especially applicable to small operations with limited budgets and in developing countries where limited resources demand creative solutions using simple technologies. Examples of the application of simple methodologies in the design and operation of small scale, low tech hatcheries are presented; including a pilot hatchery in Rhode Island, a hatchery on a floating barge and a hatchery in Zanzibar.

IS A PRECAUTIONARY APPROACH TO PERMITTING TOO CONSERVATIVE? QUANTIFYING THE IMPACTS OF OYSTER AQUACULTURE ON SUBMERGED AQUATIC VEGETATION (SAV)

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Faced with conflicting data, state and federal regulators justifiably take a precautionary approach and generally do not grant leases or permits for conducting oyster aquaculture in or over SAV beds. Conversely, many in the oyster aquaculture industry argue that their practices can enhance SAV distribution and abundance, and observational data from some farms in Chesapeake Bay support the assertion that the two can co-exist. The rapid expansion of both SAV and oyster aquaculture in Chesapeake Bay has made the resolution of this issue critical for the industry and resource managers. This project seeks to rigorously evaluate the effects of commercial-scale floating oyster aquaculture on the health and distribution of SAV, water quality, sediment characteristics and benthic macrofaunal community structure. The objectives of this project are to: 1) quantify the effects (positive and/or negative) of active commercial-scale floating oyster aquaculture on SAV health and distribution, water quality, sediment characteristics and benthic communities within SAV beds, 2) develop approaches to reduce or eliminate any observed negative impacts, and 3) disseminate the results to industry, resource managers, and the public to support environmentally responsible co-use of these critical shallow water estuarine habitats.

In 2019, SAV cover declined significantly at both experimental farms and control sites. Sampling in spring 2020 was prevented by the global pandemic. Data from summer and fall 2020 suggest that SAV had not fully recovered from the decline in 2019, limiting the conclusions that could be drawn about farm effects. Data collection and analyses are ongoing.

EFFECTS OF INTERTIDAL CULTURE PRACTICES ON THE LEVELS OF *VIBRIO PARAHAEMOLYTICUS* IN FARMED OYSTERS (*CRASSOSTREA GIGAS*) FROM THE PACIFIC NORTHWEST

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Oyster aquaculture has progressed in North America over recent decades. Farms utilize specific techniques to culture oysters for the raw half-shell market. In the Pacific Northwest, two methods are commonly used: beach culture (on-bottom) and flip bags (off-bottom). Both methods are subject to tidal patterns that expose oysters to elevated temperatures for several hours each day.

During intertidal exposures, the bacterium *Vibrio parahaemolyticus* (*Vp*) can rapidly proliferate within the oyster, creating an elevated public health risk. In this study, levels of total (*tlh*+) and pathogenic (*tdh*+ and *trh*+) *Vp* were monitored in oysters (*Crassostrea gigas*) commercially farmed in Samish Bay, Washington from both culture methods over the course of a typical tidal cycle.

In the summer of 2019, three trials were performed. For each trial, triplicate samples (15 oysters/sample) were collected from each culture method at first exposure by the receding tide, after maximum exposure, 2 and 4-hours post resubmersion by the incoming tide, and 24-hours after first exposure. Levels of total and pathogenic *Vp* were determined by MPN-real-time PCR.

In beach culture and flip bag oysters, from first exposure to maximum exposure, mean levels of *Vp* increased 1.22 log MPN/g and 1.13 log MPN/g, respectively, and then decreased 1.23 log MPN/g and 1.97 log MPN/g after 4-hours resubmersion. Pathogenic *Vp* levels followed similar trends. These preliminary data suggest that 4-hours of tidal resubmersion may be appropriate in allowing *Vp* levels in oysters under these conditions to return to background levels found at first tidal exposure.

SHIFTING PHENOLOGY OF COMMERCIAL WHITE SHRIMP LANDINGS IN SOUTH CAROLINA, USA: THE ROLES OF SHRIMP MIGRATION AND CLIMATE

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White shrimp (*Penaeus setiferus*) support a valuable (~$33 million annually) commercial fishery in the U.S. western Atlantic. The geographic range of white shrimp, however, has recently shifted northwards, with more abundant shrimp in North Carolina (NC) and Virginia (VA) leading to increases in commercial white shrimp landings in these states. In South Carolina (SC) and Georgia (GA), declines in white shrimp landings since the mid-1990s have been attributed to reductions in fishing effort, economic factors, disease, overfishing, and climate, leading to concerns over the future viability of the fishery. In NC, SC, and GA, the majority of white shrimp have historically been landed during the fall months, but recent increases in the importance of winter and spring landings in SC suggest that the phenology of the commercial white shrimp fishery may be changing. White shrimp can migrate substantial distances during their 12- to 16-month life cycle, with a southward migration in the fall/winter occurring as large shrimp migrate to warmer waters off the coasts of GA and Florida. A portion of these migrants may also move back northwards along the coast the following spring. The role that shrimp migrations play in determining spatio-temporal patterns in landings may be significant. For example, the southward migrations of shrimp in NC and VA in fall/winter may be contributing to the increasing importance of winter landings in SC. This presentation will use state and seasonal trends in commercial landings to explore a regional framework for the future of the commercial white shrimp fishery.

ASSESSING THE EFFECTS OF CULTURE METHOD AND ENVIRONMENT ON SEA SCALLOP (*PLACOPECTEN MAGELLANICUS*) GROWTH AND MORTALITY IN THE NORTHWEST ATLANTIC

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The Atlantic sea scallop (*Placopecten magellanicus*) fishery landed USD $541 million ex-vessel value of product in 2018; however, domestic demand for scallops outstrips supply, and the U.S. imports an almost equal amount, by value, of farmed scallop products. In an effort to capitalize on this trade imbalance, Maine aquaculturists are currently developing a farmed Sea Scallop industry, employing the Japanese practices of suspended net culture and the sale of whole and 'roe-on' animals; however, maximizing investments in specialized scallop grading, washing, and grow-out equipment requires a deeper understanding of the combined effects of culture method and environment on growth and mortality. In order to inform future site selection and production practices, all published scallop shell growth and mortality rates recorded in the last 45 years between southern Maine, USA and the northern shores of Newfoundland were compiled. Significant nonlinear interactions between growth, mortality, environmental condition, and culture method were identified using generalized additive models (GAM). Best-fitting growth and mortality models each explain over 50% of the deviance within the respective datasets. Results indicate that any incremental increase in stocking density severely limits growth and that temperature exerts significant nonlinear effects. Maximum mortality occurs at elevated temperatures while stocking density is only a significant predictor of product loss at very high densities. Aggregating the results of many one or two treatment experiments affords non-site-specific conclusions that can help identify potential future production and siting bottlenecks as the scallop aquaculture industry expands in the Gulf of Maine.

SCREENING OF MAJOR SHRIMP PATHOGENS IN IMPORTED WHITELEG SHRIMP (*PENAEUS VANNAMI*) TO KOREA

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Shrimp is one of the most commonly traded marine products over the world; however, imported shrimp must be strictly controlled since they may introduce new pathogens, which become potential threats to shrimp farming industry in imported countries. In this study, white leg shrimp (*Penaeus vannamei*, 60 batches, 40–50 shrimp per batch) originally imported from Vietnam, Indonesia, Malaysia, and Peru were collected from fish markets in Korea. These commodity shrimp were examined for the presence of four pathogens: infectious hypodermal and hematopoietic necrosis virus (IHHNV, recently assigned with the species name of *Decapod penstylhamaparvovirus* 1), white spot syndrome virus (WSSV), acute hepatopancreatic necrosis disease (AHPND)-causing *Vibrio* bacteria, and *Enterocytozoon hepatopenai* (EHP). Briefly, five representative shrimp were randomly sampled from each batch. Hepatopancreases or pleopods of shrimp were collected, pooled, extracted for DNA, and followed by PCR analyses. The results showed that nearly 50% of samples were positive for these four pathogens: 23 were positive for IHHNV, and two were positive for WSSV, 17 were positive for EHP, and one was positive for AHPND-*Vibrio* bacteria. In Korea, imported live and commodity shrimp must be inspected; and this includes testing for 9 OIE-listed crustacean pathogens; however, the fact that we detected four pathogens (three OIE-pathogens and EHP) from imported shrimp that had passed inspection, indicates that current testing procedures are inadequate.

IMPACT OF SPAWNING STRESS ON HEMOCYTE PARAMETERS OF BLOOD COCKLE *TEGILLARCA GRANOSA* (LINNAEUS, 1758) ON THE SOUTH COAST OF KOREA

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Blood cockles, *Tegillarca granosa*, are widely-distributed on the subsurface of intertidal mudflats in tropical, subtropical, and warm temperate areas. In Korea, *T. granosa* is harvested widely from silty-mud tidal flats on the south coast. Several studies have reported that the blood cockles on the south coast spawn during July and August when the sea surface temperature ranges 24-26°C. Spawning of bivalve molluscs is an energy-demanding process that often results in immune-depression. To understand the effects of spawning on the cellular defense system, monthly changes in hemocyte parameters of *T. granosa* from the south coast of Korea were analyzed using a histology-flow cytometry combined assay. Histology indicated that the cockles were in pre-spawning (July), spawning (August), and post-spawning (from September to December) conditions. CI decreased from July (7.33) to August (6.39), indicating that the blood cockles spawned during this period. The total hemocyte count (THC) decline from July (1.2×10^8 cells/mL) to August (1.1×10^8 cells/mL), as most of the cockles spawned. In September, massive infiltration of the hemocytes in the gonad observed coincided with the decline of the THC. The hemocyte mortality measured by the flow cytometer increased linearly from August (4%) to November (9%), as well as the reactive oxygen species (ROS) production increased from July (0.9×10^5. A.U.) to December (2.1×10^5. A.U.). The granulocyte phagocytosis capacity declined from July (13%) to September (6%), suggesting a spawning-induced immune-depression. The histology-flow cytometry combined assay applied in this study was found to be a method of choice to understand the spawning-induced immune-depression in marine bivalves.

CREATING LIVING SHORELINES TO SUPPORT HABITAT RESILIENCY AND ECOSYSTEM SERVICES IN THE URBANIZED WATERSHED OF CHARLESTON COUNTY, SOUTH CAROLINA, USA

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Estuaries form one of the dominant landscapes of the coastal zone of South Carolina, consisting of interconnected networks of intertidal salt marshes. These salt marshes support a diversity of important ecosystem services, including the provision of critical nursey habitat and feeding grounds, as well as the protection of upland habitats from storms. Coastal salt marshes are, however, currently being lost at a higher rate than any other wetland habitat. These habitat losses create both a need and an opportunity for nature-based solutions to conduct on-the-ground habitat restoration and conservation activities. In South Carolina, these activities center around the creation of intertidal oyster reef and salt marsh habitat that constitute resilient living shorelines in the face of sea level rise and future climate change.

This presentation will provide highlights from a collaborative research project supported by a competitive federal grant award to the South Carolina Department of Natural Resources from the National Oceanic and Atmospheric Administration Community-based Restoration Program. The project is focused in Charleston County, South Carolina, an area that is experiencing rapid increases in coastal development and human populations, both of which are exerting pressures on its estuarine and coastal habitats. The project involves the creation of new oyster reef habitat, using a variety of substrate supplementation techniques, and new salt marsh habitat, through the propagation and planting of seedlings on intertidal shorelines. The project is also committed to volunteer and citizen scientist engagement by providing opportunities for education and hands-on participation to enhance community-based stewardship regarding estuarine habitats.

REPURPOSING OF BRIDGE MATERIALS FOR OYSTER REEF CREATION

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The re-purposing of previously used construction materials is examined for the purposes of oyster reef creation and as a living breakwater for shoreline protection in selected estuaries. The paper examines the use of materials resulting from the demolition of transportation infrastructure such as bridges and tunnels. These materials consist of riprap, gabions, gravel, steel and re-enforced concrete. In addition to cost savings as compared to other concrete related substrate products is the added benefit of the sequestration of CO_2 already embedded in the materials eliminating the additional CO_2 emissions from the manufacture of cement. The manufacture of cement produces about 0.9 pounds of CO_2 for every pound of cement. Since cement is only a fraction of the constituents in concrete, manufacturing a cubic yard of concrete (about 3900 lbs.) is responsible for emitting about 400 lbs. of CO2. The overview also includes proprietary methods of demolition to size and process the materials to uniquely adapt them for use as reef substrate.

PHYSIOLOGICAL EFFECTS OF MICROFIBER INGESTION BY OYSTER LARVAE (*CRASSOSTREA VIRGINICA*)

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A growing body of evidence shows that microplastic ingestion negatively affects many marine organisms including bivalves, but little is understood regarding early life stage exposure, when most vulnerable to contaminants. The eastern oyster (*Crassostrea virginica*) is a valuable ecological and economic resource along the east coast of the US, making it important to understand the dynamics between microplastics and oysters. To test this, 6-7-day-old larvae were exposed to microfibers made from one of two polymers commonly found in the coastal environment: polyethylene terephthalate (PET) (14×14 and 14×28 µm) and nylon 6,6 (10×10 and 10×30 µm). Exposure concentrations of 100 and 1000 microfibers mL^{-1} were compared to controls with no microfiber additions over six days during which physiological rates (respiration, algal ingestion, carbon assimilation, and growth) were measured. Exposure to PET microfibers showed no significant differences in algal ingestion and carbon assimilation rates compared to controls; however, it showed a biphasic respiration response and larvae exposed to 1000 microfibers mL^{-1} suffered a significant growth penalty after six days. Larvae exposed to nylon microfibers showed reduced algal ingestion and carbon assimilation rates with the lowest rates at the highest microfiber concentration after three days, but no significant differences in growth or respiration. The microfiber concentrations used in this study were at and above the larval threshold of ingestion but greater than environmental concentrations. Microfibers at current environmental concentrations are unlikely to pose risks to oyster larval physiology; however, further studies are needed to understand the effects of prolonged exposure to microplastics and multistressor interactions.

AQUACULTURE AND THE PRESS: A NEW WAY FORWARD

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Another day, another report of a swimmer getting a flesh-eating bacteria wound, and another story telling the public they shouldn't eat raw oysters—despite the fact that raw oysters had nothing to do with the wound. Business is down, your relatives are telling you they'd never eat a raw oyster, and the reporters won't stop calling to talk to you about vibrio. This scenario plays out countless times each summer. it doesn't have to. In this session, we'll help you cultivate relationships with the reporters likely to cover these issues in your region, teach you how to communicate your message effectively, and stick to some key points about aquaculture that you can return to and won't get you to inadvertently say something incorrect or taken out of context (or quoted as such.) We'll explain how you can move away from the "on the one hand, but on the other" narrative that reporters often follow, and explain what is a good story that you can pitch to better get your message out. We'll talk about the issues you've encountered or may in the future: opposition to new oyster farms, regulation and legislation that restricts aquaculture operations, and myths about the danger of eating oysters. This is a chance to speak directly with members of the press and get some feedback, so we'll have lots of time for questions.

PANELISTS: Rona Kobell is a science writer and editor for Maryland Sea Grant, where she is the managing editor for the magazine Chesapeake Quarterly. She was previously a reporter for the Chesapeake Bay Journal and the Baltimore Sun. She has covered aquaculture since 2006. Rona is also an adjunct professor at the University of Maryland's Philip Merrill College of Journalism, where she is pursuing a Master's degree.

Tim Wheeler spent nearly 32 years at the Baltimore Sun as a writer and editor before joining the Chesapeake Bay Journal as an associate editor and senior writer about four years ago. He is a former president of the Society of Environmental Journalists, and spent most of his career covering the environment. He has a B.A. from the University of Virginia and a Master's in journalism from Columbia University. He has also worked at the Richmond Times-Dispatch and the Norfolk Virginian-Pilot. A West Virginia native, he's been enjoying proximity to oysters, and enjoys both covering and consuming them.

Louise Schiavone is a contributing anchor on National Public Radio, where she can be heard several days a week. She is also a senior full-time lecturer at the Johns Hopkins University Carey Business School, focusing on business leadership and human values. She is also a widely published journalist, with recent pieces in National Geographic and the Los Angeles Review of Books. She has recently completed a short documentary, "Crisis on the Half-Shell: The Chesapeake Bay."

HARD CLAM HATCHERY DEVELOPMENT: IN THE BEGINNING

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The biology of the northern quahog (= hard clam) (*Mercenaria mercenaria* Linnaeus) is unique relative to other commonly cultured bivalve species because of its low levels of recruitment. There is no possibility of economically collecting sufficient small (<10 mm) clams to provide for an aquaculture industry. This characteristic restricted earliest experiments on the field culture to small wild clams (buttons) collected while harvesting the larger individuals. Hatchery development was based on some technology transfer from academic and government hatcheries, but the private sector made many important contributions. Interest in hatchery production increased when techniques were developed to culture the species in the field. It is important to recognize that there was considerable back and forth between individuals wishing to culture this species and the academic and government researchers. Technology transfer in both the hatchery and field was based more on these personal interactions than on formal programs.

NITROGEN FILTRATION BY FRESHWATER AND SALTWATER BIVALVES: IMPORTANCE OF SESTON COMPOSITION

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Natural and cultured populations of suspension-feeding bivalves affect water quality in various ways, especially when their population size is robust relative to water residence time and seston load. The ecosystem service generating the most attention by water quality managers is the removal, transformation and sequestration of seston-associated nitrogen. Bivalves must consume sufficient nitrogen to satisfy their demands for growth (biosynthesis) and reproduction (gametogenesis). The eventual fate and form of filtered nitrogen (remineralization, sequestration) can vary widely depending the nutritional status of the animal (e.g., seasonal protein sparing) and ecological interactions (e.g., microbial processing of biodeposits), and more research is needed to discern these effects *in situ*.

An additional factor that is often overlooked is seston quantity and quality. A re-analysis of 30 years of bivalve clearance rate studies with diverse freshwater and marine species indicated that nitrogen concentrations in natural seston diets used in the experiments varied by two orders of magnitude. In contrast, clearance rate variation differed by less than one order of magnitude among species, after normalizing for body size and seasonal temperature. Nitrogen filtration rate therefore varied more with seston nitrogen concentration than bivalve species or salinity.

To promote water quality throughout coastal watersheds, a multi-species approach could include oysters, ribbed mussels and several species of freshwater mussels that live in diverse niches along the salinity gradient. Greatest nitrogen removal rates would result from restoration and enhancement tactics that promote the greatest uplift in bivalve population biomass and in geospatial niches that have highest seston nitrogen concentrations.

LOBSTER SHELL DISEASE IN THE NOAA NORTHEAST GROUNDFISH SURVEYS 2018 - 2019

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Epizootic Shell Disease (ESD) has increased in *Homarus americanus* in the Gulf of Maine. The ESD was surveyed during the NOAA Northeast Groundfish Survey and protocol consistency established with inshore surveys. Protocol was inserted in FSCS sampling routines recording ESD in lobsters using NOAA and volunteer scientists during two groundfish surveys per year. Each trawl station with lobsters was entirely evaluated or subsampled. Suspect ESD lobsters were barcoded with: location, sex, carapace length and total weight, noting any loss of legs or chela, whether egg bearing, tail notched, and barnacle presence. Carapace ESD coverage was estimated. Barcoded carapace of all ESD(+) were frozen for reevaluation on land and photogrammetry. This resulted in 3-D surface models of the carapace with descriptive metadata for each lobster and identity as true ESD or false(+). Data were found to be consistent with general observations of prior ESD studies: (1) females were more abundant in the ESD(+) category and typically had a higher level of ESD. (2) Lower ESD(+) was seen in Fall surveys, higher ESD(+) in Spring. It is concluded that the female ESD(+) class is substantially undercounted because the level 3 ESD should include deceased female lobsters.

A NEW 200K HIGH-DENSITY SNP ARRAY SPECIFICALLY DESIGNED FOR CANADIAN EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) AQUACULTURE

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The eastern oyster (*Crassostrea virginica*) inhabits highly variable environmental conditions throughout its North American east coast range, from the Gulf of Mexico to New Brunswick in Canada. Since the 2000s, eastern oyster production in Canada has increased exponentially even though twice as many growing seasons are needed to reach market size in northern locations compared to southern regions. Thus, powerful genomic resources for eastern oyster aquaculture in Canada are needed to enhance selective breeding programs. A new SNP array specifically designed for the Canadian eastern oyster will be presented. A total of 501 F1 individuals from 42 crosses bred from parental lines of 11 New Brunswick bays have been used to identify whole-genome variation among Canadian populations via three runs of NovaSeq technology. A total of 54,945,771 SNP (Minor Allelic Frequency (MAF) $>$ 0.01) were genotyped with an average coverage of 3.75 SD±1.32, on which 219,447 SNP were obtained with a preferred MAF $>$ 0.1 and no SNP inside the 30bp flanking regions but permitting MAF $>$ 0.05 and with a maximum of two SNP (MAF $<$ 0.05) inside 20pb flanking regions, distributed along the genome as the final set of functional SNP on the array. Using this array, genetic diversity observed in hatchery populations were compared with levels of diversity in wild populations. This 219K high-density SNP array represents a critical step toward the development of the first selectively bred eastern oyster strain in Canada and will be a valuable tool for aquaculture applications including accelerated production and monitoring of potential impacts on wild populations.

HISTAMINE RECEPTORS: A GENOMIC STUDY OF THE BIVALVE *CRASSOSTREA VIRGINICA*

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Histamine, a biogenic amine found in a variety of invertebrates is well studied in arthropods and gastropods. It is involved in immune responses and regulating physiological functions. Histamine also is a neurotransmitter for sensory systems. Previous work of our lab found histamine activates the sensory system of *Crassostraea virginica*, eliciting a motor response in gill. Cell biology and immunofluorescence work showed histamine and histamine receptors present in ganglia and mantle of *C. virginica*. The genome of *C. virginica* and other bivalves have begun to be mapped. To test the hypothesis *C. virginica* contains genes for histamine receptors and these receptors are similar to those in other animals, including mammals, BLAST searches of the NCBI database using DNA and protein sequences of *C. virginica* histamine receptor (H1R, H2R, H3R) genes were conducted. Gene matches for histamine receptors were found. H1R genes on chromosome 8; H2R on chromosomes 1, 2, 5 and 10; and H3R on chromosome 3. BLASTS of other animals found matches with low Expect Values and high Percent Identity, signifying similarities of H1R, H2R and H3R of *C. virginica* to those of other animals, including mammals. This study complements physiology and cell biology studies demonstrating the presence and function for histamine in *C. virginica*, and shows the genome of *C. virginica* contains genes to produce histamine receptors similar to those in other animals. This new information is valuable in showing the simple nervous system of *C. virginica* can be used to expand studies on histamine neurotransmission.

COOL WATERS RUN DEEP—PHYLOGENETIC CHARACTERIZATION OF *VIBRIO VULNIFICUS* FROM THE GREAT BAY ESTUARY OF NEW HAMPSHIRE REVEALS UNIQUE ENVIRONMENTAL SEQUENCE TYPES

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The marine opportunistic pathogen, *Vibrio vulnificus* (*Vv*), is acquired by eating contaminated seafood or dermal exposure. Though rare, infections can cause septicemia or necrotizing wound infections, and in patients with pre-existing health conditions, this is often lethal, making *Vv* the leading cause of seafood-associated death in the US. Infections caused by *Vv* are expanding into cooler regions including most of coastal New England. The Great Bay Estuary (GBE) of New Hampshire is home to a growing oyster fishing industry. To safeguard this industry there is a need to assess and monitor the population structure and virulence potential of endemic *Vv*. To this end, 123 isolates recovered from GBE oysters, water, sediment and plankton during 2009–2016 were subjected to whole genome sequencing and phylogenetic reconstruction. Phylogenetic clusters matched assignment of strains to multi-locus sequence types, together revealing considerable genetic diversity and largely unique population structure, with 89% of isolates belonging to 29 novel multi-locus sequence types. Phylogenetic clusters contained isolates from oysters, water, sediment and plankton supporting broad distribution of strains in the estuary. Some clusters contained isolates from multiple sample years, though others were single year. Though none of the isolates clustered with clinical strains, this must be interpreted with caution given recent findings that virulence might be encoded in the core genome and regulated by environmental cues. Overall, the data demonstrate a highly diverse and unique population structure for *Vv* in the GBE that expands the current understanding of environmentally occurring reservoirs of *Vv* in cooler environments.

IS THERE A RELATIONSHIP BETWEEN SEXUAL MATURITY AND EXPRESSION LEVELS OF CRUSTACEAN MALE HORMONE, INSULIN-LIKE ANDROGENIC GLAND HORMONE (IAG)?

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The Jonah crab, *Cancer borealis*, is an economically important species in the Southern New England region with a steady increasing fishery since 2000. All crustacean fisheries rely on the size of adult males, in which sexual maturity is a critical component for a fishery management perspective. A few studies have been done to provide insight into the size at which Jonah males reach maturity.

Insulin-like androgenic gland hormone (IAG) produced by the androgenic gland (AG), the male sex-gland, plays a role in the sexual development of males: secondary male-specific characteristics and spermatogenesis. The AG activity is seasonal and regulated by the neuropeptides produced in eyestalk ganglia. This study aimed to understand better if IAG relates to size of the male *C. borealis* (SM50) and if IAG is regulated by the eyestalk ganglia. To this end, the IAG cDNA sequence was isolated using gene-specific primers derived from the Jonah crab AG transcriptome.

The open reading frame encoding the full-IAG sequence was 456 nucleotides in length. The putative amino acid sequence was similar to other crustacean IAG, although a low sequence homology compared to other crustacean neuropeptides. The AG transcriptome assembly revealed higher IAG abundance in ablated males than intact. The IAG is indeed the most-upregulated gene after the eyestalk-ablation, further confirming that there is an endocrine axis between the AG and eyestalk ganglia. The male size and maturity concerning IAG (transcripts and neuropeptide) are in progress.

HISTORICAL RANGE SHIFTS AND THE INFLUENCE OF GLOBAL WARMING ON OCEAN QUAHOGS (*ARCTICA ISLANDICA*)

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Ocean quahogs (*Arctica islandica*) support one of the three largest shellfisheries on the U.S. east coast. The habitat of this species includes the Mid-Atlantic Bight, an area subjected today to rapidly warming temperatures as a consequence of climate change. These clams have a low thermal tolerance, and are found exclusively in the cold pool, a finger of cold water on the outer continental shelf where bottom temperatures rarely rise above 15°C. Evidence exists that ocean quahogs once lived inshore of their present range, suggesting a much larger footprint for the cold pool in historical times. To investigate the timing of these range shifts *Arctica* shells were collected inshore of their present southern range boundary and dated using C-14. Shells were assessed for taphonomic condition, age at death determined from growth increments, and carbonate samples extracted to estimate birthdate using C-14. Degree of color change and percentage of periostracum coverage were compared to C-14 dates to determine possible qualitative indicators of time-since-death to aid in future shell selection. Sampled shells have C-14 dates from 2000 B.C. to the past 200 years. Older shells tend to be discolored with zero periostracum. Shells that have died in the past 200 years are contemporaneous with animals alive today, indicative of a significant recent mortality event along the inshore range boundary, presumably due to regression of the cold pool. These analyses help identify the timeframe of recent ocean quahog mortality events, and record at least three earlier range transgressions and regressions inshore of their present range.

TRANSCRIPTOMIC AND EXPRESSION ANALYSIS OF THE GENES INVOLVED IN ECDYSTEROIDOGENESIS AND CHOLESTEROL UPTAKE IN THE Y-ORGAN OF THE BLUE CRAB, *CALLINECTES SAPIDUS*

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Crustacean molting is controlled by the interplay of hormones produced from the eyestalk ganglia and the Y-organs (YO). Molt-inhibiting hormone and crustacean hyperglycemic hormone that are synthesized and released by the medulla-terminalis of X-organ and sinus gland complex of eyestalk ganglia regulate the secretion levels of ecdysteroid by the YO, hence determining to hemolymph ecdysteroid concentrations during the molt cycle. It is still unknown what triggers the YO committing to elevating ecdysoteroid synthesis and release.

The purpose of this study is to highlight the ecdysteroidogenesis pathway with the changes in ecdysteroid levels occurring specifically at early premolt (ePM). To this end, the changes in the levels of the genes potentially involved in ecdysteroidogenesis in the YO at intermolt (IM) ePM stage are determined with transcriptomic and qPCR analyses. Putative cholesterol carriers are also examined for the uptake of cholesterol as the precursor molecule of ecdysteroid, in the context of the increase in the ecdysteroid levels at premolt (PM).

As expected, YO transcriptomes reveal the presence of cytochromes p450 (*Cyp450*), *Spook*, *Neverland*, and *Cyp49a1* involved in ecdysteroid synthesis. The increase in *Spook* and *Neverland* expression in the YO is seen at the induced ePM (iePM) by eyestalk-ablation, together with the concomitant increase in ecdysteroid levels. The data obtained from eyestalk-ablated animals at iePM are also congruent with those of the intact animals at the ePM stage. The present findings confirm the role of Halloween genes in the ecdysteroidogenesis in the blue crab, *C. sapidus*.

WHOLE-GENOME RESEQUENCING REVEALS GENETIC VARIATIONS AND SELECTION SIGNATURES IN EASTERN OYSTER POPULATIONS FROM THE ATLANTIC COAST AND GULF OF MEXICO

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Eleven eastern oyster populations were collected along Atlantic coast and Gulf of Mexico, including Malpeque Bay in Canada, Massachusetts, Connecticut, Delaware Bay, Chesapeake Bay, North Carolina, Florida Gulf side, and Louisiana. Equal amounts of genomic DNA from 40 animals per population were pooled for 150 bp paired-end Illumina sequencing. A total of 270.4G clean data were generated after filtering low-quality data, and 1,618 million clean reads were mapped to the reference genome. The average sequencing depth is 38.5×. Sequence alignment among 11 samples defined 42 million SNP and 11 million indels, which will be used for the development of high-density SNP array. Based on these genome-wide polymorphisms, the neighbor-joining phylogenetic tree and principal component analyses revealed strong clustering into two distinct genetic groups, Atlantic and Gulf. Selective sweep analyses were done by combing Atlantic populations and Gulf populations to detect candidate regions that have undergone selection. The average F_{st}, nucleotide diversity and neutral tests were calculated in 100 kb windows with a 10 kb shift. Using top 1% intersection, 573 genes were identified which are involved metabolic process, reproduction, response to stimulus, binding and catalytic activity according to Gene Ontology enrichment, of which 19 genes were identified as salinity-related genes in previous studies. These genes include tyrosine-protein kinase receptor, toll-like receptor, receptor-type tyrosine-protein phosphatase epsilon, organic cation transporter protein, and serine/threonine-protein kinase. The study provides insights on the adaptive evolution of oyster genomics and provides markers that could be used to trace the progeny in oyster breeding or restoration programs.

PILOTING THE FUEL EFFICIENT, LOW BYCATCH, AND HABITAT FRIENDLY N-VIRO DREDGE IN THE SOUTHERN NEW ENGLAND SEA SCALLOP FISHERY

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The Atlantic sea scallop (*Placopecten magellanicus*) fishery is worth more than $500 million per year, making it the most valuable scallop fishery in the world and the second most valuable fishery in the United States. The fishery typically uses New Bedford style dredges, which have been criticized for causing high flatfish bycatch rates and impacting benthic environments. The king (*Pecten maximus*) and queen (*Aequipecten opercularis*) scallop fisheries were criticized for similar impacts in the United Kingdom with New Haven dredges, but have increasingly been utilizing the N-Viro dredge due to its improved fuel efficiency and reduced bycatch rates and habitat impacts. The Commercial Fisheries Research Foundation, Gulf of Maine, Inc., and southern New England fishermen conducted sea-trials to determine the feasibility of the N-Viro dredge for use in the Atlantic sea scallop fishery. Through side-by-side comparisons of the N-Viro dredge and New Bedford style dredges, the N-Viro dredge showed increased fuel efficiency, reduced habitat impacts, and decreased bycatch rates of at least 50% for nearly all bycatch species. The N-Viro dredge also had decreased catch rates of scallops; however, the N-Viro dredge was more selective for the most valuable larger sized scallops. Further gear improvement work is necessary to increase the scallop catch efficiency of the N-Viro dredge to levels of traditional New Bedford dredges; however, results suggest that the N-Viro dredge has potential to serve as a tool that scallop vessels could use to access areas of sensitive habitat, juvenile scallops, or bycatch species with reduced impacts.

EPIGENETIC EFFECTS OF OCEAN ACIDIFICATION IN THE EASTERN OYSTER

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Epigenetic processes may potentially alter predictions for evolutionary responses to climate change. Here, the investigators examined the role of DNA methylation in mediating the phenotypic responses of the eastern oyster (*Crassostrea virginica*) to ocean acidification (OA), both within and across a generation. In a long-term exposure experiment, they found that ocean acidification induced only subtle shifts in gene expression and DNA methylation in the mantle (the tissue of calcification), suggesting that the ability of wild oysters to regulate calcification in response to OA may be constrained. In an intergenerational exposure experiment, they conditioned adults under control or OA conditions, and raised their larvae under control or OA conditions. Patterns of non-genetic inheritance were found, in which larvae generated from adults raised under OA conditions had overall higher growth rates, and that this effect was larger for larvae raised in OA conditions compared to control. This transgenerational effect could not be explained by maternal provisioning. The gonads of control versus OA adults show differences in the genomic landscape of DNA methylation, suggesting that this epigenetic mechanism may underlie patterns of non-genetic inheritance.

MODELING GENETIC RISKS OF NATIVE SHELLFISH AQUACULTURE

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Native shellfish aquaculture circumvents ecological risks associated with introduced species, but poses genetic risks to wild populations if wild and cultivated individuals interbreed. These genetic risks, including loss of genetic diversity, loss of fitness and erosion of population structure, are of concern to decision makers because they ultimately impact wild population viability. Assessments of these risks have often focused on salmonid systems, assuming semelparity, relatively low fecundity and negligible gamete escape; however, these assumptions are inappropriate for many native shellfish species considered for aquaculture, which exhibit overlapping generations, reach maturity before harvest, and are commonly grown in shared waters with wild conspecifics. To assess genetic risks of native shellfish aquaculture, an individual-based model was built using the *simuPOP* modeling framework in *python* to simulate shellfish production and escape to wild populations. The model was parameterized using stakeholder input, parameter estimates from the literature, and empirically gathered population genetic parameters for two species, the purple-hinged rock scallop (*Crassodema gigantea*) and the giant California sea cucumber (*Parastichopus californicus*). The model was used to evaluate the genetic impacts of alternative management scenarios and investigated their sensitivity to a range of life history parameters, representing multiple species. This study highlights the power of combining empirical data, computer modeling, and end-user input, and will be used to provide decision support to stakeholders and resource managers aiming to mitigate genetic risks.

MULTI-STRESSOR EXTREMES FOUND ON TROPICAL CORAL REEFS IMPAIR PERFORMANCE

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Global change has resulted in oceans that are warmer, more acidic, and lower in oxygen. Individually any one of these stressors can have numerous negative impacts on marine organisms, and in combination they are likely to be particularly detrimental. Understanding the interactions between these factors is important as they often co-vary, with warming promoting hypoxia and hypoxia co-occurring with acidification. Few studies have examined how all three factors interact to affect organismal performance, and information is particularly sparse for tropical environments and organisms. This study documents a strong relationship between high temperatures, low dissolved oxygen (DO), and low pH in and around a tropical bay, which are used to inform two multistressor experiments. Experimental factors represented the current average and extreme conditions experienced in the area, and sea urchin righting response was measured to assess organismal performance. Short exposure to a fully factorial combination of temperature, DO, and pH significantly depressed performance under low oxygen. Surprisingly, sea urchins acclimated to low pH for 7 days subsequent to being exposed to the same experimental 2 h exposures, had significantly increased performance compared to animals acclimated to control pH, while performance was significantly depressed under hypoxia as well as high temperature. These results show that short exposures to temperature and DO extremes that are already experience periodically have detrimental effects on their performance, and that there is a positive impact of reduced pH after longer 7 days durations, which are not currently experienced in this area.

AIDS FOR THE IDENTIFICATION OF LARVAL AND POST-LARVAL DONAX FOSSOR SAY (BIVALVIA: DONACIDAE)

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The small, marine bivalve, *Donax fossor* Say, inhabits the oceanic surf zones along the northeast coast of the United States from Long Island to northeast Florida. Sexually mature adults of this species were collected from beaches along the east coast of Assateague Island, Virginia. Spawning was induced using a variety of protocols described by various workers and the larvae and postlarvae were reared using standard hatchery techniques. Scanning electron micrograph sequences are presented of the disarticulated shell valves of the larval and post-larval stages that accurately depict the gross morphologies/morphometries and hinge (provinculum) structures of consistently-oriented shell valves of the early ontogenetic stages of this species. While these sequences were documented using a scanning electron microscope (SEM) in order to depict morphological features at high resolution, these features are readily visible using a wide range of optical compound microscopes equipped with high-intensity reflected light sources. The SEM sequences of the disarticulated shell valves of *Donax fossor* are depicted in a similar format to that presented for the 56 bivalve species included in the monograph published by Lutz et al. (2018) in Volume 37 (pp. 247-448) of the *Journal of Shellfish Research*. The presented sequences of *Donax fossor* provide researchers with invaluable aids for discriminating (using routine optical microscopic techniques) the early life-history stages of this species from those of other sympatric species of bivalves isolated from plankton and benthic samples.

IMPACTS OF SEAWATER PH BUFFERING ON LARVAL STAGE PACIFIC OYSTERS AND REPERCUSSIONS FOR SUSCEPTIBILITY OF SPAT TO SUMMER MORTALITY STRESSORS

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Ocean acidification and the resulting lowered aragonite saturation state of seawater have been linked to high levels of larval mortality in commercial Pacific oyster hatcheries. In response, major oyster seed producers along the North American west coast have resorted to seawater pH buffering (*i.e.* the addition of soda ash to increase pH). Whilst this may improve survival during larval stages, repercussions for later life stages, particularly under stressor conditions, remain largely unknown. At the same time, shellfish growers continue to observe high levels of summer mortality in commercial oyster stocks despite concentrated research efforts to pinpoint a cause and develop solutions.

In order to investigate the potential impacts of pH buffering to larvae, Pacific oysters were reared under buffered or ambient pH seawater conditions for the first 24 hours of development. At one-day post-fertilization (DPF), all larvae were placed under ambient pH conditions for the remainder of the developmental period. Larval survival, growth, microbiome and immune status (via gene expression) were assessed every two days until settlement at 19 DPF. Following, spat arising from the larval run were applied to laboratory-based challenge experiments in order to investigate potential carry-over effects to susceptibility of later life stages during stress events. Survival and immune status of spat were assessed over approximately week-long exposures to *Vibrio aestuarianus* under high temperature (24°C) conditions. Results of the larval run and spat challenge experiments will be presented and potential links to summer mortality events will be discussed.

USING PROBIOTIC BACTERIA TO REDUCE LARVAL MORTALITY AND IMPROVE METAMORPHOSIS OF *CRASSOSTREA GIGAS* DUE TO THE BACTERIAL PATHOGEN, *VIBRIO CORALLIILYTICUS*

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Increased concentrations of the pathogenic bacterium, *Vibrio coralliilyticus* (*Vcor*), are commonly associated with high mortalities of larval Pacific oysters (*Crassostrea gigas*) in hatcheries. This study examined the ability of probiotic bacteria to reduce mortality of Pacific oyster larvae in the presence of *Vcor*. Four high-performing probiotic strains were identified that significantly reduced mortality of larvae exposed to lethal concentrations of *Vcor* when added 24 hours post egg fertilization (HPF) from 99.5 ± 1.3% SD to 1.9 ± 2.4% SD with added probiotics.

The probiotics also improved larval survival and metamorphosis in the absence of *Vcor.* A natural mortality event occurred during an experiment that resulted in 82.3 ± 12.7% SE mortality in the larvae only controls, but only 38.7 ± 19.8% SD in the treatment that had received probiotics. A thirty-day experiment showed that a single addition of the probiotics to larval Pacific oyster cultures resulted in a significant increase in larval shell length 12 days post fertilization (Larvae only mean=153.0 ± 1.5µm SE, Probiotics mean=164.5 ± 2.6µm SE), and greatly increased the proportion of larvae that successfully metamorphosed and grew for at least six days as spat. A subsequent 34-day experiment found that a single addition of probiotics 24 HPF significantly increased the rate of metamorphosis in all three oyster stocks tested (Pacific *C. gigas*, Midori *C. gigas*, and Kumomoto *C. sikamea*). The ability of these probiotics to reduce larval mortality and improve metamorphosis could greatly improve the consistency and production of seed oysters in hatcheries.

MANAGING FISHERIES IN THE MID-ATLANTIC AND NEW ENGLAND REGIONS IN THE COMING DECADES—MOVING RESOURCE FOOTPRINTS, COMPETING SOCIETAL NEEDS, AND FACILITATING THE DISCUSSION

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Fisheries management is not just about the targeted living resource—it is also about the people who are economically and societally related (and I use those terms in a very broad sense) to that resource, and the challenge of engaging all parties in the management conversation. It is a communication problem. Participants are not traditionally trained to "speak the same language" in this conversation. We bring differing values sets, varied tendencies to accept risk, and willingness to the accept that current management structure must evolve to serve both (a) access for the hunter gatherer fisherman as the resource moves in response to climate change and (b) broad societal needs as the continental shelf is zoned with fixed boundaries in service of energy development, shipping, national security, sand and gravel mining, communications infrastructure, resource sanctuaries and conservation areas, and more. This is a complex and often frustrating problem. How did we get here and where do we go from here? This presentation explores the historical development of Economic Exclusion Zones, the once and future role of Public Law 94-625 (the Magnuson Stevens Fishery Conservation and Management Act), the role of the regional Fisheries Management Councils, and the immediate need for fisheries scientists (that is you!) to engage with other footprint users in securing a sustainable future for shelf based fisheries in the mid-Atlantic and New England regions.

OYSTER SHELL PRODUCTION AND REEF ACCRETION RATES: A FIRST COMPARISON OF EXTANT AND FOSSIL SHELL DATA

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Oysters are unusual amongst the bivalves in that they create their own habitat in the form of reefs. Indeed, the creation and maintenance of reef structures are essential to the perpetuation of oysters over geological time. Reefs are created by mortality of oysters, with shells contributing to accretion. Countering this accretive process are the combined processes of dissolution, breakage and burial. Reefs must accrete at rates commensurate with or in excess of relative sea level rise. Recent shell budgets have been proffered based on current day recruit, growth and mortality rates in extant populations, but these fail to address survival through periods of higher sea level rise in the Holocene. This project examines population data from fossil deposits together with more appropriate age dependent mortality rates to explain reef dynamics during periods of sea level rise far in excess of present day values.

IN SITU CLEARANCE RATES OF OLYMPIA OYSTER, *OSTREA LURID*A, HABITAT AND PACIFIC OYSTER, *CRASSOSTREA GIGAS*, AQUACULTURE IN CALIFORNIA, USA

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The Olympia oyster, *Ostrea lurida*, is the focus of restoration projects in North American Pacific coast estuaries, whereas the non-indigenous Pacific oyster, *Crassostrea gigas*, makes up the majority of oyster aquaculture in the region. Both *O. lurida* habitat and *C. gigas* aquaculture provide filtration functions as filter feeders, we investigated the contributions of both in three California bays using a whole-habitat, *in situ* approach. Upstream-downstream measurements of chlorophyll-, temperature, salinity, and turbidity were collected to estimate habitat clearance rates (HCR, L $hr^{-1}m^{-2}$). In parallel, seston total particulate matter (TPM), and organic content (OC) were estimated and existing data on bivalve density and biomass was examined. Twenty-two experimental trials and four control mudflat trials were conducted from February 2018 to June 2019. Mean HCR at *O. lurida* habitats were 166 L hr^{-1} m^{-2} ($SD = 255$) at San Rafael, -464 L hr^{-1} m^{-2} ($SD = 1420$) at Shellmaker, and 105 L hr^{-1} m^{-2} ($SD = 251$) at Deanza, while *C. gigas* aquaculture at Morro Bay was 10.3 L hr^{-1} m^{-2} ($SD = 257$). Habitat clearance rates (HCR) among sites were not significantly different. Using random forest regression, temperature (30.6%) was relatively most important to HCR, followed by turbidity (27.9%), TPM (12.0%), OC (10.8%), site (10.6%), and salinity (8.1%). The contributions of all bivalve filter feeders and natural hydrodynamics are included in whole-habitat measurements in this study, which indicates that the filtration performance of *O. lurida* habitat and *C. gigas* aquaculture are similar in California bays.

PISMO CLAMS IN CALIFORNIA: GROWTH AND REPRODUCTION OF AN ICONIC SPECIES

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Pismo clams (*Tivela stultorum*) are an iconic species in California (CA), which once supported a thriving commercial and recreational fishery. Overharvest and a shortage of fisheries management data has contributed to Pismo clam population declines statewide. Key information on the population status, reproductive cycles, and growth rates is either unknown or nearly 50 years outdated. To evaluate these populations effectively, managers require updated population and life history data. Therefore, this project aims to: 1) determine annual reproductive cycles and body condition of Pismo clams on Pismo Beach, CA; 2) identify environmental drivers of reproduction and body condition; and 3) elucidate length/age relationships between clams across California. Up to 70 clams per month were collected from Pismo Beach, CA; 40 for histological analysis to determine reproductive stage and 30 to perform a body condition index. Additional clams and shells were collected from sites north and south of Point Conception to compare growth curves between two major oceanographic zones. When available, these data were compared to historical records. Data suggest that reproductive timing deviates slightly from historical records, with clams spawning later in the year than they were decades ago. Further, clams appear to take nearly twice as long to reach a legally harvestable size than initial estimates. Collectively, these data are critical to improve stock assessments and guide management decisions for this once abundant species.

INTERNATIONAL SHIPPING (EXPORT) OF LIVE MOLLUSCS AND CRUSTACEANS

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The international movement of live molluscs and crustaceans from the United States to other countries, for non-human consumption, is overseen by the U.S. Department of Agriculture (USDA), Animal and Plant Health Inspection Service (APHIS), Veterinary Services (VS). Each destination country may have different import requirements for the same type of animal so how does one keep everything straight? This presentation will address where to find the information and requirements for export, the process of health certificate endorsement (including electronic submission), and points of contact for assistance. The pre-export requirements for an aquaculture establishment to be inspected and approved by APHIS as a Registered Aquaculture Export Facility will also be discussed, in addition to the role of an APHIS Accredited Veterinarian.

GENETIC BASIS OF EXTREME LOW SALINITY SURVIVAL IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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As oyster aquaculture increases and expands globally, there is a need for targeted breeding of oyster lines for local environmental conditions. In coastal areas where low salinity is common, large freshwater inflow events leave oysters exposed to extreme low salinity conditions (< 5) for prolonged periods of time, resulting in reduced oyster growth and subsequent mortality events. Previous work has shown that survival in extreme low salinity is a heritable trait ($h^2 \cong 0.4$), but the molecular basis of this trait is still unknown.

A low salinity exposure experiment (< 3) was conducted using four F2 families to investigate genomic regions associated with both survival and day to death in extreme low salinity. Genome-wide SNP generated for each individual via ddRADseq were used for quantitative trait mapping and joint-association analysis. For both phenotypes, the analyses reveal a highly significant QTL on chromosome 1, and genes within this region have predicted functions related to membrane transport and DNA synthesis. Using a 20%/80% testing/training validation set for both phenotypes, realized accuracy estimates from genomic prediction models are 0.45-0.57, which are similar in range to previously determined accuracies for growth-related traits in the Pacific oyster. This work provides a first glimpse into the genetic basis of survival in extreme low salinity and suggests that genomic selection is a good option when designing a breeding program for this trait, but future work must be conducted with larger sample sizes and less relatedness structure to validate these results.

TRANSMISSION OF THE SEA SCALLOP NEMATODE: TEMPORAL VARIATION AND THERMAL TOLERANCE

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In 2015, unprecedented numbers of parasitic nematodes (*Sulcascaris sulcata*) were observed in adductor muscles of sea scallops, *Placopecten magellanicus*, leaving meats unusable for the fishery due to reduced meat quality. The sea scallop is an intermediate host for the parasite, with sea turtles being the definitive host. Little more is known about *S. sulcata* basic biology, seasonality, nor transmission in the mid-Atlantic. Scallops were collected bimonthly from September 2016 to August 2017 to better understand (1) potential transmission from discards, (2) seasonality of infection prevalence, (3) the relationship among infection and scallop survival, and (4) effects of temperature on nematode survival. Co-incubated infected and uninfected scallops did not support direct transmission. Additionally, nematodes were rarely found moving freely from scallops that had been shucked, mimicking shucking and discard practices at sea. Nematode infection prevalence and intensity in scallops were highly correlated (r2=0.8), increasing throughout the sampling period, while the number of adductor muscle lesions containing nematodes varied seasonally. Infected scallops held in seawater tanks were examined daily and dead scallops were removed, measured, and lesions counted. After 60 days, survivors were sacrificed and examined. Mortality was highest in scallops from heavily infected sites, lowest in scallops from lightly infected sites, and number of lesions correlated positively with mortality regardless of site. Nematodes survived short-term freezing and remained alive in seawater for >6 weeks at 4°C. They survived 24 hrs at 18-23°C, but perished within 6 hours at 37°C and died within seconds at 95°C.

SHELLFISH FARMING AND CULTURAL SERVICES, THE OTHER ECOSYSTEM SERVICE

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Bivalve shellfish farming provides a suite of ecosystem services, including well-documented provisioning, regulating, and supporting services. A more limited body of research exists detailing cultural services, or the non-material benefits obtained from an ecosystem. Using a refined definition of cultural services - the contributions ecosystems make to human well-being in terms of the identities they frame, the experiences they enable, and the capabilities they equip (Fish et al. 2016)—this study identifies, describes, and evaluates the cultural services and benefits associated with work in shellfish aquaculture.

Fieldwork in three regions (Chesapeake Bay, Gulf of Mexico, and New England) involved participant observation, semi-structured interviews, and photovoice interviews with over 200 shellfish farmers, harvesters, and others who work in roles supportive to shellfisheries. Data were used to create a list of the cultural services provided through work with shellfish, which was further evaluated using Q methodology. Combined methods of qualitative interviews paired with structured online surveys provided rich description of cultural services as well as perceived importance of benefits acquired through work with shellfish.

Results contribute to a more complete understanding of shellfish-related ecosystem services, and have applied implications for shellfish farming. Documentation of the sociocultural benefits provided by shellfish aquaculture can be used to create more comprehensive narratives of the impacts of shellfish farming on local communities. In this way, sociocultural benefits may be more salient to some audiences and enhance industry support.

SELECTIVE INGESTION AND EGESTION OF MICROPLASTICS IN THE BLUE MUSSEL, *MYTILUS EDULIS*, AND EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Microplastics have been found throughout the marine environment and are a contaminant of emerging concern. Suspension feeding bivalve molluscs like the blue mussel, *Mytilus edulis*, and eastern oyster, *Crassostrea virginica*, interact with microplastics of different shapes and sizes suspended in the water column. Mussels and oysters are selective suspension feeders and, thus, do not consume all of the particles to which they are exposed. Past studies demonstrate that particle selection in bivalves depends on the particle shape, size and physiochemical properties. Recent work has provided evidence that these animals also ingest and egest microspheres (polystyrene) and microfibers (nylon) differently, but whether or not polymer type acts as a factor for selection has not yet been explored. To further investigate how mussels and oysters handle micro-fibers and beads of different polymer types, animals were offered aged polyester fibers of different sizes (65, 500, 1000 µm), nylon (70 µm length) and polyester (65 µm length) fibers of approximately the same size, or polyethylene (26 µm diameter) and polystyrene (31 µm diameter) microbeads during a 2h exposure. Intestinal feces and pseudofeces were collected 3h after the start of the exposure. Depuration feces and any additional pseudofeces were collected at 24h and 48h during the depuration period. The proportion of microplastics rejected in pseudofeces and egested in feces is now being determined. Selection processes occur from particle capture on the gill through digestion, so differential egestion and rejection of particles prior to ingestion will provide a more complete picture of polymer selection amongst microfibers.

WATER QUALITY BENEFITS OF A SHELLFISH-BASED LIVING SHORELINE IN MILFORD, DELAWARE, USA

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In 2014, the Partnership for the Delaware Estuary installed the first “hybrid” living shoreline along 300’ of eroding salt marsh adjacent to the DuPont Nature Center at Mispillion Harbor, Delaware. Historically, living shorelines have been installed to stem erosion, but they can also address additional goals including habitat and water quality enhancement. This site was home to populations of oysters (*Crassostrea virginica)* and mussels (*Geukensia demissa*) that filter water to satisfy their nutritional demands, cleaning it in the process. As such, an additional goal of the living shoreline was to provide water quality uplift via an increase in shellfish biomass and filtration capacity.

Oyster castles and shell bags were deployed in lower and upper treatment areas near low water and along the marsh fringe, respectively. Shellfish densities and demographics were tracked between 2014 and 2019 on all materials and the central area between them. Changes in biomass per area were integrated with seasonal measurements of seston filtration to develop allometrically scaled filtration models. Oysters primarily recruited to the low and central areas, and ribbed mussels to the high area. The filtration capacity of the shellfish increased non-linearly from 13.63kg in 2014 to 2,025.60kg in 2019, with an increased rate in biomass accumulation observed beginning in 2016. These results indicate that shellfish-based living shorelines can positively contribute to water quality, but that time is required for these benefits to develop. Additionally, in areas with a mosaic of habitats, multiple shellfish species can be utilized to expand the filtration potential.

MITOCHONDRIAL HAPLOTYPES SUGGEST GENETIC COMPONENT FOR HABITAT PREFERENCE IN BLUE CRABS

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Atlantic blue crabs (*Callinectes sapidus*) are ecologically and commercially fundamental. Life stages are punctuated with migration. Adults and juveniles live in estuaries and sounds. Larval stages develop in the coastal ocean. Juvenile and adult crabs occupy habitats from high salinities to fresh water. Whether maturing juvenile and adult blue crab habitat use is reflected in mitochondrial cytochrome oxidase 1 haplotypes was examined. High salinity crabs had lower haplotype diversity (0.7260 ± .03900) compared to spawning crabs (0.9841 ± .00021) and low salinity crabs (0.94154 ± .00118). Significant pairwise differences in haplotypes were found between high salinity and spawning crabs (Nm = 0.26018, $p < 0.001$), and between high salinity and low salinity crabs (Nm = 0.19482, $p < 0.001$) indicating a lack of gene flow. Crabs from high salinity had highly significant genetic differentiation compared to spawning crabs (Fst = 0.11830, $p < 0.001$) and low salinity crabs (Fst = 0.09689, $p < 0.001$). Results support the hypothesis that genetics influence habitat selection. Crab larvae mix in the coastal ocean but occupy specific habitats upon return to sounds and estuaries. These findings have implications for the management of fisheries.

ASSESSING OYSTER RESTORATION AS A REMEDIATION STRATEGY IN GEORGICA POND, SOUTHAMPTON, NEW YORK, USA

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Georgica Pond is a small (~300 acre) embayment located on the south shore of Long Island, NY that in recent years has experienced blooms of toxic cyanobacteria resulting in hypoxic conditions and fish and wildlife deaths. A transient inlet connects Georgica Pond to the Atlantic Ocean that is opened ~twice a year (spring and fall) and naturally closes, resulting in a broad annual salinity range (2-30). Due to the euryhaline tolerance of oysters and the refuge from Dermo provided by low salinities, this study examined the potential for introducing oysters into Georgica Pond as a restoration strategy. Two size/age classes of oysters were deployed in triplicate cages at three sites across the Pond from July 2019 to present, capturing multiple cycles of the inlet opening and closing, resulting in salinities between 7.7 and 29.6. Survivorship and growth were monitored and compared to oysters placed in Conscience Bay, a Long Island embayment with a permanent inlet and more stable salinities (~25). Additionally, water quality and disease parameters were monitored to explain differences in oyster performance. To date, survivorship is higher at Georgica Pond, while growth is higher at Conscience Bay. Fourteen months after deployment, Dermo prevalence and intensity were lower for both size classes of oysters in Georgica Pond compared to those in Conscience Bay. The observed survivorship trends in conjunction with diminished disease prevalence indicate that Georgica Pond may offer a viable habitat for introducing oyster restoration as a remediation effort.

FARM PRODUCTION OF SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) IN MAINE, USA

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Over the last twenty years, Maine fishermen, aquaculturists, scientists and others have collaborated in various ways to advance the sea scallop (*Plactopecten magellanicus*) as a candidate species for aquaculture. Many years of technology transfer with colleagues in Japan, Canada, Europe, and elsewhere, growth trials, and rulemaking on product safety and human health have allowed producers to determine feasible production systems, a workable regulatory environment, and to investigate the market potential for live and whole scallops.

Some relevant, significant developments over this time include: purchase and implementation of specialized machinery for ear-hanging production and scallop husbandry, such as graders, drills, and washing equipment; the formation of the first aquaculture cooperative in Maine, which is focused on scallop farming; the deployment of the first loan funds to a scallop farm; industry adoption and refinement of longlines and longline handling equipment; acquisition of substantial data on stocking density and growth in relation to local conditions; three years of detailed biotoxin data on several sites, which has led to regular sales of whole/live scallops; the development toward alternative methods for quantitative assessment of ASP and PSP in scallop tissues; and a growing network of producers, dealers, scientists, regulators, economic development professionals, and others, each contributing expertise toward the goal of a profitable sea scallop farming sector in the state. The presentation will review the market opportunity, history, equipment, methods, and other relevant details of this developing industry sector.

USE OF CITIZEN SCIENTISTS TO MONITOR HARMFUL ALGAL BLOOMS, CHANGES IN ENVIRONMENTAL CONDITIONS, AND ITS UTILIZATION IN AQUACULTURE

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Harmful algal blooms (HAB) occur when species of phytoplankton grow very quickly forming blooms resulting in water discolorations sometimes referred to as red tides. These blooms have been observed in every state resulting in over $1 billion in losses over the last serval decades to communities that rely on recreation, tourism, and seafood harvesting. The direct economic impact of HAB does not include the socioeconomic impact from loss of subsistence harvest activities, disruption of cultural practices, water insecurity, food insecurity, and social interaction tied to coastal resource use. 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 since they are known to cause mortality of shellfish and finfish worldwide.

The National Phytoplankton Monitoring Network (PMN) is a community-based network of volunteers monitoring phytoplankton and harmful algal blooms. Formed in 2001, PMN enhances the ability of the Nation to respond to and manage the growing threat posed by HAB by collecting important data including phytoplankton species composition and distribution as well as environmental conditions. The PMN was able to grow into a national monitoring program by use of various web-based tools such as an interactive web site and a geographic information system tool for data visualization and searchable database. This presentation will outline the use of these technologies and highlight the use of volunteer data in aquaculture settings.

IS AN APICOMPLEXAN PARASITE RESPONSIBLE FOR THE COLLAPSE OF THE BAY SCALLOP (*ARGOPECTEN IRRADIANS IRRADIANS*) POPULATION IN NEW YORK?

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In 2019 and 2020, Peconic bay scallop populations in New York suffered extensive mortality events resulting in >95% reduction in adult biomass. These events were associated with heavy infections by an undescribed apicomplexan parasite (dubbed Bay Scallop Coccidia, or BSC). The objective of this research was to characterize BSC infections and elucidate disease dynamics, including how ecologically relevant environmental factors and scallop genetic background regulate BSC disease development and associated scallop mortality.

Microscopic observations showed that BSC is highly prevalent (100% prevalence in over 1,000 scallops processed) and can infect and disrupt multiple tissues including kidney, adductor muscle, gill, and gonad. Lab experiments showed significantly lower survival rates in scallops held at 28°C as compared to those held at either 22°C or 25°C. Field investigations also showed significantly higher mortality rates in scallop habitats characterized by high temperature and low dissolved oxygen during summer. Interestingly, both laboratory and field studies showed markedly higher mortality in aquacultured stocks as compared to wild scallops. Histopathological analysis of samples collected at monthly intervals from experimental field sites is ongoing to characterize BSC life stages and disease development over the 2020 summer/fall season. In parallel, PacBio and Hi-C sequencing reads have been generated from concentrated BSC cells and parasite genome assembly is ongoing.

Overall, this study starts to shed the light on the significance of BSC infection in bay scallops and how this parasite may synergistically interact with stressful environmental conditions to impair the host and lead to mortality.

INTERACTIONS AND IMPACTS OF OFFSHORE WIND DEVELOPMENT ON EAST COAST SHELLFISH FISHERIES

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The U.S. east coast continental shelf has 1.7 million acres of federal bottom under lease for development of offshore wind energy installations, with plans underway for more than 1,500 foundations to be installed. The globally unprecedented scale of these wind farms has the potential to interact with existing coastal ocean users, with particular impacts anticipated for commercial fishing. Some commercial fishing sectors, particularly shellfish fisheries, may be excluded from wind farm areas due to gear and vessel constraints, cables in the bottom, and general limitation of fishable bottom habitat. Federal shellfish surveys may also be subject to access issues that limit data collection in these areas, which could have long-term implications and impacts for management. The fished stocks themselves may shift due to the presence of large arrays of pilings and rock foundations in areas of the ocean otherwise dominated by open sandy bottom, and the turbine fields could create turbulent mixing or changes to surface winds that may interact with important physical oceanographic features such as stratification and the cold pool. Research and monitoring efforts at wind energy installations elsewhere in the world provide insights about impacts, but the novel scale of the turbine technology, and the unique habitats and oceanography of the U.S. east coast continental shelf warrants targeted studies to identify how these wind farms may interact with and alter commercial shellfisheries.

SMALL INVERTEBRATES IN BIVALVE-CULTIVATED AND UNMODIFIED HABITATS OF NEARSHORE ECOSYSTEMS

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Many nearshore ecosystems are modified by aquaculture, including bivalve culture to produce food and restore extirpated populations. Small invertebrates in nearshore ecosystems support fundamental ecological processes, but the effects of bivalve culture on invertebrates are incompletely understood. Here, researchers compared invertebrate assemblages from multiple studies of bivalve-cultivated and unmodified nearshore habitats along the U.S. west coast. In general, unmodified eelgrass and nearby off-bottom culture habitats with eelgrass present were inhabited by a greater abundance, richness, and diversity of epibenthic invertebrates than bottom culture and bare (mud, sand) habitats that both lacked eelgrass. Findings of individual studies suggested: minor differences in epibenthic invertebrate assemblages associated with various aquaculture practices; restoring native oysters to mudflats did not detectably alter epibenthic invertebrate abundances; epibenthic invertebrates were more abundant on shell hash introduced to mudflats than unmodified mudflats; and benthic invertebrates were less abundant, rich, and diverse in habitats cultured on bottom by Manila clams. Considering the range of these patterns, there appears to be potential for coastal communities to restore extirpated bivalve populations or develop bivalve culture practices that meet objectives to grow food while maintaining nearshore ecosystems' fundamental processes supported by robust invertebrate assemblages.

COMPARING THE IMPACT OF ARTIFICIAL OYSTER REEFS AND OYSTER FARMS ON WILD OYSTER RESTORATION, AQUATIC SPECIES DIVERSITY, AND WATER QUALITY IN DELAWARE INLAND BAYS

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Oyster farms and reefs provide various ecosystem benefits such as carbon sequestration, water quality improvement, shoreline stabilization, habitat and enhancement of fishery productivity. Since the 1950s oyster population and densities have declined significantly both nationally and globally due to overharvesting, disease outbreak, eutrophication and degradation in water quality. In Delaware, restoration efforts such as artificial reef construction and oyster gardening are being implemented. Three artificial oyster reefs in Rehoboth Bay were constructed as pilot reefs. Restoration of the commercially exploited oyster population remains the principal motivation behind the restoration efforts.

The goal of this study is to compare the ability of oyster farms and oyster reefs to support new oyster recruitment, enhance local fish and invertebrate diversity, and improve water quality. Oyster recruitment, species diversity, and water quality were monitored periodically at oyster farms, artificial reef sites, and natural (non-reef) locations in Rehoboth Bay. Preliminary results suggest that artificial reefs and oyster farms tend to have higher dissolved oxygen, lower nitrogen and phosphate concentrations, and relatively higher species richness, as well as significant evidence of oyster recruitment, compared to natural areas.

EFFECTS OF OCEAN ACIDIFICATION AND CLIMATE CHANGE ON THE GROWTH AND DEVELOPMENT OF OREGON PINK SHRIMP (*PANDALUS JORDANI*) LARVAE

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Anthropogenic carbon dioxide emissions are causing ocean acidification (OA) and ocean warming, which have negative effects on the larvae of many marine invertebrates. Oregon pink shrimp (*Pandalus jordani*) currently encounter upwelling events which can result in pH as low as 7.6, and more recently marine heat waves that raise surface temperatures 2-4°C. As climate change intensifies OA and warming, pink shrimp larvae will experience more frequent and intense exposure to potentially adverse conditions. Laboratory experiments were conducted in 2018 and 2019 to determine these multi-stressor effects. In 2018, *P. jordani* larvae were exposed to pH(NBS) 7.7, 7.8, 7.9, and 8.0 at 11°C. In 2019, a fully factorial experiment with four pH levels (pH 7.6, 7.8, 8.0, 8.2) and three temperatures (8°, 11°, 14°C) was employed. Larval growth rates from 2018 decreased 17% from the highest to lowest pH. In 2019, there was a 27% and 22% decrease in growth rate between the highest and lowest pH in the 8°C and 11°C treatments, indicating a temperature-dependent effect of pH. Respiration rates were directly impacted by temperature with elevated respiration rate at pH 7.6 for both the 11°C and 14°C treatments. In addition, there was significant mortality across all 14°C treatments, suggesting a more significant impact of temperature than pH, especially within the upper range of pink shrimp thermal tolerance. These findings demonstrate the temperature dependence of OA effects in larval shrimp, indicating the complex nature of multi-stressor impacts on this commercially-important species.

IMPROVING QUANTIFICATION OF *VIBRIO VULNIFICUS* AND *VIBRIO PARAHAEMOLYTICUS* TO SUPPORT THE SHELLFISH INDUSTRY OF NORTH CAROLINA, USA

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Unlike other microbial contaminants of public health concern for shellfish that are associated with fecal contamination, *Vibrio* bacteria occur naturally in estuarine and marine waters. Currently, risk reduction to prevent *Vibrio* illnesses associated with shellfish consumption, caused in particular by V. *parahaemolyticus* and *V. vulnificus*, is regulated in a unique collaboration across the Interstate Shellfish Sanitation Conference (ISSC), Food and Drug Administration (FDA), and individual coastal states. For *Vibrio parahaemolyticus*, the recommended approach for states is to reduce the probability of illness by assessing periods that have been historically associated with illness and to implement a comprehensive program that includes time to temperature and resubmergence controls. After this, appropriate state agencies designate appropriate regulations to mitigate health issues associated with raw shellfish consumption. Even with this preventive structure, the variable nature of *Vibrio* sp. pathogen concentrations is difficult to manage because different regions, sites, oyster grow-out types, and a host of other factors complicate the management of pre- and post-harvest treatments. Furthermore, recent research conducted in North Carolina demonstrates that *Vibrio parahaemolyticus* and *Vibrio vulnificus* respond quickly to improper storage at ambient temperatures, but highlights that the risk to the consumer is likely low given the extremely low incidence of pathogenic strains. This research focuses on 1) designing and implementing improved quantitative, cost-effective molecular tools for quantification of pathogenic forms of *Vibrio* sp., 2) comparing these methods to existing culture-based methods, while understanding the changing needs of the shellfish industry, and 3) engaging the shellfish industry to learning the magnitude of *Vibrio* issues, while offering strategies that consider marketability, risk and economic value. This presentation will highlight key components from all three areas in an effort to help the shellfish industry in NC to gain a proactive, but sustainable, position on *Vibrio* sp.-related risk and increased marketability product.

REESTABLISHMENT OF A POPULATION OF ADULT QUEEN CONCH, *ALIGER GIGAS*, POPULATION IN A MARINE PROTECTED AREA IN THE BAHAMAS

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The queen conch, *Aliger gigas*, is part of the Bahamian way of life. Studies suggest that commercial stocks will be depleted in The Bahamas in 10-15 years. In response, an adult conch population was reestablished in an overfished habitat in Moriah Harbour Cay National Park, Exuma, Bahamas. The conch were purchased from the fishermen and originated from fishing grounds approximately 100 km from the study site. Conch were tagged (n=251) and stocked in a 1,385 m2 enclosure (1 conch/5.5 m^2). The site was a mixture of seagrass and macroalgae (87%) and sand and rubble (13%). For three months (May - August 2019), the site was visited every 24-48 hours to examine conch distribution and behavior, including reproductive activity. The conch acclimated to the new environment quickly as evidenced by grazing and high survival. During the study the conch moved throughout the enclosure and efficiently grazed the epiphytes from the seagrass blades. The number of fauna that were attracted to the site increased over the study period. No egg masses were laid despite environmental conditions being favorable. It was speculated that lack of egg laying was due to handling disturbances from fishing, transportation, and tagging, which may have caused the conch to resorb their gonads. It is recommended to reestablish conch in breeding areas three months prior to the spawning season. This study reinforced the ecological value of conch in seagrass habitats and showed promise as a fisheries management tool to address the decline of queen conch populations in the Caribbean.

OCCURRENCE VARIATION IN PEDUNCULATE BARNACLE *OCTOLASMIS* SP. AND GILL TISSUE DAMAGE OF MANGROVE CRABS (*SCYLLA* SP.) IN SOUTHEAST SULAWESI, INDONESIA

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Water contamination due to mining activities increase the risk of an abundance of parasites and resulting in fatal damage in aquatic animals. The study aim was to investigate the seasonal dynamics (dry and rainy seasons) of barnacle infestation on mangrove crabs (*Scylla* sp.) and their damage effect in gill tissue.

A total of 80 crabs were collected from mangroves around a former gold mining area. In the sediment, mercury (Hg) was identified with an average of 0.22 mg/kg, reinforcing the assumption that mining activities have contaminated the mangrove environment. The species of barnacle was identified based on morphological and molecular characteristics.

The results show that the dominant species of barnacle was *Octolasmis angulata*. The prevalence of *O. angulata* was (100%) during sampling period. The prevalence, mean intensity and mean abundance of *C. angulata* were significantly higher (100%, 146.78, 146.78) during the rainy season than during the dry season (100%, 69.95, 69.95). The same parameters for *O. angulata* were found to be significantly higher in female (100%, 117.97, 117.97) than in male (100%, 71.71, 71.71) respectively. Infestation levels showed a trend of high intensity at larger crab sizes. These results indicate that size and sex of host might play a secondary role in barnacle occurrence. The histological examination of the gills found encountered some damages, such as bacterial colonies, epithelial desquamation damage, and necrosis. Further studies should examine if Hg will accumulate in barnacles to prove that the they can potentially be a bioindicator of water pollution.

THE HAWAIIAN BOBTAIL SQUID, *EUPRYMNA SCOLOPES*, AS A MODEL HOST FOR UNDERSTANDING THE ROLE OF BENEFICIAL BACTERIA IN EGG DEFENSE AND DEVELOPMENT IN CEPHALOPODS

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The Hawaiian bobtail squid, *Euprymna scolopes*, serves as a model host for understanding interactions with beneficial bacteria. Female squid house a diverse bacterial community in the accessory nidamental gland (ANG), part of the reproductive system. Bacteria from the Alphaproteobacteria (*Rhodobacteraceae*), *Verrucomicrobia*, *Gammaproteobacteria*, and *Flavobacteriia* dominate the ANG and are deposited into the egg jelly coat (JC) where they are hypothesized to defend eggs from potential pathogens and biofouling during embryogenesis. Eggs treated with antibiotics developed a biomass, primarily composed of the fungus, *Fusarium keratoplasticum*, which led to the death of the embryos. ANG/JC bacterial strains and extracts inhibited *F. keratoplasticum* and/or the human pathogen *Candida albicans*. To better understand the development of the ANG symbiosis, TEM and confocal microscopy were used to show that the developing organ is poised to recruit bacteria from the environment, likely via the colonization of numerous ciliated ducts that are open to seawater. Furthermore, squid raised with sterilized substrate and artificial seawater failed to develop an ANG or had severely stunted organs (n = 15), while animals raised with substrate from the natural habitat of the squid developed normal ANG (n = 9). Taken together, these data suggest that the ANG symbiosis is environmentally transmitted, and that bacteria from the environment of the host induce development of the organ while providing for egg defense from potential pathogens in the mature association. Efforts are underway to characterize the symbiont diversity from the ANG of a number of cephalopod species from around the world.

'WHAT IS EATING YOU?': A COMPARISON OF FAUNAL COMMUNITIES AND TROPHIC STRUCTURE ON HARVESTED AND UNHARVESTED OYSTER REEFS

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Oysters are known worldwide for both their environmental and economic impact. They are extremely vital organisms, providing a wealth of services to humans with benefits ranging from water filtration to microhabitat for many marine species. In addition to these ecosystem benefits, oysters have also become commercially important as a fishery. The U.S. alone accounts for almost 200 million dollars in oyster aquaculture sales at nearly 40 million pounds harvested annually. Yet challenges to managing oyster reefs as both a habitat and a commercial fishery remain. Much of oyster aquaculture comes from destructive sampling techniques used in commercial harvest. Commercial harvest in subtidal areas in the Gulf of Mexico is typically conducted using a dredge that degrades the physical reef structure which have negative effects on associated fauna through increased sedimentation, reduced diversity and abundance of motile organisms, and lowered reproductive potential of many bivalve species.

The goal of this study is to use community and stable isotope analyses of carbon, nitrogen, and sulfur to compare the faunal community composition and food web functions of harvested and unharvested oyster reefs within Matagorda Bay, Texas. Understanding the food resources and trophic pathways supporting consumers in harvested versus unharvested reef habitats will help to clarify the characteristics that enhance habitat provision by oyster reefs and can be used to inform resource management and restoration decisions.

EFFECTS OF DIFFERENT FINANCING SCENARIOS ON MARYLAND OYSTER FARM PROFITABILITY AND SUCCESS

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After modernizing its oyster aquaculture leasing laws in 2009, Maryland launched a unique aquaculture financing program with the assistance of the Maryland Agricultural and Resource Based Industries Development Corporation (MARBIDCO). This program features an interest only payment period followed by partial loan principle forgiveness and amortization of the remaining principle balance. This approach can offer significant advantages to new operations that lack access to private funds, especially when compared to traditional financing options. The study first developed deterministic oyster farm financial models based on firm business plans to evaluate uncertainty in the deterministic estimates of net present value of cash flows using Monte Carlo analysis. Probability distributions were developed by interviewing oyster culture experts on key performance variables for bottom culture and water column culture farms of different sizes. Farms with MARBIDCO funding were also compared with farms financed with private funds and those obtained through traditional financing. Results will be presented on overall farm profitability comparing MARBIDCO funding, traditional funding and use of private funds over a 10-year period.

SUSTAINABLE OYSTER AQUACULTURE, WATER QUALITY IMPROVEMENT, AND ECOSYSTEM SERVICE VALUE POTENTIAL IN MARYLAND, CHESAPEAKE BAY, USA

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The US has a $16 billion seafood deficit that the US Department of Commerce and states are attempting to close by legislative policies encouraging expansion of aquaculture in the US. The 2011 National Shellfish Initiative recognizes the benefits to water quality of cultivation of bivalve shellfish aquaculture in addition to the provision of seafood product. More recently, research addressing these policies has resulted approval of the use of harvested oysters as a nutrient best management practice (BMP) in Chesapeake Bay region. Also discussed, but not yet implemented, is economic compensation to the oyster growers for the nutrient removal ecosystem service that the oysters provide. This study used field sampling and a local-scale oyster production model to compare water quality, oyster production, and oyster associated nitrogen removal at two bottom and four water-column Maryland Chesapeake Bay oyster farms. Objectives were to highlight differences in water quality (i.e. oyster food), resultant differences in oyster production, and differences in estimated oyster associated nutrient removal at each farm. An economic valuation analysis was done to also compare the potential payment to the oyster growers for the nutrient removal service if they were included in a nutrient-credit trading program. Production at the six sites varied from 1.78 to 25 metric tons of harvestable oysters acre^{-1} year^{-1}. Oyster filtration-related N removal was estimated to be a range of 19 - 208 kg N acre^{-1} year^{-1}. The potential economic value of N removed was estimated to be a range of $3,324 -$1,069,804 per year.

ECONOMIC TRADE-OFFS BETWEEN TRADITIONAL BOTTOM AND CONTAINER CULTURE OF OYSTERS ON MARYLAND FARMS

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The traditional method of raising oysters in Maryland is to plant spat-on-shell directly on the seafloor area of the lease. Container culture, however, has grown rapidly in Maryland. There are clear economic trade-offs between the two production methods, but these trade-offs have not been evaluated with farm-level data.

Maryland oyster farmers were interviewed in 2017 and 2018 to measure on-farm production and marketing costs for traditional bottom culture and container culture. Comparisons were made of the following economic metrics: total initial investment (facilities, infrastructure, equipment), annual costs (major costs, cost structures, variable and fixed costs, and scale effects), profitability, marketing costs, and risk.

Cost structures differed substantially between the two production methods. For example, fuel was the greatest expense for traditional bottom culture farms whereas labor was the greatest expense for container culture farms. Producers using traditional bottom culture methods tended to use primarily unpaid owner/family labor. Container culture required greater investment capital and marketing costs with overall greater startup costs than did traditional bottom culture. Per farm, the most profitable scenario was that of the larger container culture farms, followed by the larger traditional bottom culture farms. Substantial profitability risk was found across production method/scales, but was generally greater on smaller-scale and container culture farms.

APPLICATION OF MULTIPLE METHODS FOR THE DETECTION AND ENUMERATION OF PATHOGENIC *VIBRIO* SP. IN MID-ATLANTIC SEAWATER AND OYSTERS

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Both *Vibrio parahaemolyticus* (*Vp*) and *V. vulnificus* (*Vv*) infect humans through shellfish and seawater. Detection methods are tedious, expensive and time-consuming. A total of 330 oyster and 330 water samples were collected from three sites in the Delaware Bay, DE, and five sites in the Chesapeake Bay, MD, from May-October 2016 and 2017. The colony overlay procedure for peptidase (COPP) assay for total *Vibrio* (TV), direct plating (DP) on CHROMagar *Vibrio* and MPN-real-time PCR (MPN-PCR) for pathogenic *Vp* and *Vv* were compared. MPN-PCR involved assays for *tlh*, *tdh* and *trh* genes for *Vp* and *vvh*A and *vcg*C genes for *Vv*. All samples were positive for TV by the COPP assay. Positive *Vp* for seawater and oysters by MPN-PCR were 89% and 92%, respectively in MD; 100% for both in DE; and by DP were 32% and 76% in MD; and 71% and 87% in DE. Positive *Vv* for seawater and oysters by MPN-PCR were 99% and 100% in MD; 100% for both in DE; and by DP were 47% and 86% in MD and 58% and 77% in DE. TV was positively correlated ($r = 0.50\text{-}0.69$) with MPN-PCR and DP for Vv in oysters and seawater. TV was significantly correlated ($r = 0.63\text{-}0.65$) with MPN-PCR and DP for *Vp* in seawater but not in oysters. These results indicate that the COPP assay could be a viable alternative to DP or MPN-PCR to indicate total *Vp* and *Vv* levels in seawater and *Vv* in oysters, but not for monitoring pathogenic *Vibrio* sp.

SEA URCHIN HATCHERY TECHNOLOGY

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Echinoid broodstock are collected from the wild and conditioned on macroalgae or prepared diets. The sexes are separate and gametes can be collected via natural/artificial spawning or by sacrificing the adults. Female and male gametes are mixed together. After 5–10 minutes, the eggs are washed with one or more changes of filtered seawater (FSW) to remove any debris and to prevent polyspermy. Fertilized eggs are held in standing cultures at densities of ~1–2 ml of eggs per 100 ml FSW. Resultant larvae can be reared in containers of any size under either static or flow-through conditions. If the former is used, there should be some form of gentle agitation (*e.g.* stir paddles, gentle aeration) and 50–100% of the culture water should be replaced twice a week. Early-stage larval densities should be typically 1,000–1,500 inds L^{-1}, with late-stage densities reduced to 100–800 inds L^{-1}. They can be fed natural or cultured phytoplankton. Competent larvae (ready for settlement/metamorphosis) are typically placed in large tanks or raceways with vertical transparent polycarbonate plates, covered with microbial films, to induce settlement and as a food source for the recently settled juveniles. At about 50 days old, juveniles can be given soft foliose macroalgae or powdered prepared diets. The juveniles remain on these plates until they reach a test diameter of at least 5–10 mm. They are then removed from the plates and transferred to land-based or sea-based grow-out systems or the wild (for stock enhancement).

EFFECT OF TRANSPORT METHOD ON SUBSEQUENT SURVIVORSHIP AND GONAD YIELD AND QUALITY IN THE RED SEA URCHIN (*MESOCENTROTUS FRANCISCANUS*)

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Sea urchin gonad enhancement entails collecting low-gonad-yield sea urchins from the wild, placing them in land-based or sea-based captivity, and feeding them a prepared or natural diet to produce high quality/quantity gonads for marketing. Collection and transportation to the culture facility can be stressful to the urchins and cause subsequent mortalities and sub-optimal gonad yield/quality. Minimizing this handling stress is critical to ensuring maximum survivorship and optimal gonad enhancement, yet very little research has examined this, with no information being available for the red sea urchin (*Mesocentrotus franciscanus*), a candidate aquaculture species in northwestern North America. The present study examined survivorship, gonad yield, and gonad quality (lightness, redness, yellowness, and degree of colour difference) of red sea urchins two weeks after exposure to three 2-hour transport methods: (1) milk crates placed in two plastic fish totes (L × W × H: 122.9 × 109.7× x 120.1 cm, Volume: 993 L; with ten crates per fish tote) that were filled with ambient seawater ('wet crate'), (2) sealed Styrofoam boxes (L × W × H: 55.2 × 33.6 × 40.3 cm, Volume: 38 L) filled with ambient seawater ('wet box'), and (3) sealed Styrofoam boxes without seawater, but with wet burlap placed on top of the urchins ('dry box'). While no gonadal parameters significantly differed between transportation methods, percent survivorships for the wet boxes and wet crates were both 100% while the dry boxes was 58.3% after two weeks, indicating that wet transport would be preferred over dry transport for *M. franciscanus*.

SHELLFISH POISONING AND POISONING SHELLFISH: EFFECTS OF *ALEXANDRIUM CATENELLA* AND *DINOPHYSIS ACUMINATA* ON LARVAL EASTERN OYSTERS

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Paralytic shellfish poisoning (PSP) and diarrhetic shellfish poisoning (DSP) are two serious human illnesses associated with the consumption of shellfish contaminated with algal toxins. Additionally, PSP- and DSP-associated harmful algal bloom (HAB) species, *Alexandrium catenella* and *Dinophysis acuminata*, occur sequentially and simultaneously in Nauset Marsh, Massachusetts, creating a risk of co-exposure. While much study has focused on understanding the toxicity of these HAB species as they relate to human health, there is considerably less research on the effects they have on shellfish. To investigate the potential for these HAB species and their primary toxins, alone or in co-exposure, to affect larval eastern oyster (*Crassostrea virginica*) activity and mortality, 96-h laboratory HAB bioassays with seven-day-old larvae were performed. Exposure to live (10 – 1,000 cells/mL) or lysed (1,000 cells/mL equiv.) Reduced larval activity and some larval mortality was associated with *A. catenella* and *D. acuminata*. Exposure to pure saxitoxin and/or okadaic acid had little effect on larval oysters, demonstrating that these toxins were not wholly responsible for the larval effects observed during live cell and lysate exposures. Exposure to pure pectenotoxin (produced by *D. acuminata*), however, was associated with complete loss of larval activity and rapid larval mortality. Shellfish are more than just vectors for PSP and DSP, larval oysters are negatively impacted by exposure to *A. catenella* and *D. acuminata*.

TRANSCRIPTOMIC RESPONSE DURING COMPENSATORY GROWTH OF THE PACIFIC WHITE SHRIMP, *LITOPENAEUS VANNAMEI*

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The compensatory growth is ability to recover growth after a period of stress including food deprivation. New management strategies based on temporary feed restriction represents an alternative to reduce production cost by taking advantage of the shrimp compensatory growth (CG) capacity. The present work analyzes the changes in the shrimp transcriptomic response during CG. For this purpose, it was carried out a 7-week assay with four treatments: 0 (Control), 7 (R7), 14 (R14) and 21 (R21) days with 50% of feed restriction followed by a period of *ad libitum* refeeding. According to biometrics, after 7d of refeeding, specific growth rates (SGR) increased significantly compared to the control group, indicating a compensatory growth process. At the highest SGR, abdominal muscle from shrimp were sampled for RNA-seq analysis. The treatments R7 and R14 achieved a total compensatory growth compared to control treatment, with a reduction of 15% feed for R14 treatment. The transcriptional analysis showed 276 differentially expressed genes (DEG). The DEG suggest that energy metabolism was affected during CG through the use of lipids and glycogenic amino acids as a way of compensate energy demand, as well as genes associated to oxidative stress related to the accelerated growth. Immune related genes were down-regulated in response to CG. Although the temporal feed restriction allows economical cost savings without losing the final harvest size, the DEG presented in this study suggest that further research is needed to discard potential disadvantages in case of a stress event during compensatory growth of the shrimp *L. vannamei*.

THE *GUISHE* OF *AGAVE LECHUGUILLA* AS SOURCE OF NUTRITIONAL BIOMOLECULES TO PROMOTE SHRIMP PRODUCTIVITY

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Fibres of *Agave lechuguilla* are used as a raw material to make handicrafts by collectors. During the fibres extraction process results the guishe. The guishe is a bagasse and the main by-product of A. lechuguilla. It represents 85% of the total crop, and is discarded to open fields, meaning a waste and a pollution agent. Interestingly, recent studies showed that *guishe* contains molecules with nutritional properties, such as saponins, flavonoids, and sugars. Therefore, in this work, the effect of the crude extract of *guishe* as a feed additive in whiteleg shrimp diets was evaluated. The MS-HPLC analysis of the extract showed the presence of saponins such as diosgenin, smilagenin, hecogenin, manogenin, tigogenin hexose, yucagenin, chlorogenin, diosgenin, diglucoside and the flavonol, quercetin. The crude extract was included into an experimental diet in four levels; 0% (L0%), 0.1% (L0.1%), 0.3% (L0.3%) and 0.6% (L0.6%). Dietary incorporation of the extract was evaluated by zootechnical performance, haemolymph biochemistry, histomorphology, and digestive enzyme activity of shrimps. After 5-week feeding, the L0.3% diet showed significantly higher growth and better feed utilization among treatments. Besides, a significant increase in tubule epithelium height and tubule coverage area from hepatopancreas in shrimp under L0.3% diet compared with the control diet suggest an improvement of the health and nutritional status of the shrimp. In the case of digestive enzyme activity, the crude extract inclusion of L0.3% and L0.6% resulted in a reduction in amylase activity, without effect in glucose levels in the haemolymph. Thus, data suggests that *A. lechuguilla guishe* crude extract contains nutritional molecules that may be used as a feed additive to promote shrimp productivity.

‘OMIC’ TECHNOLOGIES APPLIED TO AQUACULTURE

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`Omic´ technologies refer to a range of modern methods that include genomics, transcriptomics, proteomics and metabolomics. These techniques generate numerous data that can be integrated using bioinformatics to provide information on how the organisms function and how organisms respond to various environmental conditions.

`Omic´ technology has a broad range of application. In the case of aquaculture its applications include genomic selection for selective breeding programs, identification of novel pathogens, identification of microbioma, selection of disease resistant varieties, authentication and identification of species in processed food products, molecular vaccine development, characterization of the physiological mechanisms for stress tolerance, identification of genes involved in immune responses, identification of molecules associated to defence mechanisms or to cellular networks that regulate different biological processes, among which is the elimination of biotoxins in molluscs.

`Omics´ based techniques are increasingly being applied into the study of the biology of many aquaculture species. However, the transfer of these resources to growers and industry, in areas such as hatchery production, diet and nutrition, immunology and disease and food quality and safety, has not been fully realised.

EXPERIMENTAL STUDY OF TOTAL AND POTENTIALLY PATHOGENIC *VIBRIO PARAHAEMOLYTICUS* IN TEMPERATURE-ABUSED AND RESUBMERGED OYSTERS AT SUB-TIDAL AND INTER-TIDAL AQUACULTURE SITES

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The pathogen, *Vibrio parahaemolyticus* (*Vp*), is the leading cause of seafood-borne illness in the US. Thermolabile hemolysin (*tlh*) is a *Vp* species-specific gene that is widely-used to detect *Vp* because it is present in both pathogenic and nonpathogenic strains. The genes thermostable direct hemolysin (*tdh*) and *Tdh*-related hemolysin (*trh*) are considered major *Vp* virulence factors. Common oyster aquaculture practices expose oysters to ambient air. During warm conditions, such exposure can stimulate the growth of *Vp* within oysters and may differentially increase the absolute and relative abundances of pathogenic *Vp* compared to total *Vp* in oysters.

The Massachusetts DMF conducted a temperature-abuse experiment on cultured oysters in Plymouth Harbor, MA. To assess the impact of 48 hours of exposure (typical of air drying practices for anti-fouling purposes) on the abundances of total and potentially pathogenic *Vp*, oysters from both sub-tidal and inter-tidal ‘treatments’ were exposed (abused) for two days then resubmerged at their respective source locations. *Vp* genes *tlh*, *tdh*, and *trh* were measured in initial, abused (day 0) and two, four, six and eight days resubmerged oyster samples. Total *Vp* (*tlh*) increased in abused oysters by three orders of magnitude and returned to environmental concentrations on day 8 of resubmergence in the sub-tidal treatment and day 6 of resubmergence in the inter-tidal treatment. Temperature abuse did not substantially impact *tdh* concentrations, but *trh* concentrations increased 2-3 orders of magnitude and returned to environmental concentrations on day 6 of resubmergence in the sub-tidal treatment and day 4 of resubmergence in the intertidal treatment.

MICROPLASTICS IN SANDY ENVIRONMENTS IN THE FLORIDA KEYS AND THE FLORIDA PANHANDLE, AND THE INGESTION BY SEA CUCUMBERS (ECHINODERMATA: HOLOTHUROIDEA) AND SAND DOLLARS (ECHINODERMATA: ECHINOIDEA)

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Microplastic pollution is an increasing problem in the marine environment. This study had three objectives: 1) determine if seagrass beds and adjacent sand flats in the Florida Keys differed in microplastics concentration, 2) determine if sea cucumbers from the Florida Keys and sand dollars from the panhandle of Florida contain microplastics, and 3) conduct a laboratory experiment on the sand dollar, *Mellita tenuis,* to determine if it will ingest plastic microbeads contained in sediment. Both seagrass beds and sand flats in the Florida Keys contained microplastics. Sediment near Pensacola Beach and in St. Joseph Bay contained microplastics. Sea cucumbers from the Florida Keys and sand dollars from the panhandle of Florida contained microplastics in their gut contents. In the laboratory, *M. tenuis* ingested microbeads in slightly lower proportions compared to surrounding sediment. Both sea cucumbers and sand dollars may make useful animals for monitoring sandy environments for microplastics pollution.

POPULATION GENOMIC ANALYSIS OF THE BLUE CRAB, *CALLINECTES SAPIDUS*, ACROSS ITS RANGE: INSIGHTS INTO GENE FLOW, LOCAL ADAPTATION, AND THE POTENTIAL FOR GEOGRAPHIC SOURCE TRACKING

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Advances in high-throughput sequencing are transforming our understanding of the ecology and evolution of commercially and ecologically significant marine species, such as the blue crab *Callinectes sapidus*. Here, new work is reported assessing the range-wide population structure and genomic signatures of local adaptation in the blue crab utilizing samples collected from 16 populations spanning the Caribbean, Gulf of Mexico, South America, and the east coast of the United States. Genome-wide genotyping was performed via ddRAD sequencing, aligning reads to the 3rd generation of the blue crab genome assembled with Chicago and Dovetail HiC. Approximately 8,100 high quality SNP were generated across samples, and preliminary analyses showed that populations clustered genetically by region, with Gulf of Mexico populations grouping together and distinctly from Caribbean populations and South American populations. Pairwise Fst estimates among populations were high for between-region comparisons (>0.25) indicating restricted gene flow over large geographic scales. Interesting patterns of structure were also observed within regions, particularly for the Caribbean populations. Population assignment with the entire dataset or just outlier loci was able to correctly assign most populations at a high rate except for Puerto Rico which showed admixture with Gulf and other Caribbean populations. Outlier locus analyses, genotype environment associations, and comparisons with physical oceanographic modeling-based predictions of larval dispersal will also be discussed. This is the first population genomic assessment of the blue crab across its range and results should advance understanding of how oceanography and latitudinal variation in environment shape gene flow and adaptation in this species.

EFFECT OF TIDAL RESUSPENSION WITH OYSTER BIODEPOSITS ON NUTRIENT AND OXYGEN DYNAMICS

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To test the effect of biodeposit resuspension on the nutrient and oxygen dynamics a 4-wk experiment in three 1000 L shear turbulence resuspension mesocosm (STURM) tanks (R) and three 1000 L non-resuspension tanks (NR) was performed. All tanks contained defaunated muddy sediment and brackish estuarine water, received daily additions of oyster biodeposits, and had similar water column RMS turbulent velocities (~ 1 cm s^{-1}), energy dissipation rates (~ 0.08 cm^2 s^{-3}), and tidal cycles (4h mixing-on and 2h mixing off); however, while bottom shear stress was low in NR tanks, high instantaneous bottom shear produced sediment and biodeposit resuspension in R tanks during the mixing-on cycles.

Resuspension and biodeposit addition resulted in a complex nutrient and oxygen dynamics in the water column as well as altered seabed fluxes. While in NR tanks sediment dissolved oxygen uptake was three times higher than in R tanks, water column dissolved oxygen concentrations were 2.3 times lower in the R tanks than in the NR tanks. Sediment dissolved inorganic nitrogen efflux in R tanks and uptake in NR tanks, respectively, were mediated by microphytobenthos abundance and biodeposit deposition. Concentrations of nitrite plus nitrate were significantly higher in the water column of the R tanks, suggesting nitrification in response to particulate organic matter (POM) decomposition. Seabed and bottom boundary-layer biogeochemical processes affected the nutrient and oxygen dynamics.

PROJECTED EFFECT OF FUTURE COASTAL ACIDIFICATION CONDITIONS UPON THE PHYSIOLOGY OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) AND THE ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*) THROUGH DEB MODELING

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Global carbon dioxide (CO2) emissions have increased significantly since the 1900s. The ocean absorbs one third of the CO_2 emitted, resulting in the ocean becoming less basic. Coastal ecosystems, where high nutrient levels and intense plankton production and decomposition cycles further increase pCO_2, are especially vulnerable to transient, extreme pCO_2 levels. Responding to abnormal CO_2 levels, marine organisms may expend more energy to regulate physiological chemistry. The eastern oyster and the Atlantic surfclam, two economically-important bivalves in the U.S., lower feeding rates and elevate metabolic rates, inducing a delay in growth rate, when exposed to coastal acidification (CA).

The effects of CA upon oyster and surfclam bioenergetics were explored through 3-month laboratory experiments in which juveniles were exposed to different pCO_2 treatments. Growth and physiological rates (respiration, feeding, excretion) were measured periodically to calibrate a bioenergetics model based upon the Dynamic Energy Budget (DEB) theory. DEB modeling has been applied widely to bivalves and has enabled quantification of physiological responses to environmental physicochemical conditions. The model was adapted to take into account the effects of elevated pCO_2 upon oyster and surfclam bioenergetics. Different scenarios integrating future environmental $\boldsymbol{p}CO_2$ and temperature conditions have been simulated, yielding growth projections to reveal how oyster and surfclam populations could respond to future environmental pCO_2 conditions.

OCEAN ACIDIFICATION EFFECT ON EASTERN OYSTER, SURFCLAMS, AND SEA SCALLOPS: COMMONALITIES AND DIFFERENCES

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Global carbon dioxide emissions have increased significantly since the 1900s. The ocean absorbs approximately one third of the CO2 emitted, resulting in the ocean becoming less basic. The eastern oyster (*Crassostrea virginica*), the Atlantic surf clam (*Spisula solidissima*), and the Atlantic sea scallop (*Placopeten magellanicus*) all are economically-important bivalves in the northeast and mid-Atlantic region of the United States. The possible effects of ocean and coastal acidification upon the three species were explored using physiological measurements of juveniles exposed to three different pCO_2 levels. Growth, tissue weight, shell weight, respiration, feeding rates, and excretion rates were measured to estimate scope for growth. Commonalities and differences in physiological responses will be highlighted. The results will be used to guide management of both fisheries and aquaculture as the marine environment changes.

THE CONFUSION OF COMPLEXITY VERSUS DYNAMICS: HABITAT MANAGEMENT AND SURFCLAMS OFF NANTUCKET, MASSACHUSETTS, USA

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A habitat management area (HMA) has been established east of Nantucket based on the premise that charismatic attached epifauna, supposedly part of a stable complex habitat supporting spawning of cod and other groundfish, will suffer dire impacts from surfclam dredging. The region is a location hosting expansion of the surfclam (*Spisula solidissima*) range as the North Atlantic warms up and now supports the largest surfclams in the stock. Competing for space are extensive mussel (*Mytilus edulis*) beds. Both species occupy the sandy habitat and exclude each other locally, a case of multiple stable states. A survey of the region revealed (1) surfclams first moved into the region circa 2004 and densities have continued to expand; (2) mussels are nearly entirely found living in large mats floating on sand; (3) the Great South Channel region is an area of high current flow, migrating sand dunes of many meters height, and continual scour; (4) boulders, rocks, and cobbles are continually exhumed and buried and in the process scoured clean of attached epifauna; (5) not surprisingly, charismatic attached epifauna cannot and do not live on these sedimentary particles (and neither do mussels that likewise cannot withstand continual scour). Nonetheless, the HMA continues under the surmise that any movement of a boulder, rock or cobble by a dredge risks disastrous ecological damage, a conclusion emersed in certainty as long as a failure to appreciate the dynamics and ecology of the region continues

THE POTENTIAL TO MODEL FUTURE RANGE SHIFTS OF COMMERCIAL SPECIES AND THEIR FISHERIES: A POSSIBLE NEW APPROACH

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The marine world is warming and the North Atlantic is warming at a rate faster than most of the world's oceans. Many commercial species are moving north and offshore. Competitive uses of the continental shelf, such as wind energy development, are static watchers of this northward progression. In the Mid-Atlantic, the exemplar is the Atlantic surfclam *Spisula solidissima*. Where will surfclams be in 20 years? Where too will the fishery operate? How will the interaction of the stock and fishery with wind energy development proceed? Population dynamics is usually described based on the relationship of broodstock to recruitment, modulated by a constant natural mortality rate. But, surfclams, like many commercial shellfish, do not have a broodstock-recruitment relationship (steepness ∼ 1) and more importantly, the spatial distribution of recruitment cannot easily be predicted. Future range shifts, therefore, cannot be predicted using only recruitment dynamics. We suggest that an alternative is to describe population dynamics in terms of von Bertalanffy growth and spatially variable mortality, tuning spawning stock biomass (SSB) by the strength of a negative binomial random process for recruitment. A principal hypothesis is that spatially variable SSB is primarily a product of spatially variable mortality rates, secondarily von Bertalanffy growth, and lastly patchy recruitment. The idea is developed into a coupled fishery-population dynamics model and evaluated using federal survey data and the known patchiness of fishing effort focusing on highly productive patches, both of which require accurate fine-scale distributional patterns of SSB over a dynamic latitudinal and cross-shelf range.

EFFECT OF AN ENRICHED DIET ON THE GLOBAL PERFORMANCE AND TRANSCRIPTOMIC RESPONSE IN *OCTOPUS VULGARIS*

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The culture of the common octopus, *Octopus vulgaris*, has been a big challenge for the aquaculture sector over the last decades. Animal settlement at the benthic phase was the main constraint to close the life cycle since massive mortalities occurred at the end of the planktonic stage. It is now known that diet requirements might influence the successful of settlement more than any other culturing parameter. Indeed, a proper diet was the trigger element that allowed closing the life cycle on this species.

In this study a transcriptomic comparison on 20 days post-hatching paralarvae was carried out to compare the effect of a mixed enriched diet and *Artemia*-based diet. The whole paralarvae was used for RNA extraction and subjected to RNA-sequencing using the Illumina platform.

Global performance in terms of weight and survival was significantly higher after feeding on the mixed enriched diet. A higher number of transcripts related to metabolism, biosynthesis and transport were up-regulated in *Artemia*-based diet. This might indicate that the digestion process was still ongoing at the moment of sampling or internal reserves were mobilized for energy obtaining due to a nutritionally deficient diet. Energy consuming processes seem to be largely prolonged after feeding on *Artemia*, especially considering that animals were under starvation for 12 hours before sampling. The enriched diet, on the other hand, might favor the proper development of crucial traits such as vision and neuronal development as transcripts related to crystalline formation and motor neuron preservation are higher expressed in these animals.

EASTERN OYSTER TRANSCRIPTOMIC RESPONSE TO DIFFERENT *PERKINSUS MARINUS* EXPOSURE METHODS AND INFECTION INTENSITIES

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In controlled lab challenges, *Perkinsus marinus* dosing method and infection intensity affect oyster responses. Exploring how oyster survival and gene expression vary with exposure method and parasite load can broaden our understanding of this host-parasite interaction. We compared response traits and global expression patterns over time in an Eastern oyster family exposed to *P. marinus* through suspension feeding and direct injection. All exposed oysters received a dose of 5×106 *P. marinus* cells g^{-1} wet tissue weight, but oysters in the injected group had higher initial infection intensity and reduced survival probability compared to the fed group. Using RNAseq, we identified differentially expressed transcripts between fed and control animals 6 h after exposure and between fed and injected groups at 36 h, 7 d, and 28 d post exposure. Immediately after infection, caspase-8 and transcripts associated with mediating cell damage from reactive oxygen species were upregulated in the fed group compared to unchallenged controls. Early in the infection process, increased innate immune activity and upregulation of transcripts involved in proinflammatory cytokine pathways (*e.g.* toll-like receptor 4 and TNF receptor-associated factor 6-like protein) were observed in the injected relative to the fed group. By 28 d post-exposure, the fed group expressed transcripts associated with growth, specifically microtubule-based processes, at a higher level than the injected group. This study demonstrates that dosing method impacts initial parasite load, survival, and transcriptomic response to infection with *Perkinsus marinus* and highlights the importance of considering dosing method when interpreting interactions between parasite and host.

RESPONSES OF JUVENILE *CRASSOSTREA VIRGINICA* TO FLOOD-ASSOCIATED WATER QUALITY STRESSORS

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Oyster reefs provide essential ecosystem services, but have been severely degraded worldwide due to overharvesting, habitat destruction, and disease. Extreme flooding events further threaten oyster survival by reducing salinity and introducing additional stressors into estuaries. Restoration and conservation of sustainable oyster reefs requires an understanding of where oysters can survive and thrive, especially in the face of increasing frequency of flooding disasters. We examined the effect of water quality stressors associated with flooding events on *Crassostrea virginica* growth and survival by exposing juvenile oysters to either low salinity, low pH, low dissolved oxygen, or a harmful algal bloom-associated toxin (microcystin-LR) for 24 days in the lab. There was no difference in juvenile survival between stressor treatments, but growth was 46% lower for seed exposed to low dissolved oxygen, pH, or salinity. Lab-exposed juveniles were subsequently deployed for 2 months in the field to determine how prior exposure to stressors affected growth and survival under natural settings. Survival was significantly reduced only in juveniles previously exposed to low pH, and there was no difference in growth between stressor treatments. Additionally, juvenile oysters were exposed to the same flood-associated stressors over a shorter duration (i.e., 6-day lab experiment) to provide mechanistic insights into growth and survival responses observed in the 24-day lab exposure and field experiments. Future research will assess the combined impact of these flooding-associated water quality stressors to better understand how these multiple stressors may limit the recovery and resilience of oyster reef ecosystems.

ASSESSING THE EVOLUTIONARY RESPONSE OF EASTERN OYSTER LARVAE 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 CO2. 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 CO2. 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.

AN ASSEMBLED GENOME REFERENCE FOR THE EASTERN OYSTER: A RESOURCE FOR DISCOVERY AND INNOVATION

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Genetic variation in the eastern oyster (*Crassostrea virginica*) has been studied for over half a century with questions relating to adaptation, disease tolerance, sex determination, population structure, sweepstakes reproduction and much more. Intense interest has been sustained because of this species' commercial importance in wild fisheries and aquaculture, the desire to supplement populations for fisheries or restoration purposes, and with basic research questions. Much has been learned, but many of these endeavors were limited by the genetic resources of the day. The chromosome-scale reference genome assembly for *C. virginica*, described in this talk, represents a turning point for many of these research objectives. Metrics indicating robustness of the assembly and some basic genome structure findings will be briefly described before focusing on geographic population structure and selected strain divergence as examples where genome-scale analysis of diversity provides new insights. Samples from Maine to Texas, along with five of the major selected strains, were subjected to whole genome re-sequencing. With both single nucleotide and copy number variants, the overwhelming and genomically pervasive pattern is divergence between Atlantic and Gulf of Mexico (GoM) regions, recapitulating previous inferences from lower resolution mitochondrial and nuclear marker studies. High genetic diversity has been maintained in all selected strains examined, and their divergence from source stocks is modest relative to the Atlantic - GoM divide. Evidence of selection affecting specific loci was most convincing in high and low salinity contrasts within estuaries, where background noise from genetic drift was likely reduced by high gene flow.

AN INVESTIGATION OF THE HARVEST PRACTICE OF SALTING RAZOR CLAMS IN THE INTERTIDAL FISHERY

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The intertidal fishery for razor clams, *Ensis directus*, has become increasingly important for areas of Cape Cod Bay in Massachusetts. The predominant method of harvest has been the use of brine solutions applied to razor clam 'tells' or burrows. The practice is controversial among resource managers, so basic information about the method was investigated. In a series of six post-harvest survival assessments comparing hand harvested control clams to two different size classes of salted clams, salted clam survival was the same or even higher than controls. Survival averaged 85% for hand dug controls, 89% for salted razor clams that were under the legal harvest size of 5 inches, and 97% in salted razor clams of legal size. Survival and condition in refrigerated storage following harvest was also similar between salted razor clams and those harvested by hand. Histological evaluations compared salted razor clams to controls immediately following harvest, then three days and three months after salting. Only the gills were affected by salting, with salted clams showing foci of mild epithelial erosion of the plica immediately after harvest and subsequent mild hyperplastic of the plical epithelium by three days into recovery. No histological differences were noted after three months. The survival of the salted clams along with observations in the field that the volume of brine applied is small and targeted so dissipates fairly rapidly, indicates the salting practice is not likely to be any more harmful than allowing a fishery harvested by other means.

AUTOMATING OYSTER AQUACULTURE WITH THE SUN

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Oyster aquaculture is very labor intensive, often growing less than one million oysters per acre depending on gear types and site location. Floating and off-bottom gear is typically positioned in the near-shore environment or in the upper few feet of the water column, limiting overall growth and increasing conflicts with landowners and other stakeholders.

The patent-pending Solar Oyster Production System (SOPS) was developed to take advantage of offshore space not used by other aquaculture systems. The SOPS supports a series of cages in over twenty feet of water and uses solar power to mechanically rotate each cage through the water column and up to the surface, providing desiccation/air exposure and mechanized washing, minimizing labor costs. The mooring system allows location of the SOPS in higher-energy environments, with integrated anti-poaching technology, allowing units to be placed miles off-shore, potentially minimizing stakeholder conflict. In systems with high algal density and moderate energy, the system aims to grow up to 2.4 million oysters for harvest annually on each 90 × 53 ft. (0.11 acre) SOPS unit.

The nutrient removal efficiency of oysters is well documented. State and federal regulatory agencies in the Chesapeake Bay watershed have approved procedures for nitrogen and phosphorus credits for oysters harvested from aquaculture operations that can be traded on Maryland's nutrient credit market. Oysters grown and harvested annually from one, 0.11 acre, SOPS oyster aquaculture platform will remove the same amount of nitrogen from the Bay as replacing 90 acres of impervious surface with forest.

CHARACTERIZATIONS OF THE IMMUNE-REGULATORY FUNCTION OF CSDE-1 IN *CRASSOSTREA VIRGINICA* HEMOCYTES

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Oysters, like all organisms, can respond to environmental stressors by regulating the location, availability, and rate of translation of specific mRNA to alter the available cellular proteome. The coordination of post-transcriptional events is mediated largely by RNA-binding proteins (RBP) which form protein-RNA complexes to regulate essential cellular processes. This study focused on a single RBP, Cold Shock Domain Containing Protein E1 (CSDE-1), as a model to probe translational controls by RBP in the eastern oyster, *Crassostrea virginica*. The coordinated regulation of the oyster primary immune response facilitated by hemocytes suggests hierarchical control of gene transcriptional and translational events, some of which are predicted to be locally orchestrated by CSDE-1 bound transcripts. Existing literature, *in-silico* analysis, and preliminary candidate-based protein-RNA binding assays predict hundreds of target RNA of CSDE-1 regulation known to function in the immune response, ranging from antimicrobial defensins to toll receptors. Tissues isolated from adult American oysters ubiquitously express CSDE-1, with notable enrichment in the immunocompetent hemocyte cells. In response to *E. coli* lipopolysaccharide immune stimulation of hemocytes, CSDE-1 expression and localization are modulated, and RNA Immunoprecipitation (RIP) binding assays followed by RNA sequencing confirm that CSDE-1 binds immune-related mRNA transcripts. These data implicate CSDE-1 as a driver of protein expression changes during immune challenge and indicate that translational control by RNA-binding proteins such as CSDE-1 appears to be an evolutionarily ancient, conserved mechanism with broad implications in disease and stress responses.

THE ROLE OF MITOCHONDRIAL AND LYSOSOMAL PERMEABILITZATION IN THE EASTERN OYSTER APOPTOTIC RESPONSE TO *PERKINSUS MARINUS*

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Apoptosis, or programmed cell death, is part of a complex, innate-immune response to *Perkinsus marinus* infection in the Eastern oyster, and apoptosis of infected hemocytes may reduce parasite replication. Previous studies revealed apoptosis stimulation shortly following *P. marinus* infection, but the parasite may be able to limit apoptosis as infection proceeds. Specific organelles and pathways mediating the apoptotic response to *P. marinus* are unknown. Eastern oysters were challenged *in vivo* with *P. marinus*, and hemocyte apoptosis, caspase 3/7 activation, and lysosomal permeabilization were investigated 7 d post-infection using flow cytometry. Granular hemocyte apoptosis significantly decreased in challenged oysters as compared to control oysters, indicating possible inhibition by the parasite. Caspase 3/7 activation and lysosomal permeabilization were not significantly affected by *P. marinus*, indicating likely involvement of a caspase-independent pathway in hemocyte response and no involvement of lysosomal permeabilization. Oyster hemolymph samples were challenged *in vitro* with *P. marinus* at four multiplicities of infection (MOI; *P. marinus* to hemocyte 1:1, 5:1, 10:1, and 25:1) for 1 hr, and hemocyte apoptosis and mitochondrial permeabilization were investigated with flow cytometry. Granular hemocyte apoptosis increased at all MOI compared to control, although levels of mitochondrial permeabilization did not change significantly, suggesting mitochondria are not involved in the apoptotic response to *P. marinus*. Further research explores the role of Inhibitor of Apoptosis Proteins (IAP) in modulating hemocyte apoptosis in response to *P. marinus* challenge. Uncovering pathways regulating eastern oyster apoptotic response to Dermo disease may aid in targeting genes for breeding for disease resistance.

NON-CANONICAL EPIGENETIC SYSTEM OF BACTERIAL ORIGIN IN AQUATIC MICRO-INVERTEBRATES

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Epigenetics is the study of mechanisms that have the capacity to direct regional and local activation or silencing of genes and transposons. The interest in epigenetic mechanisms has added an additional layer in the eukaryote genome complexity, which include covalent modification of histones, DNA methylation, and non-coding RNA. The genome contributes to epigenetic processes by encoding the necessary enzymatic machinery, such as methyltransferases, demethylases, or RNA-mediated silencing proteins. Altogether, with the inclusion of new sequencing techniques, it is becoming more feasible to characterize new molecular-level epigenetic factors even in non-model organisms.

Bdelloid rotifers are microscopic freshwater invertebrates able to survive desiccation at any life stage and to reproduce asexually. The genome of the bdelloid rotifer *Adineta vaga* is unusual in having over 8% of its genes originated from non-metazoan (predominantly bacterial) sources. Nevertheless, transposable elements (TE) span only about 3.5% of the *A. vaga* genome, an unusually low fraction for a eukaryote. TE content is apparently being kept at a very low level by an expanded machinery for RNA-mediated silencing, which ensures production of pi-like RNA leading to TE repression. Recently, bdelloid rotifers were found to lack the typical eukaryotic Dnmt methyltransferases responsible for 5mC DNA modifications, but instead encode an amino-methyltransferase of bacterial origin, which is fused to a eukaryotic chromodomain. It is proposed that the *A. vaga* amino-MTase may form a new layer in a genome defense system against invading TE, which do not proliferate efficiently in bdelloid genomes and could be subject to unusual forms of epigenetic regulation.

SELECTIVITY OF TWO COMMERCIAL DREDGES FISHED IN THE NORTHWEST ATLANTIC SEA SCALLOP FISHERY

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Size selectivity curves were estimated for two commercial dredges fished in the U.S. Atlantic sea scallop (*Placopecten magellanicus*) fishery. Traditionally, the New Bedford style dredge (New Bedford dredge) has been used by the commercial fleet; however, since 2013, the Coonamessett Farm Turtle Deflector dredge (turtle dredge) has been required seasonally in the Mid-Atlantic region. This analysis provides selectivity and relative efficiency estimates for both dredges. Selectivity information for the turtle dredge is currently not quantified and selectivity for the New Bedford dredge was originally assessed in 2008. The SELECT method was employed to model scallop catch-at-length data for each commercial dredge with data collected during the Virginia Institute of Marine Science fishery independent surveys in 2015 – 2017. The surveys were conducted in the Mid-Atlantic and Georges Bank regions of the resource in three distinct areas. A paired study design was employed, where a non-selective National Marine Fisheries Service sea scallop survey dredge and either a turtle dredge or New Bedford dredge were towed simultaneously at each survey station. Results indicated the 50 percent retention length was 98.2 mm, with a selection range of 28.2 mm, and a relative efficiency of 0.83 for the turtle dredge. New Bedford dredge results estimated a 50 percent retention length of 107.4 mm, selection range of 50.5 mm, and relative efficiency of 0.81. Selectivity profiles for both dredges were also compared to the 2008 results to assess for time varying changes in selectivity.

PERSPECTIVE ON DISSEMINATED NEOPLASIA IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, BASED ON ANALYSES IN VIRGINIA FROM 1999-2020

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Disseminated neoplasia (DN), a disorder characterized by the uncontrolled proliferation of abnormal cells circulating in the hemolymph of affected bivalves, has received increased attention with the observation of transmissible forms of the disease in *Mya arenaria* and *Mytilus* species. Recent reports of a high DN prevalence with possible transmission in *Mercenaria mercenaria* in particular has underscored our need to better understand DN dynamics in key commercial species. Toward this end, we reviewed diagnostic data from 1999-2020 for eastern oysters *Crassostrea virginica*, with a primary focus on lower Chesapeake Bay, for perspective on the disease in this species. DN was occasionally detected in samples of wild oysters but was not common, with mean annual prevalence in fall survey samples from 30 Virginia oyster reefs ranging from 0.0-0.2% and a maximum prevalence at any Virginia reef of 4.2%. The highest documented prevalence in any wild oyster sample we evaluated from any region was recorded from a site in Apalachicola Bay in 2007, in which DN prevalence was 13.3%. DN has more frequently been observed in aquacultured oysters, although still at generally low prevalence (≤ 12%), and with no evidence that the condition causes substantial mortality. DN in some cases was detected in several distinct aquacultured oyster lines at the same site, which is evidence for an infectious etiology, the nature of which remains to be resolved. Regardless of etiology, available data suggests that DN should not presently be viewed as representing an emerging disease threat to eastern oysters.

VIBRIO PARAHAEMOLYTICUS STRAIN-LEVEL DIVERSITY IN SEDIMENT, WATER, AND OYSTERS IN AN AQUACULTURE EMBAYMENT

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The objective of this study was to examine *Vp* diversity in a coastal aquaculture embayment and to better understand *Vp* dynamics in oyster farm conditions. Bacteria were isolated weekly from sediment, water, and oyster circulatory fluid (hemolymph) collected from Duxbury Bay, Massachusetts. Multilocus sequence typing (MLST) was performed to identify isolates to the strain level for phylogenetic analysis. Environmental *Vp* isolates were compared to environmental and clinical reference sequence types (ST) to assess the strain diversity and potential health risk *Vp* could cause from raw oyster consumption. Fifteen different ST were identified from 27 isolates confirmed as *Vp*, all originating from the same embayment. Three *Vp* isolates were identified as ST 34, an ST associated with a 2010 *Vp* outbreak in Chesapeake Bay, Maryland. Phylogenetic analysis indicated a high diversity of *Vp* strains on almost every sampling date from July to September of 2019 along with most strains potentially categorized as novel ST. Isolates were also assayed by PCR for thermostable direct hemolysin (*tdh*) and tdh-related hemolysin (*trh*) genes, which are considered virulence factors. Approximately 11% of isolates possessed *tdh*, *trh* was present in 9% of isolates, and two isolates were positive for both. Results demonstrated high diversity of *Vp* ST at any single collection date and a seasonal influence on strain diversity. Understanding *Vp* dynamics in an aquaculture embayment can mitigate potential harm to consumers who purchase raw oysters and provide an avenue to further public health efforts to curb gastroenteritis cases caused by the pathogen.

ASSESSING ECONOMIC IMPACTS TO THE US COMMERCIAL SURFCLAM FISHING INDUSTRY FROM OFFSHORE WIND ENERGY DEVELOPMENT

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The US Atlantic continental shelf supports a number of important commercial and recreational fisheries and has also been shown to hold considerable wind energy development potential. The fishery for Atlantic surfclam (*Spisula solidissima*) generates approximately US $30 million in landings revenues annually, distributed across ports throughout the mid-Atlantic and northeast US. Due to overlap between areas of surfclam harvests and potential wind energy leasing, the Atlantic surfclam fishery was identified to be among the most exposed to possible impacts from offshore wind energy development. Fishery impacts will depend upon wind array size, placement, and configuration, as well as any fishing or transit restrictions. Given the potential for novel behavioral responses to wind energy infrastructure (e.g., steaming around arrays or through without fishing), traditional spatial choice econometric models relying on existing observations of fishing behavior may yield only limited insights. In this project, an existing integrated ecological-economic agent-based model is adapted to evaluate the potential economic effects of wind energy development on the surfclam fishery. The model incorporates spatial dynamics in stock biology, heterogeneous captain and processor behavior, and federal assessment and management processes. Advisory teams representing the surfclam industry, fisheries management, and wind energy development were formed to assist in model calibration, validation, and identification of simulations for impact assessment. Model results are used to explore fishery-energy tradeoffs and evaluate impacts associated with a variety of development alternatives.

IDENTIFYING MOLECULAR MARKERS ASSOCIATED WITH RESILIENCE TO OCEAN ACIDIFICATION IN THE EASTERN OYSTER

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Natural genetic variation is a valuable source of resilience to changing environments. The eastern oyster, *Crassostrea virginica*, lives in spatio-temporally highly variable environments. This species is able to survive in a wide variety of environments due to its physiological plasticity, evolutionary adaptation to specific environments, or both. It is well-recognized that the evolution of resilience to climate related stressors depends on the standing stock of genetic variation. This study aimed at the identification of molecular pathways associated with oyster resilience to ocean acidification (OA). Adult oysters were spawned and larvae were reared in ambient $p\mathrm{CO}_2$ of ~600 ppm) or acidified (∼1200 ppm) conditions immediately upon fertilization. RNA and DNA samples were collected before larvae were moved to pCO2 treatments, after 96 hours in treatments, and after metamorphosis. Samples were processed for gene expression using RNASeq and SNP profiling by ddRADSeq. Detected variants from survivors of OA were related to biomineralization, calcium ion binding, cell differentiation, ion channel activity and hemocyte function. Upregulated genes under OA conditions included genes related to the above functions as well as response to stress. Downregulated genes were involved in immunity and cell signaling. Overall, metamorphosis appeared to be more of a selective pressure than larval development. This research indicates that resilience to OA is at least partially dictated by genetics.

ECOLOGICAL AND ENVIRONMENTAL DETERMINANTS FOR THE PATHOBIOME OF BAY SCALLOPS, *ARGOPECTEN IRRADIANS*, IN THE NORTHERN GULF OF MEXICO

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The bay scallop, *Argopecten irradians*, once supported a commercial fishery in Florida but their populations declined and the fishery was closed in 1994; however, a recreational fishery remains along the Florida gulf coast from Gulf to Pasco County despite evidence of further population decline. Therefore, characterizing potential threats beyond fishing is important to ensure fishery sustainability and the success of ongoing restoration efforts. Environmental change is one well-known threat, especially to coastal fisheries, but now disease is increasingly recognized as a prominent threat. To understand the impacts of environmental drivers and disease on the population ecology of the bay scallop we are examining their pathobiome across their fished range. The 'pathobiome' refers to an organism's pathogenic microbes, which cause disease. Three study sites were chosen within Florida's recreational scallop fishery: St. Joseph's Bay in the northern Gulf of Mexico, offshore of the Steinhatchee River in the Florida Big Bend, and offshore of Hernando County, Florida at the southern end of the fishery. Each site was visited prior to the opening of the fishery to survey the abundance and distribution of scallops, and to collect samples ($n=50$) for the creation of parasite profiles. At each location, water quality parameters were measured, and benthic type was recorded. Using a combination of traditional histological methods and molecular diagnostics we have so far identified 10 putative parasites from which to describe the geospatial distribution of their pathobiome.

IDENTIFICATION OF CHEMOSYNTHETIC SYMBIONTS IN THE LUCINID CLAM, *PILLUCINA PISIDIUM*, INHABITING A LAGOONAL SEAGRASS BED IN JEJU ISLAND ON THE SOUTH COAST OF KOREA

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Marine bivalves are often found to be associated with symbiotic microbes which provide a substantial amount of energy to the host. The marine bivalves associated with the chemotrophic bacteria have been identified from the intertidal zones to the deep-sea hydrothermal vents where the environments are enriched with reduced chemical substances. In this study, an association of chemosynthetic bacteria with a lucinid bivalve *Pillucina pisidium* occurring in a subtidal seagrass bed in a lagoon on the east coast of Jeju Island in Korea was investigated. A total of 360 clams were collected from *Zostera marina* bed for analysis. The mean shell length of *P. pisidium* was 7.0 mm and tissue wet weight was 26.2 mg. Histology revealed that *P. pisidium* has unusually thick gills, which are attributed to 16.5% of the total tissue weight. Histology also revealed that the digestive gland and the stomach were less developed compared to other bivalves, suggesting that *P. pisidium* has another source of food except for the filtered food particles from the ambient environment. Scanning electron microscopy showed symbiotic bacteria in the gills. The carbon and nitrogen stable isotope analysis indicated the bacterial fixation of carbon and nitrogen occurring in the gills. Next Generation Sequencing identified the thiotrophic and diazotrophic bacteria *Alkalispirochaeta* sp. and *Sedimenticola* sp. predominant in gill filaments. The stable isotopic and NGS analysis strongly suggested that *P. pisidium* harbors chemotrophic microbes in their gills, which use the reduced sulfur in the environment.

COMPARATIVE ANALYSIS OF HABITAT PROVISIONING BY SHELLFISH-BASED LIVING SHORELINE PROJECTS IN THE DELAWARE ESTUARY

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The development of coastal defense strategies against storms and sea-level rise are at the forefront for many vulnerable, coastal communities. Many efforts are underway to replace or improve traditional coastal defense strategies such as seawalls, bulkheads, and other structures with living shoreline (LS) tactics that integrate ecological structure and function into their design. Their aim is to restore or enhance ecosystem services provided when flora and fauna colonize shorelines, including stabilization. Living shorelines vary widely from promoting vegetation to creating biogenic reefs or a combination of grey structures with plantings and reefs. In the mid-Atlantic and elsewhere, oysters and mussels are often chosen as key elements in LS for the structural engineering they can provide. A complementary benefit to shellfish-based LS is the habitat provisioning they offer wildlife. Several studies in the Delaware Estuary have quantified this benefit by making comparisons to adjacent reference shorelines. This presentation explores a comparative analysis of these projects across the system to provide a broader perspective on the implications for habitat enhancement by employing nature-based alternatives to shoreline defense in the region.

VIDEO DOCUMENTATION OF THE MARINE COMMUNITY UTILIZING AN OYSTER FARM

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Shellfish growers routinely observe fish and invertebrates interacting with their aquaculture gear. To quantitatively assess these observed interactions, point-of-view (GoPro) cameras were used to document fish activity in and around oyster cages, floating bags, and a natural marsh habitat on an oyster farm in the Little Egg Harbor region of Barnegat Bay, New Jersey in 2018 and 2019. At least 27 species from 4 phyla were observed across all days and sites in over 100 hours of video. Nekton abundance was determined using MaxN, defined as maximum number of individuals of a given species present within each 1-minute segment of video. Species of both ecological and economic importance in the local ecosystem utilized the farm gear as habitat. MaxN values varied across sampled seasons and habitat type. Most frequently, juveniles of a given species were observed, suggesting that the oyster farm may support and enhance the natural nursery function of the marshes. Additionally, observations indicated a stochastic relationship between wildlife and human activity on the farm. This collaborative work is part of an ongoing effort underway in Long Island Sound by the NOAA Milford Lab and is a first step towards a comprehensive regional network characterizing and evaluating fish habitat provisioning on off-bottom oyster farms.

ASSESSING THE ROLE OF BLUE CRAB PREDATION IN DRIVING TOP-DOWN REGULATION OF A SALT MARSH TROPHIC CASCADE

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A trophic cascade is an interspecies interaction where a change in the abundance or behavior of one trophic level has direct and indirect impacts on the others. In the salt marsh ecosystem, the blue crab (***Callinectes sapidus***) facilitates smooth cordgrass (*Spartina alterniflora*) growth through its predation on the periwinkle snail (*Littoraria irrorata*). This project aims to confirm the cascade using a set of recently proposed criteria and also assess the role of the blue crab as a top-down predator. First, the predation pressure of *C. sapidus* on *L. irrorata* was tested with tethering. Groups of periwinkles were placed at 0m, 1m, 3m, and 5m from the marsh edge for 24 hours. Mortality rates indicate that the number of present and absent snails changes with distance ($p=0.003$). Specifically, snails at the edge of the marsh are more likely to be preyed upon than snails in the interior. Predation is equally likely at 1m, 3m, and 5m. The most frequent predation technique at all distances was shell crushing ($p<0.005$), suggesting that these snails were eaten by blue crabs. If blue crabs have restricted access to the marsh interior, only a subset of the periwinkle population may be available to them. Second, the *C. sapidus* diet will be characterized using novel genetic barcoding techniques. Stomach contents will be identified and ranked with an Index of Relative Importance (IRI) to determine the prevalence of *L. irrorata*. Thorough investigation of these interspecies interactions is critical to understanding how the salt marsh functions as an ecosystem.

DOPAMINE RECEPTORS: A GENOMIC STUDY OF THE BIVALVE MOLLUSC *CRASSOSTREA VIRGINICA*

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The gill lateral cells (GLC) of *Crassostrea virginica* are innervated by dopamine and serotonin nerves. Dopamine slows down GLC cilia beating and serotonin accelerates them. Dopamine receptors are classified as D1R and D2R. Pharmacological, cell biology and immunofluorescence work of our lab found the dopamine receptors involved in GLC cilia inhibition are D2R-like in GLC and D1R-like in cerebral and visceral ganglia. HPLC studies detected dopamine in gill, cerebral and visceral ganglia of *C. virginica*. Immunofluorescence histochemistry studies showed the presence of dopamine neurons in the ganglia, D2R-like receptors in GLC and D1R-like receptors in the ganglia. Recently the genome of *C. virginica* has begun to be mapped. To test the hypothesis *C. virginica* contains genes for dopamine receptors and these receptors are similar to those in other animals, BLAST searches of the NCBI database using DNA and protein sequences of *C. virginica* D1R and D2R genes were conducted. Gene matches for D1R genes were found on chromosome 4 and 5, and D2R genes on chromosomes 3 and 5 of *C. virginica*. BLASTS of the receptors found matches to those in other animals, including mammals. This study complements physiology and cell biology studies demonstrating the presence and function for dopamine in *C. virginica*, and shows the genome of *C. virginica* contains genes to produce dopamine receptors that are similar to those found in other animals. This new information is valuable in showing the simple nervous system of *C. virginica* can be used to expand studies on dopamine neurotransmission.

AN UPDATE CONCERNING THE ONGOING RESEARCH AND OCCURRENCE OF NEOPLASIA AND QPX IN THE NORTHERN QUAHOG (= HARD CLAM) IN MASSACHUSETTS, USA

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Hematopoietic Neoplasia (HN) has plagued northern quahog (=hard clam) (*Mercenaria mercenaria*) culturists in Wellfleet, Massachusetts (MA) for several years. It has caused significant mortality, appears to be a contagious disease, and is very similar to a disease that occurs in *Mya arenaria*. The origin of the tumorous disease in *M. mercenaria* appears to be in Wellfleet, MA, but it has recently been detected histologically in hard clams in other locations. Research indicates that HN is spread directly between clams. Additionally, a second tumor-like condition of neural tissue was noted in hard clam samples in MA during the 2019 annual clam survey. QPX, a cause of significant mortality in the past, has decreased in prevalence and severity in the last few years. But, with the resurgence in hard clam aquaculture, QPX may increase in prevalence again. Information concerning the occurrence of HN, QPX, and other diseases and results of recent research concerning HN will be presented.

MANAGEMENT STRATEGY EVALUATION SUGGESTS ATLANTIC SURFCLAM MAY BE RESISTANT TO CURRENT FISHING PRESSURE DESPITE UNCERTAINTIES

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The Atlantic surfclam (*Spisula solidissima*) is an important commercial resource in the US mid-Atlantic. Although the 2016 stock assessment found that surfclams are neither overfished nor being overfished, uncertainty in the scale of spawning stock biomass persists. As a consequence of this uncertainty, the Mid-Atlantic Fishery Management Council (MAFMC) lowered the acceptable biological catch in 2016. The risk-tolerance of that recommendation and adherence to MAFMC risk policy has not been evaluated. To address this, a management strategy evaluation was developed for Atlantic surfclam. Operating models generated simulations of the surfclam population conditioned on the 2016 stock assessment model structure, with allowance for uncertainty in steepness (h) of the stock-recruitment curve and natural mortality (M). Simulations were forecasted under a variety of management procedures and evaluated with estimation models that spanned uncertainty in h and M. Results showed current management decisions are conservative in reference to stated risk-tolerance policies, though incorrectly parameterizing natural mortality could lead to falsely characterizing the stock as overfished. Further analysis evaluated future economic viability of the fishery under alternative management procedures and biological uncertainty using a yield per recruit (YPR) analysis. Forecasted YPR was more sensitive to biological uncertainties than management decisions, with confounding effects from low h and M that forecasted low YPR. This work contributes to efforts to evaluate fishery management strategies from an environmentally and economically sustainable perspective.

COMPARATIVE TRANSCRIPTOMICS OF *MERCENARIA MERCENARIA* AND *MERCENARIA CAMPECHIENSIS* IN RESPONSE TO HEAT STRESS

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The northern quahog, *Mercenaria mercenaria* (Mm), is one of the major aquaculture species along the U.S. east coast and Gulf coast with a $55.9 million sales value. In Florida, summer heat waves, especially at low tides, resulted in massive mortality of market-sized aquaculture stocks. Understanding of the genetic basis of heat tolerance and its role in species distribution is a first step to develop heat-tolerant broodstock. The goal of this study was to develop genomic tools for heat-tolerance breeding through transcriptomic analysis. Farmed Mm samples were collected from five commercial farms in Florida. A sister species of Mm which is native in Florida, *Mercenaria campechiensis* (Mc), was collected from Tampa Bay, Florida. The farmed Mm, together with wild Mc and wild Mm collected from Maine were exposed to heat shock over a 4-week period. Heat shock was performed by increasing temperature from 24°C to 36°C with an increment of 2.5°C per week. Four different tissue types (gill, mantle, foot, and adductor muscle) from individuals in each group (N = 5) were sampled each week. RNAseq will be performed and the transcriptome of both species will be *de novo* assembled. Species-specific and population-specific signatures of gene expression will be analyzed through differential expression analysis and functional annotation. The results will elucidate the genetic basis of heat tolerance and potentially identify temperature-related gene variants between sister species. Single-cross families will be produced for each species for selection breeding and genetic analyses of the offspring for development of heat-resistance broodstock.

COUPLING OYSTER STOCK ASSESSMENTS AND SHELL-BUDGET MODELING TO DETERMINE SUSTAINABLE HARVESTS FOR THE NORTHERN GULF OF MEXICO

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A shell budget model for the estimation of sustainable harvests of oysters, management of cultch and restoration of reefs has been applied across the northern Gulf of Mexico. Oyster density and size, and cultch density are provided from surveys by State agencies. The model simulates oyster growth and mortality, and cultch loss. Reef shell mass is increased when oysters die in place and diminished when oysters are removed by fishing. Harvest is estimated as sacks of live oysters that can be removed without diminishing reef quality (i.e., reef cultch mass), or when a desired cultch mass is achieved.

Model heuristics focus discovery of negative and positive feedbacks. A negative feedback loop is setup on poor-quality reefs. Lack of cultch and a paucity of live oysters diminish recruitment and shell replenishment. In the absence of recruitment, natural shell loss ultimately drives the reef to extinction. A positive feedback loop is setup on reefs with adequate cultch and an abundance of oysters. There oysters set, survive critical early stages in boxes and reef interstices, reproduce, grow to a large size and die in place. Harvests on high-quality reefs beyond that which maintains reef cultch, and recruitment failure can cause a shift from a positive to negative feedback loop. Likewise, eliminating harvests and planting cultch on poor-quality reefs, together with successful recruitment, promotes a shift from a negative to a positive state.

INHIBITORY EFFECT OF MARINE MICROALGAE ON VIBRIO PARAHAEMOLYTICUS STRAIN CAUSING ACUTE HEPATOPANCREATIC NECROSIS DISEASE

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Marine microalgae are potential producers of antimicrobial compounds, but to date, are yet to be exploited. Monospecific, axenic co-cultures of the marine microalgae *Chaetoceros calcitrans*, *Tetraselmis suecica*, *Nannochloropsis* sp., and Thalassiosira weissflogii at the exponential phase were inoculated with two *Vibrio parahaemolyticus* strains. *Vp* M0904 strain causing acute hepatopancreatic necrosis disease and *Vp* M0702 a non-pathogenic strain, both at 1×10^5 CFU/mL. Microalgae and bacterial growth was estimated at 24, 48 y 72 h post-inoculation with bacteria. At the same time, percentage of total lipids and carbohydrates were also quantified. No microalgal cellular growth was affected by any tested bacteria during the experiment. Growth of *Vp* M0904 was significantly ($p<0.05$) inhibited in co-culture with *C. calcitrans* and *T. suecica*, while *Vp* M0702 was significantly ($p<0.05$) inhibited by all microalgae except *Nannochloropsis* sp. Minor, non significant, variations were found in the total lipids and carbohydrate metabolism of all tested microalgae inoculated with both *Vibrio* strains. Inhibitory activity of ethanolic (EE) and seawater extracts (SE) of *C. calcitrans* were also evaluated with *Vp* M0904. A lower CFU/mL of bacteria was registered with the SE at concentrations over 75 µg/mL; in contrast, the EE did not show any antibacterial activity. Bacteriostatic effect of microalgae was both microalgae and *Vibrio*-strain dependent. Compounds of *C. calcitrans* and *T. suecica* cells posse antibiotic activities on *Vp* M0904, a strain highly virulent causing AHPND, a devastating disease for farmed shrimp around world.

ON THE CO-EXISTENCE OF SUBMERGED AQUATIC VEGETATION AND CAGE-BASED OYSTER AQUACULTURE IN VIRGINIA, USA

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The intensive oyster aquaculture business continues to expand in Virginia—about one quarter of the oysters by number originating from Virginia sources are cultured. Industry expansion has encountered an exclusory approach to spatial management where SAV (*Zostera* and *Ruppia* species) habitat has priority preservation over nearly all shallow water activities including oyster culture. SAV thrives in near shore shallow waters, where suspended sediment loads are low and water quality is generally good. Where SAV is present, oyster culture is prohibited and existing operations can be required to move. This project examined the interaction between cage aquaculture operations and SAV over a six-year period using a combination of SAV aerial surveys and mandatory oyster harvest reporting. Findings are presented as a web-based viewer illustrating that this exclusory approach is unnecessary and that oyster culture and SAV can amicably co-exist on the same footprint, that oyster farm gear in the midst of SAV beds have realized footprints that will maximally cover only single digit percentages of a total lease area, and that culturists can and should be encouraged to develop culture in regions where SAV coverage is ephemeral.

EXAMINING SPATIAL HETEROGENEITY TRENDS IN OCEAN QUAHOG GROWTH AND RECRUITMENT

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Ocean quahogs (*Arctica islandica*) are a long-lived, biomass dominant species along the eastern United States continental shelf and constitute a $24 million fishery. Despite research being done on this species, very little is known about how their growth and recruitment rates change throughout their environment and over time. In 2018, Pace et al. observed different growth rates throughout different populations along the continental shelf, as well as identified temporal changes in recruitment over the last 200+ years from age frequency analyses. Results indicated that *Arctica* grow faster off the coast of New Jersey, as New Jersey represents the southernmost portion of *Arctica*'s range where they encounter warmer bottom water temperatures. Evidence indicates that a significant expansion of the population occurred in this region during the mid-1800s. To evaluate the degree to which the Pace et al. (2018) site was typical of the southern Mid-Atlantic Bight, approximately 1,500 *Arctica* specimens were collected from two New Jersey sites which were then cross-sectioned and aged to develop age-length keys. These keys will be compared to those from Long Island, southern New England, and Georges Bank, as well as the original 2018 New Jersey site. Comparisons will determine the extent of spatial heterogeneity of *Arctica* growth, age composition, and the degree to which recruitment dynamics vary regionally.

HOLDING MIRRORS UP TO NATURE: THE STRUCTURE AND FUNCTION OF THE EYES OF SCALLOPS

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The eyes of animals come in a variety of forms and some of the most unusual designs are found in molluscs. Scallops, for example, have dozens of mirror-based eyes arrayed along the edges of their valves. These eyes are among the only eyes known to use a concave mirror to focus light for image-formation and they provide scallops with high-resolution vision (at least compared to other bivalves). Two recent findings highlight the complexity and sophistication of the eyes of scallops. First, the eyes of two species of scallop demonstrate light-evoked pupillary responses. Both the bay scallop, *Argopecten irradians,* and the sea scallop, *Placopecten magellanicus,* have pupils that constrict to approximately 60% of their fully-dilated areas within several minutes of being exposed to light. At the cost of sensitivity, narrower pupils improve spatial resolution in the eyes of scallops. They do so by decreasing the influence of optical aberrations on the quality of the images formed by the mirror. Second, photonic nanostructures contribute to how the external surfaces of the eyes of scallops interact with light. Tightly-packed, nanoscale spheres are responsible for the iridescent blue appearance of the eyes of *A. irradians* and other scallop species. Computational models indicate the physical properties of these nanospheres are well-suited for scattering short wavelength light. These nanospheres are absent from black-eyed species of scallop such as *P. magellanicus*. Light-scattering nanospheres may help prevent off-axis light from degrading image contrast in the eyes of *A. irradians* and other shallow-dwelling, blue-eyed scallops.

THE SCALLOP FISHERY AND THE DEVELOPING WINDFARM INDUSTRY ON THE NORTHEAST CONTINENTAL SHELF OF NORTH AMERICA

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The development of the windfarm industry off the United States has great potential for the harvest of sustainable energy but will take up a large amount of space in an already crowded marine environment. One of the highest valued and historically productive fisheries in this same space is for the Atlantic sea scallop, (*Placopeten magellanicus*). Sea scallops are mostly sessile after their larval phase, so the location of their beds is relatively fixed in time. They are harvested offshore with a New Bedford style dredge towed behind the vessel with at least a 3 to 1 length-depth ratio. The abilities of the fishery to harvest within or next to these windfarms is under debate. The impacts extend beyond the biological to include economic, social and institutional. Fortunately, sea scallops have a large, strong scientific data base and may be one of the few fisheries where the impact of the developing windfarms industry can be assessed on a quantitative bases from scales of "individual", "population", and "community". Understanding the impacts of this new industry and suggesting ways to mitigate negative impacts is key to allowing both industries to prosper and produce a continuing supply of sustainable sea food and renewable energy to an increasingly hunger world.

NAEMO WORKSHOP: DEFINING BARRIERS AND IDENTIFYING SOLUTIONS FOR MUSSEL AQUACULTURE EXPANSION

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With a growing world population, food production is expected to increase by 60% by 2050, adding further pressures on land and water resources. Consequently, new ways of producing nutritious food in sustainable ways is needed. Aquaculture, in particular culture of low trophic species such as mussels, oysters and seaweeds, has been proposed as a solution and has been the fastest growing food production sector in the world for many years. As a seafood product, marine mussels provide healthy proteins and micronutrients, may help regenerate coastal regions which have suffered from the decline of traditional fisheries, and may contribute to a circular economy by capturing finite resources such as phosphorus. Mussel aquaculture may also enhance marine biodiversity, can reduce eutrophication effects in shallow areas, and can support restoration of threatened habitats such as biogenic reefs. There is a political agenda in many regions to enhance the production of blue mussels and other low-trophic species, yet the production of mussels has only experienced a minor growth of around 2% per year between 1974-2017. This trend is caused by a stagnation, and even decline, of both harvested and farmed mussels in the main producer countries in Europe. This is also in accordance with observations related to wild populations of blue mussels. The workshop 'Defining Barriers to Mussel Aquaculture Expansion' aims to jointly identify and discuss barriers for sustainable expansion of mussel aquaculture from different perspectives (including industry, research and policy/governance) and to summarise the findings from the workshop in a policy brief to highlight development needs to strengthen the sector. The workshop will include i) short presentations about the status and practices of the mussel industry in different geographical regions, ii) breakout groups where specific questions will be addressed, and iii) an interactive plenary session to summarise the main findings.

HATCHERIES DON'T HAVE TO BE COMPLICATED: THE CEDAR KEY SEED MODEL

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During the 1990s, federally funded job retraining programs provided an infrastructure to introduce shellfish aquaculture as an alternative employment opportunity for rural communities along the west coast of Florida. Over 200 underemployed fishermen and women in the Cedar Key area received training and aquaculture leases to start their new businesses. Adequate northern quahaog (=hard clam) *Mercenaria mercenaria* seed availability was a major concern of this emergent industry as seed plantings increased from 37 million in 1991 to 285 million in 1999. As demand increased so did the development of private-sector hatcheries throughout the state; however, it was the development of land-based nurseries in Cedar Key, over 50 at one time, that contributed to alleviating seed problems. In this decade, hatcheries experienced unacceptable losses of seed, resulting in an inconsistent and unreliable supply. By now, Cedar Key was producing over 90% of the cultured clams of Florida, about 100 million annually. To obtain adequate seed for their growout operations, several nursery operators incorporated a hatchery component. Systems and methods used by these small-scale, "pop-up" hatcheries and nurseries will be reviewed. In addition, favorable local zoning ordinances, county "green belt" property tax exemptions, and state regulations, along with extension efforts to support these facilities, will be presented.

AQUACULTURE POTENTIAL OF THE ANGELWING CLAM: THE SOUTHERN GEODUCK?

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The potential for commercial aquaculture development of the angelwing clam *Cyrtopleura costata*, a burrowing bivalve found along the US Atlantic and Gulf of Mexico coasts, was reexamined. Studies conducted in the 1980s demonstrated angelwings could be spawned using hatchery methods similar to those for commercial bivalve species. Preliminary results also indicated angelwings grow rapidly and could reach a potential harvest size in six months. However, the lack of economical production methods and harvesting techniques stymied further consideration of angelwings as an aquaculture candidate species. Despite its excellent flavor and attractive shell, another drawback was its short shelf life as most bivalves until recently were marketed as live shellstock. In the past two decades, aquaculture of the geoduck *Panopea generosa*, the largest phollad clam of North America, has advanced due to its high market value. By adapting methods developed for geoduck aquaculture, it was hypothesized that reliable production of the angelwing clam could be achieved. In this study, several field and land-based culture methods were evaluated: PVC tubes under bottom nets, submerged bottom cages, modified bottom bags, and raceways. After 23-24 weeks (six months from spawning), angelwings reared in the field averaged 59.6+13.0 mm in shell length and 26.4+9.1 grams in total weight, whereas angelwings in raceways averaged 43.5+3.4 mm and 6.8+1.9 grams. Several post-harvest processes were tested: banding and chilling to extend shelf life of shellstock, modified atmosphere packaging for live product, and frozen and vacuum skinned packaging. Preliminary evaluation of these processes for shelf life, breakage, and appearance will be presented.

A SLOW GROWING PERSPECTIVE ON MULTI-GENERATIONAL RESPONSES TO FUTURE CHANGE

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The oceans are changing, lowering in pH as atmospheric carbon dioxide (CO2) concentrations increase. Predicting how ecologically and economically important organisms will respond to these changes has become a major area of research, particularly for those species needing to maintain biomineralizing processes. In recent years there has been a shift in focus from shorter (hours-weeks) towards assessing responses over longer term exposure periods (months-years) advancing our understanding in this field. Given that predicted changes span across years and decades, and that organisms will be producing offspring, a greater consideration of multi-generational response is needed to better understand how organisms will respond under future climates. For many species, this is still in its infancy with the majority of focus on organisms with rapid life cycles. In an experimental context this is convenient as numerous generations can be achieved within weeks/months; however, they cannot be a substitute for higher trophic level organisms that have much more complex life cycle processes. High trophic levels typically comprise of slower growing organisms with longer life cycles and deferred maturity (i.e. years). With these, rearing multiple generations becomes time-consuming, difficult and almost unfundable within normal grant time-scales (i.e. 2-3 years). This presentation will address this knowledge gap by discussing the physiological, somatic, reproductive and commercially relevant responses of a slow growing benthic invertebrate, the sea urchin, bred across several generations under IPCC predicted CO2 conditions. Although this work focuses on a European species of sea urchin (*Psammechinus miliaris*), this information brings important considerations for other commercially relevant organisms.

EXPANDING PRODUCTION METHOD INFORMATION FOR SEA URCHINS

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Sea urchins are often used as model species in anthropogenic studies and their aquaculture productions has expanded in recent years. Yet basic rearing and production technique information goes largely unreported making comparability, reproducibility and translation to facilities challenging. This presentation will overview recent advances in our knowledge of this through a European case study investigating the impacts of differing seawater flow rates and stocking densities on somatic growth and physiology. It will also overview a new project funded by the Northeast Regional Aquaculture Centre (USDA) which looks at optimizing Green Sea urchin hatchery methods to make seed more competitive for grow out in the US.

THE IMPACTS OF MICROPLASTICS ON A LARGELY OVERLOOKED MARINE INVERTEBRATE—THE SEA URCHIN

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In recent years there has been an increasing effort to assess the impacts of microplastic pollution on marine organisms, yet much focus has been made on filter feeding shellfish and fish species of commercial relevance. Other ecologically and economically important groups of organisms, such as sea urchins, have still received little to no investigation. Here the first insights into assessing the effects of marine microplastics on numerous species of adult sea urchins (*Arbacia punctulata*, *Paracentrotus lividus*, and *Psammechinus miliaris*) are presented thus bringing new information into the field of microplastic pollution. Sea urchins live on the benthos grazing on food materials meaning that these organisms are at the interface for plastic exposure, through plastic loading and resuspension during events of significant water movement (e.g. storms). This study assessed the short-term influence of storm-like scenarios which could induce microplastic resuspension from sediments coupled with salinity changes associated with high precipitation during storm events. Furthermore, it assessed the longer term effects of ingesting PVC particles that can be found within the seabed environment. This study shows that numerous species of sea urchins are generally resilient to microplastic pollution even when coupled with additional parameters but species specific responses do emerge. More importantly this study shows that the urchins ingest microplastics, a phenomenon not previously documented for these species.

SEASONAL PRODUCTION OF ATRETIC OOCYTES IN THE MANILA CLAM, *RUDITAPES PHILIPPINARUM*, IN NORTHERN JAPAN

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Information on oocyte atresia is important to estimate vital egg production, but it was lacking in the *Ruditapes philippinarum* (Bivalvia: Veneridae) in the northwest Pacific region. This study aimed to elucidate seasonal production pattern of atretic oocyte in the Manila clam in northern Japan by using a trichrome staining and stereology. Three to eleven female clams were monthly sampled from April 2014 to March 2015. Dorsoventral section of generally 7-µm thick was made after fixation and embedding in paraffin. The section was stained in a modified Gomori's trichrome. In photomicrograph of the section, atretic, mature and immature oocytes that hit points of a 9 × 12 counting grid were counted to stereologically derive the volume fractions of atretic oocytes (AVF), mature healthy oocytes (MVF), immature healthy oocytes (IVF) and resorbing atretic oocytes (RVF). The AVF reached a small peak in August (spawning peak) and the largest peak in October (just after the end of spawning). From June to September (the period of active gametogenesis and spawning), MVF was high, whereas IVF and RVF were low. From October to March (the period of recovery and early gametogenesis), MVF was zero, whereas IVF and RVF were high. It was suggested that some fraction of oocytes became atretic during their development, and they would be resorbed or emitted in partial spawning event. In the post-spawning and recovery period, atretic oocytes were residues of the last gametogenic period, and most of them were to be recycled as an energy source for the forthcoming gametogenesis.

JUVENILE SEA CUCUMBER (*APOSTICHOPUS CALIFORNICUS*) FEEDING TRIALS AT WASHINGTON STATE NURSERIES AND HOME OFFICES

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A major gap in knowledge exists for growing juvenile giant red sea cucumbers (*Apostichopus californicus*) to a size that can be outplanted for potential enhancement or aquaculture. Expanded shellfish nursery growout trials of sea cucumbers were conducted at two locations in Washington State for juveniles 70 to 100mm in length. Additional work was completed at a home office targeting food sources and conditions to increase growth of small juvenile sea cucumbers averaging 1 mm in length. Proper water quality, food availability and reduced handling have led to increases in growth in all locations. In lab studies, multiple feeds have been evaluated narrowing down the list to a select few. These feeds are readily available in Washington State as waste products from shellfish and includes the invasive macroaglae, *Sargassum muticum*, that fouls shellfish gear and is abundant in Puget Sound intertidal waters. Data and Results collected here will be used to expand studies and aquaculture opportunities in the Pacific Northwest and Alaska.

ECONOMICS OF SUBTIDAL OYSTER CULTURE IN DELAWARE BAY, USA

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For more than one hundred years, the oyster aquaculture industry of New Jersey involved transplanting wild submarket oysters on thousands of acres of Delaware Bay planting grounds for subsequent harvest. This type of oyster aquaculture thrived in the mid-Bay area, reaching peak oyster harvests of nearly two million bushels per year; however, the practice effectively ended in the late 1950s when MSX disease decimated oysters on moderate to high salinity planting grounds.

The development of disease resistant oysters rejuvenated the industry, generating hundreds of oyster farms along the U.S. east coast. Consequently, intertidal oyster farming has succeeded in the lower Delaware Bay for three decades; however, subtidal oyster culture on the traditional planting grounds has yet to recover, limited by the challenging physical conditions of the Bay, a lack of capital investment, and the need for demonstrated success. Recent industry initiatives are underway to revitalize oyster culture on the planting grounds using subtidal cage production methods. This study aimed to evaluate the economic feasibility of two subtidal cage production methods deployed on the Delaware Bay.

To this end, the session talk will include a presentation of 1) the efforts to evaluate the economic feasibility of two types of subtidal cage systems in the harsh Delaware Bay environment, 2) the results of the economic analysis of the two subtidal cage systems, 3) an economic comparison of mid-Bay subtidal cage production to lower-Bay intertidal rack-and-bag production, and 4) future directions and potential for innovation in subtidal oyster culture on the Delaware Bay.

UNOCCUPIED AERIAL VEHICLES (UAV): A NEW TOOL TO IMPROVE THE RESTORATION AND MANAGEMENT OF INTERTIDAL OYSTERS (*CRASSOSTREA VIRGINICA*) IN SOUTH CAROLINA, USA

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Small, unoccupied aerial vehicles (UAV) have recently become available to natural resource professionals as effective tools that allow for the unprecedented spatial and temporal control of remote sensing data collection. Researchers at the SCDNR are exploring the capabilities of UAV platforms to inform the restoration and management practices for intertidal oyster (*Crassostrea virginica*) reefs. Products derived from these platforms can be used to estimate rates of lateral shoreline change that can in turn be used to assess the effectiveness of intertidal oyster reefs at protecting adjacent marshes. Small UAV can also be used to measure changes in reef extent and elevation, enabling managers to assess the success of intertidal loose oyster shell plantings.

This presentation will highlight key findings from over 50 UAV flights completed across 19 sites between April 2018 and October 2020 at both living shoreline sites and loose shell restoration sites. Photogrammetry software was used to produce high resolution orthomosaics and digital surface models (DSM) from UAV images. AMBUR (Analyzing Moving Boundaries Using R) software was used to estimate rates of change in the lateral position of the marsh edge, producing estimates that were comparable to those of more traditional ground surveys but with less variability. Further evaluation was conducted from orthomosiacs and DSM products by analyzing changes in both reef extent and elevation. The resultant information has the potential to detect and measure changes in the sub-decimeter range, suggesting that this method may prove useful for establishing best practices for successful plantings in the future.

OBSERVATIONS ON THE USE OF A MCDONALD FISH HATCHING JAR FOR OYSTER SEED CULTURE AND IMPROVEMENTS IN BOTTLE SILO DESIGN

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Bottle nursery systems have become commonplace in oyster hatcheries as a means to use fluidization instead of down-welling to nurse post-set and larger seed for reduced labor. The loss of commercial supply of bottle silos during 2019 initiated a preliminary investigation of a McDonald fish hatching jar as a possible replacement. Minimum flow rates to achieve fluidization were 18 and 14 seconds per gallon (sec/gal) for 1 liter (L) of < R2 grade and R2 grade *Crassostrea virginica* oyster seed, respectively. Flow >14 sec/gal resulted in unacceptable overflow down the side of the hatching jar due to the shallow top lip and discharge spout. R2 grade seed, therefore, were deemed as the maximum size for use in fish hatching jars, a limiting factor for their use in a commercial setting.

A new source of commercially-available bottle silos resulted from a new collaboration utilizing prosthetic fabrication techniques. Bottle silos (4” diameter) were constructed of PETG modified acrylic resin with the near clarity of acrylic, with more resiliency. Three designs were bench tested using 1L of microcultch, resulting in a seamless clear silo, with threaded seawater connection, increased check ball size and improved performance, and higher flow rate capacity over traditional silo design. Such silos are now commercially distributed as single or multiple units or complete systems.

PROBIOTICS FOR EASTERN OYSTER HATCHERIES: COMMERCIAL FORMULATIONS AND EFFECT ON MICROBIAL COMMUNITIES

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The rearing of larval eastern oysters, *Crassostrea virginica*, in hatcheries is necessary to supply adequate seed for the aquaculture industry. Bacterial diseases, particularly vibriosis, continue to be major causes of mortality in hatcheries. The marine bacteria *Phaeobacter inhibens* S4 (S4) and *Bacillus pumilus* RI06-95 (RI) have been demonstrated as effective probiotics conferring health benefits to larval oysters against bacterial pathogens. Commercial formulations of these probiotics have been developed for use at the hatcheries. This study sought to test and optimize the efficacy of commercially-produced formulations in protecting larval oysters in hatcheries. Four hatchery trials were carried out in 2019 (June and July) and 2020 (May and June). The probionts S4 and RI were administered to treatment tanks ($n= 3-6$) daily for 12 days. Larval survival and growth were measured in control (no probiotic) and treatment tanks. The results showed that probiotic treatment had no significant impact on larval survival or growth when provided at the targeted dose of 104 CFU/mL. Larvae from tanks treated with the S4 and RI formulations showed a significant increase in Relative Percent Survival (RPS) versus those from control tanks when exposed to the pathogen *V. coralliilyticus* RE22 (105 CFU/mL) for 24 hours in a laboratory challenge (RPS = 47 ± 10 % to 74 ± 11 % respectively, $p < 0.05$). Probiotic treatment led to subtle changes in microbial communities in hatchery tanks, as determined using 16S rRNA gene sequencing. Use of these commercial probiotic formulations show promise for enhancing larval oyster production.

DEVELOPMENT OF A CONTINGENCY PLAN FOR SHRIMP ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND)

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Acute hepatopancreatic necrosis disease (AHPND) is caused by bacteria belonging to the genus *Vibrio parahaemolyticus* and related species. These bacteria have caused substantial mortalities, up to 100%, in Pacific whiteleg shrimp, *Penaeus vannamei,* and giant tiger prawn, *P. monodon,* cultured in Asia and the Americas. The economic losses due to this disease have amounted to over USD 7 billion annually. Thus, there is an urgent need to develop a contingency plan to effectively control, contain and eradicate AHPND. This plan is designed to ensure that all needed actions, requirements, and resources are provided. Components of the contingency plan include (1) technical plans consisting of AHPND strategy manual, general procedures, and description of enterprise; (2) supporting plans in financial, resource, and legislation; (3) operational capability, such as management manuals, resources of diagnostics and field personnel, public awareness and response exercises. The AHPND-specific strategy manual, which serves as a framework for the development of national contingency plan, includes information on: (i) the nature of AHPND: its etiology, and susceptible species; (ii) diagnosis: a description of gross clinical signs and laboratory methods; (iii) treatment and prevention: the use and development of antibiotics, bacteriophages, probiotics, disease-resistant shrimp; (iv) epidemiology: the geographic distribution of AHPND, genotype, persistence in the environment, reservoir hosts, modes of transmission, and risk factors; (v) principles of control and eradication: methods for control, containment and eradication, trade and industry considerations; and (vi) policy development and implementation: specific objectives, options and strategies for eradication and control, education, funding, and compensation.

[†] The views expressed in this publication are those of the author/s and do not necessarily reflect the views of the Food and Agriculture Organization of the United Nations (FAO). Also, the designations employed and the presentation of material in this information product do not imply the expression of opinion whatsoever on the part of FAO concerning the legal status of any country, territory, city or area or of its authorities, or concerning thew delimitation of its frontiers or boundaries. Content and errors are exclusively the responsibility of the author/s.

CONJUGATIVE TRANSFER OF THE PVA1 PLASMID RESULTED IN THE FORMATION OF AHPND-CAUSING *VIBRIO* BACTERIA

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Acute hepatopancreatic necrosis disease (AHPND) has caused substantial production losses in penaid shrimp farming industries in Asia and the Americas. Strains of *Vibrio parahaemolyticus* and related species have been proved to cause AHPND; however, the mechanisms underlying the burgeoning number of *Vibrio* species that cause AHPND is unknown. AHPND-causing *Vibrio* bacteria (V_{AHPND}) harbor a pVA1 plasmid carrying $pirAB^{vp}$ toxin genes. This plasmid also contains a cluster of conjugative transfer genes, suggesting that pVA1 plasmid can be disseminated via conjugation. In this study, the pVA1 plasmid was shown to transfer from VAHPND to non-pathogenic *Vibrio* bacteria. A pVPGX1-Cm^{r} plasmid (a pVA1 plasmid) was constructed by adding a chloramphenicol resistance gene as a marker in a donor AHPND-*V. parahaemolyticus* Vp2S01. Transfer of this plasmid was successfully performed from the AHPND-Vp2S01 to a non-pathogenic strain of *V. campbellii* at a transfer efficiency of 2.6×10^{-8} transconjugant/recipient; DNase I treatment did not eliminate the transfer. The recipient *V. campbellii* acquired the pVA1 plasmid, and was shown to produce pirAB^{vp} RNA and proteins. Laboratory infection demonstrated that the transconjugant caused 100% mortality in exposed groups of *P. vannamei*. Challenged shrimp, infected with the transconjugant bacteria, showed typical gross signs and histological lesions of AHPND. The transfer of pVA1 plasmid was also demonstrated *in vivo* from AHPND-*V. campbellii* to non-pathogenic *V. owensii* present in the healthy shrimp. These studies explain the increased numbers of AHPND-causing *Vibrio* bacteria, and will be useful in the development of strategies leading to the prevention and control of AHPND.

IDENTIFICATION OF A NEW REOVIRUS IN *CALLINECTES DANAE*: WHAT DOES IT MEAN FOR SOFT-SHELL CRAB PRODUCTION IN BRAZIL?

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Crabs in aquaculture can be infected by a variety of pathogenic micro-organisms but the most damaging are viruses. *Callinectes sapidus* Reovirus 1 (CsRV1) is thought to contribute to mortality of *Callinectes sapidus* in soft crab culture in the USA. In Brazil, soft crabs are frequently produced using *Callinectes danae*, which also suffers a high mortality rate in culture. This study investigated whether CsRV1 could be detected in *Callinectes danae* from Paraná, Brazil. The study also evaluated the relationship between captivity, viral infection, and biochemical and behavioral parameters. Crabs (*C. danae*) from Paranaguá Bay were kept in a recirculation system for 14 days and subjected weekly to biochemical analysis and reflex response test. RT-qPCR assays for CsRV1 were negative for all samples; however, electrophoresis analysis of extracted RNA showed a pattern of 12 dsRNA bands that indicated intense infection by a reovirus with a genome organization different from CsRV1. The banding pattern was the same as a novel reovirus described in *C. sapidus* in Rio Grande do Sul, Brazil, called CsRV2. CsRV2 prevalence increased significantly over the time, but there was no significant difference between crabs that died and survived. CsRV2 presence corresponded to a significant reduction in the total protein concentration, reduction in glycogen, and an impairment of the kick reflex. The results obtained here contribute to a better understanding of reoviruses in south America and their effects on captive crabs. Also, it provides information that allows animals infected with CsRV2 to be quickly identified with simple behavioral or biochemical analysis.

PHYTOPLANKTON DEPLETION IN AND AROUND MUSSEL FARMS IN EUTROPHIC BALTIC COASTAL SEAS AND FJORDS

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Ecological status of coastal seas in the Baltic and Northern Europe is assessed by a number of criteria, one of the primary being phytoplankton concentrations, indicated by chlorophyll-*a* fluorescence. Commercial mussel farming designed for mitigating eutrophication are undergoing development in the Western Baltic, and the intense filtration pressure of these farms has a direct effect on this ecological indicator. Microtidal, stratified, eutrophic marine and brackish waters, characteristic of Western Baltic seas provide unique conditions to monitor interactions of mussel farms with the environment and intensity of phytoplankton depletion affecting farm performance and sub-basin scale primary production. Numerous monitoring campaigns were conducted to quantify phytoplankton depletion in different environmental conditions, and developed a farm-scale model to evaluate environmental interactions on biomass yield and depletion patterns. In a large mussel farm, synoptic fluorometric surveys, flow cytometry transects, and satellite remote sensing analyses were conducted to assess spatial characteristics of depletion patterns and local-scale impacts on the phytoplankton community structure. Methods and results from these field and model studies will be presented and discussed.

MASS DIE-OFF OF ADULT BAY SCALLOPS IN NEW YORK FOLLOWING SUCCESSFUL RESTORATION: THE LOOMING SPECTER OF CLIMATE CHANGE

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Intensive restoration efforts, conducted in the Peconic Bays of eastern Long Island since 2006, have driven order of magnitude increases in larval recruitment, benthic population densities, and commercial fishery landings of bay scallops, *Argopecten irradians irradians*. Harvest levels in 2017 and 2018 were each ∼107,000 pounds of meats: 32 times the average annual harvest during the 12 years prior to the start of restoration efforts; however, a mass die-off of adult scallops occurred between late June and early October 2019, with mortality levels of 90-100% at most sites; commercial landings similarly declined by 95%. Recruitment of juvenile scallops was still high in 2019, but mass mortality of adults recurred at even higher levels in 2020 - primarily in July and August. The primary causes of these events are hypothesized to be: (1) combined physiological stresses of high water temperature and low dissolved oxygen (DO), in conjunction with heavy infection by an apicomplexan parasite, and (2) predation by cownose rays, *Rhinoptera bonasus*, a primarily southern species which was much more abundant in local waters in 2019-2020. These scenarios are all likely driven by climate change. Results of ongoing investigations will be reported.

OYSTER METAPOPULATION DYNAMICS

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Metapopulation and source-sink dynamics are increasingly considered within spatially-explicit management of wildlife populations, yet application of these concepts are generally limited to comparisons of the performance (e.g., demographic rates) inside vs. outside protected areas, and at spatial scales that do not encompass the entire metapopulation. In the present study, a size-structured, discrete-time matrix model was applied to simulate the dynamics of an eastern oyster metapopulation in Pamlico Sound, North Carolina, USA. The model integrated empirical measures of oyster demographic rates, and represented the entire metapopulation by integrating all known oyster reefs of different types in the system: (1) restored subtidal reefs closed to harvest (i.e., protected areas), (2) restored subtidal reefs open to harvest, (3) natural subtidal reefs open to harvest, (4) natural intertidal reefs open to harvest, and (5) oyster 'reefs' on manmade, hard structures such as seawalls and pilings. Key findings included: (1) an overall stable, yet slightly declining metapopulation, (2) variable reef type-specific population trajectories depending on spatiotemporal variation in larval recruitment, (3) spatiotemporal variation in the source-sink status of reef subpopulations wherein subtidal sanctuaries and reefs located in the northeastern portion of the estuary frequently served as sources, and (4) a greater relative importance of inter-reef larval export on metapopulation dynamics relative to local larval retention processes. Resource managers should consider oysters as an interconnected metapopulation, with continued protection of existing oyster sanctuaries and conservation of other identified subpopulations that serve as frequent 'source' subpopulations, while managing harvest from 'sink' subpopulations.

PATTERNS AND DRIVERS OF FEMALE BLUE CRAB (*CALLINECTES SAPIDUS*) SIZE AT MATURITY IN SOUTH CAROLINA, USA

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The Atlantic blue crab, *Callinectes sapidus*, supports the largest crab fishery in the United States. Despite the ecological and economic value of this species to South Carolina, many aspects of blue crab life history, which are important for ensuring effective management strategies, remain unexamined. Size restrictions for harvesting blue crabs, set nearly a century ago, selectively remove the largest and most fecund crabs from the population. Evidence of both spatial and temporal variability for this species in both Atlantic and Gulf coast populations, highlights the need for characterizing patterns of mature, female blue crab demographics in South Carolina. This study incorporates a range of estuarine environments from lower saline habitat through coastal spawning grounds to cohesively investigate spatial and temporal variation in female blue crab size at maturity.

This presentation will exhibit long-term data analyzed from 40 years (1979-2018) of fishery-independent estuarine trawl surveys conducted by the South Carolina Department of Natural Resources. Generalized linear mixed modelling procedures revealed significant spatial variability in female blue crab size at maturity across South Carolina's estuaries. Patterns in temporal trends across the 40-year time series and potential drivers of spatio-temporal variability, such as temperature, salinity, and blue crab abundance will also be tested. These results will provide fishery managers with detailed information on variability in blue crab size at maturity, a life history trait that is central to effective management strategies for this species.

OPTIMIZING REMOTE SETTING ON DIFFERENT CULTCH TYPES FOR SMALL-SCALE OYSTER RESTORATION IN BARNEGAT BAY, NEW JERSEY, USA

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Restoration efforts for the eastern oyster, *Crassostrea virginica*, are often limited by sources and availability of cultch for remote setting. In southern New Jersey, a shell recycling program has been created to provide shell for restoration purposes, but the types and availability of shell can vary. Additionally, the growth of oysters on these shell types once planted may affect restoration success if set ratios are too high or low. This study evaluated the average settlement of eyed oyster larvae in circular setting tanks with mixtures of three shell types: eastern oyster (*C. virginica*), surfclam (*Spisula solidissima*), and knobbed whelk shell (*Busycon carica*). Spat settlement was assessed prior to deployment on the subtidal reef site and again four months post-planting. Initial settlement numbers (no. oysters per shell) significantly differed between each shell type and were highest for surfclam shell and lowest for whelk shell ($p<0.001$). During post-planting monitoring, oysters and surf clam shell had the largest oysters but also had the highest mortality. This study is important for optimizing aquaculture techniques for small-scale remote setting that can be restricted by both the availability of shell types and permitting requirements prohibiting certain substrates in shallow-water bays.

DIVERSITY AND GENE EXPRESSION ANALYSIS OF THIOESTER-CONTAINING PROTEINS (TEP) IN THE SQUID EUPRYMNA SCOLOPES, A MOLLUSCAN MODEL

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Thioester-containing proteins (TEP) have been identified and characterized in many metazoans. Although these molecules constitute one of the most ancient innate immune components and are present in both invertebrate and vertebrate animals, many are not well characterized. Based on amino acid homology and the presence of functional protein domains, TEP have been traditionally organized into three subgroups: complement component 3 (C3)-like subfamily, the alpha-2-macroglobulin (A2M)-like subfamily, and the insect TEP (iTEP) and CD109 subgroup. Several protein domains including the functional thioester region (TER), which has a highly reactive bond that allows proteins to covalently interact with foreign targets, and macroglobulin domains are shared by most of the members of this superfamily. This study focused on identifying the presence and characterizing the diversity and protein expression of TEP in the squid, *Euprymna scolopes*. *In silico* search revealed the presence of eight TEP in *E. scolopes*: two C3-like transcripts (Es-C3-1 and Es-C3-2), two A2M-like homologs (Es-A2M-1 and Es-A2M-2), and four molecules closely related to the iTEP (Es-TEP1–4). NCBI protein BLAST search showed that four of the *E. scolopes* TEP have a putative TER (Es-C3-1, Es-TEP-1-2, and Es-A2M-2). Protein expression studies were conducted using real-time quantitative PCR (RT-qPCR) in juvenile squid colonized by *V. fischeri* for 24 h and compared to control (uncolonized) squid. Results showed that TEP-2 is up-regulated 1.7-fold in colonized juveniles, while TEP-3 is down-regulated by 0.5-fold in colonized squid compared to uncolonized juveniles. The expression of other TEP was not affected by colonization of the symbiont *V. fischeri*.

TAKING PUBLIC OUTREACH INTO HOME KITCHENS: STUCK AT HOME? #SHUCKATHOME!

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The rapid spread of coronavirus and the resulting lockdowns led to a host of challenges when it came to traditional approaches to public outreach. Widespread restaurant closures left oyster growers without the market where about 90 percent of their product is normally distributed. Consumers, eager to eat oysters, found themselves ill-equipped to open and prepare oysters in the home. With consumers, oyster growers, and Extension agents largely limited to the confines of their own homes in the Spring of 2020, Maryland Sea Grant Extension agents pivoted to a digital approach to showcase how the public could continue to enjoy oysters in their own home by sharing easy-to-follow preparation tips and recipes.

The team engaged a range of experts, including growers, extension specialists and students to demonstrate a variety of options for at-home oyster consumption. These included various shucking techniques, shuck-less methods, as well as recipe ideas well-suited to the home chef. Recorded using the technology growers and outreach specialists had on hand–smartphones–and produced by the program's communications staff to have a consistent look and feel, the resulting 'Shuck at Home' series was planned so that episodes could be easily viewed across several social media platforms and YouTube. Optimizing the videos for this type of distribution allowed for a wider audience through social sharing and the use of targeted hashtags, as well as track shares and views through various platform analytics.

BAY SCALLOP, *ARGOPECTEN IRRADIANS*, CULTURE IN WACHAPREAGUE, VIRGINIA, USA

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Bay scallop aquaculture has been part of the VIMS ESL history since the 1960s, and past economics forestalled market development. With a greater demand for aquacultured molluscs, the economic basis for successful scallop production has changed. Work at the VIMS ESL since 2009 has focused on rearing bay scallops for ecological restoration and stock enhancement, and more recently we have been examining cultural practices with a goal to increase production efficiencies for commercial aquaculture. The major roadblock is in the nursery phase. Although the transition from hatchery to nursery is accompanied by a switch from cultured algae to 50 micron filtered natural plankton, modifications to soften the transition had no effect on survival and growth. The ESL has used vertical slats in shallow water tables for settling surfaces. Downwellers for setting did not improve nursery outcomes. Larval settling behavior was examined to provide guidance for matching settling behavior to physical structure. Estimated costs of seed scallop (5 mm) production for the two successful years using the ESL research scale system were $36 and $20 per 1000, respectively. Survival of seed scallops to market size in 11 months was about 12%, with a projected cost per scallop from fertilized egg to market of $0.53 and $0.28 in two separate production years.

A CHROMOSOME-LEVEL ASSEMBLY OF THE BLACK TIGER SHRIMP (*PENAEUS MONODON*) GENOME

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Aquaculture is an important food source for the growing population of the world as it provides the planet with more than 50 percent of fish products consumed by humans. The penaeid marine shrimps (Family Penaeidae) are the predominately cultured group. Of which, the Pacific white shrimp (*Litopenaeus vannamei*) and black tiger shrimp (*Penaeus monodon*) are the most dominant species cultured. To ensure sustainable and profitable production through genetic selective breeding programs, a high-quality genome sequence of the shrimp is mandatory. Here, the first chromosome-level whole-genome assembly of *P. monodon* using the combination of long-read Pacific Biosciences (PacBio) and long-range Chicago and Hi-C technologies will be reported. The final assembly covered 2.39 Gb and contained 44 pseudomolecules, corresponding to the haploid chromosome number. Repetitive elements occupied 62.5% of the assembly, which is highest reported among crustacean species. This high-quality genome assembly provides an invaluable resource for accelerating the development of improved shrimp strain in breeding programs and future studies on gene regulations and comparative genomics.

THE EFFECTS OF PERMITTING DELAYS ON RETURN ON INVESTMENT FOR PACIFIC COAST SHELLFISH AQUACULTURE

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A survey to assess the on-farm effects of regulations on shellfish farms on the U.S. Pacific Coast (Washington, Oregon, and California) was completed in 2017. The coverage rate for the responses was 74% of the production value of the Pacific coast shellfish industry (van Senten et al. in review). Survey responses revealed significant challenges and delays in obtaining licenses and permits for shellfish aquaculture, and costs associated with those delays. The total costs associated with obtaining permits and licenses ($6.8 million) were greater than the costs of ongoing monitoring and compliance on Pacific coast shellfish farms ($4.7 million) (van Senten et al. in review). From previous studies of regulatory costs on U.S. aquaculture sectors, it was observed that delays and challenges in permitting form a barrier to entry, expansion, and diversification (Engle et al. 2019, van Senten & Engle 2017). Using the data collected from the 2017 survey of Pacific coast shellfish producers, an analysis of the effects of permitting delays on return on investment was performed. Shellfish aquaculture requires capital investment for equipment and infrastructure, in addition to operating costs for labor and production activities. Delays in permitting have a demonstrable negative effect on the return on investment for shellfish aquaculture.

IDENTIFYING CONSUMER PREFERENCES FOR DELIVERY AND PICK UP OF AQUACULTURE FARM PRODUCTS IN VIRGINIA, MARYLAND, AND NEW YORK IN RESPONSE TO THE COVID-19 PANDEMIC

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A survey to assess consumer consumption patterns and preferences for aquaculture and seafood products was implemented in response to the COVID-19 pandemic. Using a Qualtrics panel of 100 seafood consumers (set as exclusion criteria) in three key markets in Virginia, Maryland, and New York, data was gathered by Extension personnel to assess the effect of the pandemic on seafood consumption, preferences for product type, product forms, product sizes, packaging, and delivery methods. This survey is to be repeated twice throughout the project period, in an attempt to capture changes in consumer preferences as the COVID-19 pandemic continues to evolve. Results from the first of these two surveys will be summarized and presented during this session.

THE ECONOMIC IMPACT OF SHELLFISH AQUACULTURE IN MARYLAND, USA

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An economic impact analysis of the Maryland shellfish industry was performed in 2019. Data were obtained from a survey of Maryland shellfish producers to account for the farm level expenditures of water column culture and bottom culture of shellfish. Respondent data were utilized to develop standardized enterprise budgets for water column and bottom culture farm activities, from which an industry expenditure pattern was derived. Those expenditure patterns were used to develop custom industry spending patterns for an analysis by parts (ABP) approach in IMPLAN Pro. The ABP approach was selected because IMPLAN does not contain a specific sector for aquaculture; instead grouping aquaculture with other terrestrial animal production activities. The ABP approach allows for greater flexibility and customization; which results in a better representation of shellfish aquaculture activities. Separate industry spending patterns were developed for water column and bottom culture of shellfish in Maryland. Results estimated a total economic output impact in excess of $8.1 million for 2018.

PREVALENCE AND INTENSITY OF THREE OYSTER PARASITES (*PERKINSUS MARINUS*, H*APLOSPORIDIUM NELSONI*, AND *BONAMIA* SP.) IN WILD AND CULTURED OYSTERS (*CRASSOSTREA VIRGINICA*) ON AN OYSTER FARM IN SOUTHEASTERN NORTH CAROLINA, USA

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Populations of the eastern oyster, *Crassostrea virginica*, along the Atlantic coast of the United States have been severely impacted by a variety of parasites over the past 60 years. Prevalence and intensity of three *C. virginica* protozoan parasites—*Perkinsus marinus* (Dermo), *Haplosporidium nelsoni* (MSX), and *Bonamia* sp.—were monitored in wild and cultured oysters over a five-year period using quantitative PCR (qPCR). Starting in February 2016, samples of 100 wild oysters were collected monthly from Masonboro Sound, NC. Five lines (HC5-9, CI3-14, SS5-30, MM4-30, MM6-4) of cultured oysters were also sampled monthly after deployment on an adjacent farm. Prevalence and intensity of *P. marinus* and *H. nelsoni* in wild oysters varied widely over the five-year sampling period. Peaks in prevalence of *P. marinus* occurred in summer 2017 and 2018 (93%), and in spring 2018 and summer 2019 and 2020 (100%) for *H. nelsoni*. *Bonamia* sp. was rarely detected in the wild oyster samplings, with peak prevalence observed in November 2018 (37%). Intensity of infection (estimated by Ct value) was greatest in late summer 2018 for *P. marinus* and in spring 2019 for *H. nelsoni*. Prevalence and intensity of the parasites varied among the five lines of cultured oysters, and between cultured and wild oysters. All three parasites were detected in all five lines of cultured oysters, although timing of parasite detection, prevalence and intensity of infection varied among the lines. Influence of environmental factors such as temperature, salinity, and chlorophyll-a on the occurrence of these parasites was also examined.

CHARACTERIZATION AND EXPRESSION PATTERNS OF A NEW CRUSTACEAN HYPERGLYCEMIC HORMONE (CHH) GENE FROM THE PACIFIC WHITE SHRIMP, *PENAEUS VANNAMEI*

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The crustacean hyperglycemic hormone (CHH) family is an important group of neuropeptides involved in controlling growth, reproduction, and stress response in decapod species. In this study, a new CHH containing 4 exons-3 introns was isolated from *Penaeus vannamei*. Two full-length transcripts of this CHH were isolated from eyestalk and pericardial tissue of males and females. The differences in transcripts length is a result of two polyadenylation sites present in the 3’UTR resulting in two transcription termination signals. Transcript sequences encoded one unique protein that can be classified as CHH type I, but with some particular characteristics, as a glycine insertion in the mature peptide at position 32 and no amidation is present in the C-terminal of the deduced amino acid sequence. The expression patterns show that this gene is expressed in eyestalk, supraesophageal ganglion (SoG), gill, gut, and heart, as well as in the terminal ampoule or spermatophore and *vas deferens* of males. Additionally, the expression of *Lvchh* was also analyzed throughout the molt cycle and the results indicated that it increased from early to late pre-molt in all evaluated tissues

USING A MULTI-YEAR, STATEWIDE DEMOGRAPHIC ASSESSMENT OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) IN SOUTH CAROLINA AS A TOOL TO SUPPORT RESTORATION AND MANAGEMENT

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In South Carolina, oysters (*Crassostrea virginica*) are considered substrate-limited, meaning there is plenty of larval oyster production, but the availability of suitable substrate for settlement is a limiting factor in population growth. This limitation has led to a focus on substrate supplementation-based approaches to restoration throughout the state for both their ecological and fisheries benefits. The success of these efforts could be increased through an improved understanding of the spatial and temporal variability in oyster demographics, particularly in regard to mortality, recruitment, and growth rates.

In 2015, the Shellfish Research Section at the SCDNR MRRI initiated the South Carolina Oyster Demographic Assessment (SCODA) Program to investigate oyster population demographics. By collecting oyster length-frequency data at index sites distributed throughout the coastal region, measurements of baseline natural mortality rates, relative recruitment trends, and estimates of growth parameters have been possible. This program has demonstrated spatial and temporal fluctuations in natural mortality and recruitment of oysters, and these changes appear to be related to influxes of freshwater to coastal environments. Additionally, growth rates of oysters inferred from size-frequency distributions vary spatially across the state. Identifying the causes of these variations would improve the success of restoration and management efforts in terms of site selection decision-making. By relating demographic trends in statewide oyster populations to physical and environmental conditions, the SCDNR is working to increase the understanding of the drivers of natural mortality, recruitment, and growth of oysters. Ultimately, this knowledge may serve to inform proactive management strategies that conserve the resource.

EFFECTS OF CO-CULTURE OF URCHINS, *LYTECHINUS VARIEGATUS*, WITH EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*

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The effects of overwintering co-culture of the green sea urchin, *Lytechinus variegatus*, with eastern oysters at oyster farms in Alligator Harbor (AH) and Oyster Bay (OB), Florida were evaluated. In October 2019, urchins (collected from St. Joseph's Bay, test diameter ∼25-35 mm) were deployed in clean 9 mm mesh bags (46 × 61 × 10 cm) along with ∼40 oysters (avg. shell height, 48.1 + 6.9 mm) at three urchin stocking densities (n=16/site): 0, 4 or 8 urchins. All bags were held in floating cages at commercial oyster farms at each site. As a control, urchins were also deployed without oysters at three stocking densities (n=4/site): 2, 4, or 8 urchins. In March 2020, urchins, oysters and fouling on the bags were assessed. Urchin survival was not affected by oyster presence but was significantly higher in AH than OB. All urchins grew but average weight and gonad index decreased with increasing urchin density. When gonad growth was good, color was considered excellent. In terms of oyster performance, urchins did not affect oyster survival, shell height, shell length, or the fan ratio but did produce oysters with greater shell width, deeper cup ratio, heavier shells and greater dry tissue weight. Furthermore, urchins improved oyster body condition, mantle condition and shell fullness. Finally, urchins reduced bio-fouling on the oysters. For fouling on the bags, there was a significant urchin density by site interaction, where urchins had no effect on the biofouling in OB, but significantly reduced bag biofouling in AH.

EFFECTS OF INBREEDING AND OUTCROSSING ON EARLY PERFORMANCE OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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Inbreeding can affect the performance of aquaculture stocks, and outcrossing may produce heterosis leading to improvement of production traits. In this study, effects of inbreeding and outcrossing on early performance of the eastern oysters (*Crassostrea virginica*) were investigated. Two inbred lines with different levels of inbreeding were used to produce inbred and hybrid families, along with wild control families. Mortality and size data were collected at larval and juvenile stages. At day 2, mortality of the families was mostly associated with certain female parents, indicating strong maternal effects on early larval survival. At day 20, the wild control had the lowest cumulative mortality although the differences among all groups were not statistically different ($p > 0.05$). At the pediveliger stage, larvae of hybrid families were the largest, suggesting that heterosis may be an important factor affecting larval growth. At day 133, cumulative mortality did not vary significantly among groups, but body size did. The wild families were significantly smaller than the inbred and hybrid families, and the hybrid families were intermediate between the two groups of inbred families. While preliminary, these results indicate that artificial selection in the inbred lines may have contributed to their fast growth, and juvenile growth is mostly additive. Larval and juvenile growth may be under different mechanisms of genetic determination. These families are maintained for continued evaluation and genetics analyses.

LOOKING DOWN THE BARREL OF AN ENDOSCOPE: INSIGHTS FROM THIRTY YEARS OF *IN VIVO* INVESTIGATIONS OF SUSPENSION-FEEDING MOLLUSCS

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Over the past 30 years, endoscopic examination and video-image analysis have provided a more in-depth understanding of suspension-feeding processes in bivalve molluscs and other invertebrates. Performing *in vivo* observations of the intact feeding organs of undisturbed specimens has resolved many controversies, allowed for a more integrative assessment of the particle feeding process, and uncovered some surprising behaviors. A visually appealing overview of this research will be presented focusing on several suspension-feeding processes and their mechanisms, including the capture, transport, and ingestion of natural and synthetic (plastic) particles.

INGESTION, BIOACCUMULATION, AND DEPURATION OF MICRO- AND NANOPLASTICS BY OYSTERS (*CRASSOSTREA VIRGINICA*) AND MUSSELS (*MYTILUS EDULIS*)

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Plastic debris is introduced into the oceans through anthropogenic waste. Fragmentation of this debris resulting from weathering and UV degradation produces microplastic (MP; < 1mm) and nanoplastic (NP; < 100nm) particles. Under certain laboratory conditions MP and NP can negatively affect marine animals on an organ and cellular level. Despite the potential for exposure and toxicological effects, the uptake and accumulation of MP and NP by benthic animals, such as suspension-feeding bivalves, is largely unexplored. This study examined the uptake and depuration of fluorescent polystyrene MP and NP by two bivalves, the eastern oyster (*Crassostrea virginica*), and blue mussel (*Mytilus edulis*). Bivalves were exposed to a 0.1 mg/L/hr concentration of either MP or NP for two weeks and then allowed to depurate for one week in filtered seawater. Throughout the 3-week experiment, animals were fed a standard microalgal diet. Feces were collected daily and replicate oysters and mussels sampled and frozen at the end of each week for later analysis. Tissue and feces samples were analyzed via a scanning fluorescence spectrophotometer and concentration of plastic quantified. Overall, bivalves ingested a higher mass of MP than NP, and both plastic particles were rapidly depurated over several days. No bioaccumulation of plastic particles was detected after 14 days of exposure. Results from this study will be used to develop biokinetic models of uptake and elimination of MP and NP by bivalves, and have important implications for assessing internal exposure, toxic effects, and trophic transfer.

EFFECT OF DIET AND TEMPERATURE ON GONAD ENHANCEMENT OF GREEN (*STRONGYLOCENTROTUS DROEBACHIENSIS*) AND RED (*MESOCENTROTUS FRANCISCANUS*) SEA URCHINS

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When sea urchin population growth is uncontrolled, they can over-graze and decimate macroalgal beds, creating areas termed “urchin barrens”. Sea urchin gonad enhancement is a proposed method to remove sea urchins from barren grounds, promote the re-growth of macroalgal beds, and produce a highly-valued marketable product. Prepared feeds need to be developed that not only increase gonad yield, but also impart appropriate market colour and flavour. This project assessed the effects of two prepared diets (V10.1.9 and V10.1.10) and a natural feed (bull kelp, *Nereocystis luetkeana*) and three seawater temperatures (8, 12, and 16°C) on gonad yield/quality for both the green (*Strongylocentrotus droebachiensis*) and red (*Mesocentrotus franciscanus*) sea urchin held under laboratory conditions for 12 weeks. Green urchins fed the prepared diets had overall higher gonad yields and better colour than the green urchins fed kelp at all three temperature treatments; with V10.1.9 producing the highest yields for all three temperatures and V10.1.10 producing the best colour at 16°C. Red urchins fed V10.1.10 at 12oC had the highest gonad yields out of all the treatments, while the red urchins fed kelp at 8°C had the lowest yields. The gonad colour was better overall with the red urchins fed V10.1.10, with the best colour again obtained at 16°C, which is the same trend as seen in the green urchins.

LARGE-SCALE OYSTER RESTORATION IN THE CHESAPEAKE BAY, MARYLAND, USA

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This presentation will be an overview of the large-scale, collaborative, eastern oyster (*Crassostrea virginica*) restoration effort that NOAA, US Army Corps of Engineers, state natural resource management agencies in Maryland and Virginia, and several non-governmental organizations and academic institutions have undertaken. Since 2011, the work has resulted in more than 800 acres restored, and more than $55 million has been spent. Discussion will include the process for pulling together partners behind a single large objective, setting success criteria, tributary-scale restoration goal setting, and science-driven planning, implementation, and monitoring, as well as lessons learned and evaluation of ecosystem services and economic impact for portions of the effort.

PHAGE-HOST INTERACTIONS SHAPED THE NATIVE ST36 POPULATION SUCCESSION IN THE PACIFIC AND GOVERNED SUCCESSFUL INVASIONS INTO THE NORTH ATLANTIC

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The introduction of a Pacific endemic lineage of *Vibrio parahaemolyticus* called sequence type (ST) 36 into the North Atlantic caused a steep rise in illnesses from multiple aquaculture areas along the US Atlantic coast, requiring intensive management to reduce risk. The reconstruction of the dynamic of spread and establishment of new populations was hindered by a lack of information linking infections to geographic locations. A cooperative effort of multiple agencies in the Northeast US producing an extensive collection of ST36 strains that bridge critical temporal and geographic gaps in coverage has laid a foundation to better understand the dynamic of invasion, spread, and establishment of ST36. These analyses indicate dramatic shuffling in content of filamentous prophage, viruses in the family *Inoviridae* (inoviruses) that form persistent non-lethal infections, occurred during population expansion. Elimination of a prophage that was stably maintained by the endemic ST36 clonal complex for decades likely preceded lineage diversification in the Pacific Northwest. Subsequently, at least seven distinct ST36 progenitors translocated into the Atlantic, giving rise to at least four distinct clonal, geographically stable and non-mixing subpopulations. The successful founders of two Atlantic sub-populations that have repeatedly caused infections acquired new inoviruses diagnostic for these subpopulations. These findings exemplify a potential role for filamentous phage to facilitate the adaptability and competitiveness of emergent pathogenic lineages. This study also paves the way for functional analyses to better understand the role of inoviruses in the dynamics of evolution and pandemic spread of environmentally transmitted pathogens.

SURVIVAL AND GROWTH OF SELECTED BAY SCALLOPS (*ARGOPECTEN IRRADIANS*) IN BARNEGAT BAY, NEW JERSEY, USA

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Increasing crop diversity is important for sustainable development of shellfish aquaculture. Bay scallop, *Argopecten irradians*, is a promising species for culture in high salinity (25-32) coastal waters of the northeast where bivalve aquaculture is currently dominated by eastern oysters (*Crassostrea virginica*) and northern quahogs (= hard clams) (*Mercenaria mercenaria*). In 2019, a bay scallop breeding program was initiated at Rutgers University to produce fast growing scallops that will reach a harvestable size within one year. Two groups of scallop seed were produced, selected and control, using wild collected broodstock from Peconic Bay, Long Island. The selected scallops were produced using the largest 20% of broodstock. In 2020, seed were again produced using large and randomly selected individuals from the same wild population, and from a F1 selected group produced in 2019. In both 2019 and 2020, spawns occurred in March and juvenile scallops were reared in flow-through nursery conditions until July. In both years, scallops were deployed at three farms in Barnegat Bay, New Jersey, and their growth and survival across and within sites were compared. Field survival to December was high at all sites in both years. Growth differed by site and by stocking density. At the best performing site, the two selected groups were significantly ($p<0.05$) larger than unselected controls in shell height and length. In most groups, scallops reached a harvestable size (40-50 mm) by early December of each year. Selection will be continued for three generations to determine genetic improvements.

GLIDER-BASED OBSERVATIONS REVEAL SEASONAL PH AND ARAGONITE SATURATION STATE VARIABILITY IN COASTAL U.S. MID-ATLANTIC SHELLFISHERY MANAGEMENT ZONES

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Ocean and coastal acidification alter the oceanic carbonate system, increasing potential for ecological, economic, and cultural losses. Currently, productive coastal systems lack vertically-resolved high-resolution ocean carbonate system measurements on timescales relevant to organism ecology and life history. To address this issue, a newly developed deep ISFET (Ion Sensitive Field Effect Transistor)-based pH sensor system was modified and integrated into a Slocum G2 profiling glider. From Spring 2018 to Fall 2019, seasonal pH glider deployments were conducted in Atlantic surfclam (*Spisula solidissima*) and Atlantic sea scallop (*Placopecten magellanicus*) commercial management zones in the Mid-Atlantic Bight. Simultaneous measurements from multiple sensors on the same glider allow the calculation of carbonate system parameters (e.g. aragonite saturation state) and mapping of these parameters against other variables, such as dissolved oxygen and chlorophyll. These data are being used in conjunction with shellfish stock assessments and larval dispersal models to identify times and locations where shellfish stock may be at high risk of acidification. Thoroughly resolved carbonate system dynamics in coastal systems are necessary to predict the impacts of ongoing climate change on ecosystem services and the economy.

THE USE OF SELECTIVE BREEDING TO UNDERSTAND THE GENETIC UNDERPINNINGS OF RESILIENCY TO OCEAN ACIDIFICATION IN THE PACIFIC OYSTER (*CRASSOSTREA GIGAS*)

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Ocean acidification (OA) is suspected to cause mass mortalities during larval culturing in shellfish hatcheries. The larvae of the Pacific oyster, *Crassostrea gigas*, can experience shell deformities and developmental delays when exposed to ocean acidification conditions.

Here, the expression of 24 genes involved in shell development was investigated to understand larval growth and survival in OA conditions. The parent adult oysters are from a family breeding program developed in 2019 at the Vancouver Island University Deep Bay facility. During the 2019 breeding program, oyster families were identified as being either resilient or susceptible to OA based on mortality rates and growth metrics. Using adult oysters that were "resilient" or "susceptible" to OA conditions, susceptible and resilient larval genetic lines were produced to explore the genetic underpinnings of developmental success under OA conditions. Laboratory-based OA conditions were established using seawater collected from Baynes Sound, British Columbia (BC) that is known to exhibit low pH and aragonite saturation at depths of 70 metres. Pacific oyster larvae were reared under control or OA conditions and sampled every 3 hours for 24 hours. RealTime-qPCR was used to quantify the relative gene expression of 24 selected genes believed to be involved in early shell development.

This brief presentation aims to present the key genes found to be expressed differently between 1) resilient and susceptible larvae and/or 2) control and OA conditions, and to discuss the potential applications of increased knowledge of shell development in OA conditions on selective breeding strategies in shellfish hatcheries.

CHARACTERISTICS OF THE CRUSTACEAN HYPERGLYCEMIC HORMONE (CHH) GENES AND THEIR FUNCTIONS IN THE PROCESSES OF MOLTING AND MALE SEXUAL DIFFERENTIATION IN *LITOPENAEUS VANNAMEI*

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The neuropeptides of the crustacean hyperglycemic hormone (CHH) superfamily are known to control several important functions ranging from energy metabolism, molting, osmoregulation to reproduction. Decoding the *L. vannamei* genome not only provides an insight into the genetic foundation of specific biological processes, but also provides valuable information for enhancing crustacean aquaculture. In *L. vannamei*, a striking expansion of the crustacean hyperglycemic hormone (CHH) family underpins the control of the enhanced ecdysone function. Ecdysone synthesis in the crustacean Y-organ is mainly under the negative control of the molt-inhibiting hormone (MIH), one of the type II peptides of the CHH family. Seven tandemly duplicated MIH genes with high sequence similarity were identified. This might facilitate the co-expression and co-functionality of these genes during molting. Besides, type I peptides of the CHH family are also known to suppress ecdysteroidogenesis in the Y-organ, though at a higher dose than MIH.

Recently, two CHH genes (LvCHH1 and LvCHH2) and their putative receptor guanylate cyclase (LvGC) were identified in *L. vannamei*. LvCHH1 and LvCHH2 belonged to CHH subfamily I members and LvGC was a membrane-bound guanylate cyclase. They were all differentially expressed in eyestalks and gonads of males and females. RNA interference (RNAi) of either LvCHH1 or LvCHH2 increased LvIAG expression, while injection of their recombinant protein decreased LvIAG expression, indicating that LvCHH1 and LvCHH2 are inhibitory factors of LvIAG expression.

DEVELOPING TECHNOLOGIES TO INDUCE REPRODUCTIVE STERILITY IN EASTERN OYSTERS WITHOUT CHROMOSOME SET MANIPULATION

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Triploid oysters are considered as sterile and preferred by oyster farmers because of their fast growth and premium meat quality during the summer seasons; however, recent reports revealed the phenomenon of 'triploid mortality' and found that triploid eastern oysters are more susceptible to environmental stressors than diploids even though their gonadal development was delayed and/or diminished. These results highlight the need for alternative sterilization technologies to preserve the market advantages of growing sterile oysters without altering their chromosome sets. Reproductively sterile fish have been efficiently produced using *dnd*-MO-*Vivo* to transiently silence *dead end*, an essential gene responsible for fish primordial germ cell (PGC) development, by administering Morpholino oligomer through a molecular transporter, *Vivo*.

To apply this bath-immersion technology to produce reproductively sterile eastern oyster (*Crassostrea virginica*), genes that are indispensable for oyster PGC development need to be indentifed first since no *dnd* ortholog was found in oyster. Several genes in invertebrate model organism Drosophila have been shown to be crucial for PGC development including germ plasm and germ cell formation, PGC specification and PGC migration. Loss of function mutants of these genes are reproductively sterile. The orthologs of these candidate genes have been identified and cloned in eastern oyster. Secondly, the protocol of using MO-Vivo to immerse oyster eggs and embryos has been established. The treated oyster spat were deployed to the river and sterility will be evaluated upon sexual maturity based on germ cell marker gene expression by qPCR, PGC development by *in situ* hybridization and gametogenesis by histology.

SIMPLE SEQUENCE REPEATS DRIVE GENOME PLASTICITY AND PROMOTE ADAPTIVE EVOLUTION IN PENAEID SHRIMP

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Simple sequence repeats (SSR) are rare (approximately 1%) in most genomes with unknown function and thus considered as 'junk DNA' generally; however, a growing number of genomes hold high proportion of SSR have been reported, especially for penaeid shrimp (> 23%), raising the question of whether these SSR play functional and evolutionary roles in these SSR-rich species. In this study, the chromosome-level genomes of two penaeid shrimp species, *Fenneropenaeus chinensis* and *Litopenaeus vannamei*, were assembled. Comparison of these two genomes revealed that transposons serve as carriers for SSR expansion, which is still occurring. The remarkable genome plasticity identified herein might have been shaped by significant SSR expansions, and a major expansion occurred in the penaeid shrimp ancestral genome, consistent with the rapid evolution of penaeid shrimp after a mass extinction event. It was also found that SSR regulate gene expression by multi-omics analyses, and be responsible for driving adaptive evolution, such as the variable osmoregulatory capacities of these shrimp under low-salinity stress. For the first time, these data provide strong evidence that SSR are an important driver of the genome plasticity and adaptive evolution in penaeid shrimp. Since they are widely-distributed in the genome, SSR should serve as new key elements to regulate various biological processes in SSR-rich species.

COMPARISON OF THE PEARL QUALITY OF MABÈ *PTERIA PENGUI*N CULTURED IN BAY AND STRAIT IN THE PROVINCE OF SOUTHEAST SULAWESI, INDONESIA

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Pearl oysters are cultivated for mabe pearl production. The research objective was to compare the quality of mabè pearls reared in different water conditions, the Kendari Bay and Buton Strait in the Southeast Sulawesi Province, Indonesia.

The shells were implanted with two pearl nuclei in each shell. The shells were reared by a rope system with a floating raft. Each hanger contains 20 shells. Oysters were cultivated for 4 mo during rainy season; February-May 2020. Water quality parameters were measured. After harvested shells, 62 pearls were observed for each location. Pearls were classified based on their quality, there are 5 categories: AAA (Very high luster, quite symmetrical, smooth surface and even); AA (High luster, smooth but uneven surface, no surface defects, symmetry); A (Good luster, uneven surface slightly deformed, less symmetry); B (The sparkle is quite a bit blurry, the surface is uneven, not symmetry); and N/C (Bad luster, thin, speckled, not symmetrical defects).

Classification of mabè pearls produced from the waters of Kendari Bay were quality of AAA (22.58%); AA (24.^{2}9%); A (30.65%); B (14.5^{2}%) and N/C (8.06%). Meanwhile, the results of the Buton Strait waters were AAA (29.03%); AA (27.4^{2}%); A (29.57%); B (8.06%) and N/C (5.91%). During the cultivation period, the percentage of quality mabè pearls (AAA-A) tended to be higher from Buton Strait waters than from Kendari Bay waters. The waves and currents in the waters of the Buton Strait were higher than in Kendari Bay. This indicates that pearl formation could be influenced by water conditions.

REVERSE TRANSCRIPTASE-RELATED GENES AND THEIR POSSIBLE ROLE IN THE HOST CELL RESPONSE TO TRANSITION METAL POLLUTION

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Reverse transcriptase-related (*RVT*) genes represent a remarkable class of reverse transcriptases (RT) found in bacteria, fungi, protists, plants, and invertebrates from aquatic and soil-dwelling environments. These are cellular single-copy genes preserved by natural selection. Their occurrence in prokaryotic and eukaryotic representatives suggests a conserved biological function that is applicable to both prokaryotes and eukaryotes.

Reverse transcriptase-related proteins from the filamentous gliding bacterium, *Herpetosiphon aurantiacus*, and the ascomycete fungus *Neurospora crassa* display a peculiar property of initiating polymerization via protein priming. Thus, *RVT* proteins represent the first known case of protein-primed RT encoded by a chromosomal non-selfish gene. Moreover, the N-terminal coiled-coil domain allows *RVT* proteins to form multimers and could potentially interact with metal ions. Since most free-living organisms can be frequently exposed to hazardous pollutants including transition metals, they therefore need potent mechanisms to cope with such stresses.

Three free-living organisms with active *RVT* genes in their genome (*H. aurantiacus*, *N. crassa*, and the bdelloid rotifer, *Adineta vaga*) not only display signs of altered growth and behavior after treatment with varying concentrations of several metal ions (Ni2+, Co^{2+}, Fe^{2+} etc.), but also display strongly induced expression of *RVT* genes under metal stress conditions. Interestingly, all examined organisms demonstrate specificity of *RVT* response to a specific metal ion. When recombinant bacterial HaRVT is expressed in *E. coli*, it apparently provides an advantage for survival in iron-rich environments. Participation of domesticated RT in metal stress response could reveal an ancient function of these genes in early evolution and novel pathways to environmental adaptation.

GENOMIC SIGNATURES OF SELECTION ON OYSTERS WITHIN A SINGLE ESTUARY

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Local adaptation is a multigenerational process that increases mean population fitness and occurs at spatial scales where gene flow presents a weak countering force. When habitat heterogeneity creates strong selection at microgeographic scales relative to dispersal distances, the evolution of adaptive phenotypic plasticity is expected and well-documented. Sometimes these two adaptive mechanisms are not sufficient to describe the realized distribution of genotypes and phenotypes at small spatial scales. Specifically, sedentary species with high fecundity, early dispersal and high early mortality have enhanced capacity for differential selection to operate at small spatial scales within each generation. Within-generation selection contributes to microgeographic differentiation and produces a dynamic, non-equilibrium means of local cohort adaptation. Different from classical local adaptation, the hallmarks of this ‘cohort adaptation’ are microgeographic substructure increasing over time in a cohort, spatial genotype associations with environmental drivers, and in some cases repeatable genomic change at loci under selection. Using eastern oyster as a model, this study seeks to demonstrate the genomic and phenotypic consequences of cohort adaptation along the Delaware Bay salinity gradient. Results on initial efforts with adults, comparing changes in whole genome sequences resulting from an experimental hyposalinity challenge versus differences among wild transect samples after extreme precipitation-associated mortalities up-bay will be presented. Moderate, directional allele frequency changes were observed at multiple candidate loci. Tests for genetic/environment associations will be presented based on location-specific indices of salinity exposure. Understanding the cohort adaptation dynamic is important for interpreting population substructure snapshots and predicting adaptive responses to environmental change.

ASSOCIATION OF CLIMATE AND SEASON WITH THE PREVALENCE AND DISTRIBUTION OF A PATHOGENIC VIRUS AFFECTING THE ATLANTIC BLUE CRAB ACROSS ITS TRANS-HEMISPHERIC RANGE

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The Atlantic blue crab, *Callinectes sapidus*, is an estuarine keystone species that functions as both predator and prey in food webs and supports a multimillion dollar fishery along the western Atlantic coast from the US mid-Atlantic to southern Brazil. It has a broad latitudinal distribution encompassing both tropical and temperate climates. Its life history varies latitudinally, from extended overwintering at high latitudes to year-round activity in tropical locations. *Callinectes sapidus* reovirus 1 (CsRV1) is a pathogenic virus first described in the North Atlantic *C. sapidus* and has recently been detected in southern Brazil. Little information exists about CsRV1 prevalence at intervening latitudes, or in overwintering blue crabs. The goal of the study was to investigate the CsRV1 prevalence in *C. sapidus* across latitudinal differences in temperature and crab life history as well as in additional *Callinectes* spp and within overwintering *C. sapidus* using a quantitative reverse transcription PCR (RT-qPCR) method. Three major findings of the study are: 1) CsRV1 prevalence in *C. sapidus* was significantly higher at temperate than tropical latitudes; 2) Prevalence of CsRV1 in *C. sapidus* on the mid-Atlantic coast was significantly lower in winter than in summer; 3) CsRV1 infections were not detected in other *Callinectes* spp. This presentation will lead into a discussion about the association between the climate/temperature and host life history and the prevalence of CsRV1, which will help to better understand the underlying mechanisms that drive marine virus dynamics and how it might affect blue crab fishery under changing environmental conditions.

INVESTIGATING THE EFFECTS OF COASTAL STRESSORS ON THE GENOMIC VARIATION OF OYSTER POPULATIONS IN NARRAGANSETT BAY, RHODE ISLAND, USA

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Coastal environments are characterized by the presence of multiple stressors that may be occurring simultaneously and linked through biological processes. These stressors can have negative effects on the survival and development of important coastal species like the eastern oyster, *Crassostrea virginica*. Oysters have a sessile adult stage with low dispersal potential making them dependent on their pelagic larval stage for long-distance dispersal to increase gene flow across populations. Larvae are more sensitive than adults to a variety of natural and anthropogenic stressors making them a natural conduit for adaptation to environmental stressors. Multiple co-occurring coastal stressors may act as barriers to gene flow, limiting larval exchange by selective mortality (only letting resistant larvae pass), structuring populations through reduced connectivity. To investigate the effects of coastal stressors on the genomic variation of oyster populations, adult oysters were collected from multiple sites in Narragansett Bay varying in environmental conditions, including dissolved oxygen, pH, and sewage effluent. Sequence capture probes were generated from mRNA extracted from larval oysters exposed to coastal stressor treatments. These probes were used to capture regions of the adult genome highly expressed in response to these stressors. Population and seascape genomic analyses revealed high genetic differentiation of oysters from a site characterized by low salinity and higher temperatures compared to the other populations. Sampling of additional oyster populations within Narragansett Bay and collecting more long-term environmental data will further reveal how coastal stressors shape the genomic variation of oyster populations in Narragansett Bay.

USING BASELINE DATA FROM A BEFORE-AFTER-CONTROL-IMPACT (BACI) SURVEY OF AMERICAN LOBSTER (*HOMARUS AMERICANUS*) AND JONAH CRAB (*CANCER BOREALIS*) TO EXPLAIN RELATIVE ABUNDANCE AND SIZE STRUCTURE IN OFFSHORE SOUTHERN NEW ENGLAND (SNE)

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Scheduled offshore wind development in the United States will alter the surrounding ecosystem, potentially impacting the species that co-occur there. A lasting effect will be scour protection; the large volume of stones placed around each turbine structure. This will turn soft sediments into complex habitats, possibly preferable to structure-oriented species.

To establish a year-one baseline for a before-after-control-impact (BACI) survey within the Vineyard Wind (VW) 501N lease area, we employed coastwide ventless trap survey protocol that is also utilized by the Northeast coastal states. The 501N area and an adjacent control site were sampled for American lobster and Jonah crab relative abundance and size structure. An influx of smaller males influenced the size distribution of Jonah crab in the 501N area. Both species' relative abundance was seasonal and greater in the 501N area, but trap type specific catch rates were opposite compared to state data, where ventless trap catches observed in RI and MA surveys exceeded vented trap CPUE.

Generalized linear models (GLM) were used to relate environmental and survey characteristics to species presence. Time, depth, and temperature explained the seasonal variability for lobsters caught in vented traps, while trap saturation by *C. irroratus* bycatch negatively affected the abundance of lobster in ventless traps. Trap type, time, temperature, depth, latitude, and an interaction between temperature and depth best described *C. borealis* presence. Changes in temperature corresponded to abundance changes for both species, but an affinity for greater depths explained localized distribution and contributed to the difference in abundance between areas.

DEVELOPMENTAL AND BEHAVIORAL CHANGES OF THE WHITE SHRIMP, LITOPENAEEUS SETIFERUS, UNDER THE EXPOSURE OF PHENYLPYRAZOLE FIPRONIL

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Chemical pesticides are commonly used world-wide, and they can flow into estuaries and affect non-targeted organisms. The effects of six concentrations of the phenylpyrazole fipronil were evaluated (0.0, 0.005, 0.01, 0.1, 1.0, and 3.0 μg/L), which were previously observed in the environment, on white shrimp *Litopenaeus setiferus* (initially averaging 0.80 ± 0.08 g/shrimp). Compared with the control, survivorship of shrimp over 45 days declined significantly at the higher concentration treatments. Growth was affected at all concentrations, and the percent weight gain decreased significantly. Inter-molt intervals were longer in all treatments. Changes in swimming and feeding behavior of shrimp were observed under all treatments and change in body color was observed at higher concentration treatments. Lipid content in shrimp decreased significantly while ash content increased with fipronil concentration. Fipronil adversely affected white shrimp under the concentrations observed in the environment and monitoring of fipronil use is needed in coastal areas.

EFFECTS OF THE INSECTICIDES FIPRONIL AND IMIDACLOPRID ON THE GROWTH, SURVIVAL, AND BEHAVIOR OF BROWN SHRIMP, *FARFANTEPENAEUS AZTECUS*

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Increased use of pesticide is causing detrimental effects on non-target species worldwide. In this study, lethal and sub-lethal effects of fipronil and imidacloprid were examined on juvenile brown shrimp (*Farfantepenaeus aztecus*). The effects of six concentrations of fipronil (0.0, 0.005, 0.01, 0.1, 1.0, and 3.0 μg/L) and six concentrations of imidacloprid (0.0, 0.5, 1.0, 15.0, 34.5, 320.0 μg/L) were tested in a laboratory. Five different endpoints: growth, molting interval, survivorship, behavioral change, and body color change were evaluated. Growth of shrimp was reduced significantly under higher concentrations of both insecticides. Under fipronil exposure, shrimp in control showed the shortest inter-molt interval (7.57 ± 2.17 day) compared with other treatments; similarly, in the imidacloprid experiment, molting increased from 8.43 ± 2.52 day in control to 11.95 ± 4.9 day in 0.5 μg/L treatment. Higher concentrations of fipronil (1.0 and 3.0 μg/L) showed a 0.0% survival rate compared with 100% survival in the control and 0.005 μg/L treatment. Under imidacloprid, survivorship decreased from 100% in the control to 33.33% in the 320.0 μg/L treatment. The 96-h LC50 of fipronil was 0.12 μg/L, which makes brown shrimp one of the most sensitive invertebrates to the pesticide. Changes in behavior and body color were observed under both insecticides after different durations of exposures depending on concentrations. As a conclusion, at the corresponding EPA benchmark concentrations, fipronil had more lethal effects than imidacloprid, and imidacloprid had more sub-lethal effects than fipronil. Both effects are of serious concern, and monitoring is necessary in estuaries.

COMPARISON OF GENOMIC DNA EXTRACTION METHODS IN BLACK TIGER SHRIMP (PENAEUS MONODON) FOR LONG-READ GENOME SEQUENCING

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Aquatic animals are important to human nutritional and economic needs. The availability of genome sequences will undoubtedly improve the aquatic animal production; however, only few reports of high-quality genome sequence of aquatic animals, especially crustaceans, are available. One of the key challenge for the success of genome sequencing in crustaceans is the difficulty in isolating high quantities of pure, intact, and high molecular weight (HMW) genomic DNA. In this study, five DNA extraction protocols (CTAB, Genomic-tip, Mollusc DNA, TIANamp Marine Animals DNA, and Sbeadex livestock kits) were evaluated for their effectiveness in extracting genomic DNA from black tiger shrimp (*Penaeus monodon*) for long-read sequencing platform. The quality and quantity of the differentially extracted DNA were assessed by NanoDrop spectrophotometer, Qubit fluorometer and pulsed-field gel electrophoresis. Among the five DNA extraction protocols, Genomic-tip kit gave high yielded genomic DNA with the highest quality. To evaluate whether the obtained genomic DNA could be used for the long-read sequencing platform, the DNA samples from top three extraction methods (CTAB method, Genomic-tip and Mollusc DNA kits) were used for Pacific Biosciences (PacBio) sequencing. While the genomic DNA form Genomic-tip and Mollusc DNA kits allowed successful library construction, the genomic DNA obtained from CTAB method did not. The sequencing of genomic DNA obtained from Genomic-tip kit yielded a higher number of long reads (N50 of 14.57 Kb) than those obtained from Mollusc DNA kit (N50 of 9.74 Kb). Therefore, an effective DNA extraction protocol could be further applied for extracting high quality genomic DNA for long-read sequencing of other aquatic animals.

DIRECT COMPARISON OF THE FECAL AND GUT MICROBIOME OF THE BLUE MUSSEL (*MYTILUS EDULIS*)

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Shellfish have been studied for centuries; however, the microbes that reside inside of them have been largely overlooked. This study explored the potential differences between the resident gut microbiome and the transient fecal microbiome of bivalves. The fecal microbiome of the blue mussel (*Mytilus edulis*) was directly compared to the gut microbiome of isolated individuals to detect any differences in microbial community composition. Mussels were collected *in situ* from Long Island Sound and housed in individualized sterile microcosms for six hours to allow for fecal egestion. For each mussel, fecal and gut samples were collected and analyzed by sequencing prokaryotic community 16S rRNA amplicons. Fecal communities of different mussels resembled each other but did not resemble gut communities, likely reflecting the similarity in local conditions and environmental microbe pool. Fecal communities were significantly more diverse, in terms of amplicon sequence variant (ASV) richness and evenness, than gut communities. These results serve as preliminary evidence that mussels maintain a robust resident gut microbiome after fecal egestion that is dominated by ASV belonging to *Mycoplasma*. These results also indicate that, for mussels, the fecal microbiome is not a reliable proxy for the gut microbiome, unlike the gut and fecal microbiomes of many mammals. This discovery suggests that long-term microbiome manipulation will continue to be limited by the requirement for invasive gut sampling. Experiments that aim to study solely resident bivalve gut microbiota should employ an egestion period prior to gut sampling to allow time for voidance of transient microbes. Acknowledgement: This research was funded by a National Science Foundation (NSF) Research Experience for Undergraduate (REU) site grant to Mystic Aquarium and UConn; Award # 1559180.

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

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

THE INCORPORATION OF EPIGENETIC EFFECTS IN ENVIRONMENTAL AND HUMAN HEALTH RISK ASSESSMENT: APPROACHES FOR NON MODEL SPECIES

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Epigenetic mechanisms have gained relevance in human health and environmental studies, due to their pivotal role in disease, gene × environment interactions and adaptation to environmental change and/or contamination. Epigenetic mechanisms are highly responsive to external stimuli and a wide range of chemicals has been shown to determine specific epigenetic patterns in several organisms. Furthermore, the mitotic/meiotic inheritance of such epigenetic marks as well as the resulting changes in gene expression and cell/organismal phenotypes has now been demonstrated. Therefore, epigenetic signatures are interesting candidates for linking environmental exposures to disease as well as informing on past exposures to stressors. Currently, methodologies that study the entire epigenome, which refers to all chemical modifcations added to the DNA code, are routinely used to investigate potential epigenetic effects. While these technologies are increasingly applied in studies with model species, they remain challenging to apply to non model species. Here, the potential of these technologies in non model species will be discussed.

QUANTIFYING FARM-SCALE ECOSYSTEM SERVICES ASSOCIATED WITH EASTERN OYSTER AQUACULTURE IN THE NORTHEAST

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The eastern oyster (*Crassostrea virginica*) is a commercially important aquaculture species and food resource along the Atlantic and Gulf coasts of the United States (U.S.). Oyster aquaculture is the most common form of molluscan farming in the world and U.S. oyster production is valued at $192 million annually. In addition to its economic value, oyster aquaculture provides ecological value such as water quality improvement; however, the east coast of the U.S. is projected to experience increases in the frequency and intensity of freshwater events (i.e., storms and precipitation) with climate change. These climate change stressors may alter oysters' ability to provide these water quality benefits. The purpose of this research is to provide a scientifically rigorous account of an ecosystem service provided by oyster farms in the northeast. Specifically, this project aims to (1) estimate farm-level year-round filtration and nitrogen removal occurring at three oyster farms in the Delaware Bay region to quantify local farm contributions to improved water quality and (2) estimate impacts of low-salinity events to oyster farm filtration. Experiments to estimate individual oyster in-situ filtration and nitrogen removal are being conducted using a flow-through filtration chamber, from which, oyster biodeposits are collected for analysis. These methods capture variations in seasonal temperature, food quality and quantity, oyster size and energetic demands, among other conditions to accurately characterize annual filtration. These results may support the development of nutrient management programs in the Delaware Bay region similar to those in the Chesapeake Bay and elsewhere in the world.

ROGER WILLIAMS UNIVERSITY (RWU): CENTER FOR ECONOMIC AND ENVIRONMENTAL DEVELOPMENT (CEED)

Skylar Bayer, Bradford Bourque, Allex Gourlay, Matthew Griffin, Robbie Hudson, Jacqueline Mitchell, Andrew Rhyne, Alicia Schickle, Timothy M. Scott*, Abby Scro, Koty Sharp, and Roxanna Smolowitz

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On a waterfront campus in Bristol, Rhode Island, the Center for Economic and Environmental Development (CEED) includes 7,000 ft.2 of marine laboratories; three research vessels and a 200' dock on Mt. Hope Bay. CEED offers an exceptional opportunity to study all aspects of aquaculture and applied marine science. A full-scale Shellfish Hatchery (Dr. Skylar Bayer), produces shellfish and algal species for research, education and restoration, always with a focus on expanding the regional aquaculture industry. Research facilities include a nursery and experimental aquaculture farm providing hands-on experience while aiding the development of improved culture technologies. An Aquatic Diagnostic Laboratory (Dr. Roxanna Smolowitz), blends traditional diagnostic methods with cutting-edge molecular techniques, with a focus on the diseases of aquatic animals. The Marine Ornamental Research Facility (Dr. Andy Rhyne), emphasizes the culture of marine species and the international marine ornamental trade. Working in collaboration with several Public Aquariums, the lab investigates bottlenecks inhibiting commercial production and the establishment of a sustainable aquarium trade. The Sharp Lab (Dr. Koty Sharp), examines the microbial ecology of marine invertebrates (corals, sponges, tunicates, bryozoans, and bivalves) employing techniques from molecular biology, microbiology, chemical ecology and advanced microscopy.

THE EASTERNMOST MARINE SCIENCE FIELD STATION IN THE US: A PARTNERSHIP BETWEEN THE UNIVERSITY OF MAINE AT MACHIAS AND THE DOWNEAST INSTITUTE

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Marine science research and education are stronger and more active than ever in the easternmost coastal U.S. After 19 years of planning and development the University of Maine at Machias and its nonprofit partner, the Downeast Institute (DEI), are proud to announce that the newest marine science field station (MSFS) in the U.S. is open for business. Located on a 16-acre campus and adjacent to a 1200-acre preserve owned by The Nature Conservancy, this pristine setting is located 40 miles east of Acadia National Park in a traditional fishing community in Washington County, Maine. The marine research laboratory and adjacent shellfish production and development center are only 100-ft from deep water that covers nearly 3,000 ft rocky intertidal shoreline where tides vary 12- to 14-ft every six hours. Visiting scientists and their students have access to a 30-seat classroom equipped with running seawater, moveable tables/ benches, microscopes, seawater holding tanks, and Polycom communication capabilities. Six offices look out upon the Western Bay where spectacular sunsets are the norm, and where lobster fishermen ply their trade so close to shore during early mornings that you can almost reach out and touch their boats. A 1,000 ft2 ecology wet lab can be used for experimental work, or to hold organisms prior to field trials. Adjacent to the wet lab is a business incubator, quarantine lab, and climate control chamber. In addition, we have constructed a state-of-the-art ocean acidification lab to examine effects of current and future levels of CO2 on calcifying organisms.

USING A SCLEROCHRONOLOGICAL APPROACH TO DETERMINE A CLIMATE-GROWTH RELATIONSHIP FOR WAVED WHELK, BUCCINUM UNDATUM, IN THE U.S. MID-ATLANTIC

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Using growth rings observed in statoliths, the size-at-age relationship was modeled for waved whelk (*Buccinum undatum*) populations within the Mid-Atlantic Bight. A total of 45 sites in the mid-Atlantic were sampled between 2016-2019 using a scallop dredge, and a subset of the whelk collected were aged (n=318). Lab-reared individuals and back-calculation methods were used to fill missing juvenile observations. The Mid-Atlantic Bight population appears to differ in the fit of growth curves, compared to other assessed populations, due to a timing difference in hatching. Growth curves for whelk from this region show that maturity is reached between 4 and 6 years of age. A statolith chronology spanning a 10-year period was developed using a mixed-effects modeling approach. The chronology was used to explore the influence of temperature variation on growth during ecologically relevant periods. Growth increased with higher annual temperatures however specific seasonal bottom temperature had varying effects on growth. Increasing bottom temperature during summer, the anticipated egg-development and hatching period, resulted in an age-dependent decline in growth with a positive effect on younger whelk and a negative effect on older whelk growth. Higher summer temperatures provide larger time-windows for growth, facilitating increased growth in early life stages. It appears that whelk in this region possess sufficient growth plasticity to adapt to warmer conditions throughout the year, but increased warming during specific seasons may depress growth in older individuals, potentially affecting fitness and population persistence. Understanding these temperature-growth dynamics are critical for disentangling the effects of climate change on whelk growth, allowing for population predictions in the future.

ASSESSING THE DISTRIBUTION OF HORSESHOE CRAB EGGS IN RELATION TO INTERTIDAL OYSTER AQUACULTURE IN DELAWARE BAY AND RED KNOT FORAGING DISTRIBUTION

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The resurgent eastern oyster (*Crassostrea virginica*) aquaculture industry in Delaware Bay may influence the ecological relationship between horseshoe crabs (*Limulus polyphemus*) and the threatened rufa red knot (*Calidris canutus rufus*). Delaware Bay hosts the largest spawning population of horseshoe crabs in the world and red knots feed on the abundant eggs to fuel their annual circumpolar migration. Because intertidal oyster aquaculture in lower Delaware Bay overlaps portions of the spawning and foraging habitat, it may disrupt this trophic interaction to the detriment of these species. Prior research shows that oyster aquaculture does not impact the ability of horseshoe crabs to access spawning habitat on the beach, however, it is unknown how aquaculture may impact the distribution of horseshoe crab eggs available to the birds. The red knot distribution in Delaware Bay is driven primarily by horseshoe crab egg abundance, and while foraging behavior is not impacted by the presence of farms, red knot abundance is reduced by 2-7% while farms are actively being tended, so the relative abundance and distribution of horseshoe crab eggs in relation to oyster farms may significantly impact this shorebird species. Throughout the Spring 2021 and 2022 spawning and migration seasons, transect surveys using both sediment cores and quantitative photographs will be conducted overnight during the ebbing tide to determine the relative abundance of surficial eggs across the region containing oyster farms. The objective is to determine the effect of oyster farms on the distribution of horseshoe crab eggs and, consequently, on foraging red knots.

HURRICANE IMPACTS ON OYSTER REEFS OF NORTH CAROLINA, USA: IS THIS THE NEW PARADIGM?

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North Carolina is second only to Florida on the United States east coast for most impacted by hurricane tracks since 1850. These storms can bring widespread flooding, coastal storm surge, and devastating winds, but opportunistic studies and field observations suggest that their impact may have further reaching ecological consequences. The impacts of a series of hurricanes from 2016-2019 were documented on a set of subtidal oyster reefs in Pamlico Sound, North Carolina. These observations included changes in water quality, reef habitat characteristics, and oyster density and demographics. Widespread sedimentation, prolonged hypoxic conditions (DO $<$ 2 mg/L), low salinity environments, strong water column stratification, and turbulent displacement of reef material occurred on deep, natural reefs in the southwest and northern Pamlico Sound following Hurricane Florence (2018) and Dorian (2019), respectively. The resulting conditions at these sites correlated with increased oyster mortality. Comparatively, oyster populations at restored cultch reefs in shallow bays in the western Pamlico Sound experienced minimal impacts from Hurricane Matthew (2016) and Florence (2018). The oyster reefs of North Carolina support a multimillion-dollar commercial fishery, and they provide invaluable ecological services such as water filtration, bottom and shoreline stabilization, and vital nursery habitats. These findings highlight potential management implications for coastal oyster growing states that face increased threats from frequent hurricanes. Additional evaluation of oyster habitat, consideration of higher reef profiles and larger reef footprints, improved reef siting methods, and rotational harvest systems are encouraged as they may provide practical solutions to mitigate mortality in the face of increasing storm frequency.

MANGANESE TOXICITY, MITOCHONDRIAL DYSFUNCTION, AND THE POTENTIAL THERAPEUTIC VALUE OF P-AMINOSALICYLIC ACID, TAURINE, AND CARNOSINE

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Manganese is an essential metal. Toxic exposure causes accumulation in human brain and Manganism, which is similar to Parkinson's disease. Manganese disrupts dopamine neurotransmission. The neurotoxic mechanism is not fully understood. Proposed mechanisms include elevated oxidative stress and mitochondria dysfunction. Studies using the oyster, *Crassostrea virginica* showed manganese interferes with dopamine's cilio-inhibitory effect in gill cells, and reduces gill mitochondria O2 consumption and membrane potential. P-aminosalicylic acid, taurine and carnosine reduced the toxic effects. To test the hypothesis p-aminosalicylic acid, taurine and carnosine protect against manganese induced mitochondria dysfunction in other animals, published data of other labs on manganese induced mitochondria dysfunction and the effectiveness of p-aminosalicylic acid, taurine and carnosine's in alleviating the damage were reviewed. Manganese caused mitochondria dysfunction in other animals, including: inhibition of electron transport, decreased O_2 consumption, interference of ATP synthase, altered mitochondria permeability, decreased membrane potential, disruption of Ca^{2+} homeostasis and swelling. Less was available on p-aminosalicylic acid, taurine and carnosine. P-aminosalicylic acid reduced neuro-inflammation, oxidative stress and intracellular reactive O_2 species generation, prevented loss of mitochondria membrane potential and protected O2 consumption. Taurine preserved mitochondria ATP and membrane potential, and prevented swelling. Carnosine regulated mitochondria matrix pH, preserved membrane potential, increased respiratory chain activity and enhanced energy production. These findings concur with studies on oyster mitochondria, and support the hypothesis. They generate new information to assist in designing future experiments, the results of which should be of interest to those exploring possible agents in the prevention or therapeutic treatment of Manganism.

MICROPLASTICS AND ORGANIC POLLUTANTS IN MANGROVE SEDIMENTS AND MARSH CLAM (*POLYMESODA EXPANSA*) FROM SELECTED COASTAL AREAS OF NEGROS ORIENTAL, PHILIPPINES, AS INDICATORS OF COASTAL POLLUTION

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The Philippines is currently ranked as the third top producer of plastic wastes, yet little research has been conducted on marine plastic pollution in this fishery-dependent, developing country. This study quantified and characterized microplastics and organic pollutants such as polyaromatic hydrocarbons (PAH, n=17, e.g., benzo[ghi]pyrelene, dibenz(a,h)anthracene, indeno[1,2,3-cd]pyrene, and benzo[a]pyrene), phthalates, polychlorinated biphenyls (PCB), and pesticides (n=18, e.g., Chloroneb, Carbaryl, Ethion) found in the mangrove sediments and edible marsh clam (*Polymesoda expansa*) tissues from selected (3 for mangrove sediments; 3 for marsh clam) coastal areas of Negros Oriental, central Philippines. Of the 30 clam samples, microplastic density ranged from 4.1-6.1 particles/clam but did not differ significantly between sites. Microplastics in both sediment and clam samples were mainly composed of fibers. Using gas chromatography-mass spectroscopy (GC-MS), 45 different chemical contaminants were identified in the mangrove sediments while 27 chemical contaminants in the marsh clam tissues. Among the sites, concentration of PCB and PAH were highest in the mangroves in Bindoy while pesticides and phthalates were highest in the mangroves in Bais Bay, an urbanized area surrounded by extensive sugarcane plantations and proximate to industries (e.g., sugarmills and an ethanol processing plant). Concentration of phthalates, PAH, and pesticides were also highest in the clam samples from Bais and Tanjay cities while concentration of PCB was highest in Ayungon. This study confirms for the first time the presence of microplastics and organic pollutants in mangrove sediments in the Philippines and demonstrates the potential for these pollutants to reach other filter-feeding shellfish (e.g., shrimps and crabs).

JACKSON ESTUARINE LABORATORY: 50 YEARS OF DISCOVERY, EDUCATION, AND OUTREACH

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The Jackson Estuarine Laboratory (JEL) opened 50 years ago in 1970. It is part of the University of New Hampshire School of Marine Science and Ocean Engineering. Named after Dr. Floyd Jackson, early marine ecologist and champion of Great Bay, the lab is dedicated to the study of estuarine and marine ecology. Over the years, resident and visiting researchers with disciplines from hydrodynamics and water quality to shellfish ecology and habitat restoration have discovered how estuaries work and how they provide ecosystem services to us all. These investigators have helped train hundreds of undergraduate and graduate students, and investigators have published more than 500 peer reviewed journal articles as part of the JEL Contribution Series, accessible through the UNH Scholars Repository. Each year a variety of K-12 classes and other visitors learn about estuaries and research at JEL, and the faculty bring their new research findings into their classrooms at UNH. Most of the research at JEL is supported by grants from state and federal agencies, hence the results are used in support of natural resource management at local, state and national scales. Researchers from other institutions and agencies also take advantage of the lab facilities and unique setting to conduct their own or collaborative studies. Emergent research and monitoring challenges are being tackled by faculty and students using new technology (e.g. DNA sequencing, drones) to collect, transmit and share information about New Hampshire and New England estuaries.

RUTGERS UNIVERSITY HASKIN SHELLFISH RESEARCH LABORATORIES

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The Haskin Shellfish Research Laboratory (HSRL) is a New Jersey Agricultural Experiment Station and a field station for the Department of Marine and Coastal Sciences at Rutgers University. Its primary mission is to support fisheries and aquaculture through basic and applied research and outreach. The station has been disseminating research results while working cooperatively with the fisheries and aquaculture communities and regulatory agencies in New Jersey and beyond since 1888.

The HSRL has been home to a number of ‘Shellfish Pioneers’ celebrated by the National Shellfisheries Association (NSA), multiple recipients of NSA awards and several past Presidents of the NSA. With a year-round staff of about 30, the HSRL generates and disseminates research information directly applicable to all aspects of fisheries and aquaculture science, concentrating on species of commercial importance to the New Jersey region.

The HSRL maintains four facilities in southern New Jersey. The Bivalve Laboratory in Port Norris is a modern research laboratory with a high salinity recirculating wet laboratory and ready access to Delaware Bay. The Cape Shore Laboratory in Green Creek is a shellfish research hatchery with nursery and growout capacity that can also support a variety of ecological field studies. The Aquaculture Innovation Center in North Cape May is a large production-scale hatchery with a modular design to support innovation and demonstration. The Fisheries Cooperative Center is situated near the fishing port of Cape May providing ready access to the expansive mid-Atlantic fishing industry. Each facility provides a variety of opportunities for collaboration, internships, training and experience.

ASSESSING THE PRESENCE OF MICROPLASTICS IN MARINE MACROPHYTES FOR THE POSSIBLE USE IN BIOREMEDIATION

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Plastic pollution has become a threat to the oceans worldwide. Microplastics (MP) can reach the marine environment through different anthropogenic and industrial inputs. Bioavailability of MP has made them part of the intake for many organisms, but transmission via the food chain is not well understood yet, principally because its accumulation in marine primary producers has been scarcely studied. Macroalgae and seagrasses have the capacity to uptake nutrients and environmental pollutants, including MP. Beyond contamination from the trophic chain bottom; such capacity could be used in bioremediation - the use of living organisms to reduce contaminants from soil or water for the restoration of the ecosystem. Different species of marine macrophytes were explored through literature search to qualitatively assess their suitability for MP bioremediation. The macroalga, *Ulva prolifera*, and the seagrass, *Zostera marina*, were the best candidates for their use in bioremediation. *In situ* experimental studies are recommended before real implementation of bioremediation treatments using these and other marine macrophytes.

AN *IN SITU* STUDY OF THE ROLE OF PARTICLE SHAPE IN THE CAPTURE EFFICIENCY OF BIVALVES AND ASCIDIANS

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Benthic suspension feeders play an essential role in trophic dynamics of near-shore waters. Their feeding process removes planktonic cells and suspended particles from the water column significantly contributing to benthic-pelagic coupling. The types of cells and particles that are captured has been the subject of much study because of its importance in understanding the animals' nutrition and the effects on top-down control of plankton composition. Particle size is a well-studied factor that influences capture efficiency. A less studied factor is particle shape. The goal of the present study was to understand how particle shape influences capture in four suspension feeders that are common in Long Island Sound coastal communities. Capture efficiency was measured *in situ* using the InEx method to collect cleanly paired of water inhaled and exhaled by the blue mussel, *Mytilus edulis*, the ribbed mussel, *Geukensia demissa*, the clubbed tunicate, *Styela clava*, and the vase tunicate, *Ciona intestinalis*. The shape of the sampled particles in the InEx water pairs was analyzed by means of a FlowCAM-based automated technique to examine how particle shape, in particular aspect ratio and circularity, affects capture efficiency by the four species.

USE OF SHELL DIMENSIONS AS SIMPLE INDICES TO EVALUATE THE MARKETABILITY OF DIPLOD AND TRIPLOID PACIFIC OYSTER, *CRASSOSTREA GIGAS*, CULTURED USING SUBTIDAL SUSPENDED LONG-LINES AND HEXAGONAL PLASTIC CONTAINERS ON THE WEST COAST OF KOREA

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There is consensus among oyster farmers and consumers that good-looking oysters have a high market value; however, a few studies suggested guidelines and reference values for evaluating the oyster shape using simple indices such as shell length/shell height (SL/SH) ratio. To evaluate the martetability, a total of 888 oysters from the south coast of Korea, including diploid oyster reared by subtidal suspended long-line culture (2-yrs-old, 113.9±18.5mm SL), diploid (1-yr-old, 79.5±11.7mm SL) and triploid (3-yrs-old, 152.7±22.6mm SL) oysters reared individually in subtidal hexagonal plastic containers were collected. For the evaluation, the shell dimensions (SH, SL) and tissue dried weight were measured. Condition Index (CI) was determined as the dried tissue weight to the internal cavity volume ratio. Pearson's correlation coefficient was applied to test relationship between the CI and the shell dimensions. Positive correlations were found between the CI and and SH/SL ratio in the diploid and triploid oysters reared in the suspend hexagonal containers. In contrast, no clear correlation was observed between the CI and the shell demensions among the oysters rasied in the suspended long-lines. According to the oyster grade suggested by the Canadian local government, oysters with SL/SH ratio less than 1.5 have a high market value, while the ratio more than 2.0 have a low marketability. When this grade was applied, 47% of the oysters reared using a long-line culture exhibited low marketability, while 80% of the oysters reared in the subtidal hexagonal containers showed a relatively high marketability. The data indicated that the subtidal hexagonal containers are more useful method to enhance marketability of the diploid and triploid oysters.

THE EFFECT OF DENSITY ON REPRODUCTIVE EFFORT IN THE ATLANTIC SEA SCALLOP, *PLACOPECTEN MAGELLANICUS*

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The Atlantic sea scallop fishery employs a rotational area management strategy designed to increase future yield-per-recruit and spawning potential due to fast growth observed by scallops afforded protection from fishing pressure; however, it is unclear how well the analytical models that underpin this strategy hold under conditions that deviate from long-term averages, such as the high-density recruitment events observed in 2012 in the Nantucket Lightship and 2013 in the Elephant Trunk. The scallops at these sites have persisted at high densities and appear to be exhibiting varying degrees of impacted performance. The effect of scallop density on growth, yield, and reproduction was investigated through quarterly sampling trips in 2018 and 2019 with sampling at 21 sites divided among high, medium, and low-density scallop beds. In addition to total catch and length data, 30 scallops were retained at each site to determine meat, viscera, and gonad weights along with sex and reproductive stage. Reproductive effort was quantified as the ratio of gamete production estimated as gonad weight to total production in meat weight and viscera weight to determine how this metric differs across population density. Responses varied between sampling locations. In the Nantucket Lightship, scallops at high densities exhibited lower reproductive effort than those at medium or low densities, which is consistent with a density-dependent effect as resources become limiting. In the Elephant Trunk, the response of reproductive effort to population density was more mixed, suggesting that other factors such as food availability may be operating between these two regions.

THE BOCAS DEL TORO RESEARCH STATION

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Located on the Caribbean coast of Panama, the Bocas del Toro Research Station (BRS) offers a sophisticated platform from which to investigate the unique environment and biota of a Caribbean ecosystem with continental influence. The station provides easy access to iconic Caribbean coral reefs, mangroves and seagrass, as well as swamp forests all within easy reach of a well-equipped laboratory platform. Inaugurated in 2003, the BRS hosts approximately 300 visiting students and researchers each year. The BRS is part of the Smithsonian Institution MarineGEO network of coastal observing systems. As part of this program technicians conduct network experiments to document ecosystem functions, and monitor environmental conditions weekly. The BRS welcomes researchers from all branches of science but ~60% of the visitors focus on marine biology. Active areas of research include, climate stressors (temperature, acidification and hypoxia), biodiversity (discovery, description and training), coral reef ecology, and conservation.

PRELIMINARY EVALUATION OF *IN-SITU* BIOFOULING OF CULTURED BAY SCALLOPS, *ARGOPECTEN IRRADIANS*, ON COMMERCIAL SHELLFISH WATER COLUMN LEASES IN TAMPA BAY, FLORIDA, USA

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The Florida bay scallop (*Argopecten irradians*) is currently produced via aquaculture for restoration and research purposes, but commercial production for consumption faces several challenges. One of these is the extensive biofouling that occurs when scallops are confined to enclosures necessary for aquaculture grow-out in the natural environment. The west coast of Florida offers excellent growing conditions and ample shellfish harvest areas, but a market for larger sized whole scallops would be economically realistic only *in situ*ations where production systems maximize growth and minimize labor in order to generate the greatest net return.

This project aimed to collect preliminary data to inform future efforts aimed at enhanced production. Extension faculty worked with industry members to evaluate how biofouling related to survival and growth of caged bay scallops deployed on an existing water column lease in Tampa Bay, Florida. Scallops were assigned randomly to one of two groups (*treatment*: shells cleaned or *control*: shells uncleaned). Treatment and control groups displayed similar survival and growth rates, but the control group had a significantly higher meat: shell ratio at the termination of this project.

This pilot demonstrated that fouled scallops could survive to marketable size when grown in suspended cages. In addition to informing the potential for a commercial market, these results are valuable to ongoing bay scallop restoration efforts on the west coast of Florida, which often request larger animals. This design may provide an economically feasible template for providing older, larger bay scallops to ongoing and future restoration efforts.

INTRASPECIFIC COMPARISON OF OYSTER GENE EXPRESSION RESPONSE TO LOW OXYGEN

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Hypoxia, defined as oxygen concentrations below 2.0 mg L^{-1}, is an increasing threat both to coastal waters and their inhabitants worldwide. There is great interest in understanding the mechanisms that organisms employ to tolerate current extremes in environmental stressors, such as hypoxia, as these can provide insights into their capacity to tolerate projected changes. Intraspecific comparisons of gene expression in response to hypoxic exposure provide a useful tool to elucidate tolerance differences and the genetic underpinnings to tolerance. The eastern oyster, *Crassostrea virginica*, is an ecologically and economically important sessile bivalve that resides in coastal environments prone to hypoxic events. While much is known about hypoxia tolerance in oysters generally, less is known about intraspecific differences in molecular response to hypoxia that might give rise to different tolerances. To better understand this knowledge gap, oysters from six different sites—three that experience seasonal hypoxia and three that experience annual normoxic conditions—throughout the Maryland portion of the Chesapeake Bay were collected. After six months of common garden acclimation, oysters were brought into the laboratory and exposed to either a hypoxic or normoxic treatment for 96 hours. RNA was extracted from dissected gill tissue from each oyster, sequenced, and differential gene expression analysis was conducted on the resulting reads. Preliminary results showed significant differences in gene expression between oysters in normoxic and hypoxic treatments and an indication of site-specific intraspecific patterns of gene expression. Results are expected to provide novel insights into the gene expression response of *C. virginica* to hypoxia.

THE JACQUES COUSTEAU NATIONAL ESTUARINE RESEARCH RESERVE: AN EXEMPLAR IN SCIENCE-BASED MANAGEMENT

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The Jacques Cousteau National Estuarine Research Reserve (JC NERR), is one of 29 National Estuarine Research Reserves (NERRS) created to promote the responsible use and management of the estuaries of the US through an integrated program of scientific research, education, and stewardship. Serving as a sentinel site in southern New Jersey, the JC NERR conducts a variety of collaborative research and long-term projects such as understanding coastal marsh sustainability, early detection of environmental change, and development of web-based tools to inform coastal decision making. Long-term monitoring of physical, biological and meteorological processes in the Mullica River-Great Bay Estuary system is supported by waterside facilities at the Rutgers University Marine Field Station.

Emerging coastal management priorities identified collaboratively by the JC NERR staff and partners include:

- Changes in abiotic parameters driven by natural and anthropogenic factors
- Range Shifts in organisms and habitats including invasive species
- Role of Marsh ponds in ecosystem dynamics
- Impact/disturbance from closing of power plant cooling flow
- Microplastics in coastal areas

The place-based monitoring approach allows study of episodic events that would be missed by short-term, question-driven programs. Education and outreach activities focus on research opportunities for undergraduate and graduate students, as well as science education programs for teachers, K-12 students and community members. Available summer internships are modeled after the NSF Research Experiences for Undergraduates program. A new Margaret A. Davidson Graduate Research Fellowship Program will be initiated in 2020 at all 29 NERRS.

FRIDAY HARBOR LABORATORY: JEWEL OF THE PACIFIC NORTHWEST

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The Friday Harbor Laboratory (FHL) is a marine station located on San Juan Island, about 70 miles NW of Seattle in the inland waters of Washington State. It has supported research and education in the marine sciences for almost 120 years in an egalitarian, collaborative culture where every student is a scientist worthy of respect. Part of the University of Washington College of the Environment, the FHL is open year-round to researchers from around the globe, working in fields from physical oceanography to conservation, from genetics and development to anatomy and ecology. One active current research program is Dr. Adam Summers' project to 'Scan All Fishes', bringing researchers from all over the globe for free use of a CT scanner, from which all data and images are made publicly available. Infectious marine diseases are also a current research topic. In spring, summer, and fall, FHL offers graduate and undergraduate courses on similarly diverse topics. Generous private donors help to defray costs for students. The FHL facilities include 13 lab buildings, most of which have running seawater tables for maintaining marine organisms; a variety of modern equipment for shared use; several classrooms; a full-service Dining Hall; and roughly 200 beds in housing units ranging from student dormitories to private apartments. Also on the FHL campus, the Helen Riaboff Whiteley Center provides a refuge (seven cottages and a study center) for established scholars and artists to create and interact in a peaceful environment. As space allows, FHL also rents its facilities for workshops and conferences.

ASSESSMENT OF THE OXIDATIVE STRESS AND BIO-TRANSFORMATION ENZYMATIC EFFECTS OF GLYPHOSATE EXPOSURE ON THE PACIFIC WHITELEG SHRIMP, PENAEUS (*LITOPENAEUS) VANNAMEI*)

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Naturally, aquatic organisms have self-defense mechanisms that protect them from the actions of chemicals such as the herbicide and antimicrobial Glyphosate. The changes in expression levels of different types of enzymes could be used as biomarkers of exposure such as hepatopancreatic cytochrome P450-associated enzyme activity. It is also possible that the rate of release of reactive oxygen species (ROS) increased during exposure and the defense mechanisms occurred in the cell because of rapid oxidation, reduction, hydroxylation and dealkylation reactions. Glyphosate 41% S.L. (I.P.A salt) is manufactured by Monsanto India Limited, Mumbai, India. Total quantity of this herbicide bottle is 500 mL which was purchased from Theni District, Tamilnadu. The 41% Glyphosate make up to 100% for stock then serially diluted to different concentrations. The effect of Glyphosate exposure was examined to assess the oxidative stress and biotransformationon *P. vannamei*. Post larval stage (PL12–PL15) were collected from a commercial farm near Pattukottai, Thanjavur District, Tamilnadu and acclimatized for one day after the experiment was statred. After measuring body length (1.760 ± 0.197cm) using a verniorcolibor and weight (0.629 ± 0.081g), they were divided into groups (n=25/tank): control, 10 ppm, 20 ppm, 30 ppm, 40 ppm, and 50 ppm Glyphosate concentrations for 24 hours. Water quality was maintained at a pH of 7.8, a salinity range of 28-32, and temperature of 27-28ºC throughout the study. Tissue samples were collected every 6 hr and the hepatopancreas removed for enzymatic reactions. The levels of antioxidant [superoxide dismutase (SOD), catalase (CAT) and glutathione reductase (GR)] and biotransformation enzymes (CYP450 isoform-EROD, MROD, BROD and GST) increased at 6 hr and 12 hr in the 10-30 ppm groups, their activity decreased afterwards. In the 40-50 ppm groups, the antioxidant and biotransformation enzymes increased up to 24 hr. Results suggested that (a) antioxidant enzymes were elevated at early stages of exposure in 10-30 ppm groups, (b) GSH, SOD, and CAT play a role against ROS and neutralized it, (c) enzymatic biotransformation is essential to eliminate Glyphosate, and (d) the cellular enzyme defense mechanism protect shrimp at certain levels of exposure.

THE “KEYSTONEIN” MOLECULE IN THE MEDITERRANEAN MUSSEL - AFFECTED BY COASTAL ACIDIFICATION

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Keystone species such as *Mytilus galloprovincialis* play a special role in the structure of ecological communities and in determining biodiversity. A glycoprotein named KEYSTONEin was characterized in *M. galloprovincialis*, *M. edulis*, and *M. californianus*. Its role is crucial since it constitutes a cue of predation for sea stars. In this work KEYSTONEin expression was analyzed under a predictable ocean acidification (1200 CO_2 ppm) regarding the current situation (400 ppm) to determine if it could be affected by climate change.

Mussels were acclimated to the experimental pCO_2 concentrations (400 and 1200 µatm) for a month in 9-L tanks with semi-static system. After that, half population was exposed to crushed conspecifics for a three-week period. Four individuals were collected from each experimental group and dissected. Several tissues were sampled for RNA and/or protein isolation and qPCR was carried out for KEYSTONEin expression.

There is a tendency towards downregulation of KEYSTONEin under acidification conditions without the faux prey. These results seem to suggest that ocean acidification could play a detrimental role in keystone molecules expression. This might lead to important ecological effects such us spatial distribution not only for foundation species but also for other species. Nonetheless, when the faux prey is introduced, the predation signal seems to be strong enough to mask the effect of acidification.

OYSTER AQUACULTURE AND OYSTER REEFS HAVE COMPARABLE SEDIMENT DENITRIFICATION RATES

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Oyster populations have decreased globally from overharvesting and disease, leading to loss of associated ecosystem services such as nitrogen (N) removal. At the same time, an increase in N load from watersheds has led to eutrophication and impaired coastal waterbodies. Oyster aquaculture and oyster reef restoration may help remove N by enhancing sediment denitrification, the microbial conversion of bioavailable N to inert N^2 gas. Yet, it is unknown if oyster aquaculture and oyster reefs have different effects on sediment N cycling. Sediment fluxes of N^2, nitrate + nitrite (NOx), ammonium (NH_4^+), and sediment oxygen demand (SOD) were measured from an oyster aquaculture farm, a restored oyster reef, and respective reference sites in the Rappahannock River, Virginia, USA. It was hypothesized that oyster sites would have higher rates of denitrification (net positive N_2 fluxes) compared to reference sites but that denitrification rates would differ between aquaculture and reefs. This study found that oyster aquaculture and oyster reefs enhanced sediment denitrification compared to reference sites, but the enhancement was not different between the oyster sites. Oyster aquaculture and oyster reefs had higher SOD, NO_x, and NH_4^+ fluxes compared to reference sites, though the increase was not significant. Results demonstrate that oyster aquaculture and oyster reefs affect sediment N cycling, and both provide comparable N removal benefits via enhanced denitrification.

AQUACULTURE FACILITIES AND FIELD STATIONS IN THE UNIVERSITY OF MAINE SYSTEM

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The Aquaculture Research Institute (ARI) at the University of Maine (UMaine) is an interdisciplinary institute that coordinates the UMaine aquaculture facilities and assets. The ARI supports a broad range of aquaculture research and education programs and has the ability to access resources across the UMaine System to offer a unique training platform comprised of five aquaculture facilities and a field based Aquaculture Experimentation and Outreach Station (AquEOuS). Each of the UMaine aquaculture facilities can support unique research and experiential learning opportunities using both the facility location on the Maine coast as well as its staff and equipment. The following are brief description of each facility:

- Aquatic Animal Health Laboratory (AAHL), Orono, ME: a new, state-of-the art, high containment aquatic animal health research facility;
- Darling Marine Center (DMC), Walpole, ME: a marine station with flowing seawater labs, a business incubator and a research farm;
- Center for Cooperative Aquaculture Research (CCAR), Franklin, ME: a compound with industrial RAS systems and a business incubator;
- Downeast Institute (DEI), Beals, ME: a non-profit acting the UMaine Machias Marine Science Field Station with flowing seawater labs, a commercial-scale shellfish hatchery, and an ocean acidification laboratory.

The poster will include in depth descriptions and photos of research resources, housing and staff available at each site as well as examples of recent research projects that have benefited from these facilities.

THE NORTH CAROLINA STATE UNIVERSITY CENTER FOR MARINE SCIENCES AND TECHNOLOGY

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The principal mission of the North Carolina State University Center for Marine Sciences and Technology (CMAST), located in Morehead City, NC, is to discover innovative solutions to questions and problems in marine systems, and provide effective communication of these discoveries by promoting multidisciplinary studies among research scientists, educators and extension specialists. The CMAST programs also enhance interaction with other educational institutions and agencies, and a broad range of stakeholders and the general public.

The co-location of faculty, staff and students from five different departments and a K-12 STEM Program, promote creative collisions among disciplines that support solutions to such grand challenges as *Ocean Health and Food Security*. The CMAST faculty and staff are researching a wide range of topics that affect the health and well-being of humans, animals and the environment, ranging from monitoring aquatic animal health as an indicator of human health risks, to seafood safety, to improving water quality of coastal waters that are critical to tourism. Applied fisheries programs are informing sustainable harvest of wild and aquaculture species, as well as a range of coastal habitat restoration initiatives.

Academic programming is providing leaders for the state, nation, and the world through a Summer Fellows and Intern Program, Graduate, and Undergraduate training that emphasizes hands-on research, as well as K-12 educational outreach. The CMAST hosts partnerships with the North Carolina Aquarium System, North Carolina Sea Grant, the North Carolina Division of Marine Fisheries, North Carolina Cooperative Extension, and the local Community College.

NOT SO SHELLFISH AFTER ALL: HOW NATIVE OYSTERS (*OSTREA LURIDA*) MAY AID EELGRASS (*ZOSTERA MARINA*) RESTORATION BY NITROGEN FILTRATION

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Eelgrass (*Zostera marina*) is a foundation species in coastal waters that provide vital ecosystem services ranging from habitat provision to trophic support; however, populations have declined globally at alarming rates including within Upper Newport Bay, CA. A multi-habitat restoration approach with native oysters (*Ostrea lurida*) may be the key to promoting more successful eelgrass restoration. Oysters may increase nitrogenous nutrients within sediment porewater for uptake by eelgrass by mediating nitrogen transfer from the water column via filter-feeding and subsequently depositing nitrogenous waste into sediments. Resource managers are concerned about the efficacy of co-restoration with native oysters due to potential negative interactions with eelgrass as a protected species. Little research has been conducted to date to address the efficacy of restoring these species together. In summer 2019, eelgrass shoots were collected from four restored sites within Upper Newport Bay using a factorial block design, with eelgrass alone, eelgrass with oysters, oysters alone, and a mudflat control at each site. Shoots were processed for leaf and rhizome growth rates, and above and below ground dry weight. Response metrics were analyzed in relation to distance from and density of respective oyster beds using two-way mixed ANOVA and linear regressions. Preliminary results indicated no significant associations suggesting a neutral relationship. Further research will be conducted to measure ammonium and nitrate within porewater samples, and percent total nitrogen in eelgrass tissue.

STOCKTON UNIVERSITY MARINE FIELD STATION

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The Stockton University Marine Field Station (MFS) is in Port Republic, New Jersey and is located within the Jacques Cousteau National Estuarine Research Reserve. The location of the MFS is central to its offerings; less than 15 minutes from the main campus, only 7 nm from the Atlantic Ocean and just minutes by vessel to estuarine habitats and sampling sites. The MFS offers dockage and modest laboratories with access to an array of resources including vessels, sampling equipment, and marine technology instrumentation. Visitor housing is available in the summer months on the main campus (15-minute drive). The inshore research fleet consists of shallow-draft vessels ranging from 16’—24’ and the flagship vessel of the program is the 36’ × −14’ *R/V Petrel*. The marine technology program includes a 300m-rated remotely operated vehicle, side scan sonar, multiphase echo-sounder, mobile LiDAR, acoustic doppler current profilers, and a magnetometer. The marine operations staff provide support services and oversee the maintenance and use of the facilities, vessels, instrumentation and sampling equipment.

The faculty associated with the MFS have active research and teaching programs in fisheries, marine debris, oyster monitoring and restoration, SAV monitoring and restoration, marine geology, marine chemistry and several areas of oceanography including estuarine/near-coastal circulation and sea floor mapping programs. The MFS is a UNOLS - member laboratory and organizational member of multiple professional societies, including National Association of Marine Laboratories, Organization of Biological Field Stations, Scientific Boating Safety Association, Marine Technology Society, and the Hydrographic Society of America.

GENOMIC STUDY OF GABA RECEPTORS IN THE BIVALVE *CRASSOSTREA VIRGINICA*

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GABA, an inhibitory neurotransmitter in molluscs and other animals, has not been well studied in bivalves. GABA neurotransmission impairment in humans causes epilepsy. In the bivalve *Crassostrea virginica* serotonin is an excitatory neurotransmitter accelerating gill lateral cell (GLC) cilia beating. This serotonin innervation originates in the cerebral and visceral ganglia. Previous studies demonstrated applying GABA to visceral or cerebral ganglia blocked serotonin's action on accelerating *C. virginica* GLC cilia beating. Additionally, the GABAa receptor antagonist bicuculline methchloride blocked the action of GABA. HPLC detected GABA in ng amounts in *C. virginica* ganglia. Immunofluorescence histochemistry showed GABA neurons present in the ganglia and that some serotonin neurons had GABA receptors on their soma. The *C. virginica* genome has begun to be mapped. To test the hypothesis *C. virginica* contains GABA receptor genes and these receptors are similar to those of other animals, BLAST searches of the NCBI database were conducted using DNA and protein sequences from *C. virginica* for GABAa and GABAb receptor genes. Matches for GABAa and GABAb receptor genes were found on *C. virginica* chromosomes 3 and 5, respectively. BLASTS of other animals found matches with similarities to GABAa and GABAb receptors of *C. virginica*. This study complements the studies demonstrating the presence and function for GABA in *C. virginica*. It shows *C. virginica* genome contains genes for GABA receptors similar to other animals. This information is valuable as it shows the simple nervous system of *C. virginica* can be used to conduct studies on GABA neurotransmission.

LONG-DISTANCE TRANSMISSION OF PATHOGENIC *VIBRIO* SPECIES BY MIGRATORY WATERBIRDS: A POTENTIAL THREAT TO PUBLIC HEALTH

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A potential mechanism for the global distribution of waterborne pathogens is through carriage by the migratory waterbirds; however, this mode of transmission has yet been confirmed epidemiologically. The whole genome sequence of *Vibrio* spp. collected from waterbirds, sediments, and molluscs in the estuary of the Liaohe River in China was carried out to investigate this transmission mode. It was found that a *V. parahaemolyticus* strain isolated from a waterbird was clonally related to the other *V. parahaemolyticus* strains obtained from the sediments and molluscs, and three *V. mimicus* strains isolated from bird feces were genomically related to those found in the molluscs and upstream groundwater, suggesting that the bird-carried *Vibrio* strains were acquired through the direct predation of the local molluscs. Surprisingly, two bird-carried *V. parahaemolyticus* strains belonging to the same clone were identified in Panjin and Shanghai, which are over 1,150 km apart, and another two were found at two locations 50 km apart, further supporting that waterbirds are capable of carrying and disseminating these pathogens over long distances. Molluscs, crustaceans, crabs, and oysters are the common food resources of waterbirds, and the majority of waterbird species are long-distance migratory birds. Results provide the first evidence of direct transmission from molluscs to waterbirds and confirm that waterbirds act as disseminating vehicles of waterborne pathogens. To prevent the rapid spread of pathogens, public health authorities must strengthen their active surveillance of birds and monitor their exact migration routes. Further studies need to focus on the epidemiological links between *Vibrio* species in waterbirds and *Vibrio* species in contaminated fish. Effective surveillance of migratory waterbirds

OCTOPUS AQUACULTURE: SEARCHING FOR A SUCCESSFUL PRODUCTION DRIVEN BY NUTRIGENOMIC AND EPIGENETIC INTERACTION STUDIES

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The common octopus (*Octopus vulgaris*) is a highly-valued species of great commercial interest, and it is an excellent candidate for aquaculture diversification. However, the massive mortalities during the early life-cycle stages (paralarvae) have hampered its commercial production. In recent years great progress has been made in achieving its life cycle under captive conditions, but its commercial aquaculture practice is still in the experimental period. Therefore, efforts to improve it, and specifically search for biomarker genes to optimize the culture, are currently a priority.

The Octomics project aims to deepen the study of the first developmental stages of the common octopus in order to gain a greater understanding of the biological processes occur in these early stages of life under different cultivation conditions through nutrigenomic and epigenetic analyses.

Octopus embryonic developmental stages, as well as paralarvae in their early stages of development, cultivated under different conditions and fed on different diets have been examined. A wide range of genes and proteins identified by transcriptomic (RNA-seq), proteomic (SWATCH) and epigenomic (RRBS) tools, involved in different signaling cascades related to metabolism, stress and immune response were analyzed. The selection of specific genes and proteins, together with functional biochemical validation assays, allow the identification of candidates for biomarkers to evaluate welfare and health in early stages of *O. vulgaris* development under cultivation conditions. This approach will provide new perspectives and will open new opportunities to deepen the requirements and improve the culture of the species.

BIVALVE BODYGUARDS: EELGRASS MEADOWS BUFFER HIGH ENERGY BOAT WAKES AND REDUCE SEDIMENTATION STRESS ON OLYMPIA OYSTER (*OSTREA LURIDA*) BEDS CONSTRUCTED FOR A LIVING SHORELINES PROJECT

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Significant development in Southern California coastal areas has removed marine habitat that would normally buffer wave energy, leaving shorelines vulnerable to erosion. Living Shorelines projects seek to address this problem by restoring native habitat with the goal of rebuilding ecosystems in a way that provides ecosystem services such as shoreline stabilization. Foundation species such as oysters and eelgrass are increasingly used in these projects because they provision habitat via their three-dimensional structure and reduce erosion. Native Olympia oyster beds and eelgrass beds were restored at four sites in Upper Newport Bay in 2016 as part of the Upper Newport Bay Living Shorelines Project to explore the possible combined benefits of restoring two foundation species. All sites have seen differential success since initial restoration in terms of oyster density and bed growth. Human activity such as trampling and wave energy has been previously linked to mussel and oyster bed degradation, so to understand the impacts of human activity on restored oyster beds 30-minute human use surveys were conducted at all sites and all instances of human activity including recreation, fisher activity, boating, and the size of wakes produced by each passing boat were documented. Preliminary analyses show a trend for reduced oyster density with increased frequency of large boat wakes and a trend for decreased sedimentation and burial of beds constructed next to a restored eelgrass meadow versus an unmanipulated mudflat. This suggests that eelgrass ameliorates a portion of the boat wake energy and may protect oyster beds from sedimentation stress.

WHITE SPOT SYNDROME VIRUS (WSSV) ALLOWS ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) TO CAUSE FASTER AND HIGHER MORTALITY IN PACIFIC WHITE SHRIMP (*PENAEUS VANNAMEI*)

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In this study, the co-infection with WSSV- and AHPND-causing *V. parahaemolyticus* (VpAHPND) was simulated in juvenile Pacific white shrimp (*Penaeus vannamei*) under laboratory condition. The experimental shrimp (average 0.5g, N=80) were divided into four groups (Group 1: WSSV only; Group 2: Vp_{AHPND} only; Group 3: WSSV + *Vp*AHPND; Group 4: not challenged), and for the co-infection, shrimp were challenged with dual pathogens (initially exposed to WSSV and subsequently exposed to Vp_{AHPND}) by immersion method. The mortality rate was significantly increased in Group 3 (WSSV + Vp_{AHPND}) compared with the other groups (Group 1, 2 and 4). Also, shrimp in Group 3 (WSSV + Vp_{AHPND}) showed typical histopathology signs of AHPND in the hepatopancreas, with sloughing of hepatopancreatic tubule epithelial cells (G4), and strong WSSV positive reaction in gill by immunohistochemistry examination (brown coloration). On the other hand, shrimp in Group 1 (WSSV only) did not show WSSV lesions in gills, and shrimp in Group 2 (Vp_{AHPND} only) did not show typical histopathology signs of AHPND in the hepatopancreas. This study demonstrated that shrimp initially exposed to WSSV allows Vp_{AHPND} to cause faster and higher mortality than shrimp infected with Vp_{AHPND} alone, and also leads to severe WSSV infection. This indicates that WSSV is a risk factor for Vp_{AHPND} in shrimp ponds.

SURVIVAL AND GROWTH OF EASTERN OYSTER SPAT, *CRASSOSTREA VIRGINICA*, WHEN EXPOSED TO LOW SALINITY FOR PROLONGED PERIODS IF GIVEN SHORT INTERVALS OF RECOVERY AT HIGHER SALINITY

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The hydrology of Caloosahatchee River Estuary has been dramatically altered by dredging, channelization, construction of several lock and dams, and an artificial connection to Lake Okeechobee. Prolonged discharges from the lake along with flashy discharges from the C-43 and tidal basins have altered the salinity regimes in the estuary which create osmotic challenges for the organisms that live there. The eastern oyster, *Crassostrea virginica*, is a keystone species and, as such, a valued ecosystem component. As part of a larger study to develop a decision matrix for managing high-flow discharges without undermining the sustainability of oyster reefs, this presentation reports on oyster spat survival and growth when cultured under low salinity if given repeated short intervals of higher salinity to recovery. To date only two rounds of experiments have been conducted. Each round of experiments consisted of multiple tests with spat exposed to a combination of different conditions: low salinity (e.g., 0 and 5‰), stress duration (e.g., 2, 7 and 10 days), recovery salinity (5 and 10‰), duration of recovery period (3, 7, 14 days). The first round of experiments was done both at 20°C and 30°C for a total of 30 days. The second set of experiments were only done at the more stressful 30°C for a total of 72 days. The results of these experiments will be discussed in the context of protocols selected for the next round of experiments and the ultimate objective of improving survivorship during long-duration, high flow events.

DETERMINING READER PRECISION AND BIAS WHEN AGING *ARCTICA ISLANDICA*, THE OLDEST-LIVING BIVALVE ON EARTH

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The ocean quahog, *Arctica islandica*, is the longest-lived bivalve on Earth. Individuals on the deep continental shelf of Georges Bank can survive for centuries, and when found in the colder, boreal waters of Iceland, ages over 500 years can be reached. Ocean quahog age-at-length data are famously inconsistent both within and across regions preventing the development of a comprehensive age-length key, an essential component to understanding the population dynamics of a species. When developing an age-length key, the validity of such a key is only as credible as the age determinations used to create it. Understanding the precision of each age reader and any underlying bias present in the age estimates allows researchers to report error and identify age drifts produced by such biases. A sample of 648 *A. islandica* collected from Georges Bank, US were employed to develop an age precision and bias protocol for both new and experienced age readers, and to create a preliminary reference collection which consists of relative ages using a two-lab consensus. Crossdating was also performed on a subset of Georges Bank samples to validate annual growth patterns and chronologies.

MONITORING AND RECOVERY OF NATIVE SHELLFISH USING CLAM GARDENING IN SOUTHCENTRAL ALASKA

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Clam populations in southcentral Alaska have been on a steady decline for many years. Clams are an important subsistence food source for residents in native communities in coastal Alaska. In support of these communities, the Tribally operated Chugach Regional Resources Commission Alutiiq Pride Shellfish Hatchery (APSH) has been developing shellfish enhancement tools utilizing the sanctuary concept. The purpose is twofold: provide clam resources for subsistence harvest and attempt to identify the bottleneck for population recovery. This project seeks to establish native shellfish sanctuaries throughout several intertidal habitats in southcentral Alaska. These sanctuaries will be used to 1) monitor the growth and mortality of seeded shellfish *in situ* and 2) re-establish healthy native populations for future subsistence use. Adult clams are collected and aggregated to understand the Allee effect and monitored for sexual maturation and spawn timing. Juveniles produced at APSH are seeded in the sanctuary and monitored for growth and survival. In addition to scientific efforts, a major goal of this program is the involvement of trained tribal members as citizen scientists. Sanctuary maintenance, and all beach surveys, juvenile out-plantings, and monitoring efforts are conducted at the local level to ensure the efficacy of future tribally led shellfish programs. Data collected during this project are being used 1) to enhance the current body of scientific knowledge with respect to shellfish growth and 2) in the development of local shellfish management plans. The adult clams produced by APSH are harvested and shared with elders and others in the communities.

MODELING AND MONITORING A SUSTAINABLE ISLAND STATION: INTEGRATING EDUCATION AND RESEARCH

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The Hurricane Island Center for Science and Leadership integrates science education, applied research, and leadership development through year-round educational programs and a seasonal, environmentally-sustainable island community. Ten miles offshore in the Fox Islands Archipelago in Penobscot Bay, Maine, Hurricane Island offers access to unique terrestrial and marine environments for middle and high school students, researchers, college and university faculty and students, and adult learners from around the world May through October. Committed to sustainability, the Island is solar-powered, utilizes composting toilet systems, cultivates a growing garden to increase on-Island food production, and is breaking ground on a new state-of-the-art Passive House Design research facility in Spring of 2020. The Island itself consists of lower elevation spruce-fir forest, cattail marsh, granite outcrops, seaside goldenrod/ goosetongue open headland, and rose/bayberry maritime shrubland. The marine subtidal bottom habitat around Hurricane is rugged, high-relief seafloor, dominated by bedrock outcrops with accumulations of coarse-grained sediment in low-lying areas. The intertidal zone includes areas with dense rockweed, exposed high-impact beaches, small sand deposits, and artificially built-up granite faces from the quarrying-era. Situated at the confluence of the Eastern Maine and Western Maine Coastal Currents Hurricane sits in the heart of lobster country, perfectly positioned to participate in monitoring studies and research on climate change, alterations in the Gulf of Maine ecosystem, and fisheries biology and management. With a 3.2-acre aquaculture site growing scallops, kelp, oysters, and mussels, the Center leads research, workforce development, and education efforts focused on the growing aquaculture industry in Maine.

HEAVY METAL POLLUTION AND ECOLOGICAL RISK ASSESSMENT IN THE MAOWEI SEA MANGROVE, CHINA

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Studies on heavy metal pollution and potential ecological impacts in the Maowei Sea mangroves, China, are relatively sparse. In this study, the vertical distribution and ecological risk of heavy metals in Maowei Sea mangrove sediments were investigated. The concentrations of Cd, Co, Cr, Cu, Mn, Ni, Pb and Zn were determined using inductively coupled plasma mass spectrometry (ICP-MS). The results showed that heavy metals mainly accumulated in the top 10 cm in the mangrove sediments. Vertical distributions showed that heavy metals declined from the surface to 20 cm depth, afterwards they turned relatively constant. Exceptionally, significant increase in Mn concentration with depth in the mudflat were observed. The degree of metal contamination and resulting potential impacts on biota were comprehensively assessed using Geo-accumulation Index (I_{geo}), Pollution Load Index (PLI), Potential ecological risk index (RI), mean-PEL-quotient, mean-ERM-quotient, and the Total unit toxic index (ΣTU). Multiple environmental risk indices indicated that the investigated area was broadly contaminated by heavy metals and that Cd was the dominant contributor to potential ecological risks; however, the biological toxicity posed by these metals was negligible. Multivariate analyses implied that Cd, Co, Cr, Cu, Ni, Pb, and Zn originated mainly from anthropogenic sources, whereas Mn was primarily from natural processes. These findings provide insightful information for future management of the Maowei Sea mangroves from China.

IDENTIFICATION OF DEFENSIN-LIKE GENES FROM THE *CRASSOSTREA VIRGINICA* TRANSCRIPTOME

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Bivalve molluscs have an innate immune system used to combat viral, bacterial, and protozoan infections. Among the immune effectors are antimicrobial peptides (AMP) including defensins, a prolific family of AMP that associate with bacterial membranes and can inhibit peptidoglycan synthesis or disrupt membrane integrity. This study focuses on the β-like *cis*-defensins in eastern oysters, *Crassostrea virginica*. Because of the short length, gene structure, and possible use of alternate start sites, defensins evade annotation by standard algorithms used to computationally predict protein-coding genes in a genome. Previous proteomic and genomic studies revealed multiple β-like defensins in *C. gigas* and in other oysters. Although the complete genome is available for *C. virginica*, no β-like defensins have been annotated, but one has been characterized from a proteomics study. A bioinformatic approach was applied to search the *C. virginica* transcriptome for defensin cysteine motifs and signal peptide sequences. A multigenic cluster of β-like defensins previously described as noncoding RNA was identified. Molecular phylogenetic analyses reveal the evolutionary relationships and diversity of β-like defensins in this species. Quantitative gene expression analyses confirm differences in defensin mRNA expression among tissues and following immune stimulation. These data provide insight into mechanisms of pathogen resistance and adaptation to immune challenges in the eastern oyster and allow for comparison of these important antimicrobial peptides among oyster species.

SUMMER ASSESSMENT OF WILD PACIFIC OYSTER (*CRASSOSTREA GIGAS*) PATHOGENS AND OTHER MICROBIAL CONSTITUENTS IN SAN DIEGO BAY, CALIFORNIA, USA

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In order to assess viability of oyster aquaculture operations in San Diego Bay, this study investigates the presence and severity of pathogens that accumulate in wild *Crassostrea gigas* populations during the summer. In October 2020, adult wild oysters were collected from San Diego Bay. TCBS (Thiosulfate-citrate-bile salts-sucrose) Agar plates were used to culture viable microbial cells from oyster gill, gut and hemolymph. These TCBS plates are selective for *Vibrio* species. *Vibrio* grew from all body sites as confirmed by 16S rRNA Sanger sequencing; colonies grew at temperatures of 25°C, 30°C and, for gut samples, in an anaerobic box. These results demonstrate presence of *Vibrio*, but do not confirm pathogenicity or total load of the community. To further explore the microbial community present in oyster hemolymph, more oysters ($n = 7$) were collected in early November 2020 for 16S rRNA sequencing of the hemolymph. Additionally, a cohort of oysters collected from San Diego Bay in the summer of 2020 will be monitored for OsHV-1 presence and viral load using qPCR of the ORF100 gene.

HISTAMINE RECEPTORS: A GENOMIC STUDY OF THE BIVALVE *CRASSOSTREA VIRGINICA*

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Histamine, a biogenic amine found in a variety of invertebrates is well studied in arthropods and gastropods. It is involved in immune responses and regulating physiological functions. Histamine also is a neurotransmitter for sensory systems. Previous work of our lab found histamine activates the sensory system of Crassostraea virginica, eliciting a motor response in gill. Cell biology and immunofluorescence work showed histamine and histamine receptors present in ganglia and mantle of *C. virginica*. The genome of *C. virginica* and other bivalves have begun to be mapped. To test the hypothesis *C. virginica* contains genes for histamine receptors and these receptors are similar to those in other animals, including mammals, BLAST searches of the NCBI database using DNA and protein sequences of *C. virginica* histamine receptor (H1R, H2R, H3R) genes were conducted. Gene matches for histamine receptors were found. H1R genes on chromosome 8; H2R on chromosomes 1, 2, 5 and 10; and H3R on chromosome 3. BLASTS of other animals found matches with low Expect Values and high Percent Identity, signifying similarities of H1R, H2R and H3R of *C. virginica* to those of other animals, including mammals. This study complements physiology and cell biology studies demonstrating the presence and function for histamine in *C. virginica*, and shows the genome of *C. virginica* contains genes to produce histamine receptors similar to those in other animals. This new information is valuable in showing the simple nervous system of *C. virginica* can be used to expand studies on histamine neurotransmission.

THE EFFECTS OF L-GLUTAMINE AND L-GLUTAMATE ON THE LATE LARVAL DEVELOPMENT OF THE SEA URCHIN, *LYTECHINUS VARIEGATUS*

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Metamorphosing from a larva to a juvenile urchin is a vital transition in the sea urchin life cycle; however, few larvae complete this metamorphosis (about 2% in mass culture). Histamine, a common excitatory neurotransmitter, has been shown to be a modulator of metamorphic competence in larvae. The role of histamine in metamorphosis brings into question the role of other excitatory neurotransmitters. This study investigates the effects of exposure to L-glutamate, another excitatory neurotransmitter, or L-glutamine, an L-glutamate precursor, on the metamorphosis of *Lytechinus variegatus*. Larvae were raised at a density of 1 larva/mL in six-well plates containing 10 mL artificial sea water and fed a diet of the single celled algae *Rhodomonas salina* and *Dunaliella tertiolecta* at a concentration of 4500 cells/larva for each (9000 cells/larva in total). Water changes occurred before feeding and before chemical exposure. When larvae reached metamorphic competence at approximately 14 days after fertilization, they were exposed to either 1 mM, 0.1 mM, or 0.01 mM concentrations of L-glutamine or L-glutamate, *in situ*, for 24 hours. No metamorphosis was observed in any group; however, in the L-glutamine treatment, arm loss was observed in more larvae exposed to 0.1 mM and 1 mM L-glutamine (61.67 and 91.38% of larvae lost arms, respectively) compared to controls (3x2 Pearson χ^2 test, $\chi^2 = 379$, $P < 0.001$, d.f $= 6$). Arm loss was not observed for larvae exposed to L-glutamate. These results demonstrate that while L-glutamine may not trigger metamorphosis in sea urchins, it may play a role in apoptosis associated with metamorphosis.

MOLECULAR DETECTION OF PROTOZOAN PARASITE INFECTIONS IN MARINE BIVALVES IN KOREAN WATERS

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Several species of protozoan parasites, including the members in the genus Perkinsus, Marteilia, and *Bonamia* are listed and regulated by the world organization for animal health (OIE), as they often cause mass mortalities of the host organisms. Small bays on the south coast of Korea are used as major culture grounds of the Pacific oyster, *Crassostrea gigas*, where approximately 150,000 MT of oysters are produced annually. The Pacific oysters on the south coast of Korea are known to be infected by *Marteillioides chungmuensis*, while infection by other OIE-listed protozoan parasites is unknown. In this study, possible infections by *Bonamia ostreae*, *B. exitiosa*, *Marteilia refringens*, *Perkinsus marinus*, and *P. olseni* in the Pacific oysters from the south coast were surveyed. A total of 1,860 oysters from 31 sites on the south coast were collected in spring and fall for the analysis. The OIE-listed five protozoan parasites in the oysters was examined using PCR with the species-specific primers recommended by the OIE. Of the 1,860 oysters examined in this study, *B. ostrea*, *B. exitiosa*, *M. refringens*, and *P. marinus* were not detected from any individual oyster. *Perkinsus olseni* was detected from 5 individuals out of 600 oysters collected from intertidal areas, and quantification by q-PCR indicated that the infection intensities were below 100 cells. The PCR also indicated that none of the oysters collected from subtidal long-lines were positive for *P. olseni*.

DARLING MARINE CENTER: CONNECTING PEOPLE TO THE OCEAN THROUGH RESEARCH, EDUCATION, AND PUBLIC SERVICE

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Darling Marine Center (DMC) was established in 1965 as the marine laboratory of the University of Maine. This unique facility in Walpole, Maine delivers distinctive research, education, and community and industry engagement programs, transforming knowledge into solutions to meet the needs of coastal communities in Maine and beyond. As a hub for marine research and education in the region, the DMC is a destination for professional and community scientists from throughout the state and nation. The waterfront facilities of the DMC—which include a newly renovated flowing seawater system, research vessel fleet, and shellfish hatchery—allow researchers to conduct controlled laboratory experiments in close proximity to field sites. In addition, the DMC hosts the University of Maine System scientific diving program and has housing and event space for groups as large as 100. Faculty in residence conduct research in Maine and around the world and engage graduate and undergraduate students in active exploration of coastal and ocean environments. Through Semester By the Sea and research internships in the summer, undergraduates have diverse opportunities to immerse themselves in hands-on education. As engaged community partners, Darling Marine Center researchers, staff and students work with fishermen, aquaculture entrepreneurs and other community members to advance workforce development and education through fundamental and applied research, product development and commercialization, and business incubation. The DMC also hosts programs for visiting college students and has a long tradition of informal education programs for the public and local schoolchildren. Learn more at http://dmc.umaine.edu/

IMPROVEMENT OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*) SETTLEMENT USING PROBIOTIC-TREATED SUBSTRATES

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Shellfish hatcheries are producing high-quality oyster spat for farmers; however, even under optimized conditions, oyster larvae can sporadically display poor settling during their transition from larvae to spat, leading to low yields. Consequently, this study focuses on improving spat settlement with the use of probiotics.

Four probiotic strains were selected for the pre-treatment of a setting substrate (ceramic tiles). These strains have previously shown to increase larval survival upon challenge with the shellfish pathogen, *Vibrio coralliilyticus*. The substrate was soaked in combined cultures of the four probiotic strains for two treatment groups of 24 hours and 48 hours, respectively. Subsequently, settlement was assessed by placing the treated substrates into well-plates and adding settlement-ready oyster larvae in seawater to the wells.

After the 24-hour soak in probiotics, spat settlement on the ceramic tiles was 2.5X higher (26.8 ± SD 4.3%) than on control tiles soaked in sterile seawater (10.7 ± SD 6.2%). After a 48-hour probiotic soak, the highest settlement rates were 43.3 ± SD 10.2%, compared to 26.2 ± SD 0.8% on tiles not treated with any probiotics; however, due to the large standard deviations observed for most treatments, none of the differences were statistically significant. Consequently, to better elucidate the differences in settlement rates, larger-scale trials have been planned. In conclusion, improved oyster larval settlement through the use of probiotic-treated substrates could significantly improve spat production yields in hatcheries.

A COMPARISON OF SHELL AGING METHODOLOGIES FOR THE PISMO CLAM (*TIVELA STULTORUM*)

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Pismo clams (*Tivela stultorum*) are an ecologically and economically important species in California. Populations have dramatically declined in recent years; legal size individuals (114 millimeters in length) are extremely rare. Prior research indicates that Pismo clam growth rates have declined compared to historical records, with individuals taking nearly twice as long to reach legal size. Historical age estimates used external growth rings, whereas modern studies use internal annuli. The observed discrepancies in growth rates may be due to changes in the environment, in Pismo clam physiology, or methodological differences. The objective of this project is to determine if the observed disparity in age-size relationships is a product of methodological differences. A total of 632 Pismo clams and shells were collected throughout California. Two independent readers counted external surface annuli for each individual and—following a minimum interval of one week—counted the internal annuli in shell cross sections. External and internal age estimates were compared using a paired t-test. Initial findings indicate that internal and external aging strategies provide similar age estimates, suggesting that historical estimates were accurate, and the discrepancy is due to one or multiple other factors. Understanding how methodological techniques influence the accuracy of growth rate and age estimates is critical for the effective management and conservation of this iconic species.

APPLICATION OF STABLE CARBON AND NITROGEN ISOTOPES TO EXAMINE FEEDING HABITS IN BLUE CRABS (*CALLINECTES SAPIDUS*) ACROSS VARIOUS VEGETATION ZONES IN BLACKBIRD CREEK, DELAWARE, USA

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Blue crabs (*Callinectes sapidus*) are crucial to the economy of Delaware as they account for $15 million of the state revenue. Evaluating the feeding habits of commercially relevant aquatic species such as blue crabs is necessary to manage and conserve those species. In this study, stable Carbon (C) and Nitrogen (N) isotope ratios were compared in blue crabs collected from sites along Blackbird Creek, Delaware, to examine their feeding habitats. C and N isotopes are used as tracers of nutrient flow in food webs. The carbon isotope δ^{13}C is used primarily to trace the food source mainly from primary producers, while the nitrogen isotope δ^{15}N indicates the trophic level of species and dietary shifts. Different sampling sites were distinguished by the existent dominant vegetation along the creek: *Sporobolus alterniflorus* dominant, *Phragmites australis* dominant or mixed vegetation. Based on preliminary results, no significant difference for the C isotope was found among the blue crabs collected from different sites with a reported average range of −19.47 ‰ to ±21.28 ‰. In contrast, there was a significant difference in the N values, which ranged from 9.32 ‰ to 13.44 ‰ in blue crab tissues. These preliminary results suggest that blue crabs collected from the various vegetation zones are opportunistically feeding on locally available food sources that differ across sites.

INITIAL SETTLEMENT HABITAT HAS IMPLICATIONS FOR GROWTH OF JUVENILE OYSTERS IN DIFFERENT SALINITIES

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Estuaries provide valuable habitat for the eastern oyster (*Crassostrea virginica*). While salinity at a given location fluctuates regularly with tides and precipitation, there are stark environmental differences upbay and downbay controlled by the salinity gradient. High salinity habitats downbay support higher oyster growth, while lower salinity upbay is a refuge from predation and disease. Three experiments were performed to investigate the effect of initial salinity conditions on subsequent growth in different salinities. Two experiments were performed with oyster spat collected from distinct Delaware Bay salinity zones, then transplanted into various salinity conditions in the laboratory where growth was monitored. Transplanting into low salinity led to significant decreases in growth compared to transplanting to higher salinity, and growth of oyster spat differed based on their salinity zone source. An additional experiment was performed using hatchery reared larvae. Upon reaching competency, larvae were placed in one of four different salinity conditions to settle, and they were maintained for three weeks post-settlement, then measured. Spat were then transferred into new salinity conditions where they remained for three weeks and measured again. As before, lower salinity treatments were associated with lower growth, with final size depending more on initial settlement salinity than transplanted salinity. Consequently, environmental conditions at settlement can impact subsequent oyster growth, in addition to changes in salinity. As increased freshwater events due to climate change are expected in the Delaware Bay, these differences in early oyster growth in response to settlement habitat and salinity changes are important for oyster stock resilience.

POST-SETTLEMENT SURVIVAL IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) TO INFORM MANAGEMENT AND RESTORATION IN THE CHESAPEAKE BAY

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Oysters are a dominant species, important ecosystem engineers, and provide critical ecosystems services in estuaries. Despite their importance, oyster populations have declined 85% globally and are at $<$1% their historic harvest levels in Virginia. Many invertebrates exhibit high mortality in their early post-settlement life stages, but there is limited quantitative information on post-settlement mortality and its relationship with recruitment due to the small size of settlers. This project aims to understand post-recruitment early life history dynamics of oysters in the Chesapeake Bay, specifically growth and mortality rates during the first 3-4 months post-settlement. Shellstrings were deployed at two long-term monitoring sites in the James River. At each site, 6 serial deployments of 4-10 shellstrings were set at 2-week intervals. Every 2 weeks, 2 shellstrings were collected from each deployment. The number of recent oyster recruits were counted, up to 250 recruits were photographed per shellstring, and individual recruits were measured using ImageJ software. The length data was used to generate a growth curve for the first 3-4 months post-settlement and provide a unique dataset. Given that oysters have multiple spawning events throughout the summer, this approach identifies optimal time windows or conditions that improve settlement success and survival. An improved understanding of early life history recruitment, growth and mortality rates can help guide shell replenishment and oyster population management in the Chesapeake Bay.

LARVAL TRANSPORT AND SETTLEMENT OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) IN SAN CARLOS BAY, FLORIDA, USA

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Eastern oyster populations in San Carlos Bay, near Fort Myers, FL, have seen drastic decreases in recent years as the result of coastal development and alteration of freshwater flows through the Caloosahatchee River as part of the Comprehensive Everglades Restoration Plan. As a result, restoration and monitoring programs have been implemented in the last 20 years to assess and mitigate the effects of altered hydrology (specifically salinity regimes) on the heath of oyster reefs. Oysters, like many other bivalve species, have a multiphasic life cycle and spend the early stages of their life as plankton before settlement occurs. Larvae are more sensitive to changes in their environment than juveniles or adults, so successful recruitment (and reseeding natural or restored reefs) depends on the ability of larvae to tolerate extreme salinity changes. Furthermore, altered flow rates from the Caloosahatchee River during the spawning season affects transport of larvae through the estuary and may result in advection out of San Carlos Bay. Thus, a better understanding of larval transport and settlement patterns will be necessary for successful restoration efforts and for water management plans. As such, we monitored patterns of larval dispersal and settlement biweekly at 10 locations in San Carlos Bay from June to October 2020. Preliminary analysis suggests that upriver sites serve as sources of oyster larvae for sites near the mouth of San Carlos Bay and connected water bodies, but that recruitment is heavily influenced by tidal patterns and flow regimes within the estuary.

AQUACULTURE FACILITIES IN THE UC DAVIS COASTAL AND MARINE SCIENCES INSTITUTE BODEGA MARINE LABORATORY

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The Bodega Marine Laboratory (BML), was established in 1966 by UC Berkeley and acquired by UC Davis in 1983. It is a multidisciplinary research institution capable of hosting visiting aquaculture researchers year-round. Numerous indoor and outdoor aquaculture facilities are utilized for crustacean, molluscan and fishery aquaculture, as well as barren urchin ranching and algal culture. Abalone and native oyster aquaculture are current focal points. In collaboration with industry partners, the BML develops SOP for native and non-native oyster culture, producing "spat" for commercial and restorative out-planting of underutilized oyster species. The abalone aquaculture project includes efforts to save an endangered species.

White abalone (*Haliotis sorenseni*) once supported a lucrative commercial fishery in California. Commercial overharvesting quickly decimated stock, triggering a harvest ban in 1993. White abalone became the first marine invertebrate listed as an endangered species in 2001. In coordination with NOAA Fisheries, California Sea Grant and the California Department of Fish and Wildlife, BML houses a captive breeding program. The White Abalone Restoration Consortium (WARC), consisting of 10 agencies, collaborate to spawn and raise captive bred abalone for out-planting. Culturing viable abalone larvae requires year-round brood stock conditioning, feeding, induced spawning, and rearing of juvenile abalone. The white abalone captive breeding program has been successful, increasing larval production from dozens in 2012 to thousands in 2014. The first out-planting of 3,200 captive bred white abalone occurred during November 2019 in southern California.

Facilities and staffing include: the Aquatic Resources Group - Facility-wide animal care and life support services, Anadromous Fish Facility, Climate Change Facility, Fluorescence Imaging Facility, Invasive Species/Pathogen Facilities, Bivalve Hatchery, Algae Culture Greenhouse, Abalone Culture Facility, Housing/Conference Facilities, Vessel Operations, and the Boating/Dive Program.

OVERWINTERING ALTERNATIVES FOR EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) FARMED IN DELAWARE BAY, NEW JERSEY, USA

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Oysters farmed intertidally in Delaware Bay, New Jersey are susceptible to freezing, ice damage and increasingly unpredictable freeze-thaw cycles that can all lead to significant losses. Oyster grown subtidally are not susceptible to these risks while oysters grown in more northern regions are often overwintered in cold storage. Because subtidal access is limited in Delaware Bay, most intertidal farms leave oysters in place during winter exposing them to considerable risk. This study compared survival, condition and disease among oysters held intertidally, subtidally and under refrigeration during winter. Two year classes of the Rutgers NEH™ line representing sub-market and market-size oysters were deployed under each method in five replicate bags from December 2019 through mid-March 2020 then returned to the intertidal farm. Survival was measured monthly, while size, weight and condition were measured quarterly through October 2020. Oysters were assessed for dermo and MSX diseases at the start of the study and subsequently in June and October. Results indicated no significant differences in any parameters measured among overwintering methods. Winter weather during the study was mild and did not pose significant risk to intertidal stocks, but the fact that other methods performed equally well suggests that refridgeration provides a viable alternative in years when intertidal conditions are harmful.

SCEMFIS 2020: A YEAR IN REVIEW

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The Science Center for Marine Fisheries (SCEMFIS) is a National Science Foundation (NSF) funded industry/university collaborative research center (I/UCRC) established in June 2013. The SCEMFIS has two sites: The University of Southern Mississippi (USM) and Virginia Institute of Marine Science (VIMS). Since 2013, the SCEMFIS has grown to include researchers from USM, VIMS, Cornell University, Rutgers University, University of Rhode Island, University of Maryland Center for Environmental Science, The University of Massachusetts Dartmouth, and Old Dominion University, along with other U.S. and Canadian academics and consultants and 12 industrial partners. The SCEMFIS provides NSF sanctioned research to meet the needs of industry partners with the ultimate goal being sustainability of both the shellfish and fish stocks and their associated fisheries. Achievements for SCEMFIS graduate students in 2020 include two non-academic research internships and a Knauss Fellowship. Additionally, the SCEMFIS was awarded an NSF breakthrough award for ocean quahog ageing methods. Current projects include carrying out research on surfclam and ocean quahog growth and age-frequency distributions, the influence of wind energy development on mid-Atlantic shellfish fisheries, several forage fish projects, and many other topics. The SCEMFIS is looking back at a successful year and forward to more progress in 2021 as more academics and industries become involved with the Center and its ongoing projects.

THE POTENTIAL FOR BLUE CRAB PREY TO BE A HOST OF THE CRAB PATHOGEN, CSRV1

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Predation of reservoir hosts and alternate hosts can be an important route for transmission of pathogens to a target species. The commercially and ecologically important blue crab, *Callinectes sapidus* Rathbun, 1896, is infected by *C. sapidus* Reovirus 1 (CsRV1) throughout its geographic range from New England to Uruguay. CsRV1 causes mortality in captive crabs in soft crab production, and experimental infection with CsRV1 is lethal to blue crabs in 2-4 weeks. The prevalence of CsRV1 in temperate latitudes averages ~20%, while it is below 5% in the tropics. Very little is known about how blue crabs in the environment acquire CsRV1 infections. In this study, we look at the potential for three blue crab prey species in the family Panopeidae to become infected with CsRV1: *Rhithropanopeus harrisii*, *Panopeus herbstii*, and *Eurypanopeus depressus.* Wild-caught crabs were divided into experimental and control groups that were injected with CsRV1 and saline, respectively, and held in individual vessels for 14 days. Using an RT-qPCR assay to detect CsRV1, virus replication was seen in 60% of CsRV1- injected, but not saline injected, *P. harrisii* and 9% of *P. herbstii*. Virus replication was observed in 42% of *E. depressus* injected with CsRV1, but also in 40% of the control group. These preliminary results illustrate that CsRV1 can infect and replicate in blue crab prey, raising the possibility that these crabs can serve as vectors of the virus to blue crabs. Further work is needed to investigate the prevalence and transmission dynamics of CsRV1 in wild Panopeidae.

EFFECT OF MICROALGAL (SPECIES) ON SUNRAY VENUS CLAM (*MACROCALLISTA NIMBOSA*) AND NORTHERN QUAHOG (= HARD CLAM) (*MERCENARIA* SP.) POST-SET PRODUCTION

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Diversification within the shellfish aquaculture industry in Florida is needed to increase economic stability. Previous research concluded that the sunray venus clam (SRV) could be cultured similarly to the northern quahog (=hard clam). Despite these efforts, a lack of available SRV seed supply remains an issue and additional research focused on optimizing culture methods still needs to be conducted. A post-set feed study was performed to address whether various combinations of live microalgae would differentially effect post-set production of SRV and hard clams.

The six-week feed experiment compared bi-, tri-, and quad-live microalgae combinations. The experiment consisted of six treatment groups, consisting of three replicates each, stocked with 1079 (±43) 2-week post-set clams. With respect to growth, SRV and hard clams both showed an increase of 8%-22% and 2%-18% higher growth respectively and statistical significance ($p<0.05$) when fed the quad-algae combination of equal proportions of *T-Isochrysis galbana*, *Chaetoceros gracilis*, *Pavlova lutheri*, and *Thalassiosora weissflogii* compared to the other dietary treatments. With respect to the survival of the hard clams, the results showed no statistical significance among treatments (90-95%) while the SRV clams showed an increase of 9%-22% higher survival percentage ($p<0.05$) when fed the bi-algae combination of equal proportions *T-Iso*, and *C. gracilis*. These results may be used to inform industry concerning dietary treatments that may increase production for post-set of both clam species.

OSHV-1 SURVEY IN SEA WATER AND *CRASSOSTREA GIGAS* TISSUES IN TWO AREAS USING DIFFERENT CULTURING SYSTEMS

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The incidence of OsHV-1 is highly associated with sea water temperature being 16ºC the threshold for disease development and oyster mortality. Culturing methods also influence the disease progression as higher density of animals and direct contact favour viral transmissions. In order to minimize the impact of the disease in culturing areas, it is also important to know the specific oceanographic and environmental conditions which could facilitate disease management strategies.

One stock of oysters was split in two groups and settled in two culturing sites where massive mortalities were previously detected. Oysters were grown in trestles at one site and on rope rafts at the other site. Oyster tissues and sea water were collected regularly over a two-month period. 200 mL of sea water were filtered through 40, 10, 5, 1.2 and 0.22 µm. Oyster mortality and sea water temperature were also recorded. OsHV-1 was detected by standard PCR and quantitative PCR in mantle oyster tissues and 1.2 µm and 0.22 µm filters.

One peak of abnormal mortality associated with a rapid increase in sea water temperature was observed in oysters grown in trestles. Prevalence of infection increased to 57% and quantification of viral load in sea water reached a maximum value of 4.5x10E4 viral DNA copies/µL before the mortality episode; however, no abnormal mortalities were observed in rope rafts although sea water temperature was constantly over 16ºC and prevalence of infection reached 40%.

EFFECT OF DIFFERENT PATHOGENS ON THE TRANSCRIPTOMIC RESPONSE OF *OCTOPUS VULGARIS*

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The need for species diversification is crucial to satisfy the global demand on aquaculture products. The common octopus, *Octopus vulgaris,* is a species with a high interest for human consumption. Octopus physiological characteristics make this specie very interesting for culture due to fast growth and short life cycle. Recent investigations have achieved to close the life cycle under captivity. For a profitable culture, next issue to be addressed should focus on the incidence of pathogens especially at the first stages.

In this study we have evaluated at transcriptomic level the effect of two marine pathogens: the ostreid herpes virus OsHV-1 and the bacteria *Vibrio lentus*, which has caused mortalities in this species. Paralarvae at 0 and 40 days post-hatching was exposed *in vitro* to pathogen suspensions for 24 hours. Samples were collected at 24 h post-exposure and RNA was extracted for RNA-sequencing.

Genes related to cell adhesion, cellular and vesicle traffic and membrane organization were up-regulated after *V. lentus* exposure. Virus exposed paralarvae overexpressed genes related to apoptosis regulation and also antiviral defences. Regarding cell interactions, different protocadherins were up-regulated in both experimental trials suggesting a different pattern of expression for each host-pathogen interaction.

IDENTIFICATION OF MOLECULAR MARKERS ASSOCIATED TO OSHV-1 RESISTANCE IN CRASSOSTREA GIGAS

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Significant mortalities have been regularly occurring in the Pacific oyster, *Crassostrea gigas*, associated with the incidence of OsHV-1 and impacting the aquaculture production at a global level. Long-term solutions such as the selection of resistant strains and the identification of molecular markers have been postulated as prioritizing strategies by the scientific community. In this context, the information gathered by novel sequencing methodologies offers new perspectives for the study of non-model species.

RNA-seq data previously carried out for comparison of *C. gigas* spat with different susceptibility was further analysed for potential molecular markers examination. For that, read mappings corresponding to differently expressed transcripts were manually checked for variant localization. Validation of potential polymorphisms was carried out in oyster families produced by single pair matting of adult animals with different susceptibility to OsHV-1. Families were naturally exposed to OsHV-1 in a culturing raft and after a mortality outbreak; survivors were collected and compared to initial samples. A total of 461 animals were genotyped by sequencing using individual barcoding identification for multiplex amplification.

Twelve transcripts containing 30 nucleotide variants were analysed. Among them, 18 variants were real single nucleotide polymorphisms (SNP). The allele frequencies significantly varied in 10 loci on resistant families and 5 loci on susceptible families. Moreover, two linked SNP were also significantly different attending to the disease susceptibility features of the broodstock. These results showed the identification of two linked molecular markers that can be used in selective breeding programmes.

MANGROVE ACTION PROJECT—STANDING AT THE ROOTS OF THE SEA

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Today there is a growing urgency to recognize the importance of conserving and restoring protective mangrove greenbelts to lessen the dangers from future natural catastrophe. As sea levels rise, so will the frequency and intensity of hurricanes and storm surges. Mangroves can buffer against the fury of such destructive natural events, potentially protecting those settlements, livelihoods and lives located behind a healthy mangrove fringe. Mangroves are also vital to curb climate change and to help restore our threatened marine biodiversity.

Though there are good reasons aplenty to conserve and restore mangroves, so why are we still losing around 60,000 ha of mangroves a year, and how can we halt this trend? More than that, why are we not taking more effective actions? Since its inception in 1992, the Mangrove Action Project (MAP) has been countering the adverse threats to mangroves posed by industrial shrimp aquaculture, tourism, golf courses, urban and agriculture expansion and now climate change and rising sea levels.

Over the last two decades, MAP has set off on a unique course to combat mangrove loss. The MAP 'roadmap' for the future of our planet's mangroves interweaves a multi-faceted approach where all 'roads' lead to a common solution. This five-pronged approach to long-term mangrove conservation involves: education, advocacy, networking and collaboration, conservation and restoration, and sustainable community-based development. In this presentation, I will better define the major routes that MAP takes and how these connect to the overall mission of MAP to conserve and restore the mangroves.

EFFECTS OF EELGRASS DENSITY ON FILTER FEEDER BIOMASS AND CONDITION INDEX IN A MULTI-HABITAT LIVING SHORELINE

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Over two decades, estuarine ecosystems have suffered 50% habitat loss. Implementation of multi-habitat living shorelines (MHLS) can restore lost habitat function. Researchers constructed a MHLS in 2016 in Newport Bay, California by restoring eelgrass and oyster beds together and in isolation. Increased sedimentation from eelgrass could threaten oysters and other filter feeders. This study will investigate how eelgrass impacts filter feeder biomass and condition index. To compare short-term and longer-term success of oysters restored with varying densities of adjacent eelgrass, the total biomass and per capita condition indices of native and non-native filter feeders on restored oyster beds one- and three-years post-restoration will be calculated. It is hypothesized that increased eelgrass density will increase sedimentation rates onto adjacent oyster beds, causing declines in filter feeder biomass and per capita condition indices, biomass will increase, and condition index will decline with increasing filter feeder density, and there will be no interannual variation in the effect eelgrass density has on response factors. I will use previously collected data on these factors. Filter feeders from quadrats on oyster beds will be excavated, identified, and weighed to determine wet and dry tissue and shell weight, and quantify condition index. Sedimentation will be quantified by measuring mud deposition on oyster beds via point-contact and filter feeder and eelgrass densities will be measured using quadrat surveys. Predicted results support the hypotheses mentioned. Increasing understanding of the relationship filter feeders share with eelgrass will inform future management decisions about whether to restore MHLS together or in isolation.

MORPHOMETRIC CHANGE WITH GROWTH IN THE SCALLOP, *PLACOPECTEN MAGELLANICUS*

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The sea scallop, *Placopecten magellanicus*, displays a subtle change in morphometry as it increases in size and age. Previously, Dadswell and Weihs (1990, Can J. Zool 68: 778-785) related these changes to hydrodynamics and swimming capability in scallops from Passamaquoddy Bay, Canada and indicated a three stage adult life history of early sedentary, mid-life mobile and a later second sedentary stage. Herein, the examination of size and age related morphometry was extended to collections from the Georges Bank and mid-Atlantic shelf regions of the U.S. east coast. The project aims to compare the morphological transitions associated with life history stages and adds the important function of age to these transitions and stages. It includes a discussion of the time sequence of morphological change in terms of the role of scallops as benthic dominants in their bathymetric range, temporal and spatial stock stability, and implications for fishery management.

COMMUNITY ASSEMBLAGE AND DEMOGRAPHICS OF INVERTEBRATES IN URBANIZED MANGROVES

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The strong physical and biotic alterations associated to urbanization in tropical coastal areas are prompting mangrove loss or degradation worldwide, with unknown consequences for mangrove-associated fauna. In these systems, most species are declining and being replaced by a less diverse set of species —often composed of non-natives— able to capitalize on the new conditions, which dictates the balance between 'winners' and 'losers' of human actions in mangrove forests. While previous studies have identified cormorants (Phalacrocoracidae) and toadfish (Batrachoididae) has been suggested as synanthropic species in urban mangroves, invertebrates such as periwinkles (Littorinidae), fiddler crabs (Ocypodidae) and non-native bristle worms (Polychaetes) are seemingly outperforming in these environments. These species assemblages and the ecosystems they form are seemingly due to the newly built environment and the abundance of materials and pollutants provided by humans. At the species level, urbanization acts as a strong selective pressure for "urban phenotypes". Urban seascapes in the Pacific and Atlantic coast of Colombia present shifted thermal regimes, the provision of anthropogenic materials such as waste waters, heavy metals and plastic materials that have persisted during nearly a century. The quality of these habitats seems to be good enough as to support high-density populations often displaying smaller size ranges and behavioural adjustments to cope with the novel conditions.

EFFECTS OF A NON-INDIGENOUS BRYOZOAN ON THE RECRUITMENT OF THE NATIVE OLYMPIA OYSTER, *OSTREA LURIDA*

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Non-indigenous fouling organisms settling onto artificial and natural hard substrata in estuaries can negatively impact native species via space competition, predation, or other mechanisms. The effects of *Zoobotryon verticillatum*, and other fouling organisms on the recruitment of *Ostrea lurida*, were studied to determine whether their presence, biomass, and abundance affect oyster recruitment. Terracotta tiles, proxies for available hard substrata, were deployed in Newport Bay, California at tidal elevations between −0.4 and +0.1 feet MLLW, April-October 2020, during the spawning and recruitment season of the oyster. Five treatment groups (n=5 replicates per tile) were established to examine the effects of *Z. verticillatum* and other fouling organisms on recruitment of *O. lurida*: unmanipulated controls, *Z. verticillatum* removals, *Z. verticillatum* plus other fouler removals, other fouler removals with *Z. verticillatum* additions, and other fouler removals with 2X *Z. verticillatum* additions. The treatment groups were maintained by adding or removing *Z. verticillatum* foulers as appropriate per treatment; all removals were quantified via volume displacement as a proxy for biomass. During tile retrieval, the volume displacement and wet weight of *Z. verticillatum* and other foulers were recorded. Oysters recruiting to the tiles were measured for length and width, identified, and counted. Percent cover of all species recruiting to the tiles using point contact techniques was recorded. Preliminary results suggest that *Z. verticillatum* is facilitating *O. lurida* recruitment as *Z. verticillatum* removals had lower oyster recruitment. Some non-indigenous fouling organisms may not be as problematic as predicted when restoring native species in estuarine communities.

SHRIMP ENDOGENOUS VIRAL ELEMENTS (EVE) OF INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS (IHHNV) AND THEIR IMPLICATIONS FOR SHRIMP DIAGNOSIS

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Integration of non-retroviral fragments into animal genomes has been found for a few decades as a result of infection and completion of their life cycles. To date, ‘endogenous viral elements’ (EVE) of infectious hypodermal and hematopoietic necrosis virus (IHHNV) and white spot syndrome virus (WSSV) have been found in penaeid shrimp. For practical diagnostic approach, it necessitated a change in the routine method to distinguish between infected shrimp and EVE-containing samples. In the case of IHHNV, infected shrimp species have been developing resistance to the virus, thus it is a challenge to separate shrimp carrying both infectious form of virus and EVE from those that are infected only (i.e. the former and latter would be recognized by conventional PCR testing). Discard of domesticated shrimp breeding stocks based on such false positive results might have negative consequences, if such inserts are related to shrimp viral disease tolerance according to ‘viral accommodation hypothesis’. It is thus necessary to improve accuracy in diagnosis of IHHNV infection. For example, multiplex PCR analysis is developed to amplify the entire IHHNV genome, ensuring the accurate diagnosis, and the technique must be convenient for practical application. More recently, isothermal nucleic acid amplification techniques such as loop-mediated isothermal amplification (LAMP) comprises primers targeting OIE-recommended region and the 3’end of the viral genome that has been reported to be less occurrence of EVE in the shrimp genome.

THE EFFECT OF ENVIRONMENTAL PARAMETERS ON *CRASSOSTREA VIRGINICA* SHELL SIZES IN NARRAGANSETT BAY, RHODE ISLAND, USA

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Along the coastline of Narragansett Bay, Rhode Island, there is variation in environmental parameters as well as *Crassostrea virginica* (eastern oyster) shell sizes. In Rhode Island, the population of *C. virginica* was almost completely diminished due to harmful human impacts. In order to understand how the wild oyster population is doing today, shell measurements of lengths and widths as well as environmental data were collected and compared across six sites in Narragansett Bay. Data were collected over the summer months in order to estimate the environment during the most stressful part of the year. These analyses will help suggest which environmental parameter played the largest role in wild oyster shell sizes. Conclusions will inform how oysters perform in varying environments as well as aiding in future restoration projects.

DUKE UNIVERSITY MARINE LABORATORY

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The Duke University Marine Lab (https://nicholas.duke.edu/marinelab) is a satellite campus of Duke University located on Pivers Island in coastal North Carolina. The campus is a full-service campus operating year round and offering courses four terms per year (Fall, Spring, and two Summer Terms). There are approximately 15 full-time faculty based at the marine lab. The marine lab has a vibrant student community consisting of undergraduate, professional Masters, and PhD students. Facilities at the marine lab include dorms (5), a dining hall, a library, an auditorium, a student activity center, teaching classrooms, teaching and research laboratories, running sea water, docks, boats (in- and off-shore capabilities). Faculty at the marine lab maintain active research programs and engage students at all levels. Multiple programs are currently supported by the marine lab. The Duke Aquafarm is a shellfish aquaculture farm that provides students with volunteer opportunities for doing oyster culture. The Marine Robotics and Remote Sensing Facility (aka. ‘Drone’ Lab) employs multiple platforms for remote sensing of the marine environment. The Pivers Island Coastal Observatory (PICO) is a long-term physical and biological monitoring program for coastal oceanography. The Marine AlGae Industrialization Consortium (MAGIC) is a DOE-funded project focused on growing algae at industrial scales for biofuels. These programs and the facilities at the Duke Marine Lab provide both students and faculty with numerous opportunities for participating in cutting-edge research in marine science.

FOLLOWING THE BIG BEND SHELLFISH TRAIL IN FLORIDA

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The Big Bend region of Florida has a long history of natural resource dependence. Oysters, crabs, shrimp and fish have all crossed the docks of rural communities in this region at one time or another in abundance. To highlight the unique and diverse shellfish resources the Gulf of Mexico supports, a tourism initiative, “Follow the Big Bend Shellfish Trail”, was implemented in 2016. In partnership with visitors’ bureaus and chambers of commerce in four coastal counties and with support by The Conservation Fund, a map identifying local businesses where visitors can buy, eat, and, sometimes, harvest local shellfish was developed. With National Maritime Heritage Grant Program funding, the map was recently expanded to an actual trail through the placement of colorful, interpretive signage kiosks in the area. These kiosks serve as points of interest and convey cultural and historical information about the shellfish harvested and processed at each working waterfront location. An interactive website, www.floridashellfishtrail.org, provides information on kiosk locations, suggested road trips, infographics of each shellfish species (bay scallop, blue crab, hard clam, oyster, shrimp, and stone crab), recreational and commercial harvesting, importance of water quality, recipes, and more. The Big Bend Shellfish Trail, the largest trail of its kind in the United States, has the potential of being a valuable public educational tool that will simultaneously enhance the authenticity and sustainability of the destinations as well as being economically beneficial for the working waterfront communities in the region.

SYNERGISTIC EFFECTS OF FEEDING AND EYESTALK ABLATION ON OVARIAN MATURATION OF THE BLACK TIGER SHRIMP

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Unilateral ablation of eyestalk in female black tiger shrimp *Penaeus monodon* is known to induce ovarian maturation; however, without feeding the female broodstock with live feeds, the inductive effect cannot be realized. Thus, the synergistic effects of feeding with live feeds and the ablation must be elucidated. This study was conducted when the high-quality genome assembly was not available, thus it constructed the first high-quality ovarian reference transcriptome in *P. monodon* using short-read Illumina RNA sequencing and long-read Pacific Biosciences (PacBio) isoform sequencing (Iso-seq). This transcriptome assembly allowed us to dissect the effects of feeds and eyestalk ablation and reveal their synergistic effects at the transcriptomic level. It was found the regulation of important genes involved in fatty acid regulation, energy production, and hormone-mediated oocyte maturation pathways. These findings shed the light on molecular mechanisms and key molecular pathways which may lead to means to induce ovarian maturation without having to perform eyestalk ablation in the future.

COOPERATIVE OXFORD LABORATORY—A BIRD'S EYE VIEW

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The Cooperative Oxford Laboratory (COL) is a unique combination of scientific, response and management capabilities of National Oceanic and Atmospheric Administration, Maryland Department of Natural Resources (DNR), and U.S. Coast Guard. All three organizations collaborate to meet their respective missions and address science.

The laboratory was established in 1960 to investigate oyster diseases in Chesapeake and Delaware Bays. The year 2021 marks the 82nd anniversary of the Maryland Fall Oyster Survey, an annual assessment by DNR to provide managers with reproduction, mortality and disease data. Health assessments at the COL have since expanded to multiple fish and shellfish species as well as marine mammals and sea turtles. Research priorities have also broadened to help better inform local, state, and federal decision-making. Current priorities address coastal habitat assessment and restoration, pathogen forecasting, fish recruitment and habitat modeling for ecosystems-based fisheries management, ecosystem services evaluation, and climate related risk vulnerability. The COL scientists continue to expand our understanding of estuaries and improve community resilience by developing and applying novel techniques and by transforming research into products used by people every day.

The laboratory is located in the town of Oxford on the Tred Avon River, a tributary of Choptank River in Chesapeake Bay. It has 16,000 square feet of laboratory and office space, including wet labs, quarantine facilities, and a 58' research vessel and smaller boats to support research operations. The COL employs about 50 federal, state, and contractual staff and operates chiefly via telework during the on-going COVID-19 pandemic. The COL has a long history of welcoming visiting scientists and students and expects onsite opportunities to resume when the laboratory re-opens to the public. Availability and financial support of internships varies among the COL partners and are currently limited. Information about student opportunities across NOAA may be found at https://www.noaa.gov/education/opportunities/student-opportunities

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PREDATION OF THE PERIWINKLE SNAIL, *LITTORARIA IRRORATA*, IN THE SALT MARSH INTERTIDAL ZONE

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The periwinkle snail (*Littoraria irrorata*) is a ubiquitous grazer in Atlantic salt marshes. In extremely high densities, periwinkles can defoliate patches of salt marsh habitat. Predation is critical for controlling periwinkle populations, thus facilitating the growth of *Spartina alterniflora*, the dominant marsh vegetation. This study assesses how predation intensity varies across the intertidal zone of the salt marsh. Groups of periwinkles ($n=5$) were tethered in place at 0m, 1m, 3m, and 5m from the marsh edge for 24 hours. Mortality rates varied as a function of distance into the marsh ($p=0.003$) with tethered snails at the marsh edge more likely to be preyed upon than snails in the interior. These data suggest that the marsh interior serves as an important spatial refuge for periwinkles, but predation was equally likely within the 1-5m zone. Additionally, predated snails were classified by predation strategy using the characteristic patterns of snail remains. The most frequent predation technique at all distances was shell crushing ($p<0.005$), which suggests that blue crabs are the primary predator of periwinkles. At 0m, cut lines were more frequent than empty intact shells, and the reverse was observed for 1-5m. Empty shells are indicative of predators that suck or scrape out the snail, like gastropods and fish. According to the trophic cascade model, blue crab predation is a top-down regulator of periwinkle grazing. Even though escaping into the marsh provides spatial refuge for periwinkles, blue crabs can still access the intertidal zone of this habitat and exert predation pressure.

DOPAMINE RECEPTORS: A GENOMIC STUDY OF THE BIVALVE MOLLUSC *CRASSOSTREA VIRGINICA*

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The gill lateral cells (GLC) of *Crassostrea virginica* are innervated by dopamine and serotonin nerves. Dopamine slows down GLC cilia beating and serotonin accelerates them. Dopamine receptors are classified as D1R and D2R. Pharmacological, cell biology and immunofluorescence work of our lab found the dopamine receptors involved in GLC cilia inhibition are D2R-like in GLC and D1R-like in cerebral and visceral ganglia. HPLC studies detected dopamine in gill, cerebral and visceral ganglia of *C. virginica*. Immunofluorescence histochemistry studies showed the presence of dopamine neurons in the ganglia, D2R-like receptors in GLC and D1R-like receptors in the ganglia. Recently the genome of *C. virginica* has begun to be mapped. To test the hypothesis *C. virginica* contains genes for dopamine receptors and these receptors are similar to those in other animals, BLAST searches of the NCBI database using DNA and protein sequences of *C. virginica* D1R and D2R genes were conducted. Gene matches for D1R genes were found on chromosome 4 and 5, and D2R genes on chromosomes 3 and 5 of *C. virginica*. BLASTS of the receptors found matches to those in other animals, including mammals. This study complements physiology and cell biology studies demonstrating the presence and function for dopamine in *C. virginica*, and shows the genome of *C. virginica* contains genes to produce dopamine receptors that are similar to those found in other animals. This new information is valuable in showing the simple nervous system of *C. virginica* can be used to expand studies on dopamine neurotransmission.

MANAGEMENT STRATEGY EVALUATION SUGGESTS ATLANTIC SURFCLAM IS RESISTANT TO CURRENT FISHING PRESSURE DESPITE UNCERTAINTIES

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The Atlantic surfclam (*Spisula solidissima*) is an important commercial resource in the US Mid-Atlantic. Although the 2016 stock assessment found that surfclams are neither overfished nor is overfishing occurring, uncertainty in the scale of spawning stock biomass persists. As a consequence of this uncertainty, the Mid-Atlantic Fishery Management Council (MAFMC) lowered the acceptable biological catch in 2016. The risk-tolerance of that recommendation and adherence to MAFMC risk policy has not been evaluated. To address this, a management strategy evaluation was developed for Atlantic surfclam. Operating models generated simulations of the surfclam population conditioned on the 2016 stock assessment model structure, with allowance for uncertainty in steepness (h) of the stock-recruitment curve and natural mortality (M). Simulations were forecasted under a variety of management procedures and evaluated with estimation models that spanned uncertainty in h and M. Results showed current management decisions are conservative in reference to stated risk-tolerance policies, though incorrectly parameterizing natural mortality could lead to falsely characterizing the stock as overfished. Further analysis evaluated future economic viability of the fishery under alternative management procedures and biological uncertainty using a yield per recruit (YPR) analysis. Forecasted YPR was more sensitive to biological uncertainties than management decisions, with confounding effects from low h and M that forecasted low YPR. This work contributes to efforts to evaluate fishery management strategies from an environmentally and economically sustainable perspective.

IN-DEPTH INVESTIGATION INTO PATHOPHYSIOLOGY OF THE GUT METAGENOME AND HOST RESPONSE TO *VP*$_{\text{AHPND}}$ IN MADAGASCAR–MALAYSIA CROSSBRED BLACK TIGER SHRIMP, *PENAEUS MONODON*, COHORT STOCKS

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A recently emerged lethal shrimp bacterial infection known as Acute Hepatopancreatic Necrosis Disease (AHPND) has led to massive, farmed shrimp mortalities including the black tiger shrimp, *Penaeus monodon*. This disease is mainly caused by *Vibrio parahaemolyticus* AHPND strain (*Vp*$_{\text{AHPND}}$) bacteria. During *Vp*$_{\text{AHPND}}$ infection, an intriguing matter would be the possibility of synergistic co-infection or secondary infection of other bacterial species and colonization in the shrimp gut. The biochemical changes of shrimp hepatopancreas during different stages of toxin damage or site colonization by *Vp*$_{\text{AHPND}}$ are also vital for understanding the host-pathogen interaction. The present study aims to provide an insight into the alterations of *P. monodon* gut metagenome and hepatopancreas biochemical activity when challenged with *Vp*$_{\text{AHPND}}$. 16S metagenomic analysis was conducted for both control and infected gut samples. Different bacterial diversity was determined between the control and infected samples. Pathogenic bacterial species potentially involved in co-infection or secondary infection together with *Vp*$_{\text{AHPND}}$ were identified. This assists in understanding host-associated and environment-specific microbial communities influenced by *P. monodon* farming. Biochemical tests including Phenoloxidase (PO) Test, Superoxide Dismutase (SOD) Test, and Nitric Oxide (NO) Test were conducted using challenged shrimp hepatopancreas samples. Statistically significant biochemical activity increments were observed across different post-AHPND infection time points especially in the middle time points (6- and 12- hours post-infection). In conclusion, besides the observation of empty gut, the underlying *P. monodon* gut metagenome and host biochemical response were also affected during *Vp*$_{\text{AHPND}}$ infection.

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The infrastructure, location, and people of the University of New England Marine Science Center (MSC) uniquely position the UNE to address issues of high scientific and economic value in marine and coastal systems.

The assets that make the MSC unique include interdisciplinary inter-agency research programs, high quality seawater facilities, and access to the Saco River and the Gulf of Maine allow the UNE to offer collaborative opportunities to interested researchers. The MSC facility plays an integral role in aquaponics, marine and estuarine research, and instruction.

Assets include a fleet of research vessels: a 23-foot fiberglass Maritime Skiff, an 18-foot fiberglass Carolina Skiff, a 35-foot Marlin fishing vessel and a 30 passenger research landing craft vessel. This fleet of research vessels allows for water access year round and facilitates access to the UNE owned Ram Island, a one-acre island that serves as a 'living laboratory'. In addition, the UNE manages an ocean-based kelp farm just off the coast of campus in Saco Bay. The island and surrounding waters are home to migrating songbirds, harbor seals, gray seals, and various intertidal flora and fauna.

The MSC floor area is 27,550 ft^2 (2560 m^2) with two floors that consists of a flow-through seawater system, classrooms, offices and laboratories. Individual equipment includes a Deep Trekker ROV, a flow cam, and a suite of water quality instruments. Individual rooms include a phytoplankton culture lab, a Macroalgae Nursery and Research Lab, a Recirculating Aquaculture System, a tropical fish and coral growing lab, and an Aquaponics Lab.

DISCOVERY OF GENES AND PATHWAYS RELATED TO REPRODUCTION OF THE BLACK TIGER SHRIMP (*PENAEUS MONODON*) THROUGH TRANSCRIPTOME ANALYSIS

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The black tiger shrimp (*P. monodon*) is a significant aquatic species contributing to global food supply and national economic profit. Poor reproductive maturation in captivity of *P. monodon* has hindered sustainability of the shrimp farmining industry. Eyestalk ablation is still a common practice to induce the maturation of female shrimp. To overcome this problem, genetic knowledge of reproduction is essential. In this study, transcriptomic analysis yielded 25,777 and 26,293 transcripts of ovaries from wild and domesticated shrimp, and 9,598 and 9,775 transcripts of testis from wild and domesticated shrimp, respectively. KEGG pathway mapping showed that most genes in pathways related to reproduction such as oocyte meiosis, progesterone-mediated oocyte maturation and gonadotropin-releasing hormone (GnRH) signalling pathway could be filled. For example, identified genes that are essential for reproduction were *GnRH receptor*, c*alcium voltage-gated channel* and epidermal growth factor recepto. A new a putative *vigillin* encoding for an estrogen–induced polysome-associated protein which has not been reported in penaeid shrimp was also identified. The functional genes and pathways identified here provide a valuable genetic resource for understanding reproduction in *P. monodon*.

CYTOTOXIC RESPONSES TO THE PERFLUORINATED XENOBIOTIC, GENX OF ATP-BINDING CASSETTE PROTEIN AND CELLULAR ACTIVITIES IN *CRASSOSTREA VIRGINICA* HEMOCYTES: IMPLICATIONS FOR GLOBAL CLIMATE CHANGE

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GenX is a perfluorinated compound that has been contaminating the Cape Fear River, NC for over 20 years. When organisms are exposed to GenX, it can enter their cells and cause toxicity. ABC proteins are responsible for removing xenobiotics like GenX from cells; however, when these proteins are inhibited, cellular toxicity increases. This project tested the hypotheses that: 1) GenX will inhibit ABC transporters thus increasing mitochondrial membrane potential, cytotoxicity and hypoxia and 2) incubation of hemolymph at a higher temperature to mimic climate change will cause increased inhibition of ABC transporters, and will cause increased mitochondrial membrane potential, cytotoxicity, and hypoxia. Hemolymph from wild adult oysters was exposed to filtered seawater, a protein inhibitor, Reversine, and two concentrations of the xenobiotic, GenX (1.5µM and 15µM). Samples were incubated in 5 replicates at 21°C, and at 30°C to mimic global climate change. The hemolymph was then exposed to various dyes to determine mitochondrial membrane potential, cytotoxicity, hypoxia, and cell mortality. Samples were analyzed using flowcytometry. Though not statistically significant, mitochondrial membrane potential increased in both GenX treatments compared to the control. When compared with the control, cytotoxicity increased in both GenX treatments. Hypoxia also increased in both GenX treatments, indicating that GenX is inhibiting the function of ABC proteins. While no effects of GenX on hemocyte viability were observed, hemocyte mortality after incubation at 30°C was higher than at 21°C. Cytotoxicity and mitochondrial membrane potential both decreased after incubation temperature was raised while hypoxia increased.

MONITORING PHYSIOLOGICAL CONDITION OF *MYTILUS EDULIS* AND *DONAX VARIABILIS* THROUGH TIME ON THE EASTERN SHORE OF VIRGINIA, USA

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Climate change and its impact on calcifying organisms is presently a vigorous area of study. To assert that climate change is causing significant changes in study organisms, a baseline of organism condition is needed. Furthermore, organism condition needs to be monitored through time, to detect any changes in physiological condition. It is well-documented that the eastern shore of Virginia has been and will continue to experience significant changes in water temperature and carbonate chemistry in the coming years. This study operates under the assumption that water quality changes have a significant effect on bivalve species' condition. The goal of this study is to affirm whether there have been significant changes in the physiological condition of two bivalve species through time and between barrier islands on the Virginia eastern shore. The research questions being answered are as follows: Have there been directional changes in the physiology of *M. edulis* and *D. variabilis*, specifically in shell length and condition index, within the last 13 years? Do these trends vary among islands? To answer these questions, a historical archive containing blue mussels and coquina clam recruits, sampled on Virginia barrier islands from the years 2005-2018 is being used. Condition index and shell height are calculated for bivalve species collected from three islands: Metompkin, Myrtle, and Smith (blue mussels) and Hog, Metompkin, and Wreck (coquina clams). Significant differences were observed in the condition and shell length of mussels and clams in response to variation in water quality among years and islands.

THEORETICAL MORPHOLOGIC ANALYSIS OF THE 'CURL-BACK' HINGE SHELL ABNORMALITY IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*)

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The 'curl-back' shell abnormality, present in many stocks of farm raised eastern oysters, is characterized by a sharp, downward curvature of the right valve and plane of commissure close to the hinge. The trait is undesirable to consumers and can result in extra work on farms or decreases in sales. To better understand the 'curl-back' trait, a group of 3-year-old cultured oysters of wild stock origin were sorted into two groups based on whether or not they exhibited the curl-back hinge trait and crossed amongst each other. The progeny from each of the two four by four crosses (16 families per culture) were grown separately in a common garden experiment, and, in the following year, the crosses were repeated using selected F1s (9 families per culture), resulting in two generations of selection for 'flat' and for 'curled-back' oysters. Comparisons of the relative lengths or heights of right and left valves of 100 four-month-old F2s per group showed that the curl-back trait has a genetic component. To more accurately describe the trait and better visualize the effects of selection, forty eleven-month-old F2s per group were used to estimate the tangent angle of the logarithmic spiral, alpha, of the valves of the shells and these values were plotted in a two-dimensional theoretical morphopspace. Calculated alpha angles of right valves between the two groups were found to be significantly different ($p < 0.0001$), while the differences between left valves, likely due to occlusion, was not as strong ($p = 0.057$).

EFFECTS OF LIVE FEED *PERINEREIS NUNTIA* ON PROSTAGLANDIN BIOSYNTHESIS AND FATTY ACID REGULATORY PATHWAYS IN THE BLACK TIGER SHRIMP, *PENAEUS MONODON*

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The female black tiger shrimp, *Penaeus monodon*, is commonly fed with the polychaete, *Perinereis nuntia*, during larvae production. The large amounts of prostaglandin E_2 (PGE2) in polychaetes are believed to enhance shrimp ovarian development; however, the effects of polychaete feeding on shrimp prostaglandin biosynthesis pathway remained unclear. In this study, *P. monodon* broodstock were fed with feed pellets or polychaetes for four weeks. Unilateral eyestalk ablation was performed to induce ovarian development, revealing that polychaete-fed shrimp reached higher ovarian maturation stages than pellet-fed shrimp. The most prominent effect of shrimp feed was the increases in PGE_2 and prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) levels, which were 15 and 12 times higher in the hepatopancreas of polychaete-fed shrimp than those of pellet-fed shrimp, respectively. Polychaete feeding also increased the transcription levels of *cyclooxygenase* (COX) and *prostaglandin F synthase* in shrimp ovaries. As feed pellets and polychaetes contained different fatty acid composition, the transcription levels of fatty acid regulatory genes were examined. In intact shrimp, higher transcription levels of fatty acid regulatory genes were detected in ovaries of polychaete-fed shrimp compared to those of pellet-fed shrimp while the reverse pattern was observed in the eyestalk-ablated samples. As ovarian maturation progressed, the transcription levels of prostaglandin biosynthesis and fatty acid regulatory genes increased in ovaries but decreased in hepatopancreas. These findings not only provide the first characterization of the prostaglandin biosynthesis and fatty acid regulatory pathways as affected by shrimp feeds, but also reveal the dynamics of these pathways in shrimp ovaries and hepatopancreas during ovarian development.

MICROPLASTICS FROM SELECTED SEAFOOD PRODUCTS OF CENTRAL VISAYAS, PHILIPPINES

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The occurrence of microplastics (MP) in marketed seafood products in the four provinces (Negros Oriental, Siquijor, Cebu, and Bohol) in Central Visayas, Philippines was assessed. Products examined included three species of dried rabbitfish, *Siganus fuscescens* (n=90), sardine, *Sardinella pacifica* (n=120), and scad, *Decapterus* sp.(n=30), fermented anchovies/sprats (n=12), bottled mussel, *Perna viridis* (n=12), and sea urchin, *Tripneustes gratilla,* roe (n=3). A total of 778 microplastic particles were isolated using microscopic examination and hot-needle tests. Microplastics were dominated by fibers and only a few fragments and foams. Quantities of MP from dried fish (2.7-4 particles/fish) and fermented anchovies (1.3-4 particles/25g sample) did not differ significantly between sampling locations. Among samples of bottled mussel, only those from Negros Oriental had microplastics with mean density of 0.3 particles/25g sample. Sea urchin roe samples obtained from Siquijor also tested positive for microplastics (density=1 particle/25g sample), despite having low human population density. Out of the 66 particles subjected to Fourier-Transformed Infrared (FTIR) Spectroscopy, only 24 were identified to specific polymer types (correlation >0.6), dominated by regenerated cellulose (e.g., rayon) followed by alginate, and few particles identified as polyvinyl chloride (PVC) and polyester. These marketed seafood products may have been contaminated by microplastics through ingestion, during processing, and open display in the market. There is a need to quantify microplastics and organic contaminants in other shellfish products (e.g., bottled shrimp pastes) in the Philippine market and refine the processing of these products to minimize exposure to microplastics.

DEVELOPMENT OF CRYOPRESERVATION PROTOCOLS FOR MICROALGAE—*TETRASELMIS STRIATA*

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Microalgae is an essential source of nutrients and lipids for aquaculture of molluscan shellfish, and the industry is dependent on reliable stocks of culture. Over time, microalgae cultures are at risk for contamination, degradation, and mutation. The algal species, *Tetraselmis striata*, is commonly used in aquaculture due to its biochemical composition of high levels of EPA, ARA, and 24-meth sterols, and starches. Cryopreservation of cells at ultra-low temperatures (-196°C) using liquid nitrogen has become a standard for many agriculture and aquaculture species for long-term storage.

The goal of this study is to develop a cryopreservation protocol for *Tetraselmis striata* through systematic evaluations of factors at each cryopreservation procedure. Objectives are to: 1) Identify optimum staining concentration and time of neutral red to label alive cells for accurate determination of cell survival; 2) Estimate the acute toxicity of DMSO, PG, EG, Methanol, and Glycerol as cryoprotectants at concentrations up to 25%, after incubation with fresh cells for up to 2 hours at culture temperature of 22°C on post-thaw survival; 3) Evaluate the effect of varying cooling rates in °C per minute from culture temperature to −40°C in 2-mL cryovials and 0.5-ml straws; 4) Evaluate effects of different thawing temperatures on post-thaw survival; and 5) Verify cryopreservation protocol by cryopreserving multiple cultures of from different stocks. This project is ongoing and anticipated that this study will identify optimal factors throughout the cryopreservation process for *Tetraselmis striata* to advance the process. The results from this study will be useful for the aquaculture production and beyond.

INTERACTIVE INFLUENCES OF DERMO DISEASE AND THE MICROBIOME ON *CRASSOSTREA VIRGINICA* DISEASE SUSCEPTIBILITY AND MICROBIAL DYNAMICS

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The dramatic impact of Dermo disease on eastern oysters warrants a better understanding of factors contributing to infection susceptibility, resistance and tolerance. Recent studies of the oyster microbiome suggest that the bacterial community living on and within oysters plays an important role in health akin to other organisms. This study explored how the bacterial fraction of the oyster microbiome influences oyster susceptibility, resistance and tolerance to infection. In a factorial experiment, wild oysters were dosed or not with antibiotics and/or *in vitro* cultured *Perkinsus marinus* over a five-week period. Weekly hemolymph withdrawals as well as end-point dissected tissues were analyzed via Ray's fluid thioglycollate medium (RFTM) assays and 16S rRNA sequencing. Dermo infections varied among challenged oysters with a significant difference between groups with intact and perturbed microbiomes. The natural microbiota appears to have exacerbated Dermo disease, resulting in an improved resistance among oysters with perturbed microbiota. Future experiments may help elucidate the curious microbial dynamics underpinning these findings.

A NOVEL INTRIGUING MOLECULAR MECHANISM OF RESPONSE TO TRANSITION METALS IN DIVERSE ENVIRONMENTS

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Reverse-transcriptase related (*rvt*) genes represent a remarkable class of reverse transcriptases (RT) found in bacteria, fungi, protists, plants and invertebrates from aquatic and soil-dwelling environments. These are cellular single-copy genes, which are preserved by natural selection. Their occurrence in prokaryotic and eukaryotic representatives, previously unknown for any RT, suggests a conserved biological function that is applicable to both prokaryotes and eukaryotes.

The RVT proteins from filamentous gliding bacterium, *Herpetosiphon aurantiacus*, and the ascomycete fungus, *Neurospora crassa*, display a peculiar property of initiating polymerization via protein priming, which is abolished by site-directed mutagenesis of the catalytic aspartate in the RT domain. Thus, RVT represent the first known case of protein-primed RT encoded by a chromosomal non-selfish gene. Also, the N-terminal coiled-coil domain allows RVT proteins to form multimers and could be a good candidate for interacting with metal ions, such as Ni^{2+}, Co2+, Fe^{2+}, Cu^{2+}, Zn^{2+}, etc. This is important because most free-living organisms can be frequently exposed to transition metals and may therefore need potent mechanisms to cope with such stresses. In addition to the well-known general stress response mechanisms (eg. heat shock proteins), there may be additional systems to alleviate transition metal-induced stresses. It is of special interest to uncover an ancient molecular mechanism which is common to different Kingdoms and operates in environments which may be contaminated by hazardous pollutants.

ESTABLISHMENT OF IMMUNOLOGICAL ASSAYS OF HEMOCYTES IN NORTHERN QUAHOGS, *MERCENARIA MERCENARIA*

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Aquaculture of the northern quahogs, *Mercenaria mercenaria* is a $65 million industry in the U. S. Often, environmental stresses, such as such as the hot summers in Florida and harmful algal bloom, affects this industry greatly. Molluscan bivalves are poikilothermic with open circulatory system and hemocytes can function as multiple-purpose defense system through inmate immune responses to protect host against natural environmental stresses, diseases, and toxins.

The goal of this study was to establish immunological assays of hemocytes in the northern quahog (= hard clam) by use of flow cytometry for evaluation of environmental and disease stresses. The objectives are: 1) develop a non-lethal method for hemocyte sampling from the hard clams and determine the pH and osmolality of hemolymph; 2) measure the hemocyte size and classify cell types through microscopic observation after making slides and staining with Wright – Giemsa (Camco Quik Stain® II); 3) evaluate hemocyte viability and morphology with fluorescent stains of SYBR Green and propidium iodide and compared with that recorded through microscope observation, of different types through microscopic observation flow cytometry; 4) develop methodologies for hemocyte phagocytosis with artificial 2-um fluorescent beads and ROS with specific staining of cell permeant reagent 2’,7’ –dichlorofluorescin diacetate (DCFDA), a fluorogenic dye that measures reactive oxygen species (ROS) activity within the cell; and 5) develop non-lethal methodologies for hemocyte collection for these immunoassays. It is expected that the assays to be established in current study will be applied to further investigation of hard clam immunological responses to environmental and disease stresses.

MENDOCINO COLLEGE COASTAL FIELD STATION

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The Mendocino College Coastal Field Station near Point Arena, about 150 miles north of San Francisco, is a 15-acre property with cliffs that overlook the Pacific Ocean and with access to the intertidal zone of a relatively protected cove. The site, surrounded by the California Coastal National Monument, provides unique opportunities for studying marine life, coastal prairie flora, and the geological features which abound.

The facility was created in 1981 when the US government transferred the former Coast Guard facility to Mendocino College. The facility offers dorm houses with kitchen amenities and beds to comfortably accommodate about 20 guests at a time. On site is an education building with space for class meetings and a dry lab room.

Mendocino College students visit the field station as part of courses such as Environmental Science, Botany, Zoology, and Marine Biology. Students have established vegetation plots and participate in intertidal zone transect surveys, plankton surveys, and other experiential opportunities.

When Mendocino students are not utilizing the station, the facility is used by university classes such as UC Berkeley Jepson Herbarium, CSU East Bay, and the UC Field Ecology Supercourse. It has also been a base for researchers from Humboldt State and UC Santa Cruz, as well as non-profit organizations such as ReefCheck California. In addition, the facility hosts research equipment of UC Davis (monitoring coastal currents) and UNAVCO (GPS ground motion). With our current nominal fee structure, the facility is a great choice in a unique location for research and educational activities.

INVESTIGATING THE EFFECTS OF COASTAL STRESSORS ON THE GENOMIC VARIATION OF OYSTER POPULATIONS IN NARRAGANSETT BAY, RHODE ISLAND, USA

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Coastal environments are characterized by the presence of multiple stressors that may be occurring simultaneously and linked through biological processes. These stressors can have negative effects on the survival and development of important coastal species like the eastern oyster, *Crassostrea virginica*. Oysters have a sessile adult stage with low dispersal potential making them dependent on their pelagic larval stage for long-distance dispersal to increase gene flow across populations. Larvae are more sensitive than adults to a variety of natural and anthropogenic stressors making them a natural conduit for adaptation to environmental stressors. Multiple co-occurring coastal stressors may act as barriers to gene flow, limiting larval exchange by selective mortality (only letting resistant larvae pass), structuring populations through reduced connectivity. To investigate the effects of coastal stressors on the genomic variation of oyster populations, adult oysters were collected from multiple sites in Narragansett Bay varying in environmental conditions, including dissolved oxygen, pH, and sewage effluent. Sequence capture probes were generated from mRNA extracted from larval oysters exposed to coastal stressor treatments. These probes were used to capture regions of the adult genome highly expressed in response to these stressors. Population and seascape genomic analyses revealed high genetic differentiation of oysters from a site characterized by low salinity and higher temperatures compared to the other populations. Sampling of additional oyster populations within Narragansett Bay and collecting more long-term environmental data will further reveal how coastal stressors shape the genomic variation of oyster populations in Narragansett Bay.

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