National Shellfisheries Association

Program and Abstracts
of the
118th Annual Meeting

March 22–26, 2026
Portland, Oregon

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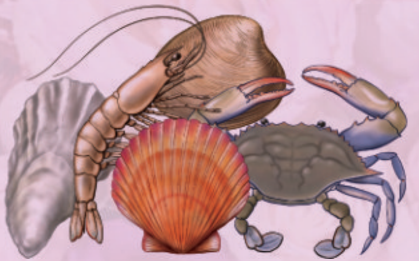

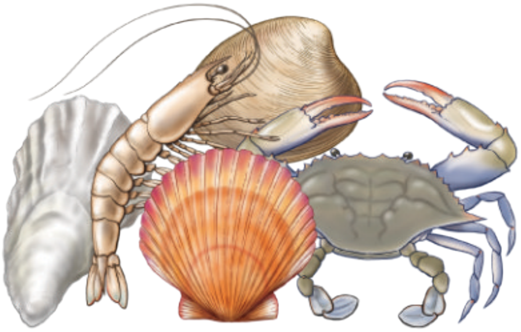

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NSA 118th ANNUAL MEETING
National Shellfisheries Association
Marriott Portland Downtown Waterfront - Portland, Oregon
March 22-26, 2026

SUNDAY, MARCH 22, 2026

6:30 PM	STUDENT ORIENTATION Mount Hood/Mt. Saint Helen Foyer
7:00 PM	PRESIDENT'S RECEPTION Mount Hood/Mt. Saint Helen

MONDAY, MARCH 23, 2026

6:30-7:45 AM	STUDENT MENTOR-MENTEE BREAKFAST (NSA student members only – advanced sign-up required) Mt. Saint Helen				
8:00-8:50 AM	PLENARY LECTURE: Madonna Moss (University of Oregon) Salon G/H/I				
ALL DAY	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS Salon A				
	Salon H	Salon G	Salon I	Salon D	Salon B
9:15-10:30 AM		REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP) WORKSHOP	OYSTERS I	NASA AQUACULTURE WORKSHOP	ONE HEALTH EPIGENOMES & MICROBIOMES
10:30-11:00 AM	MORNING BREAK				
11:00-12:30 AM		DOWN ON THE FARM	BIVALVE HATCHERY HEALTH CONSORTIUM	NASA AQUACULTURE WORKSHOP	ONE HEALTH EPIGENOMES & MICROBIOMES
12:30-1:30 PM	LUNCH BREAK				
1:30-2:30 PM	HARMFUL ALGAL BLOOMS	SHELLFISH RESTORATION & CONSERVATION	COMMERCIAL SHELLFISHERIES	ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS	ONE HEALTH EPIGENOMES & MICROBIOMES
2:30-3:00 PM	GENERAL CONTRIBUTED I	SHELLFISH RESTORATION & CONSERVATION	COMMERCIAL SHELLFISHERIES	ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS	ONE HEALTH EPIGENOMES & MICROBIOMES
3:00-3:30 PM	AFTERNOON BREAK				
3:30-5:00 PM	GENERAL CONTRIBUTED I	SHELLFISH RESTORATION & CONSERVATION	GENERAL CONTRIBUTED II	ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS	ONE HEALTH EPIGENOMES & MICROBIOMES

TUESDAY, MARCH 24, 2026

8:00-8:50 AM	PLENARY LECTURE: Robert Rheault (East Coast Shellfish Growers Association) Salon G/H/I				
ALL DAY	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS Salon A				
	Salon I	Salon G	Salon H	Salon D	Salon B
9:15-10:30 AM	OYSTERS II	SHELLFISH AND THEIR (GOOD & BAD) MICROBES	RIBBED MUSSELS		MANGROVE SHELLFISH
10:30-11:00 AM	MORNING BREAK				
11:00-11:45 AM	OYSTERS II	BIVALVE DISEASE	ANTHROPOGENIC CONTAMINANTS		MANGROVE SHELLFISH
11:45 AM-12:30 PM	OYSTERS II	BIVALVE DISEASE	ANTHROPOGENIC CONTAMINANTS		MANGROVE SHELLFISH
12:30-1:30 PM	LUNCH BREAK				
1:30-3:00 PM	OYSTERS II	OSHV-1	GREEN CRABS	GASTROPODS	MANGROVE SHELLFISH
3:00-4:00 PM	OYSTERS II	SUMMER MORTALITY	GREEN CRABS	GASTROPODS	MANGROVE SHELLFISH
4:00-6:00 PM	POSTER SESSION AND HAPPY HOUR Salon E/F				
7:00–10:00 PM	STUDENT ENDOWMENT FUND AUCTION Exhibit Hall Lower Level 2				

WEDNESDAY, MARCH 25, 2026

8:00-8:50 AM	PLENARY LECTURE: Chris Langdon (Oregon State University) Salon G/H/I			
ALL DAY	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS Salon A			
	Salon G	Salon H	Salon C	Salon I
9:00-10:30 AM	VIBRIO	WILD SHELLFISHERIES	NOAA GRANT WRITING WORKSHOP	AQUACULTURE EDUCATION, EXTENSION & INFORMATION TRANSFER
10:30-11:00 AM	MORNING BREAK			
11:00-12:30 PM	BIRDS & SHELLFISH SANITATION	WILD SHELLFISHERIES	NOAA GRANT WRITING WORKSHOP	AQUACULTURE EDUCATION, EXTENSION & INFORMATION TRANSFER
12:30-2:00 PM	NSA BUSINESS LUNCHEON Exhibit Hall Lower Level 2			
2:00-5:00 PM	Gyotaku Workshop (fish print art) – Bruce Koike (advanced sign-up required - additional fee) Salon D			
2:30-4:30 PM	SCALLOP GALLOP 5K RUN/WALK EXPLORE PORTLAND!!			
4:30-6:00 PM	POSTER SESSION AND HAPPY HOUR Salon E/F			

THURSDAY, MARCH 26, 2026

	Salon I	Salon G	Salon H	Salon B
8:00-8:50 AM	PLENARY LECTURE: Andrew Suhrbier (Pacific Shellfish Institute) Salon G/H/I			
ALL DAY	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS Salon A			
9:00-10:15 AM	SHELLFISH GENETICS/GENOMICS	ADVANCES IN HATCHERY TECHNOLOGY	CLAMS	SHRIMP ENCODE
10:15-10:45 AM	MORNING BREAK			
10:45-11:30 AM	SHELLFISH GENETICS/GENOMICS	ADVANCES IN HATCHERY TECHNOLOGY	CLAMS	SHRIMP ENCODE
11:30 AM-12:00 PM	SHELLFISH GENETICS/GENOMICS	ADVANCES IN HATCHERY TECHNOLOGY		SHRIMP ENCODE
12:00-1:00 PM	LUNCH BREAK			
1:00-3:30 PM	SHELLFISH GENETICS/GENOMICS	SEAWEED-BIVALVE CO-CULTIVATION	SOCIAL-ECOLOGICAL SYSTEMS	SHRIMP ENCODE
3:30-5:00 PM	CLOSING HAPPY HOUR Salon E/F			

POSTERS and All BREAKS are in Salon E/F.

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

PLEASE REMOVE YOUR POSTERS BY NOON ON THURSDAY

MONDAY
March 23, 2026

6:30-7:45AM	**STUDENT MENTOR-MENTEE BREAKFAST (NSA STUDENT MEMBERS ONLY – *Advanced sign-up is required*)** **Mt. Saint Helen**			
8:00-8:50 AM	**PLENARY: Madonna Moss (University of Oregon) - *The archaeology of indigenous shellfisheries on the northwest coast of North America*** **Salon G/H/I**			
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Salon A**			
ROOM	**Salon D**	**Salon G**	**Salon I**	**Salon B**
SESSION TITLE	**NASA AQUACULTURE WORKSHOP** **Erin Urquhart, Kelly Luis, Melanie Cook & Amita Mehta**	**REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM (RSSBP) WORKSHOP: WEST COAST SHELLFISH SEED BIOSECURITY STATUS AND NEEDS** **David Bushek**	**OYSTERS I** **Bill Fisher & Jessica Pruett**	**ONE HEALTH EPIGENOMES & MICROBIOMES** **Acacia Alcivar-Warren**
9:15 AM	This 3-hour introductory workshop will provide an overview of NASA remote sensing data and its applications in supporting shellfishery activities in both marine and freshwater environments. Participants will be introduced to remote sensing observations from multiple satellites that offer frequent and enhanced spatial coverage of coastal and freshwater areas for monitoring algal blooms. No prior knowledge or experience in remote sensing is required to attend this training. Attendees should bring their laptops to participate in provided hands-on exercises. Click here to register	This workshop aims to identify and prioritize the key steps, considerations, and prerequisites needed to support potential expansion of the RSSBP to the Pacific Coast. Topics include assessment of regional disease profiles, evaluation of existing state and federal regulatory frameworks, alignment with tribal authorities, and identification of data gaps in shellfish health monitoring.	Shell color and pattern variation in the eastern oyster, *Crassostrea virginica*: insights for selective breeding **O'Hala*, Ratcliff, Jamieson, Coyne, Guo**	ONE HEALTH epigenomes and microbiomes: from soil to people - recognition to students and "Outstanding ONE HEALTH Researchers in Fisheries and Aquaculture" awardees **Alcivar-Warren, DeWitt**
9:30 AM			Genotype x environment x ploidy interactions impact the performance of Pacific oysters in aquaculture **Norrie, Busch, Chang, Davis, Dockery, Jackson, Legros, McElhany, Sorren, Padilla-Gamiño**	Microplastics and molluscs – a brief overview of a flawed field **Shumway, Ward, Mladinich, Holohan, Blaschik**
9:45 AM			The impact of feeding and feeding delay on larval eastern oysters (*Crassostrea virginica*) **Griffith, Salimeno**	One Health, EcoHealth, Planetary Health: New definitions for a sustainable and healthy future for all by conserving healthy mangroves and shellfish to protect human health **Alcivar-Warren, DeWitt, Puttock, Rico, Jorquera, Valenzuela**
10:00 AM			Evaluating conservation aquaculture for Olympia oyster restoration in Morro Bay, California **Baldwin, Johnson**	Unraveling the mystery of the mechanism by which feeding beneficial microorganisms to shrimp reduces mortality from microbial infections **Hirono**
10:15 AM			Aquaculture feasibility in Fort Bragg, California, USA **Miller, Johnson^{P}, Gardner**	
10:30-11:00 AM	**MORNING BREAK**			
SESSION TITLE	**NASA AQUACULTURE WORKSHOP** **Erin Urquhart, Kelly Luis, Melanie Cook & Amita Mehta**	**DOWN ON THE FARM** **Alex Marquardt & Kevin Marquez**	**BIVALVE HATCHERY HEALTH CONSORTIUM** **Marta Gomez-Chiarri & Robbie Hudson**	**ONE HEALTH EPIGENOMES & MICROBIOMES** **Acacia Alcivar-Warren**
11:00 AM		Coordinated multi-estuary farm trials to further understanding of Pacific oyster performance and survival in California and Washington **Johnson, Fleener, Panneno, Villarete, Hill, Tweet, Carrion, Ng, Hanshaw, Hardy**	The objectives of this interactive workshop are to: 1) share lessons learned from the BHHC enrollment and sampling process; 2) report findings from the 2024 sampling season, 3) engage participants in interpreting the data collected so far, and 4) discuss further steps. Members of the BHHC coordinating team, including pathologists, ecologists, hatchery managers, and extension specialists, will answer questions and gather feedback from those interested in the program on how to address this critical issue of larval crashes.	Some advances on the characterization of microbial communities in aquatic ecosystems of southern Chile **Jorquera**
11:15 AM		Pilot testing the timing and effectiveness of tidal exposure and two dip treatments for control of shell pests in cultured oysters **Hutchinson, Archer, Reitsma**		
11:30 AM		Immobilization of burrowing shrimp (*Neotrypaea californiensis*) via subsurface sediment vibration as a pest control strategy for shellfish farms **Trimble, Ruesink^{P}**		Evaluation of the combined effects of ammonia and nitrite on the survival and growth of juvenile Pacific white shrimp, *Penaeus vannamei* **Ishimwe*, Chhetri, Ray**
11:45 AM		Drones for sustainable shellfish farm management **Houle**		Biological aspects that enhance the growth of the pathogen bacterium, *Vibrio parahaemolyticus* **Vargas-Aguilar, Chavarín-Meza, Caña-Bozada, Soto-Rodríguez, Gomez-Gil**
12:00 NOON		Ecological interactions of shellfish aquaculture in Puget Sound nearshore habitats and a review of relevant tools, models, and calculators **McDowell, Kiffney, Sanderson**		Trained immunity and immune priming in plants (mangroves) and invertebrates (shellfish) **Arteaga-Cordero*, Alcivar-Warren, Alcivar-Herrera, Romero-Arteaga, Arteaga-Cedeno, Alcivar-Arteaga**
12:15 PM		Washington and Oregon shellfish aquaculture permitting guides **King**		
12:30-1:30 PM	**LUNCH BREAK**			

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

MONDAY March 23, 2026					
NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Salon A**					
ROOM	**Salon H**	**Salon G**	**Salon D**	**Salon I**	**Salon B**
SESSION TITLE	**HARMFUL ALGAL BLOOMS** **Steve Morton**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS WORKSHOP** **Eric Heupel**	**COMMERCIAL SHELLFISHERIES** **David Rudders & Kevin Stokesbury**	**ONE HEALTH EPIGENOMES & MICROBIOMES** **Acacia Alcivar-Warren**
1:30 PM	Differentiation of microbial communities in coastal waters during harmful algal blooms in Chile **Jorquera**	Recruitment rhythms: understanding spatial and temporal variability in the eastern oyster, *Crassostrea virginica*, recruitment in South Carolina, USA **Mitchell, Faulk, Sundin, Hawk, Kingsley-Smith**	As scientists and researchers, we all have two jobs – do the science and communicate the science. We receive a great deal of training (and build experience) to conduct research and innovate, but - except for journal publications - little to no training in communicating our science. Join Eric (a scientist and scientific illustrator/communicator) for tips on becoming a more effective visual communicator followed by an "Ask Me Anything" session.	Understanding long-term change in the Atlantic bay scallop fishery **Tomasetti, Novara**	Community Action for Fresh Water (CAFW): A Rotary International and United Nations Environment Program (UNEP) initiative to restore, protect, and sustain freshwater ecosystems **Rico**
1:45 PM	Behavioral changes in larval eastern oysters (*Crassostrea virginica*) when exposed to the dinoflagellate, *Margalefidinium polykrikoides* **Scro, Collins, Brosnahan, Chamberlin, Sharon, Scott, Smolowitz**	Thinking outside the shell: alternative methods and materials to accelerate and expand oyster restoration in South Carolina **Hollis, Czwartacki, Hodges, Sommers, Swain, Sundin, and Ownby-Connolly**		The peculiar case of the Virginia "conch": challenges confronting a small-scale commercial fishery **Jackson***	
2:00 PM	Marine biotoxin depuration rates: management applications, research priorities, and predictions for unstudied species **Free, Fang**	Increasing coastal resiliency around South Fenwick Island, South Carolina, USA: A case study of eastern oyster reef restoration **Kingsley-Smith, Sundin, Faulk, Mitchell, Hodges, Hollis, Sanger**		Partnership for Research Excellence in Sustainable Seafood (PRESS): lessons learned **Gomez-Chiarri, Cygler, Hudson**	Effects of antifoulant Irgarol 1051 and microplastics on the attachment performance of thick-shelled mussels (*Mytilus coruscus*) **Pan*, Hu, Wang**
2:15 PM	Participatory science approach to monitor harmful algal blooms, water quality, and changes in environmental conditions with the aquaculture industry **Morton, Shuler**	Mansions in the marsh: monitoring the performance of Oyster Castles® in coastal South Carolina, USA **Faulk, Sundin, Mitchell, Hawk, Fly, Pehl, Kingsley-Smith**		Engaging commercial fishermen to advance knowledge of Atlantic sea scallop physiology and recruitment events **Smoak, Bethoney**	Disruption of the gill-gut-hemolymph axis in thick-shelled mussels (*Mytilus coruscus*) induced by co-exposure to polystyrene microplastics and di(2-ethylhexyl) phthalate **Gao*, Pang, Hu, Wang**
SESSION TITLE	**GENERAL CONTRIBUTED I** **Stephen Tomasetti**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS WORKSHOP** **Eric Heupel**	**COMMERCIAL SHELLFISHERIES** **David Rudders & Kevin Stokesbury**	**ONE HEALTH EPIGENOMES & MICROBIOMES** **Acacia Alcivar-Warren**
2:30 PM	Timing is everything: energetic tradeoff with early gonad development with ocean acidification **Padilla, McFarland, Gurr, Bernatchez, Dixon, Keith, Mayo, Milke, Novara, Poach, Hart, Plough, Redman, Sennefelder, Stiles, Veilleux, Anderson, Wikfors, Meseck**	Performance of subtidal and intertidal alternative reefs at Naval Weapons Station Yorktown, Virginia **Seitz, Burke, Knick, Saluta, Seebo, Smith, Lipcius**		Development of a GRTS survey approach for the VIMS sea scallop dredge survey **Roman, Rudders**	Epigenetic-like regulators shape strain-level differences in *Vibrio parahaemolyticus* AHPND pathogenicity **Bermudez*, Yuasa, Mwamburi, Guzman, Homsombat, Konishi, Nozaki, Kondo, Hirono, Koiwai**
2:45 PM	Mothers know best: maternal signaling boosts larval resilience under ocean acidification conditions **Timmins-Schiffman, Root, Crim, Middleton, Ewing, Winnikoff, Ham, Goetz, Roberts, Gavery**	Habitat use of artificial oyster reefs by crabs, fish, and diamondback terrapin: Performance and analysis of a novel video technique in turbid waters **Lipcius, Seitz, Burke, Knick, Saluta, Seebo, Smith**			Epigenetic mechanisms of crustaceans and molluscs from marine and freshwater ecosystems under environmental stress: A One Health approach **Rosas-Anaya*, Yepiz-Plascencia, Alcivar-Warren**
3:00 – 3:30 PM	**AFTERNOON BREAK**				
SESSION TITLE	**GENERAL CONTRIBUTED I** **Stephen Tomasetti**	**SHELLFISH RESTORATION & CONSERVATION** **Peter Kingsley-Smith**	**ART & DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS WORKSHOP** **Eric Heupel**	**GENERAL CONTRIBUTED II** **Eric Schott**	**ONE HEALTH EPIGENOMES & MICROBIOMES** **Acacia Alcivar-Warren**
3:30 PM	Physiological responses of *Mytilus edulis* to single and recurrent heatwave events **Chilvers*, Del Valle, Ignatz, Perron, Filgueira**	Does Olympia oyster, *Ostrea lurida*, restoration impact community composition and juvenile salmon prey? **Barber, McKeegan, Cordell, Grossman, Harrington, Hunter, LeMoine, McArdle**		Oyster restoration and blue carbon: Leveraging oyster reef ecosystem services for salt marsh conservation **Czoer*, Boydstun, Medders, Brinton, Carroll**	Antioxidant system and oxidative stress responses in shrimp under environmental changes **Yepiz-Plascencia**
3:45 PM	Shellfish Sensitivity Index: A sustainability tool for estuaries facing low oxygen and warming **Novara*, Gobler, Tomasetti**	Moving beyond the baseline: oysters as a performance metric for the Comprehensive Everglades Restoration Plan **Geiger, Levine, Kirby**		Safeguarding a resilient tribal Dungeness crab fishery through improved biological monitoring and adaptive management **Gately, Tobin, Buckner, Sund, Bosley**	
4:00 PM	Assessing the thermal tolerance of Atlantic sea scallop (*Placopecten magellanicus*) early life stages **Easton*, Houston, Beal, Cowles, Stokesbury, Zavell**	Field evaluation of eastern oysters (*Crassostrea virginica*) genomically selected for enhanced dermo resilience and growth **Williams*, Rikard, Casas, La Peyre, Ngo, Wang, Coyne, Guo, Tarnecki, Bushek**		Analysis of new size-length models for the sea cucumber, *Apostichopus californicus*, and their effectiveness in a management context **Vetak**	Citizen science approach to mitigate the effects of harmful algal blooms in Costa Rica **Morton, Vanopdenbosch, Shumway**
4:15 PM	Describing the identity and impacts of shell blister in Atlantic sea scallops **Miller*, Rudders, McDowell, Roman**	Direct setting of eastern oyster larvae (*Crassostrea virginica*) in Mississippi coastal waters **Schweiss, Spires, Russell**		Suspension-feeders to clear the waters in urban estuaries **Schott, Kido, Casagrande, Mansfield**	The Environmental Sustainability Rotary Action Group (ESRAG): Helping to implement sustainable practices on biodiversity, circular economy, food systems, sustainability, climate, and pollution **DeWitt**
4:30 PM	The multiple stressors of a multiple-stressor system: engineering a budget-conscious experimental system **Hainey*, Jennings, Bauer, Langdon**	Widespread demographic supplementation of Connecticut wild oysters by aquaculture farms **Chen, Getchis, Hart, Proestou, Hare^{p}**		Boring into benthic fluxes: in situ measurements of pumping and organic matter processing by a rock-boring bivalve **Ray*, Miller**	How to write effective global grants to apply for funding for your project by Rotary International **DeWitt, Puttock, Rico**
4:45 PM		Hurricane impacts on water quality and oyster reef habitat in a large, wind-driven estuary **Bowling, Caretti, Eggleston^{p}**			

* denotes student presenter

^{p} denotes non first-author presenter

	TUESDAY **March 24, 2026**			
8:00-8:50 AM	**PLENARY: Robert Rheault (East Coast Shellfish Growers Assocation) – *Shellfish farming, obstacles, and opportunities*** **Salon G/H/I**			
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY **Salon A**			
ROOM	**Salon I**	**Salon G**	**Salon H**	**Salon B**
SESSION TITLE	**OYSTERS II** **Bill Fisher & Jessica Pruett**	**SHELLFISH & THEIR (GOOD & BAD) MICROBES** **Steph Smith**	**RIBBED MUSSELS** **Michael Acquafredda**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren** **& Caroline DeWitt**
9:15 AM	Genetic tracking of oyster spat on a restoration site **Wilcox*, Plough, North**	Oyster microbiome insights: exploring relationships between bacterial communities and host health metrics **Colacicco*, Brunelle, Kim, Tracy**	The Ribbed Mussel Aquaculture Collaborative (RMAC) **Acquafredda, Towers, Gilpin, Zarnoch, Green-Beach, Sclafani, Udelson, Caroussos**	Mangrove Shellfish session: From carbon storage to epigenetics - recognition to students and "2026 Outstanding ONE HEALTH Researchers in Fisheries and Aquaculture" awardees **Alcivar-Warren, DeWitt^{p}**
9:30 AM	Assessing restoration of the Olympia oyster in Sequim Bay, Washington **Raymond, Burns, Harrington, Mahan, Tobin**	Microbiomes under stress – Tolerance of the blue mussel (*Mytilus edulis*) and its gut microbiome to toxic pharmaceutical exposure **Naik, Holohan, Nyholm, Ward**	Advancing ribbed mussel (*Geukensia demissa*) spawning protocols to accelerate commercialization and meet growing demand **Towers, Gilpin, Acquafredda**	Pesticides, ecosystems pollution, shellfish, environmental health, and planetary boundaries - an urgent challenge **Alcivar-Herrera*, Alcivar-Warren, Romero-Arteaga, Arteaga-Cedeno, Arteaga-Cordero, Alcivar-Arteaga**
9:45 AM	Oyster reef building success on alternative restoration substrate in a high salinity estuary **Kirby, Geiger**	Probiotic strategies to mitigate bacterial-induced mortalities of Pacific oyster larvae: insights from hatchery trials **Thorstenson, Barton, Schubiger, Mueller, Langdon**	Ribbed mussel (*Geukensia demissa*) aquaculture techniques: investigating an alternative diet **Barrett, Towers, Acquafredda^{p}**	Restoring clean water to the Chesapeake Bay 2012-2025: Rotary oyster reef at St. Mary's River, Maryland **Puttock**
10:00 AM	Adaptive management in the face of uncertainty: Lessons learned from a native oyster, *Ostrea lurida*, restoration project in the Salish Sea **McArdle, Barber, Grossman**	Multi-strain probiotic cocktail improves bivalve larval survival against pathogens **Samson*, Quay, Rowley, Gomez-Chiarri**	From plankton to population: linking settlement, recruitment, and community assembly in a key salt marsh species **Anderson*, Padilla**	Acute Hepatopancreatic Necrosis Disease (AHPND): an outcome of *Vibrio parahaemolyticus* niche colonization **Victorio-De los Santos*, Gutiérrez-Franco, Alvarado-Verdin, Venegas-de la Paz Pérez, Soto-Díaz, Vázquez-Reyes, Ayón-Pérez, Rodríguez-Ocampo, Ramos-Ramírez, Golzález-Reyes, Cano-Sánchez**
10:15 AM	Development of a habitat suitability model for the eastern oyster (*Crassostrea virginica*) in Florida estuaries **Levine**		Ribbed mussels at the edge: surviving (but not thriving) in living shorelines **Rose*, Bilkovic, Isdell**	
10:30-11:00 AM	**MORNING BREAK**			
SESSION TITLE	**OYSTERS II** **Bill Fisher & Jessica Pruett**	**BIVALVE DISEASE** **Marta Gomez-Chiarri, Tal Ben-Horin** **& Steph Smith**	**ANTHROPOGENIC CONTAMINANTS & THEIR INTERACTIONS & IMPACTS ON SHELLFISH BIOLOGY & ECOLOGY** **Evan Ward & Anne Gilewski**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren** **& Caroline DeWitt**
11:00 AM	Reduced water flow and increased stocking density exacerbate hypoxia risk in oysters **Leuchtenberger*, Carrington**	Tracking seasonal oyster mortality and MSX disease prevalence in the eastern oyster, *Crassostrea virginica*, in the Maryland portion of the Chesapeake Bay from 2023 to 2025 **Preziosi**	Ingestion and egestion of cryo-milled tire tread particles by oysters (*Crassostrea virginica*) and mussels (*Mytilus edulis*) **Gilewski*, Holohan, Shumway, Ward**	Cesium-137 and microplastics: potential health risks to shellfish and other marine life **Arteaga-Cordero*, Alcivar-Arteaga, Alcivar-Herrera, Romero-Arteaga, Arteaga-Cedeno, Alcivar-Warren**
11:15 AM	Transcriptomic responses to temperature and oxygen in two populations of Olympia oysters **BuyanUrt*, Hollister, Hardy, Johnson**	Two decades of parasitism trends in Connecticut oysters **Bienlien, Carey**	Size-based ingestion of microspheres and microfibers by two freshwater mussel species (*Dreissena bugensis* and *Elliptio complanata*): Implications for removal of microplastic pollution **Collins*, Olatunji, Shor, Ward**	Environmental quality of mangroves in the northern Ecuadorian coast **Rebolledo-Monsalve**
11:30 AM	Molecular signatures of resilience: Evaluating stress priming in juvenile eastern oysters (*Crassostrea virginica*) using heat shock protein 70 expression **Fowler*, Gray, Plough**	Comparative thermal responses of *Perkinsus marinus* isolates from the Gulf of Saint Lawrence, Canada, and the Gulf of Mexico, USA **Johnson*, Casas, La Peyre, Filgueira**	Disruption of the gill-gut-hemolymph axis in thick-shelled mussels (*Mytilus coruscus*) induced by co-exposure to polystyrene microplastics and di(2-ethylhexyl) phthalate **Gao*, Pang, Hu, Wang**	The Galapagos mangroves of Ecuador are in danger despite conservation efforts **Romero-Arteaga*, Alcivar-Arteaga, Alcivar-Herrera, Arteaga-Cedeno, Arteaga-Cordero, Alcivar-Warren**
11:45 AM	Comparative analysis of mitochondrial activity in triploid and diploid oysters **Feole*, La Peyre, Rikard, Allam**	High resolution environmental surveillance contextualizes molecular signals to reveal microbial dynamics during oyster disease outbreak **Ciesielski, Schubert, Noble, Ben-Horin**	Effects of antifoulant Irgarol 1051 and microplastics on the attachment performance of thick-shelled mussels (*Mytilus coruscus*) **Pan*, Hu, Wang**	The Mangrove Epigenome (MangroveENCODE) project of the FUCOBI Foundation of Ecuador: A ONE HEALTH approach to conserving mangroves biodiversity and avoid climate disaster **Arteaga-Cedeno*, Alcivar-Arteaga, Alcivar-Herrera, Arteaga-Cordero, Romero-Arteaga, Rodriguez-Flores, Alcivar-Warren**
12:00 NOON	Establishing baseline immune parameters to investigate Sudden Unusual Mortality Syndrome (SUMS) in eastern oysters (*Crassostrea virginica*) **Handley, Tarnecki**	Immune priming defense across distinct life stages in eastern oysters (*Crassostrea virginica*) **Calhoun, Gomez-Chiarri**	Bioindicators of microplastics: Are bivalves the best choice? (Spoiler, they are not) **Mladinich, Holohan, Shumway, Ward^{p}**	Bioprospecting mangrove microbiomes: identification of bacterial strains capable of tumor cell inhibition and bioremediation **Pileggi**
12:15 PM	Inducible defenses in oysters: how age, size, and predator exposure shape physiological and transcriptomic responses **Barry*, Bushek, Guo**		Persistence of the pathogen, *Vibrio parahaemolyticus*, on microplastic surfaces and transmission into the Pacific oyster **Wiggin, Allard, Gilbert**	
12:30-1:30 PM	**LUNCH BREAK**			

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

TUESDAY
March 24, 2026

NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Salon A

ROOM	Salon I	Salon G	Salon H	Salon D	Salon B
SESSION TITLE	**OYSTERS II** **Bill Fisher & Jessica Pruett**	**OsHV-1** **Colleen Burge & Don Webster**	**GREEN CRABS** **Brian Beal & Sylvia Yamada**	**GASTROPODS** **Max Zavell & Dianna Padilla**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren & Caroline DeWitt**
1:30 PM	Pathogenic *Vibrio* monitoring in shellfish farms in Maryland and Delaware and development of colorimetric method for pathogenic *Vibrio* detection **Ozbay, Parveen, Parsaeimehr**	Monitoring for OsHV-1 in juvenile Pacific oysters on the U.S. West Coast **Burge, Prado-Zapata, Evans, Garcia, Dumbauld**	Green crab recruitment dynamics in the soft-bottom intertidal along the Maine coast (2020-2025) **Beal, Houston, Randall, Greene**	Consequences of differing maturity definitions on management regulations for a gastropod fishery **Zavell, Calabrese, Delargy, Merhoff, Morgan, Painten, Shumway, Wachala, Stokesbury**	A transposable element–epigenetics One Health perspective to understand antimicrobial resistance and contamination by pesticides acting as endocrine disrupting chemicals, glyphosate, metals-biocides, microplastics, bisphenol A, bis(2-ethylhexyl) phthalate, and per- and poly-fluoroalkyl substances in shellfish **Alcivar-Warren, Romero-Arteaga, Arteaga-Cedeno, Arteaga-Cordero, Alcivar-Herrera, Alcivar-Arteaga**
1:45 PM	Structural elements and neighborhood mosaic influence nekton community similarity across eelgrass and oyster-culture habitats **McDonald, Ruesink, Houle, Hudson, Boardman**	Modeling OsHV-1µvar transmission risk in Pacific oysters on the U.S. West Coast using innovative biological models **van Berkel, Birkeland, Mortensen, Bell, Saw, Simpson, Wikfors, Kachmar, Parikh, Burge**	Wrangling, tangling, and following invasive green monsters in coastal Maine waters **Goldstein, Burke, Crane, Gutzler, Furey**	A national effort to understand, mitigate, and manage invasive terrestrial gastropods in U.S. cropping systems **Baker, Beattie, Diepenbrock, Borrero, Martini, McDonnell, Roda, Quinn, Emery, Warner**	Enhancing marine and freshwater ecosystems and promoting sustainable aquaculture: the ESRAG commitment to a healthier planet **DeWitt**
2:00 PM	Influence of Alaskan oyster farms on benthic communities **O'Neil*, Konar, Long**	A quantitative genetic evaluation of multiple Pacific oyster populations response to OsHV-1 microvariant (San Diego Bay) exposure in laboratory trials **Thompson, Dotterweich, Burge**	Multiple larval sources for Oregon and coastal Washington green crab populations **Yamada, Tepolt, Shanks**	Are *Crepidula fornicata* larvae phenotypically plastic? **Padilla, Nungaray, Anderson**	How to write effective global grants to apply for funding for your project by Rotary International **DeWitt, Puttock, Rico**
2:15 PM	Predictors of the habitat value of oysters – a global meta-analysis **Garcia*, Vivas-Ackenhausen, Doshi, Wilson, Ruesink**	Characterizing OsHV-1 infection in Midori and Miyagi Pacific oysters using lineage-specific transcriptomics **Calla, Thompson, Burge**	Impacts of European green crab (*Carcinus maenas*) foraging and temperature on eelgrass, *Zostera marina* **Swanson*, de Rivera**	Assessing the role of plasticity in determining thermal risk across the life cycle of an intertidal gastropod **Litle*, Rollins, Carrington**	Dengue vectors co-infecting shrimp viruses: epidemiological control challenges in the context of climate change and contamination by insecticides and pesticides used for combating insects **Arteaga-Cordero*, Arteaga-Cedeno, Asuncion, Galindo, Alcivar-Arteaga, Alcivar-Warren**
2:30 PM	Matsushima Bay: Revisiting the ancestral home of (nearly) all Pacific oysters in the world **Fleener**	Differential susceptibility of eastern oyster families and lines to OsHV-1 variants **Burge, Small, Varney, Agnew, Macintyre, Scott, Reece**	Beyond predation: green crabs (*Carcinus maenas*) disrupt juvenile Pacific oyster (*Crassostrea gigas*) function through both consumptive and non-consumptive pathways **Mize*, de Rivera**	Temperature-dependent energy flow and growth in pinto abalone (*Haliotis kamtschatkana*) through a dynamic energy budget framework **Umanzor, Montiel, Pinchuk, Charlotte Springer**	Epigenetic mechanisms of Penaeid shrimp – examples of environmental traits associated with DNA methylation, histone modifications, and non-coding RNA and recommendations for future research to enhance sustainability **Alcivar-Warren**
2:45 PM	Six decades of observations of oyster recruitment in the Chesapeake Bay: what have we learned? **Southworth, Otto, Marquardt, Mann**	Geographic and seasonal surveillance finds no OsHV-1 in Atlantic and Gulf bivalves **Burge, Prado-Zapata, Garcia, MacIntyre, Hudson, Webster, Carnegie, Reece^{P}**	The trophic relationships of invasive green crabs in the Coos Bay estuary are revealed using fatty acids as biomarkers **Diehl*, Galloway, Schooler**	Circasemilunar foraging activity of a predatory whelk: cues and consequences revealed by tidal emersion experiments **Carrington, Hayford**	Shrimp Scampi: A Citizen Science Project - Educating people about microbes and endocrine disrupting chemicals (EDC) such as metals and glyphosate using foldscopes **Warren*, Warren, Alcivar-Arteaga, Alcivar-Warren**
SESSION TITLE	**OYSTERS II** **Bill Fisher & Jessica Pruett**	**SUMMER MORTALITY** **Tim Green**	**GREEN CRABS** **Brian Beal & Sylvia Yamada**	**GASTROPODS** **Max Zavell & Dianna Padilla**	**MANGROVE SHELLFISH** **Acacia Alcivar-Warren & Caroline DeWitt**
3:00 PM	Supporting sustainable oyster restoration and resource management in Mississippi using structured decision making **Pruett, Fisher, Bernard, Olmi-Graham, Sempier, Darnell**	A needle in a haystack - recognizing yessotoxins and their role in shellfish mortality **King**	Invasive European green crab (*Carcinus maenas*) predation in a Washington State estuary revealed with DNA metabarcoding **Fisher, Grason, Stote, Kelly, Litle, McDonald**	Movement ecology of the channeled whelk (*Busycotypus canaliculatus*) during the development of an offshore wind lease site **Jackson*, Runde, Wilke, Lipsky, Methratta, van Hoeck, Smith, van Parijs, Rudders**	
3:15PM	Translating oyster quality across markets and food cultures **Yoshida**	Mass mortality of cultured juvenile Yesso scallops caused by extreme summer water temperatures and effects of deep-water culture on survival **Natsuike, Mizukami**	Investigating river otter predation on invasive European green crab within the estuaries of Makah Bay, Washington **Little*, Akmajian, Acevedo-Gutiérrez, Schwarz**	Establishing a reliable milk conch, *Macrostrombus costatus*, captive breeding program **Matthews, Bazurto, Gronley, Beswick-Seidl, Davis**	
3:30 PM	U.S. oyster production: recent trends and market potential **Hudson, Rheault, Parker, Rubino**	An update on Sudden Unusual Mortality Syndrome (SUMS) on the U.S. Gulf Coast **Tarnecki**	Protecting subsistence resources: management of European green crab on the Annette Islands Reserve in southeast Alaska and beyond **Hudson, Reynolds, Winter, Winter**		
3:45 PM		Can Pacific oyster condition be related to environmental shifts, reproductive state, and mortality events in a U.S. Pacific coast estuary? **Dumbauld, McIntyre, Du, Evans, George, Forster**	European green crab management plan for Washington: lessons learned and looking forward **Parker, Flannery**		
4:00 – 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Salon E/F**				
7:00 – 10:00 PM	**STUDENT ENDOWMENT FUND AUCTION** **Exhibit Hall Lower Level 2**				

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WEDNESDAY
March 25, 2026

8:00-8:50 AM	**PLENARY: Chris Langdon (Oregon State University) – *Taming the Pacific oyster in the "Wild West"* Salon G/H/I**			
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY Salon A			
ROOM	**Salon G**	**Salon H**	**Salon C**	**Salon I**
SESSION TITLE	**VIBRIO SPECIES IN SHELLFISH & HUMAN HEALTH Stephen Jones**	**WILD SHELLFISHERIES Courtney Hart & Christopher Biggs**	**NOAA GRANT WRITING WORKSHOP Cliff Cosgrove**	**AQUACULTURE EDUCATION, EXTENSION & INFORMATION TRANSFER Katie Houle**
9:00 AM	Contribution of distinctive VPaI effectors associated *Vibrio parahaemolyticus* lineages that dominate infections in the U.S. Northeast to environmental fitness **Whistler, Early, Eggert, Xu, Foxall, Jones**	Climate-driven recruitment dynamics in the Washington coastal razor clam fishery **George**	This 3-hour workshop subject matter experts from NOAA Fisheries will cover everything you will need to know about the new registration process for all federal grants, how to write a competitive grant application, submit a federal grant application, the do's and don'ts preparing a proposal and the best practices to incorporate when applying	Building a skilled, connected, and resilient mariculture workforce: an integrated outreach model for shellfish farming in Alaska **Jones, Good, Chrimp, Whitney, Eckert**
9:15 AM	Bias enhanced electro photocatalysis: Novel therapy for *Vibrio parahaemolyticus* infections in shrimp aquaculture **Hayden, Thind, DePaola**	Body condition index of a pandalid shrimp, a novel method for assessing ocean shrimp populations **Groth, Anderson^{P}, Rasmuson**		Development and assessment of an industry-led apprenticeship program **Tarnecki, Grice**
9:30 AM	Protective *Vibrio mediterranei* lineages rescue oyster larvae from pathogen-induced mortality **Smith, Wilbur, Samson, De La Flor, Gomez-Chiarri, Ushijima, Noble**	Variability in somatic growth over time and space determines optimal season-opening date in the Oregon ocean shrimp (*Pandalus jordani*) fishery **Oken, Groth, Holland, Punt, Ward**		Beyond the basics for businesses and practitioners **Hudson*, Cygler, Dalton**
9:45 AM	Evaluating novel *Vibrio* assays against approved methods **Hess*, DePaola, Kim, Tarnecki**	Red abalone in Oregon: Seascape genomics, survey methods, and management applications **Smith, Griffiths, Groth, Whitehead**		Strengthening partnerships to expand oyster shell recycling in the South Carolina SCORE program **Sommers*, Hollis, Hodges, Czwartacki, Swain**
10:00 AM	Long-term seasonal ecology of *Vibrio* spp. population ecology in New Hampshire oysters **Jones, Eid, Foxall, Petit, Ivanyi, Meyer, Batchelor, Young, Whistler**	Flat abalone: From robust fishery to risk of extirpation **Groth, Rogers-Bennett, Smith, Carlton**		Workforce training in shellfish aquaculture at Bellingham Technical College - curriculum and hatchery updates **Palm-Flawd, Pomerleau, Smith**
10:15 AM	Quantitative risk assessment of individual oyster harvests using industry observations can expand Vibrio risk management options **DePaola**	A collaborative Dungeness crab larval monitoring network in the Pacific Northwest provides long-term, fishery-relevant data **Galiotto, Buckner, Grossman, Cook, Brownlee, Barber, Earle, Becker, Bosley, Harrington, McDonald, Paul, Homerding, Houle, Pantaleo, Paul**		Seeding the future of aquaculture: Youth engagement through the NOAA Science Camp Aquaculture Session **Sullivan, Epps, Naar, Ewald, Love, Ralston, Lepori-Bui, Petrich, Chadsey, David, Grant, Kowaleski^{P}**
10:30-11:00 AM	**MORNING BREAK**			
SESSION TITLE	**BIRDS & SHELLFISH SANITATION Robert Rheault**	**WILD SHELLFISHERIES Courtney Hart & Christopher Biggs**	**NOAA GRANT WRITING WORKSHOP Cliff Cosgrove**	**AQUACULTURE EDUCATION, EXTENSION & INFORMATION TRANSFER Katie Houle**
11:00 AM	Bird-related pathogen risk in shellfish aquaculture **Rheault**	New insights into population structure and phenotypic variation in Salish Sea Dungeness crab **Dimond, Grossman, Bosley, Buckner, Cook, Tobin, Barber**		Investigating oysters: 4-H guide to underwater science activities for youth **Bissell, Christy, Pattillo, Wood, Lantz**
11:15 AM	Bird-related pathogen contamination in shellfish aquaculture: A comprehensive literature review **Pruente, Fitzpatrick, Martin**	Using tribal commercial fishers to survey Dungeness crab biomass in Puget Sound, Washington State **Hart, Buckner, Bosley, Sund, Gallioto**		Expanding engagement of underrepresented communities and alternative learning institutions in coastal habitat restoration and recreational fishing in South Carolina **Hodges, Swain, Plaisted, Treon**
11:30 AM	Evaluating an acoustic deterrent for birds on floating oyster aquaculture gear **McCarty, Siemann**	Carapace width-weight relationships as indicators of biological condition in recreationally harvested Dungeness crab (*Metacarcinus magister*) on the Washington coast **Berry-Powell, George**		Shellfish aquaculture education in the classroom and on the tide flats **Christy, Bissell**
11:45 AM	Assessing the influence of birds and site-specific characteristics of oyster farms on fecal coliform levels in southern New England **Lavoie*, McWilliams, Gomez-Chiarri**	Climate-adaptive management of the U.S. West Coast Dungeness crab fishery using projections of distribution shifts and catch forecasts **Free, Oken, Richerson, Zhu, Siedlecki**		
12:00 NOON	Assessing depuration of *Campylobacter* spp. from oysters **Richard, Ezeama, Gomez-Chiarri, Rheault, Nobel, Clerkin, Smith**	Sea surface temperature and upwelling as predictors for Dungeness crab recruitment success, fishery landings, and population abundance **Biggs**		
12:15 PM	Fecal coliform measures elucidate inconsequential risk from resident and migrating birds on surface culture in Willapa Bay, Washington, USA **Hudson, Suhrbier, Boldt**			
12:30-2:00 PM	**NSA BUSINESS LUNCHEON Exhibit Hall Lower Level 2**			
2:00 – 5:00 PM	***Gyotaku* (fish print art) Workshop – Bruce Koike – Salon D (*advanced sign-up required, cost: $115 for professionals and $95 for students*) Email Bruce to sign up: koike.bruce@gmail.com**			
2:30 - 4:30 PM	**SCALLOP GALLOP 5K run/walk – meet at hotel lobby EXPLORE Portland!!**			
4:30 - 6:00 PM	**POSTER SESSION AND HAPPY HOUR Salon E/F**			

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THURSDAY
March 26, 2026

8:00-8:50AM	**PLENARY: Andrew Suhrbier (Pacific Shellfish Institute) – *Echinoderm aquaculture, fisheries, and their intersections with bivalves* Salon G/H/I**			
	NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY Salon A			
ROOM	**Salon I**	**Salon G**	**Salon H**	**Salon B**
SESSION TITLE	**SHELLFISH GENETICS/GENOMICS Louis Plough**	**ADVANCES IN HATCHERY TECHNOLOGY Vengatesen Thiyagarajan & Karen Hudson**	**CLAMS Brian Beal & John Kraeuter**	**SHRIMP ENCODE – SHRIMP GENOMES & EPIGENOMES Acacia Alcivar-Warren & Kathy Tang**
9:00 AM	Marker-assisted selection for resistance to OsHV-1 in the Pacific oyster, *Crassostrea gigas* **Langdon, Green, Sutherland, Divilov, Lunda, Jennings, Mueller**	Oxylipins, PUA, and larvae: Bioactive byproducts of phytoplankton are an emerging concern for the shellfish aquaculture industry **Sanderson, Glover, Menegay, Edwards, Carnegie, Smith**	Single-cell transcriptomics reveals immune evasion and growth reprogramming in transmissible cancer of northern quahog (= hard clam) (*Mercenaria mercenaria*) **Samson*, Murphy, Paz, Fisk, Reitsma, Smolowitz, Gomez-Chiarri**	Shrimp Genomes and Epigenomes (ShrimpENCODE) Session: From repetitive sequences and epigenetics to genomic selection - Recognition to students and "Outstanding ONE HEALTH Researchers in Aquaculture and Fisheries" awardees **Alcivar-Warren, Tang^{p}**
9:15 AM	Causes of triploid oyster mortality in the U.S. Pacific Northwest **Hedgecock, Page, Romersa, Davis**	The status of bivalve shellfish hatcheries on the Atlantic coast of the United States: A report from the Bivalve Hatchery Health Consortium **Hudson*, Gray, Gomez-Chiarri**	Investigating drivers of northern quahog (*Mercenaria mercenaria*) growth following coastal limestone application in a Rhode Island estuary **Schwemmer, Fontaine, Pimenta, Anderson, Gibson, Teevan-Kamhawi, Foster, Nestory, Schwartz, Wang, Palter, Grear**	Domestication and selective breeding drive intestinal microbiota stabilization in the shrimp, *Penaeus vannamei* **Cervantes-Echeverría*, Ochoa-Leyva**
9:30 AM	Enhancement of polyploid breeding strategies for the eastern oyster, *Crassostrea virginica* **Small, Katsuki, Varney**	Hidden hearts: Screening assays suggest involvement of toxins, pollutants, or viruses in some bivalve hatchery larval crashes in the Atlantic coast **Murphy*, Blustajn, Hudson, Gomez-Chiarri**	Harnessing northern quahog (= hard clam) (*Mercenaria mercenaria*) burial behavior for eelgrass (*Zostera marina*) restoration: Preliminary evidence for effectiveness **Collins*, Collins, Guernsey, Beard, Roberts, Zhang, Rittschof**	Repetitive sequences from the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, produced in the United States: Characterization of the *Outcast-1_LVa* non-LTR retrotransposon, putatively associated with Abdominal Segment Deformity Disease (ASDD) of farmed *P. vannamei* from Thailand **Bao, Alcivar-Warren^{p}, Yuan**
9:45 AM	Comparative transcriptomic responses of full-siblings diploid and triploid Pacific oysters under extreme salinity stress **Chancellor, Laroche, Delisle, Scholtens, Bandaranayake, Vignier^{p}**	The use of probiotics to mitigate Atlantic sea scallop (*Placopecten magellanicus*) mortality following challenge with pathogenic *Vibrio* species **Brennan*, Perry, Beal, Bowden**	Characterizing the distribution, abundance, and habitat associations of tideflat shellfish populations in Tillamook Bay, Oregon, USA: Implications for resource management **D'Andrea, Felde, May III, Gellhaus**	
10:00 AM	Advancing the development of a novel sterility method in shellfish **Gavery, Vandepas, Saunders, Vadopalas, Luckenbach, Trapnell, Roberts**	Optimum microalgal combination diets for larvae and spat of the Pacific calico scallop, *Argopecten ventricosus* **Huo, Pritzl, Roy, Drawbridge**	Manila clam aquaculture in Puget Sound: Estimating nutrient removal from harvests **Chan*, Kresge, Kiffney, Sanderson, McDowell**	Molecular cloning and protein modelling of thioredoxin glutathione reductase from the shrimp, *Penaeus vannamei* **Morán-Yañez*, Peregrino-Uriarte, Camacho-Jiménez, Yepiz-Plascencia**
10:15-10:45 AM	**MORNING BREAK**			
SESSION TITLE	**SHELLFISH GENETICS/GENOMICS Louis Plough**	**ADVANCES IN HATCHERY TECHNOLOGY Vengatesen Thiyagarajan & Karen Hudson**	**CLAMS Brian Beal & John Kraeuter**	**SHRIMP ENCODE – SHRIMP GENOMES & EPIGENOMES Acacia Alcivar-Warren & Kathy Tang**
10:45 AM	Integrating genomics into Pacific oyster breeding: Development and deployment of an operational selection framework **Hewish, Verbyla, May^{p}, Kokkinias, Trotter, Chuku**	Physiological responses to extended winter holding periods and subsequent warm-up in eastern oyster (*Crassostrea virginica*) seed **Congrove, Glover^{p}, Rivest, Abbas, Thomas, McDermott, Allen, Jr.**	Growth of Atlantic surfclam, *Spisula solidissima solidissima*, populations at intertidal sites around Massachusetts, USA **Poach, Roberts, Bernatchez, Hare, Meseck, Hennen, Shoemaker**	Current and emerging diagnostic techniques for shrimp diseases **Tang, Alcivar-Warren**
11:00 AM	Multigenerational genome-wide association study for Dermo resistance in the eastern oyster, *Crassostrea virginica* **Coyne*, Wang, Sun, Casas, La Peyre, Williams, Rikard, Bushek, Guo**	Combating climate-linked oyster mass mortality: Genomic and hatchery solutions for China and Southeast Asia **Thiyagarajan, Yu, Xiao, Zhang, Li, You, Wang, Wang, Song, Chung, Hwai, Vu, Guo, Li**	Atlantic surfclam subspecies (*Spisula solidissima solidissima* and *S. s. similis*) can produce fertile hybrid offspring **Acquafredda, Allam, Guo, Munroe**	
11:15 AM	Improved genomic prediction for Dermo resistance in eastern oysters (*Crassostrea virginica*) using machine learning and rare variants **Sun*, Coyne, Wang, Casas, La Peyre, Williams, Rikard, Bushek, Wong, Guo**	Sea cucumber aquaculture in Hawaii: Project status, challenges, and opportunities **Anderson, Mason, Haws**		Long terminal repeat (LTR) retrotransposons and DNA transposons in the genome of the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, produced in the United States **Alcivar-Warren**
11:30 AM	Fine-tuning breeding strategies: Field performance and disease acquisition of selectively bred eastern oyster families in a breeding program **Nichols*, Varney, Carnegie, Small**	Spawning, larvae rearing, and juvenile nursery culturing of warty sea cucumber, *Apostichopus parvimensis* **Huo, Roy, Drawbridge**		Sex determination of Pacific white shrimp, *Penaeus vannamei* **Alcivar-Warren, Guo**
11:45 AM	From productivity to resilience: An industry-engaged model for shellfish breeding in New Zealand **Vignier, Scholtens, Symonds, Ericson, King**	High-speed imaging microscopy in shellfish hatchery research **Gibala-Smith, Veilleux, Acquafredda, Houston, White**		
12:00-1:00 PM	**LUNCH BREAK**			

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THURSDAY
March 26, 2026

NSA AT THE MOVIES – FILM FESTIVAL – CONTINUOUS SHOWINGS ALL DAY
Salon A

ROOM	**Salon I**	**Salon G**	**Salon H**	**Salon B**
SESSION TITLE	**SHELLFISH GENETICS/GENOMICS** **Louis Plough**	**SEAWEED-BIVALVE CO-CULTIVATION** **Michael Doall**	**SOCIAL-ECOLOGICAL SYSTEMS** **Kaitlyn Kowaleski**	**SHRIMP ENCODE – SHRIMP GENOMES & EPIGENOMES** **Acacia Alcivar-Warren & Kathy Tang**
1:00 PM	First Marosporida nuclear genome: a draft genome assembly of bay scallop Marosporida (BSM) associated with bay scallop mortality in New York **Grouzdev, Pales-Espinosa, Alam, Savastano, Cacot, Tettelbach, Tobi, Green-Beach, Allam**	The Halo Effect: The ability of seaweeds to transform bivalve aquaculture in the Anthropocene **Gobler, Sylvers, Doall**	Can submerged aquatic vegetation and shellfish aquaculture co-exist in Maryland? A case study of interactions at Choptank Oyster Co. **Gray, Cornwell, Palinkas, Skirtich, Tomasetti**	Unlocking the genetic potential of the shrimp, *Penaeus vannamei*, through genomic selection and prediction **Bedhane, Alcivar-Warren**
1:15 PM	Comparative genomics of bay scallop (*Argopecten irradians*) populations exhibiting contrasting infection outcomes to an emerging protist parasite Bay Scallop Marosporida **Alam*, Tanguy, Boutet-Tanguy, Pales-Espinosa, Allam**	Dulse seaweed, *Devaleraea mollis*, mitigates effects of ocean acidification on larval Pacific oysters, *Crassostrea gigas* **Wessler*, Niemann, Clark, Green, Frommel**	Socio-ecological change in a modern clam garden **Barber, Greiner, Williams, Donatuto, Fisher**	
1:30 PM	Genome-wide association study for heat stress tolerance in northern quahogs (= hard clams), *Mercenaria mercenaria* **Coyne*, Guo**	Seaweeds (*Ulva* sp., *Gracilaria* sp.) significantly increase the growth rates of North Atlantic oysters, scallops, and clams grown in an aquaculture setting **Banik*, Seo, Sylvers, Doall, Gobler**	Exploring unintended outcomes from climate adaptation for the well-being of fishers **Fisher, Nelson, Francis, Levin, Samhouri, Harvey, Dee, Marshall, Miller, Moore, Barnes, Cha, Cinner, Gray, Punt, Ridings, Simon**	Putative endogenous viral elements (EVE) identified in three whole reference genome assemblies available for the Pacific whiteleg shrimp, *Penaeus vannamei* **Alcivar-Warren**
1:45 PM	Decoding environmental stress tolerance in Alaskan crab fisheries **Spencer, Long, Gardner, Roberts, Spies**	Seaweeds as a supplemental food source for eastern oysters grown in an aquaculture setting **Seo*, Sylvers, Banik, Doall, Gobler**	Exploring grower perceptions of stressors in the North Carolina oyster farming industry **Eimers*, Murray, Noble**	Endogenous virus elements (EVE) of Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV-EVE) found in the genomes of the shrimp, *Penaeus vannamei* and P. monodon **Asunción*, Alcivar-Arteaga, Romero-Arteaga, Alcivar-Herrera, Arteaga-Cedeno, Arteaga-Cordero, Galindo, Alcivar-Warren**
2:00 PM	An improved genome assembly and transcriptomic resources for the eastern oyster, *Crassostrea virginica* **Guo, Wang, Ratcliff, Jamieson, Coyne**	The mitigation of harmful algal blooms by cultivable seaweeds **Sylvers, Gobler**	Collaborative modeling and oral history to support resilient shellfish aquaculture **Kowaleski, Naar, Magel, McDonald, Poe**	Endogenous viral elements (EVE) of white spot syndrome virus (WSSV-EVE) are found in transcriptomes of the first specific pathogen free (SPF) shrimp (*Penaeus vannamei*) produced in the United States – WSSV genomes from Ecuador, Peru, China, and Mexico are not integrated in the genomes of five penaeid shrimp species **Galindo, Alcivar-Arteaga, Romero-Arteaga, Alcivar-Herrera, Arteaga-Cedeno, Arteaga-Cordero, Alcivar-Warren**
2:15 PM	Presence-absence variation (PAV) shapes genomic signatures in bivalves: a comparative study **Gallardo-Escárate, Valenzuela-Miranda, Valenzuela-Múñoz, Saco, Figueras, Novoa, Roberts**	Second harvest: biofouling macroalgal yield in California oyster farms **Campbell*, Fleener, Johnson, Froehlich, Miller, Kroeker**	Network analysis of oyster restoration and management at the Elkhorn Slough National Estuarine Research Reserve in California **Creedon***	*Ternstroemia dentisepala*: a Mexican plant as novel resource of metabolites against the bacterium, *Vibrio parahaemolyticus* **Soto-Díaz*, Taketa, Victorio-De los Santos**
2:30 PM	A chromosome-level genome assembly and organ transcriptomes of the Atlantic surfclam, *Spisula solidissima* **Guo, Coyne, Sun, Munroe**	Maximizing nitrogen bioextraction through the co-cultivation of seaweed with oysters **Doall, Eckstein, Curtin, Morrell, Meichenbaum, Kraemer, Gobler**		Chromosomal locations of developmentally and differentially expressed AT-rich cDNA of specific pathogen-free (SPF) shrimp, *Penaeus vannamei* **Alcivar-Warren**
2:45PM	Monitoring the genetic diversity of the European flat oyster, *Ostrea edulis*, for restoration: a comprehensive genomic framework **Alves Monteiro, Saurel, Bekkevold, Hemmer-Hansen**	DISCUSSION		The shrimp epigenome (ShrimpENCODE) of the first specific pathogen-free (SPF) *Penaeus vannamei* produced in the United States: founder stocks used to develop the selective breeding program, genome sizes, and epigenetic mechanisms of penaeid shrimp **Alcivar-Warren**
3:00 PM	Identifying native and introduced oysters in Hawai'i **Mason***			How to produce healthy shrimp free of the contaminated glyphosate-based feeds (soybeans, corn) used to produce balanced shrimp foods - recommendations from the World Economic Forum, Rotary International-ESRAG, and the Foundation for Conservation of Biodiversity of Ecuador **Rodriguez*, DeWitt, Alcivar-Arteaga, Alcivar-Warren**
3:15 PM				
3:30 – 5:00 PM	**CLOSING HAPPY HOUR** **Salon E/F**			

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ORAL PRESENTATIONS

ATLANTIC SURFCLAM SUBSPECIES (*SPISULA SOLIDISSIMA SOLIDISSIMA* AND *S.S. SIMILIS*) CAN PRODUCE FERTILE HYBRID OFFSPRING

Michael Acquafredda*[1], Bassem Allam[2], Ximing Guo[1], and Daphne Munroe[1]

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There are two Atlantic surfclam subspecies. The northern subspecies (*Spisula solidissima solidissima*) supports the federal fishery and is abundant on the continental shelf of the northeastern United States. The southern subspecies (*S.s. similis*) is predominantly found south of Cape Hatteras, but is also found in shallow, patchy, northern areas, such as coastal Virginia, Long Island Sound, and southern Massachusetts; however, the taxonomic rankings of these clams remain controversial. Recent genetic evidence suggests they could be distinct, but closely related species. The goal of this project was to determine whether these genetically distinct surfclams can produce fertile hybrid offspring. Surfclams were collected from commercial fishing grounds off New Jersey (*S.s. solidissima*) and from a known *S.s. similis* bed in Massachusetts. F1 progenies were bred in October 2023 and May/June 2024, and F2 progenies were bred in April 2025. Genetic samples were collected from each of the parental and offspring groups to confirm genetic lineage. Fertilization rates across F1 and F2 groups ranged from 85-95%. Larvae from all groups metamorphosed, with most reaching competency at approximately 21±5 days post fertilization. Juvenile performance was also evaluated under ambient and elevated (+1.2°C) temperature conditions. Results from the juvenile study indicate that similis-female F1 hybrids exhibited heterosis (i.e., hybrid vigor). Under both conditions, similis-female hybrids grew at significantly greater rates than *S.s. solidissima* purebreds, and notably, the hybrids in the heated condition grew as well as the *S.s. solidissima* purebreds grew in the ambient condition. Together, this work demonstrates that *S.s. solidissima* and *S.s. similis* are indeed capable of hybridizing, the hybrid offspring are fertile. and under certain conditions, hybrids may outperform purebreds. Results from this work will support future surfclam aquaculture breeding programs and provide valuable information about how wild surfclams may evolve in response to ocean warming.

THE RIBBED MUSSEL AQUACULTURE COLLABORATIVE (RMAC)

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Demand for cultured ribbed mussels (*Geukensia demissa*) has grown exponentially in recent years due to their use in a wide range of ecological engineering projects, such as bacterial remediation, bioextraction, ecosystem stabilization, living shoreline development, and coastal resiliency; however, consistent ribbed mussel seed production has remained challenging and unreliable. Unlike the well-established husbandry techniques for the eastern oyster (*Crassostrea virginica*) and the northern quahog (= hard clam) (*Mercenaria mercenaria*), culture techniques for ribbed mussels remain severely underdeveloped. Founded in 2022, the Ribbed Mussel Aquaculture Collaborative (RMAC) became the first organized, multi-institution research initiative focused solely on advancing ribbed mussel aquaculture. The RMAC has explored major aspects of ribbed mussel hatchery production, including broodstock conditioning, spawning, larviculture, and juvenile culture. They have also carried out studies aimed at developing methods for wild-spat collection. Through the efforts of the RMAC to date, a valuable set of protocols are being developed to publish and share with commercial and public hatcheries.

COMPARATIVE GENOMICS OF BAY SCALLOP (*ARGOPECTEN IRRADIANS*) POPULATIONS EXHIBITING CONTRASTING INFECTION OUTCOMES TO AN EMERGING PROTIST PARASITE BAY SCALLOP MAROSPORIDA

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Since 2019, recurrent summer mass mortality events in bay scallops have been associated with infection by the protist parasite Bay Scallop Marosporida (BSM); however, infection intensity and mortality are not always tightly coupled, suggesting that host-level mechanisms may modulate disease outcomes. To investigate the genomic underpinnings of these contrasting responses, a comparative genomic analysis was conducted across scallop populations representing distinct infection scenarios. These populations capture naturally occurring contrasts in exposure, susceptibility, and disease outcome across environments and life-history contexts.

For example, scallops from Martha's Vineyard, Massachusetts and New York experience comparable BSM infection levels, yet differ markedly in mortality susceptibility. In addition, a unique New York fall-spawned cohort escapes peak summer infection during its first year, while New York scallops deployed in Virginia remain uninfected due to the absence of BSM at that location. Bulk mRNA sequencing was integrated with whole-genome bisulfite sequencing to compare transcriptional and epigenetic landscapes across these populations. By examining genomic states associated with tolerance, temporal escape, and lack of exposure, this work aims to identify regulatory features linked to differential disease outcomes. This comparative framework provides a foundation for understanding how environmental history and host genomic regulation interact to shape susceptibility to BSM-associated mortality, with broader implications for scallop health and disease resilience.

PESTICIDES, ECOSYSTEMS POLLUTION, SHELLFISH, ENVIRONMENTAL HEALTH, AND PLANETARY BOUNDARIES - AN URGENT CHALLENGE

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Pesticides (insecticide, herbicide, fungicide) act as endocrine disrupting chemicals (EDC), developmental and reproductive toxicants. They affect a diverse range of non-target species and may be linked to global biodiversity loss. Challenges associated with pesticide production and use put the health of human and wildlife populations at risk, including: high pesticide production and use, increasing rates of release into the environment; adverse effects on non-target species - including humans and shellfish; pesticides that are persistent organic pollutants (POP) do not stay where they are used, contributing to ecosystem pollution far from their intended areas of application; climate change can exacerbate the use of pesticides, and social determinants of health (equity and justice). The framework of planetary boundaries evaluates how human activities impact earth systems and prevent the biophysical systems of the Earth from being maintained sustainably. The nine planetary boundaries framework (climate change, ocean acidification, ozone depletion, nitrogen and phosphorous cycles, biosphere integrity, freshwater use, land system use, atmospheric aerosol loading, novel entities) makes clear that failure to act against the most concerning chemicals, including pesticides, ultimately puts the survival of human populations at risk. Human activities have significant and sometimes irreversible effects on key aspects of environmental health. When considering the global impact of pesticides, products can disrupt several planetary boundaries including biogeochemical cycles, biosphere integrity (e.g., measures of biodiversity), and the availability of clean freshwater, but the greatest challenge posed by pesticides is the "novel entities" boundary (i.e., the introduction of synthetic chemicals and materials into the environment). A summary of pesticides negatively impacting growth, reproduction, behaviour, and other physiological biomarkers within terrestrial and aquatic systems on multiple non-target organisms across trophic levels is presented. The sustainability of current pesticide use is questionable, there is a need for enhanced risk assessments to reduce risks to biodiversity and ecosystems.

CHROMOSOMAL LOCATIONS OF DEVELOPMENTALLY AND DIFFERENTIALLY EXPRESSED AT-RICH cDNA OF SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS VANNAMEI*

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AT-rich elements of SPF *Penaeus vannamei* were previously identified in three cDNA amplified by vertebrate interleukin-1 (IL-1) alpha primers. Sequence analysis revealed that all three clones were AT-rich with 64.5%, 67.4% and 64.2% for ShIL1-21 (U94689, 954bp), ShIL1-28 (U94690, 864bp) and ShIL1-J17 (U94691, 182bp), respectively. The cDNA are developmentally and differentially expressed in SPF *P. vannamei.*

Availability of five whole genome sequences (WGS) for *P. vannamei* allowed us to explore the chromosome locations of these cDNAs. Homology searches were performed using the following NCBI databases: WGS, Core_nt, Blastx (ClusteredNR), and EST. Results from WGS showed that the three cDNA are present in the five draft genome sequences available for *P. vannamei* (JANIEY010000002.1, QWLK01006167.1, QCYY01000591.1, JBFNAF010000002.1, DAWKWD010002199.1). Interestingly, cDNA U94690 is present in JANIEY010000002.1 which is the current NCBI Reference Genome; however, this reference genome did not contain the endogenous nimavirus *Nimav-1_LVa* (279,905 bp) identified in the first Reference Genome for *P. vannamei* (QCYY01000591.1) which was produced using cultured SPF shrimp (farmed in China) developed by the U.S. Marine Shrimp Farming Program (USMSFP).

Core_nt results showed that cDNA U94690 is 95% identical to PREDICTED: *Penaeus vannamei* transmembrane protein 179 (LOC113829339) mRNA (XM_070130224.1, 5333-bp). Blastx ClusteredNR results found no significant similarity. The other two cDNA, U94689 and U94691, remain uncharacterized, perhaps due to the lack of a complete genome sequence. There is a need for a new, chromosome-based, reference genome for *P. vannamei* that will allow better characterization of immune system and disease resistant genes, transcriptomes and epigenomes, endogenous viruses, and repetitive sequences.

EPIGENETIC MECHANISMS OF PENAEID SHRIMP – EXAMPLES OF ENVIRONMENTAL TRAITS ASSOCIATED WITH DNA METHYLATION, HISTONE MODIFICATIONS, AND NON-CODING RNA AND RECOMMENDATIONS FOR FUTURE RESEARCH TO ENHANCE SUSTAINABILITY

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The role of epigenetic mechanisms on gene expression of Penaeid shrimp throughout development and adaptation to environmental stressors is summarized. Epigenetic mechanisms include DNA methylation, histone modifications and non-coding RNA (ncRNA): microRNA, piRNA, siRNA, lncRNA, circRNA, tRNA-derived small RNA. Examples of epigenetic mechanisms of *P. vannamei* are presented with focus on 1) DNA methylation associated with ammonia nitrogen stress, growth traits, white spot syndrome virus (WSSV) resistance, environment, and cold tolerance; 2) Histone modifications associated with acute hepatopancreatic necrosis disease (AHPND), WSSV ICPII, and embryonic development; and 3) non-coding RNA such as lncRNA associated with alkaline stress, AHPND, *Vibrio parahaemolyticus*, *Spiroplasma eriocheiris,* and WSSV; circRNA associated with high alkaline and high pH; and piRNA associated with AHPND and WSSV.

Recommendations are suggested for future research on shrimp genomics and epigenomics to understand complex traits inheritance by harnessing advanced technologies to enhance sustainability and disease resistance and help the shrimp industry worldwide. They include (1) advance reference genome assembly quality – a new chromosome-based reference genome for *P. vannamei* is needed to characterize its repeatome. (2) Integrate multi-omics data - to enhance analysis of production and performance traits; develop resources for collection and integration of phenomics data; reduce reliance on chemicals and antibiotics, promote sustainable and eco-friendly farming practices; study potential of targeted epigenetic modulation through pharmacological agents, dietary supplements, environmental interventions, or gene-centric methodologies to enhance immunity and disease management; avoid using feeds prepared with glyphosate-based-herbicides (GBH)-produced soybeans, these feeds may lead to development of AMR in the offspring and food safety issues. (3) Address foundational research needs: improve techniques for chromosome analysis; map the sex-determining locus - towards 'all-female' stocks; invest in training, extension, and outreach programs to support the application and integration of genomic and epigenomic sciences into shrimp aquaculture operations, fostering a skilled workforce for the future.

LONG TERMINAL REPEAT (LTR) RETROTRANSPOSONS AND DNA TRANSPOSONS IN THE GENOME OF THE FIRST SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS VANNAMEI,* PRODUCED IN THE UNITED STATES

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A total of 269 long terminal repeat (LTR) retrotransposon and 134 DNA transposon families were identified in a small-scale genomic sequence (479-Mb) obtained from the genome of the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, from the Kona Line produced by the breeding program of the U.S. Marine Shrimp Farming Program (USMSFP). All sequences are deposited in Repbase (www.girinst.org). The 269 LTR retrotransposons include 25 *BEL*, 2 *Copia*, 232 *Gypsy*, and 10 *LTR* families. The 134 DNA transposons consist of 42 *DNA*, 7 *DNAV*, 1 *EnSpm*, 11 *Harbinger*, 14 *hAT*, 2 *Kolobok*, 4 *L2*, 10 *Mariner*, 13 *Merlin*, 1 *MuDR,* 1 *P*, 9 *piggyBac*, 3 *Polinton*, 5 *Sat*, 8 *TE*, 2 *Transib*, and 1 *Zator* families. The seven *DNAV* correspond to seven smaller segments/entries in Repbase (*DNAV-1a_LVa* to *DNAV-1g_LVa)* of a reconstructed 279,384-bp long consensus sequence (*DNAV-1_LVa)* representing the complete genome of a WSSV-like virus. Some *Sat* transposons show similarity to microsatellites (SSR) from SPF *P. vannamei*, including the telomeric pentanucleotide repeat (TAACC/GGTTA)$_n$, the insertion site of a large DNA virus, a nimavirus (*Nimav-1_LVa)*.

The five whole genome sequence (WGS) databases available for *P. vannamei* confirm that the telomeric pentanucleotide repeat (TAACC/GGTTA)n is highly abundant and widely distributed in intron and intergenic regions of *P. vannamei* (similar to telomeric repeats (TTAGG)n of insects). The wide interstitial distribution of telomeric repeats in the shrimp genome may represent extensive, recent, or active invasion by the pentanucleotide repeat. Considering that the estimated genome size of SPF *P. vannamei* from the United States is 2.89-Gb, while the current NCBI reference genome of *P vannamei* is 1.64-Gb, a new contiguous, whole reference genome for *P. vannamei* is needed to fully characterize telomeric repeats and the repeatome.

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

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Five whole genome sequence (WGS) assemblies are available for *Penaeus vannamei*. In addition, a small sequence (470-Mb) from the first specific pathogen-free (SPF) *P. vannamei* produced in the United States generated hundreds of repetitive elements (RE). Among these RE are DNA transposons (TE) and simple sequence repeats (SSR) homologous to endogenous viruses like *Nimav-1_LVa* (279,905-bp) and a white spot syndrome virus (WSSV)-like (*DNAV-1_LVa*, 279,384-bp). Some SSRs show similarity to *P. vannamei* microsatellites including the telomeric pentanucleotide (TAACC)n, the insertion site of *Nimav-1_LVa*.

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

THE SHRIMP EPIGENOME (ShrimpENCODE) OF THE FIRST SPECIFIC PATHOGEN-FREE (SPF) *PENAEUS VANNAMEI* PRODUCED IN THE UNITED STATES: FOUNDER STOCKS USED TO DEVELOP THE SELECTIVE BREEDING PROGRAM, GENOME SIZES, AND EPIGENETIC MECHANISMS OF PENAEID SHRIMP

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The founder stocks used to develop the selective breeding program of the first specific pathogen-free (SPF) shrimp, *Penaeus vannamei*, by the U.S. Marine Shrimp Farming Program (USMSFP), the genome sizes of *Penaeus* species, and the epigenetic mechanisms of Penaeid shrimp will be summarized. The USMSFP founder stocks were from the Kona and Taura Syndrome Virus (TSV)-resistant Lines. The genome size estimate for SPF *P. vannamei* is 2,890.00-Mb. Genome sizes for five Penaeus species (*P. chinensis, P. indicus, P. japonicus, P. monodon, P. vannamei*) are available in the NCBI Genome Database, sizes ranging from 96.78-Mb for *P. vannamei* farmed in China to 2,391-Mb for *P. monodon* from Thailand. Only one (ASM378908v1) of the five *P. vannamei* genome assemblies contain the nimavirus *Nimav-1_LVa* (279,905-bp).

The role of epigenetic mechanisms on gene expression throughout development and adaptation to environmental stressors is summarized. Epigenetic mechanisms include DNA methylation, histone modifications and non-coding RNA (microRNA, piRNA, siRNA, lncRNA, circRNA, tRNA-derived small RNA). Examples of epigenetic mechanisms of *P. vannamei* are presented. Recommendations are suggested for future research on Penaeid shrimp aquaculture genomics and epigenomics to understand complex traits inheritance by harnessing advanced technologies to enhance sustainability and disease resistance and help the shrimp aquaculture industry worldwide.

SEX DETERMINATION OF PACIFIC WHITE SHRIMP, *PENAEUS VANNAMEI*

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Sexual dimorphism exists in the shrimp, *P. vannamei* (ZZ/ZW determination system) with females having a higher growth rate than males. A mono-sex culture program (ALL-FEMALE SHRIMP) may increase the economic return of shrimp farming by mapping the sex-determination region in this species, which may assist in improving economic relevant traits like reproduction and growth, and study recombination rates and transposable elements (TE). Part of a nonLTR retrotransposon has been identified as a potential female sex marker in SPF *P. vannamei*. A genetic map that yielded 15,256 single nucleotide polymorphisms (SNP) assigned to 44 linkage groups (LG) identified a sex-determining region in LG31 with 21 statistically significant SNP, the most important SNP was previously identified as a sex-linked marker and was able to identify 99% of the males and 88% of the females. A sex-determining locus was identified in LG18 of the first reference genome. Two microsatellites we identified as sex-linked markers in LG4 are similar as the sex-linked marker in LG18.

To confirm the ZZ/ZW determination system, efforts are underway to sequence the genome of a wild female *P. vannamei* from Ecuador using long-read sequencing to assemble 45 chromosomes, even if it will be more challenging to assemble than ZZ males. Considering that there are only five draft genome assemblies available for *P. vannamei*, and some of them do not contain the sequences published as potential sex-determining genes, a new chromosome-based whole reference genome sequence is urgently needed for *P. vannamei*.

SHRIMP GENOMES AND EPIGENOMES (ShrimpENCODE) – A ONE HEALTH APPROACH

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Shrimp, a popular seafood of Americans, is mostly imported, causing a ~$4.5 billion trade deficit. The Pacific white shrimp, *Penaeus vannamei*, is one of the most valuable aquaculture species in the world but has suffered major economic losses from outbreaks of viral, bacterial and parasitic diseases such as those caused by white spot syndrome virus (WSSV), Taura syndrome virus (TSV), acute hepatopancreatic necrosis disease-causing *Vibrio* bacteria (V_{AHPND}), *Ecytonucleospora hepatopenaei* (EHP), among others. Environmental stressors may impact on the health of imported shrimp, posing safety concerns due to potential contaminations with banned antibiotics with potential for antimicrobial resistance (AMR) and pollutants that contaminate water. Pollutants include endocrine disrupting chemicals (EDC) such as bisphenol A, phthalates, persistent organic pollutants (PCB, Dioxin, organochlorine pesticides), per- and polyfluoroalkyl substances, microplastics and nanomaterials, metals and pesticides like glyphosate-based herbicides, among others. While the FDA has some measures in place (i.e. HACCP), the imported shrimp still contains unsafe levels of these substances. How environmental chemicals are harming shrimp and human health, and how they interact with the genome and epigenome is unknown.

The ShrimpENCODE session will provide a platform for students and researchers to discuss the use of molecular, genomic, and epigenomic tools in penaeid shrimp research to fill critical data gaps in health, management and conservation of wild and cultured shrimp, and study the effects of genome and epigenome interactions on disease and AMR resistance based on the ONE HEALTH Approach. Speakers will address advances in refining the genome of *P. vannamei* and how to use it for developing disease resistant lines with potential of breeding through genomic selection. Topics on biotechnology, genome editing, antivirals, epidemiology, pathogenesis, diagnosis, and EDC and microplastic pollution in marine environment will be addressed.

ONE HEALTH, ECOHEALTH, PLANETARY HEALTH: NEW DEFINITIONS FOR A SUSTAINABLE AND HEALTHY FUTURE FOR ALL BY CONSERVING HEALTHY MANGROVES AND SHELLFISH TO PROTECT HUMAN HEALTH

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A scientific review of One Health, EcoHealth, and Planetary Health is presented relative to conserving healthy mangroves and shellfish and how those actions will also protect human health.

One Health is defined by its inclusion of environmental, ecosystem, animal, human and plant health. An integrated, unifying approach that recognizes that the health of animals, the wider environment, humans and plants is closely linked and interdependent. The approach mobilizes multiple sectors, disciplines (shellfish and mangrove researchers), and communities at varying levels of society to work together to foster well-being and tackle threats to the health of all, including humans and ecosystems, addressing the collective need for healthy food (shellfish, fish), clean water, energy, and air, acting on climate change, preserving biodiversity, and contributing to sustainable development by tackling the systems that have forced us into disciplinary silos. ***EcoHealth*** is a transdisciplinary approach addressing the intricate connections between humans, wildlife, and ecosystems health - defining health as more than just the absence of disease, but rather as a state of 'complete physical, mental, and social well-being that is dependent on the health of ecosystems and society'. It emphasizes systemic and participatory methods, integrating social, ecological, economic factors to address complex health challenges and promote well-being - relevant for understanding and preventing zoonotic diseases. ***Planetary Health*** is mostly focused on human-environmental interactions, seeking to alert humanity to the risks to civilization, and thus to human health, on the global scale and in the near and midterm future. These risks arise from human impacts on the environment, critical erosion of ecosystem services, and manifest in phenomena like climate change and the loss of species. It identifies steps toward a fairer world, rapid decarbonization, and for health workers to become part of a movement for global social justice that must consider and seek to reduce pressures on the Earth's systems.

MONITORING THE GENETIC DIVERSITY OF THE EUROPEAN FLAT OYSTER, *OSTREA EDULIS,* FOR RESTORATION: A COMPREHENSIVE GENOMIC FRAMEWORK

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The native European flat oyster (*Ostrea edulis*) has suffered centuries of decline from overfishing, disease, and habitat loss, making genetic diversity monitoring essential for successful restoration efforts. Effective restoration of *O. edulis* requires integrated genetic monitoring across both wild and hatchery populations. The research establishes a genomic foundation and practical tools necessary for evidence-based restoration programs.

Leveraging the chromosome-level *O. edulis* genome of a Brittany individual, genomic analysis unveiled hidden genetic clusters in Scandinavia and identified three large putative structural variants (SV) in the last remnant wild populations of the species. These findings provide critical guidance for source collection and distribution strategies in restoration programs notably by adding another layer of complexity regarding SV genotype distribution between populations. The study also developed field-tested methods for assessing parentage, relatedness, and genetic variation across wild and hatchery contexts. Three years of testing across different broodstock sizes, without prior sex determination, revealed the challenges of predicting breeding outcomes and managing sex-changing broodstock. Finally, analysis of third-generation hatchery samples from distinct populations shows that domestication effects rapidly pervade the genome, with implicated genetic pathways varying by geographical origin. This emphasizes the need for population-specific hatchery protocols for conservation and management strategies of native oysters. This integrated approach provides restoration programs with the genomic tools and guidelines necessary to maintain genetic diversity while optimizing supplementation strategies for long-term population recovery.

SEA CUCUMBER AQUACULTURE IN HAWAII: PROJECT STATUS, CHALLENGES, AND OPPORTUNITIES

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Aquaculture represents roughly 80% of global sea cucumber production, yet the United States has no farmed output despite strong export demand established by wild fisheries. Sea cucumbers are low-trophic, benthic detritivores that are well-suited for integrated multitrophic production on existing aquaculture sites. Hawai‘i's loko i‘a (traditional fishponds) offer a unique opportunity to develop this opportunity. These cultural resources are being actively restored for food production and provide permitted space where secondary crops like sea cucumbers can both enhance water quality and generate revenue to support restoration. Kaua‘i Sea Farm and the Pacific Aquaculture and Coastal Resources Center (PACRC) are collaboratively developing *Stichopus horrens* aquaculture for scalable production in fishponds, with implications for broader regions. Our work has identified a promising native species, established a novel grow-out system, and improved reproductive conditioning to achieve high year-round fecundity. Key challenges remain in producing reliable seedstock at commercial scale, but the opportunity for U.S. expansion is substantial across Hawai‘i and beyond. This presentation will share current research progress, bottlenecks, and next steps toward establishing the first sea cucumber aquaculture industry in the United States.

FROM PLANKTON TO POPULATION: LINKING SETTLEMENT, RECRUITMENT, AND COMMUNITY ASSEMBLY IN A KEY SALT MARSH SPECIES

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Community assembly arises through the combined effects of dispersal, abiotic filtering, and biotic interactions that determine which species persist locally. For marine invertebrates with complex life histories, understanding factors that affect settlement of larvae and recruitment of juveniles is critical for linking across life stages to adult distributions, but is rarely examined in the field. The ribbed mussel (*Geukensia demissa*) is a key species in north-western Atlantic salt marshes that affects salt marsh health and is the target of restoration efforts. The settlement (arrival and attachment of larvae) and recruitment (survival and persistence) dynamics of this species were therefore investigated across an elevation gradient and in the presence/absence of conspecifics. No individuals settled in the high marsh, which experienced the highest temperatures and longest periods of aerial exposure, and the presence of adult conspecifics at low and mid elevations did not affect settlement. In contrast, recruitment was over six times higher within aggregations of adult mussels across low and mid elevations. These results suggest that adult mussels may modify the environment in ways that enhance juvenile survival by providing refuge from desiccation, thermal stress, and/or predation. A sequential assembly process in which abiotic filters affect the transition from settlement to recruitment and biotic facilitation governs persistence of juveniles in the community is likely. Physiological stress, positive species interactions, and phenology can all shape community assembly, and illustrate the importance of integrating across life stages to understand community assembly and species persistence under changing environmental conditions.

THE MANGROVE EPIGENOME (MangroveENCODE) PROJECT OF THE FUCOBI FOUNDATION OF ECUADOR: A ONE HEALTH APPROACH TO CONSERVING MANGROVES BIODIVERSITY AND AVOID CLIMATE DISASTER

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Mangrove forests are natural laboratories for studying epigenetics and climate change. They are salt-tolerant plant species that grow in coastal saline water and are adapted to harsh environmental conditions such as high ultraviolet light, low nutrition, and fluctuating salinity in coastal zones. Mangroves are highly productive and biologically diverse wetlands that serve as nurseries and habitats to many juvenile fishes and shellfish (molluscs, crustaceans (shrimp)); and sequester large quantities of carbon that become significant sources of greenhouse gases when disturbed through land-use change. Some mangroves began disappearing due to ozone depletion, freshwater diversion, ocean acidification, atmospheric aerosol pollution, shrimp farming, and the introduction of exotic chemicals and modified organisms in the shrimp farms near mangrove habitats. Mangroves support diverse microorganisms such as fungi, and bacteria associated with biogeochemical transformations of nutrients. They trap sediments and assimilate nutrients along with associated sediment contaminants such as antibiotics, EDC and glyphosate-based herbicides. Mangrove species have very low genetic diversity caused by their stressful living conditions, suggesting that epigenetic variation is likely a vital source for them to respond to environmental changes.

The long-term goal of MangroveENCODE is to study the epigenetic mechanisms associated with the interactions of CO_2 uptake, EDC in sentinel species (shellfish), and microbial communities considering environmental degradation-related health issues. The plan is to obtain baseline information for future studies to test mechanism-driven hypotheses to study the interactions of CO_2, EDC, and microbial diversity. Short-term goals: characterize the microbiome, CO_2 uptake, and EDC concentrations in mangrove sediment and shrimp; and review available studies on epigenetic regulation and adaptation of mangroves. This talk will summarize (a) best technologies to assess the microbiome and CO_2 stocks from > 1-meter-deep sediment, and (b) genome sizes, microbiomes, epigenome, and transposable elements of mangroves.

CESIUM-137 AND MICROPLASTICS: POTENTIAL HEALTH RISKS TO SHELLFISH AND OTHER MARINE LIFE

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Cesium is the heaviest and most reactively stable of the alkali metals. Contaminated metal at an Indonesian industrial site likely caused radioactive contamination that prompted recalls from the U.S. Food and Drug Administration of more than 61,000 packages of imported shrimp. Microplastics (MP) can act as carriers for radioactive cesium, posing risks to aquatic ecosystems, shellfish and other marine life, and human health. MP can absorb radionuclides such as cesium-137, facilitating their transport and entry into the food chain via adsorption, biofilm enhancement, vector for migration, and particle size. The environmental and biological consequences of cesium exposure will be discussed, including bioaccumulation and biomagnification (contamination could move up the food chain higher trophic levels, including humans who consume seafood); changes in buoyancy (accumulation of biofilms and other materials, including radionuclides, can increase the MP density and cause them to sink, transferring radioactive contaminants to deeper layers of the water column and seabed sediments); and widespread pollution (the buoyant and mobile nature of MP allows them to carry contaminants over long distances via ocean currents, spreading radioactive pollution globally). Factors influencing cesium adsorption include microplastic properties, environmental conditions, and comparison to sediments.

Areas of concern include nuclear incidents and limited research. Events such as the Fukushima Daiichi nuclear accident have released large amounts of cesium-137 into the ocean. The interaction between cesium and the growing abundance of MP highlights a novel and serious contamination risk. The combined effects of MP and radionuclides on marine life and the long-term ecological risks are still not fully understood. More research is needed to investigate these synergistic effects and develop effective mitigation strategies.

TRAINED IMMUNITY AND IMMUNE PRIMING IN PLANTS (MANGROVES) AND INVERTEBRATES (SHELLFISH)

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This presentation provides examples of the concept of trained immunity in mangroves and shellfish (shrimp, molluscs) after exposure to viruses and environmental stressors. Immune memory has long been thought to be restricted to the adaptive immune system of vertebrates, but several lines of evidence have changed our understanding of immune memory and have shattered the strict separation between innate and adaptive immunity. In vertebrates, a form of innate immunity called ‘trained immunity’ has been studied for over ten years. Studies in plants and an increasing number of invertebrate taxa have demonstrated that these organisms also possess ‘immune memory’, despite the absence of an adaptive immune system. These phenomena are mostly known as ‘immune priming’. The mechanisms of immune priming vary across taxa and may or may not partially include the epigenetic and metabolic mechanisms involved in trained immunity. An evolutionary perspective on immune priming, uniquely integrating key aspects across plants and invertebrates for the first time was presented by Kurtz et al. (2025) providing a conceptual clarification regarding the terms ‘trained immunity’ and ‘immune priming’ and offered a brief overview of these phenomena across taxa. They analyzed which processes of immune priming share potentially evolutionary conserved epigenetic and metabolic processes with trained immunity and explore signaling processes involved in immune priming. Specificity is a key defining criteria for immune memory and the potential role of soil and gut microbiota for acquiring innate immune memory in plants and invertebrates was addressed. Trained immunity in *Penaeus japonicus* induced by inactivated white spot syndrome virus (WSSV), and in Artemia during a transgenerational study as a model system will be discussed.

DENGUE VECTORS CO-INFECTING SHRIMP VIRUSES: EPIDEMIOLOGICAL CONTROL CHALLENGES IN THE CONTEXT OF CLIMATE CHANGE AND CONTAMINATION BY INSECTICIDES AND PESTICIDES USED FOR COMBATING INSECTS SUCH AS GLYPHOSATE-BASED HERBICIDES

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Arboviruses are an important group of pathogens that cause diseases of medical and veterinary concern worldwide. Dengue, a mosquito-borne virus transmitted mainly by *Aedes aegypti,* is a major public health issue in Latin America. In Ecuador, 50,408 confirmed cases of Dengue were reported in 2024. The interactions of arboviruses with their host cells are complex, and frequently, the coexistence of two different viruses in the same cell results in the inhibition of replication in one of the viruses, which is a phenomenon called 'viral interference' and can be exploited to develop antiviral strategies. Persistent viral co-infections in arthropods have been studied by many researchers, producing stable, persistently infected mosquito cell cultures by serial passage of exponentially growing whole cells infected with either a Densovirus (AalDNV) or Dengue virus (DEN-2), suggesting that the capacity to support stable, viral co-infections may be a general phenomenon for arthropod cells.

Anti-viral immunity in crustaceans and insects has been studied since 2004 by Dr. Tim Flegel reporting that mosquito cells accommodate balanced, persistent co-infections with a Densovirus and Dengue, and proposed the hypothesis for "heritable, anti-viral immunity in crustaceans and insects." The Densovirus Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV) causes IHHN and runt deformity syndrome and mortalities in *Penaeus stylirostris* but not in *P. vannamei.* Co-infection of IHHNV with WSSV showed the typical clinical symptoms of WSSV infection, but co-infected shrimps did not have any other external deformities. Results of a literature review on molecular, genetic, and epigenetic mechanisms involved in Densovirus-Dengue interactions in shrimp will be presented, addressing potential challenges for epidemiological control in the context of climate change and contamination by insecticides and pesticides (like glyphosate-based herbicides) used for combating pests and insects in crops.

ENDOGENOUS VIRUS ELEMENTS (EVE) OF INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS (IHHNV-EVE) FOUND IN THE GENOMES OF THE SHRIMP, *PENAEUS VANNAMEI* AND *P. MONODON*

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Viral diseases cause major economic losses to the shrimp industry, including diseases caused by white spot syndrome virus (WSSV), infectious hypodermal and hematopoietic necrosis virus (IHHNV; renamed *Decapod penstylhamaparvovirus 1*), among others.

Endogenous virus elements (EVE) of IHHNV and WSSV have been reported. The IHHNV genome (AF218266.2; 3,909-bp) is integrated in various chromosomes of *P. monodon* genome from China (PM-nanhai2-001_Lachesis_group23__306, JACBPZ010000025.1) and *P. monodon* from Thailand (JABERT 010000007.1) both 95-97% identical. Fragments of AF218266.2 are also present in two genomes of *P. vannamei* farmed in China [(QCYY01000759.1, *Penaeus vannamei* breed Kehai No.1 LVANscaffold_759, nucleotides 87-1851 and 936-2058, 95-96% identity) and *P. vannamei* isolate Guihai-1-2017-001_HiC_scaffold_2, JANIEY010000002.1, nucleotides 1294-2575, 68% identity).

Three IHHNV sequences have been reported in cultured *P. vannamei* of Ecuador [(AY362548.1) 3,775-bp), (OL598344.2) 3,203-bp, and (OM728642.1) 3,902-bp] and portions of these genomes are also integrated in the genomes of *P. monodon* from Thailand (GCA_015228065.1, isolate SGIC_2016 chromosome 7) and *P. vannamei* from China (GCA_003789085.1, breed Kehai No.1 LVANscaffold_759). IHHNV isolates from Peru (like OM728641 4,122-bp) are also integrated in *P. monodon* chromosomes 7 and 35, the number of fragments varying per chromosome, 10 and 51, respectively. Results suggest that the currently farmed *P. vannamei* lines in Ecuador are tolerant to circulating IHHNV genotypes, prompting the industry to request delisting of IHHN disease by the World Organization for Animal Health (WHOA). A new reference genome for *P. vannamei* is needed to determine the integration sites and evolution of IHHNV-EVE, and their association with simple sequence repeats and non-coding RNA potentially associated with slow growth and disease resistance/tolerance.

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

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Limited information is available regarding the content of repetitive sequences [transposable elements (TE), and satellite DNA, also called SSR or microsatellites] in *Penaeus* species. A pilot genome sequence (470-Mb) from the first SPF *P. vannamei* produced in the United States generated 479 repetitive sequences representing 345 TE [269 long terminal repeat (LTR) retrotransposons and 76 non-LTR retrotransposons] and 134 DNA transposons, they are deposited in the RepBase database (www.girinst.org).

Some repetitive sequences show similarity to SSR from SPF *P. vannamei*, such as the telomeric pentanucleotide $(TAACC/GGTTA)_n$ repeat, the insertion site of *Nimav-1_LVa*. The *Outcast-1_LVa* non-LTR retrotransposon (6,180-bp) was further characterized. A genomic locus [KC179708, 4101-bp] derived from nucleotides 1,974-6,062 of *Outcast-1_LVa* shows 96.9% identity to the consensus sequence of *Outcast-1_LVa* in Repbase. KC179708 was putatively associated with ASDD of farmed *P. vannamei* from Thailand, authors suggested that ASDD may be caused by use of eyestalk ablation (EA) in female broodstock and inbreeding. *Outcast-1_LVa* is expressed in SPF *P. vannamei* transcriptomes from various developmental stages and adult tissues, expression changes observed in ovaries six-days after EA. Considering that the genome size of SPF *P. vannamei* is estimated at 2.89-Gb, a new, contiguous whole reference genome sequence for *P. vannamei* is needed to fully characterize its repeatome, study the molecular and epigenetics mechanisms involved in growth and disease susceptibility/tolerance, and determine whether expression of *Outcast-1_LVa* gene is indeed associated with EA and inbreeding.

A NATIONAL EFFORT TO UNDERSTAND, MITIGATE, AND MANAGE INVASIVE TERRESTRIAL GASTROPODS IN U.S. CROPPING SYSTEMS

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Invasive terrestrial gastropods are an emerging threat to U.S. specialty crops, row crops, and nursery systems, yet their distribution, impacts, and management challenges remain poorly documented. In 2019, personnel from southeastern universities and state agencies identified increasing reports of *Bulimulus cf. bonariensis* in peanuts, cotton, soybeans, and citrus, prompting the formation of a multi-state Working Group to assess impacts and coordinate research. Since then, collaboration has expanded to include partners from western and northeastern states as well as federal agencies, supporting studies on gastropod biology, sampling techniques, novel attractants, trapping methods, chemical control, biocontrol, and deterrents. To better understand stakeholder needs and guide research priorities, a national needs-assessment survey of growers, extension professionals, and agricultural consultants was conducted. Respondents reported frequent problems with snails and slugs, substantial labor requirements for management, and variable levels of economic damage across crops. Gastropods were documented in multiple commodities, and respondents rated severity, manageability, and economic impact of these issues. Although growers relied on cultural, mechanical, and chemical practices, many indicated a gap between the importance of effective gastropod management and their own confidence or capacity to implement it. Collectively, these findings reveal significant knowledge gaps, inconsistent management success, and a clear need for integrated crop-specific strategies. Survey outcomes are now shaping Working Group priorities. Together, these efforts aim to advance coordinated research, extension, and evidence-based management of invasive terrestrial gastropods across U.S. agricultural systems.

EVALUATING CONSERVATION AQUACULTURE FOR OLYMPIA OYSTER RESTORATION IN MORRO BAY, CALIFORNIA

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Olympia oysters (*Ostrea lurida*), the only native oyster on the west coast of North America, have declined to less than 1% of their historical abundance, with recruitment limitation remaining a major barrier to population recovery. Morro Bay has been identified as a high-priority estuary for restoration, yet limited information exists on which aquaculture methods or estuary locations best support Olympia oyster performance. This study implemented a conservation aquaculture experiment comparing on-bottom bags and suspended SEAPA baskets, paired with intertidal and subtidal deployments across three sites within Morro Bay. Growth, survival, condition index, reproductive development, and natural recruitment were monitored over a 12-month period.

SEAPA gear supported faster growth, with rates approximately 15–20% higher than in on-bottom bags. Survival was also higher in SEAPA baskets (82% vs. 62%), although the difference was not statistically significant due to low replication. Condition index displayed a similar positive but non-significant trend favoring SEAPA gear. Histological analysis revealed a significant association between gear type and gonadal stage (Fisher's exact test, $p = 0.0347$), with SEAPA oysters showing a greater proportion of female and transitional stages, indicating more advanced reproductive development. Intertidal and subtidal deployments further demonstrated spatial and tidal variation in growth, survival, and recruitment. Overall, SEAPA gear enhanced growth and reproductive progression relative to on-bottom bags, and recruitment varied across locations and tidal elevations. These findings provide estuary-specific guidance for applying conservation aquaculture to Olympia oyster restoration in Morro Bay.

SEAWEEDS (*ULVA* SP., *GRACILARIA* SP.) SIGNIFICANTLY INCREASE THE GROWTH RATES OF NORTH ATLANTIC OYSTERS, SCALLOPS, AND CLAMS GROWN IN AN AQUACULTURE SETTING

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While bivalve populations are threatened by climate change stressors including ocean acidification and hypoxia, the photosynthetic activity of seaweeds can raise the pH and dissolved oxygen (DO) of seawater, combatting these stressors. Here, three commercially important North Atlantic bivalves (eastern oysters, *Crassostrea virginica*; northern quahogs (= hard clams), *Mercenaria mercenaria,* and bay scallops, *Argopecten irradians*) were grown in the presence and absence of two common seaweeds (*Ulva* sp. and *Gracilaria* sp.) in replicated 300-L outdoor aquaculture tables with flow-through seawater. Environmental conditions including pH, DO, and chlorophyll *a* were continuously monitored and levels of dissolved inorganic carbon and the complete carbonate chemistry of seawater quantified. The presence of seaweeds significantly increased shell- and tissue-based growth rates of oysters by 20-70%, of clams by 60-70%, and of scallops by 130-140% ($p < 0.05$) with both seaweeds being similarly effective. Both seaweed species caused significant increases in pH, DO, and the saturation state of calcium carbonate (Ω) during the day ($p < 0.05$) whereas differences at night were muted with night-time $\Omega_{\text{aragonite}}$ levels being at or below saturation in all treatments. In some experiments, the presence of seaweeds caused a significant increase in the concentrations of suspended chlorophyll *a*, suggesting that seaweeds increased the total amount and diversity of food available to bivalves. Collectively, this study demonstrates that the co-culture of seaweeds with bivalves in a land-based aquaculture setting can significantly accelerate the growth rate of bivalves by increasing pH, DO, Ω, and food availability.

SOCIO-ECOLOGICAL CHANGE IN A MODERN CLAM GARDEN

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Clam gardens are engineered intertidal landscapes created by Northwest Coastal Indigenous peoples to expand and enhance clam habitat and productivity. In response to declining clam populations and community concerns related to climate change, the Swinomish Tribe initiated a clam garden project. The project integrates traditional ecological knowledge, modern resource management, and climate adaptation approaches to support food security, food sovereignty, and sustainable shellfish production. As the first clam garden constructed in the United States in modern times, the Swinomish Tribe implemented a long-term monitoring program to evaluate both ecological trajectories of the developing clam garden and socio-cultural outcomes within the community. Ecological responses were assessed using a before–after control–restoration design, with the restored site represented by the newly constructed clam garden and the control site by a nearby, unmodified beach. “Before” and “after” conditions were defined by sampling conducted prior to and following rock wall construction and beach tending. Socio-cultural outcomes were evaluated through intercept surveys designed to assess objectives including access to Swinomish First Foods; community education grounded in Indigenous intergenerational knowledge and values; opportunities for cultural practice; strengthening community connections; exercising self-determination; and supporting the socio-emotional resilience of participants. Invertebrate community composition varied significantly between the clam garden and control site. Clam density varied among species and did not change synchronously across sites or through time. Although limited in temporal scope, socio-cultural findings to date indicate positive progress toward project objectives and strong community engagement.

DOES OLYMPIA OYSTER, *OSTREA LURIDA*, RESTORATION IMPACT COMMUNITY COMPOSITION AND JUVENILE SALMON PREY?

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Restoration of Olympia oysters (*Ostrea lurida*) is expanding throughout the Salish Sea, yet most research focuses on oyster performance rather than ecosystem-level outcomes. Notably, it remains unclear whether native oyster restoration alters small invertebrate community structure or enhances prey resources for juvenile salmon. This study evaluates whether restored Olympia oyster beds influence invertebrate assemblages and whether these changes translate into prey subsidies for juvenile salmon. Differences in invertebrate communities on and off restored oyster beds were assessed, juvenile salmon diets within restoration areas were characterized, and relationships between consumed prey taxa and invertebrate communities were examined. Small invertebrates were sampled using suction sampling at four restoration sites, with replicate samples collected on and off oyster beds during spring outmigration periods (March–April) between 2015 and 2023. Samples were sieved, preserved, and identified to the lowest practical taxonomic level. Juvenile salmon were collected concurrently using beach seines, and gut contents were identified in the laboratory. Restored oyster beds did not increase invertebrate species richness, diversity, or evenness relative to adjacent areas without oysters; however, invertebrate community composition differed between oyster and non-oyster plots across sites, with several prey taxa occurring at higher relative abundance on oyster beds. Gut content analyses indicated that juvenile Chinook consumed proportionally more Diptera, bivalves, and amphipods, whereas chum salmon consumed more harpacticoid copepods. These results demonstrate that Olympia oyster restoration can influence community assemblage structure and prey availability in a site-specific manner, suggesting that ecosystem services provided by this species may vary at localized spatial scales.

RIBBED MUSSEL (*GEUKENSIA DEMISSA*) AQUACULTURE TECHNIQUES: INVESTIGATING AN ALTERNATIVE DIET

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Ribbed mussels (*Geukensia demissa*) are understudied bivalves that play a critical role in U.S. East coast marshes. They are in high demand due to their ecological engineering applications, but aquaculture for the species is underdeveloped. Ribbed mussels are one of the few bivalves capable of feeding on small-sized bacterioplankton. Due to their ability to feed upon small particles, it was hypothesized that *Nannochloropsis oculata* (Nanno), a relatively small green microalgae with high lipid content, would be a beneficial supplement to the standard diet of *Tisochrysis lutea* (Tiso), improving survival and growth. The results of feeding larval and juvenile ribbed mussels a controlled diet of 100% Tiso and an experimental diet of 2:1 Nanno:Tiso were compared. Diet did not significantly influence larval ribbed mussel survival, but did influence larval growth, with larvae fed the Nanno mix treatment growing significantly slower. Larvae fed the Tiso diet exhibited a negatively skewed distribution of final shell lengths, while those fed the Nanno mix diet exhibited a bimodal distribution with a noticeable overlap between the right peak and the unimodal distribution of the Tiso-fed larvae. In contrast to the larval experiment, diet had a significant effect on juvenile survival but did not have a significant influence on juvenile growth. Juveniles fed the more diverse Nanno mix diet demonstrated statistically higher survival than juveniles that were solely fed Tiso. Unlike the larval experiment, juveniles from the two diet treatments exhibited broadly overlapping final shell length distributions. The difference in performance between larvae and juveniles may suggest intraspecific niche partitioning related to the particle selection efficiency of this species.

INDUCIBLE DEFENSES IN OYSTERS: HOW AGE, SIZE, AND PREDATOR EXPOSURE SHAPE PHYSIOLOGICAL AND TRANSCRIPTOMIC RESPONSES

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Inducible defenses occur when an organism responds to predator presence by changing its phenotype to reduce predation risk. Oysters induce defenses in response to chemical cues from predators like blue crabs, mud crabs, and drills, by developing stronger shells. Their response is proportional to predator type and biomass. Older and larger oysters may respond less to predators if they have outgrown predation threats. This research explored the phenotypic and transcriptomic responses of oysters to predators through two experiments.

The first experiment explored the responses of different age and size classes of oysters to blue crabs. Three starting size classes (2.5, 4, and 8 mm) for three different aged cohorts (5, 12, and 17 months) were exposed to blue crabs for six weeks at the Rutgers Aquaculture Innovation Center. Following exposure, oyster shell strength was measured. Results showed larger starting sizes (8 mm) and 12-month-old oysters responded most to predators. This was unexpected and could be due to differences in cohorts or higher energetic reserves in the 8 mm oysters. The second experiment examined transcriptomic responses of oysters with and without previous predator exposure. After 24h of blue crab exposure, RNA-sequencing of mantle tissue showed oysters with previous predator exposure upregulated more shell formation genes providing evidence for genetic memory in oysters.

Identifying genes responsible for predator response in oysters can provide valuable insights into defense mechanisms and possibly facilitate breeding of oysters with stronger shells. These findings can help develop effective ways to induce stronger shells in oyster for aquaculture and restoration.

GREEN CRAB RECRUITMENT DYNAMICS IN THE SOFT-BOTTOM INTERTIDAL ALONG THE MAINE COAST (2020-2025)

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Green crabs (*Carcinus maenas*) first appeared in North America in 1817 in Long Island Sound and reached Casco Bay, Maine, by 1905 (Rathbun). Populations expanded Downeast and into New Brunswick by the 1950s, with two major explosions. Glude (1955) tied the first increase to warm Gulf of Maine (GOM) winters boosting crab survival, as cold typically kills crabs and eggs; soft-shell clam (*Mya arenaria*) landings then plunged 79% from 33.7 million pounds (1950) to a historic low of 7.1 million (1959). Colder winters spurred clam recovery to 38.4 million pounds by 1977, but populations have since fallen 85%, hitting three more record lows post-2017 amid rising GOM seawater temperatures accompanied by a second explosion of green crabs.

Since 2020, passive collectors (1-ft × 2-ft × 3-in units with mesh excluding organisms >2.1 mm) have been deployed on lower mid-intertidal mudflats across 12 Maine communities, spanning the coastline. Placed in spring (< 10°C seawater, pre-spawning) and retrieved in late October/early November (post-settlement), these monitor soft-shell clam recruitment dynamics. They also capture juveniles of other taxa (12 bivalves, 2 polychaetes, 5 gastropods, 2 crustaceans), including green crabs.

Green crab recruitment varied significantly across southern, midcoast, and eastern Maine from 2020–2025, with regional shifts in density, size, and presence. Southern sites showed increasing densities over time; midcoast sites had extreme localized abundance and yearly fluctuations in density and size; green crabs nearly vanished in the past two years at Downeast sites. These trends signal ongoing challenges for the clam fishery of Maine amid climate shifts.

UNLOCKING THE GENETIC POTENTIAL OF THE SHRIMP, *PENAEUS VANNAMEI,* THROUGH GENOMIC SELECTION AND PREDICTION

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The shrimp, *Penaeus vannamei,* is widely farmed worldwide and is a cornerstone of food security and livelihoods in developing regions of Africa, southeast Asia, the Pacific coast of Latin America, from northern Peru to northern Mexico, and the Caribbean. Although naturally associated with coastal and estuarine ecosystems, the species is increasingly cultured in low-salinity and freshwater-influenced inland systems, expanding production while raising concerns related to genetic erosion, disease emergence, and ecosystem sustainability. Intensifying pressures from overutilization of broodstock, recurrent disease outbreaks, habitat degradation, and unsustainable freshwater management practices pose growing risks to long-term population viability and resilience, underscoring the need for integrated environmental sustainability research alongside genetic improvement efforts.

Genomic selection (GS) provides a promising framework to address these challenges by accelerating genetic gain while reducing dependence on wild and founder populations. Current genomic prediction (GP) approaches in *P. vannamei* primarily employ genomic best linear unbiased prediction (GBLUP) and single-step GBLUP, with Bayesian and multi-trait models offering improved accuracy for growth, survival, and disease resistance traits. Advances in reference genome quality, SNP discovery, and low-cost genotyping have enabled practical deployment of GP in commercial breeding programs. Nonetheless, major challenges persist, including variable phenotype quality, destructive disease challenge testing, rapid linkage disequilibrium decay, and strong genotype-by-environment interactions across diverse farming systems. Despite these constraints, the species' high fecundity, short generation interval, and large family sizes create exceptional opportunities for rapid genetic progress. Integrating genomic prediction with conservation-oriented breeding strategies, functional genomics, and environmentally sustainable aquaculture practices will be critical for ensuring resilient and responsible shrimp production in emerging regions worldwide.

PATHWAYS FOR EXPANDING THE REGIONAL SHELLFISH SEED BIOSECURITY PROGRAM TO U.S. PACIFIC COAST STATES

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The transfer of shellfish seed is critical to aquaculture production and restoration efforts, but it presents biosecurity risks associated with the spread of pathogens, parasites, and non-native species. The Regional Shellfish Seed Biosecurity Program (RSSBP) was established to provide a coordinated, science-based framework for managing these risks while supporting responsible shellfish seed movement. While the program has been implemented in other regions, interest is growing in extending this approach to U.S. Pacific Coast States.

This workshop aims to identify and prioritize the key steps, considerations, and prerequisites needed to support potential expansion of the RSSBP to the Pacific Coast. Topics include assessment of regional disease profiles, evaluation of existing state and federal regulatory frameworks, alignment with tribal authorities, and identification of data gaps in shellfish health monitoring. The presentation also highlights the importance of stakeholder engagement, including growers, hatcheries, resource managers, and researchers, to ensure that any future expansion is both scientifically robust and operationally practical.

Lessons learned from the existing structure of the program will be used to identify opportunities and challenges unique to the Pacific Coast, such as diverse species assemblages, varied production systems, and long-distance seed transfers. By describing a clear pathway for expansion, this workshop aims to support informed discussion among key stakeholders and NSA members and contribute to the development of a regionally coordinated biosecurity framework that protects shellfish resources while sustaining aquaculture and restoration activities along the U.S. Pacific Coast.

CARAPACE WIDTH-WEIGHT RELATIONSHIPS AS INDICATORS OF BIOLOGICAL CONDITION IN RECREATIONALLY HARVESTED DUNGENESS CRAB (*METACARCINUS MAGISTER*) ON THE WASHINGTON COAST

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Dungeness crab (*Metacarcinus magister*) can be found along the 157 miles of the Pacific coastline of Washington and within the estuarine waters of Grays Harbor, Willapa Bay, and Columbia River. Recreational harvest expanded during the 20th century with effort concentrated in protected coastal waters. Management of the recreational fishery follows the “3-S” approach, size, sex, and season, to protect crab health and reproductive vitality. Under this strategy, recreational management measures include licensing requirements, harvest and size limits, prohibition on retention of female crabs, legal gear specifications, seasonal gear restrictions, and gear marking rules. The recreational fishery is open year-round with short seasonal pot closures to reduce handling mortality of soft-shelled crab. These regulations are intended to support sustainable harvest while maintaining broad access for coastal communities and visitors. Biological data collected during recreational creel interviews were analyzed to evaluate patterns in the biological condition of recreationally harvested crab across seasons and areas. Carapace width-weight relationships were assessed using log-transformed regression models, with comparisons across shell hardness and season to examine variability in crab condition potentially associated with molt stage and harvest timing. This analysis highlights the value of biological data collected through recreational creel surveys and demonstrates how such information can improve understanding the biological condition of harvested crab. Results provide a foundation for future integration of biological metrics with fishery-dependent estimates.

EPIGENETIC-LIKE REGULATORS SHAPE STRAIN-LEVEL DIFFERENCES IN *VIBRIO PARAHAEMOLYTICUS* AHPND PATHOGENICITY

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Epigenetic-like regulation in bacteria, such as histone-like nucleoid-associated proteins (NAP) and RNA regulators, influence DNA organization, gene activity, and host interaction. Their roles in *Vibrio parahaemolyticus* strains that cause Acute Hepatopancreatic Necrosis Disease (AHPND) are not yet well defined, despite clear differences in virulence among isolates.

This study examined two AHPND-positive strains, D6 and the more virulent E1, through comparative genomics and RNA sequencing at 4, 9, and 16 hours. Six major groups of nucleoid-associated regulators: H-NS, HU/IHF, Fis, Lrp/AsnC, Dps, and Hfq, were identified across chromosomes and plasmids in both strains. Transcriptomic analysis showed that E1 consistently expressed several histone-like proteins and RNA chaperones at higher levels than D6, especially during later growth.

When NAP expressions were compared with genome-wide transcription patterns, a distinct group of E1-specific genes located on plasmids showed strong positive correlation with these regulatory proteins. Several chromosomal genes, in contrast, displayed negative correlation, suggesting transcriptional silencing through DNA structuring. These patterns match phenotypic observations: E1 produces more colonies, shows stronger colonization ability, and maintains higher CFU counts than D6 despite similar overall growth.

The findings highlight a regulatory system in *V. parahaemolyticus* that behaves in an epigenetic-like manner. Differences in NAP activity appear to shape strain behavior and may help explain why some AHPND strains are more virulent. This work adds new insight into *Vibrio* regulatory biology.

TWO DECADES OF PARASITISM TRENDS IN CONNECTICUT OYSTERS

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The eastern oyster (*Crassostrea virginica*) is a commercially and ecologically significant oyster species that has long been a food source for coastal populations. In many locations, overharvesting, pollution, and disease has led to declining wild populations. Significant research and monitoring have been done on this species, especially following epizootic outbreaks of the important oyster parasites, *Haplosporidium nelsoni* (MSX) and *Perkinsus marinus* (Dermo). Comparatively little focus has been given to other common, but less lethal, oyster parasites. Yet, parasite diversity and load are increasingly recognized as ecological indicators of population health. Perspective on overall oyster parasite dynamics could be beneficial to resource managers by shedding light on trends impacted by changing environmental conditions.

The Connecticut Department of Agriculture Bureau of Aquaculture has monitored oyster populations along its coastline since 1997. This program has recorded the presence of multiple oyster parasites through histological methods. The prevalence of several oyster parasites (i.e., *Nematopsis* sp., *Stegotricha* sp.) in adult oysters collected in the fall or winter season from 1997 to 2016 will be presented. Results will be paired with available Long Island Sound water temperature and salinity data to provide context on concurrent environmental trends. Additionally, recent data (2024) will give insight into where these often-overlooked parasites currently stand. Preliminary analyses indicate complex and species-specific trends. The oyster parasitome undoubtedly impacts individual oyster health and resiliency and incorporating a more holistic understanding of oyster parasitism could lead to better outcomes in oyster management.

SEA SURFACE TEMPERATURE AND UPWELLING AS PREDICTORS FOR DUNGENESS CRAB RECRUITMENT SUCCESS, FISHERY LANDINGS, AND POPULATION ABUNDANCE

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The coastal Dungeness crab (*Metacarcinus magister*) fishery is the most productive fishery in Washington State over the last 15 years in terms of biomass landed and revenue generated. Despite the importance of Dungeness crab to both state and Tribal co-managers in Washington, there is a lack of fisheries independent data and little to no ability to predict abundance for upcoming fishing seasons. Instead, managers utilize the "3-S" management framework by setting a minimum "Size" of 159 mm, constraining harvest to a single "Sex" (males), and setting harvest "Seasons" to avoid fisheries during the peak molting period of male crabs. The lack of fisheries independent data and lack of abundance estimates hinders the ability of co-managers to attain harvest sharing goals. Recognizing that larval survival likely determines adult abundance and that annual landings serve as a reliable proxy for the total population, this study examined generalized additive models and species distribution models to assess the impact of ocean and climate drivers on population abundance. The fishery primarily catches four-year-old crab, so ocean and climate conditions were lagged four years and used to predict annual fisheries landings. The most parsimonious models of relative abundance were based on water temperature and upwelling during larval development and settlement, which significantly correlated with fisheries landings four years later. This information can enhance co-management negotiations, harvest regulations, and entanglement risk reduction measures.

INVESTIGATING OYSTERS: 4-H GUIDE TO UNDERWATER SCIENCE ACTIVITIES FOR YOUTH

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The "Investigating Oysters" Underwater Science Activity Booklet is an exciting educational resource developed as part of the Smart, Sustainable Shellfish Aquaculture Management (S3AM) program. S3AM is a nationwide, multi-institutional initiative funded by the USDA that leverages smart technologies to improve the efficiency, economic viability, and environmental sustainability of oyster farming. By integrating innovation with aquaculture practices, the program aims to support a thriving shellfish industry while protecting marine ecosystems.

This booklet introduces young learners to the fascinating world of oysters and the cutting-edge technologies shaping the future of aquaculture. Through hands-on, inquiry-based activities, participants explore topics ranging from oyster biology to underwater robotics. The activities are designed to spark curiosity and build STEM skills, making complex concepts accessible and fun.

Highlights of the booklet include:

- **Virtual Oyster Dissection** – A guided digital experience that teaches anatomy and the ecological role of oysters in marine environments.
- **Buoyancy and Propulsion Experiments** – Interactive lessons that explain the principles of underwater movement and stability.
- **4-H SAM Robot Build Guide** – Step-by-step instructions for constructing the Shellfish Aquaculture Management (SAM) robot, an entry-level underwater Remotely Operated Vehicle (ROV). The SAM robot was specifically designed for youth ages 8–16, allowing them to easily assemble and operate a functional underwater robot.

By combining marine science with robotics, this resource empowers the next generation to explore aquaculture careers and understand how technology can make oyster farming smarter and more sustainable.

HURRICANE IMPACTS ON WATER QUALITY AND OYSTER REEF HABITAT IN A LARGE, WIND-DRIVEN ESTUARY

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This study examined differential impacts of three sequential tropical cyclones – Hurricanes Florence and Dorian, and Tropical Storm Michael – on water quality and natural versus constructed oyster reefs in Pamlico Sound, North Carolina, USA. Long-term monitoring data collected before and after storm events found that reef type, water depth, reef vertical relief, and location mediated reef stability, oyster density and size-structure, sedimentation, and water-quality responses to storms. Deep-water reefs (~ 4.5-7m) experienced extensive sediment burial, hypoxia, and oyster mortality, whereas shallower reefs located in protected embayment (~ 1.5-3m) and reefs with high vertical relief (> 0.5m) displayed minimal structural change and short-term recovery. Management and restoration strategies aimed at resilience to tropical cyclones should explicitly account for reef setting and structure. Incorporating storm vulnerability into restoration planning, preserving no-harvest sanctuaries, and prioritizing resilient reef settings will be key to sustaining oyster populations in dynamic estuarine environments under increasing tropical storm frequency and intensity.

THE USE OF PROBIOTICS TO MITIGATE ATLANTIC SEA SCALLOP (*PLACOPECTEN MAGELLANICUS*) MORTALITY FOLLOWING CHALLENGE WITH PATHOGENIC *VIBRIO* SPECIES

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The Atlantic sea scallop (*Placopecten magellanicus*) supports one of the most economically important fisheries in the northeastern United States. Scallop farmers rely on the acquisition of juvenile sea scallops to continue production, but wild spat collection is inconsistent. Hatcheries in the state of Maine could reliably produce spat year-round, but struggle with mortality events. Probiotics have decreased mortality amongst bivalve larvae in other industries and could be implemented to decrease larval sea scallop mortality.

Seven probiotic bacteria were identified from the literature and screened *in vitro* for potential benefits to sea scallop larvae. Bacterial competition assays were used to examine the inhibition of a model pathogen, *Vibrio pectenicida*, by probiotic candidates. Challenge trials involving larval sea scallops and *V. pectenicida* (10^5 CFU/mL) were also conducted to test the effectiveness of applied probiotics on challenged and non-challenged larvae. *Alteromonas macleodii* (10^5 CFU/mL) increased survival amongst challenged larvae (RPS 46% ± 11) and *Pseudoalteromonas espejiana* (10^4 CFU/mL) amongst non-challenged larvae (RPS 46%). Both treatments were tested at a hatchery scale with *in vivo* challenge trials. *A. macleodii* had a negative impact on larvae growth and survival. *P. espejiana* improved the rate of larval sea scallop growth and development during the late straight hinge to early pediveliger stage, where larvae mortality typically occurs.

Results from this study can improve hatchery protocols through the implementation of the probiotic *P. espejiana*. Further investigation into potentially problematic *Pseudomonas* and *Vibrio* species is underway in tandem with the isolation of lytic bacteriophages to explore phage therapy in the hatchery.

MONITORING FOR OsHV-1 IN JUVENILE PACIFIC OYSTERS ON THE U.S. WEST COAST

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Ostreid herpesvirus-1 (OsHV-1) poses a global threat to Pacific oyster (*Crassostrea gigas*) production, with viral emergence causing significant mortality and economic losses in some regions. On the U.S. West Coast, oyster aquaculture spans Alaska to Southern California, and Hawaii, with stock transfers governed by state biosecurity regulations. To date, OsHV-1 has been detected only in limited areas of northern California and San Diego Bay, with routine testing conducted during health examinations and mortality events. In 2020, a sentinel monitoring program was initiated to monitor and characterize OsHV-1 outbreaks on the U.S. West Coast in collaboration with commercial oyster farms in Washington, Oregon, and California. This program provides multi-year, seasonally resolved data on OsHV-1 presence. From 2020 to 2024, two oyster families predicted to have low and high survival were outplanted and monitored during their first summer of field growth, when OsHV-1 infection and mortality risk are highest. Across all sites, OsHV-1 was consistently detected at only one location—Tomales Bay, California - where OsHV-1 - associated mortalities occur annually. Cox proportional hazards models are being used to evaluate whether mortality risk is associated with (1) oyster family and outplant timing, (2) viral load (when present) and oyster size at mortality, and (3) temperature.

DIFFERENTIAL SUSCEPTIBILITY OF EASTERN OYSTER FAMILIES AND LINES TO OsHV-1 VARIANTS

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Given concerns about potential impacts to East and Gulf coast shellfish industries should OsHV-1 emerge in the region, laboratory trials were conducted to assess susceptibility of eastern oyster (*Crassostrea virginica*, *Cv*) families and lines to viral variants. Spat from 30 families and two lines exposed to a French µvar via bath challenge, resulted in mortality ranging from 0–50% (mean 15%). Juveniles from eight families spanning low to high survival were subsequently challenged by injection with French and San Diego µvars, with mortality ranging from 0 – 87% (mean ~ 23%). Survival across bath and injection challenges was highly correlated (R = 0.9 – 0.99). Viral loads were positively associated with mortality, with poorly performing families having higher viral DNA concentrations and lower levels in families exhibiting little or no mortality. Survivors in susceptible families also had higher levels of viral DNA. Using progeny from these families, a dose–response experiment with the San Diego variant was conducted using progeny from two *Cv* families predicted to have high (*Cv* high) and moderate (*Cv* moderate) survival, along with a Pacific oyster control. Survival was as predicated for *Cv* high while *Cv* moderate had similar survival to the Pacific oyster control at the high dose but higher survival at all other doses. Results indicate that while some *Cv* families are susceptible to OsHV-1, many exhibit tolerance, suggesting that selective breeding could be an effective mitigation strategy. Multi-trial genetic parameter analysis assessing the heritability of OsHV-1 resistance in *C. virginica* will be presented.

GEOGRAPHIC AND SEASONAL SURVEILLANCE FINDS NO OsHV-1 IN ATLANTIC AND GULF BIVALVES

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Disease outbreaks and mass mortality events have increasingly affected shellfish fisheries and aquaculture. Effective disease management depends on strong biosecurity and clear knowledge of pathogen distributions across regions and host species. A major emerging threat to bivalve aquaculture is Ostreid herpesvirus 1 (OsHV-1), particularly the globally distributed µvars that have caused severe mortalities in Pacific oysters since 2008. Despite this risk, OsHV-1 is not routinely monitored in susceptible Atlantic and Gulf of Mexico species, and the most recent geographic survey predated the emergence of µvars. A broad geographic survey was conducted to assess OsHV-1 presence in eastern oysters (*Crassostrea virginica*), northern quahog (= hard clams) (*Mercenaria mercenaria*), and bay scallops (*Argopecten irradians*) across the U.S. East and Gulf coasts. Samples of 1–2 cm bivalves (n = 150 per site; ~ 2,700 total) were collected from 16 sites in 13 states by academic, State, and Federal colleagues and tested using OsHV-1–specific qPCR in 2023–2024. A targeted seasonal survey was also conducted at four sites/states (Virginia, North Carolina, Florida, and Alabama) during spring–summer (3-4 time points), when viral activity is most likely. OsHV-1 was not detected in any samples collected during the geographic or seasonal survey. These results, together with the absence of OsHV-1–associated mortality events in Atlantic and Gulf species, indicate that OsHV-1 is not present in U.S. East and Gulf coast waters.

TRANSCRIPTOMIC RESPONSES TO TEMPERATURE AND OXYGEN IN TWO POPULATIONS OF OLYMPIA OYSTERS

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Olympia oysters (*Ostrea lurida*) are the only oyster species native to the North American west coast. Restoration and conservation efforts for these species are important for maintaining the ecological, economic, and cultural value of coastal ecosystems as well as mitigating the effects of climate change. As sessile invertebrates inhabiting estuaries along the coast, Olympia oysters are subject to frequent and intense environmental stressors, particularly marine heatwaves and hypoxia events. In this study, survival and transcriptome-level responses in hatchery-reared *O. lurida* oysters from two populations were evaluated following exposure to elevated temperature and low oxygen. Survival results showed that during combined elevated temperature and anoxia stress, the Morro Bay oyster population survived longer (LT_{50} = 28.5d) compared to those from Elkhorn Slough (LT_{50} = 18.5d). Transcriptomic responses to these stressors were assessed after 48 hours of treatment exposure using RNAseq. Two approaches used in the transcriptomic analysis included pair-wise assessments of differential gene expression (DGE) and a weighted gene correlation network analysis (WGCNA). DGE analysis in response to the fixed effects of population, temperature, oxygen, and their interactions found 45 significantly differentially expressed genes. WGCNA identified 18 unique gene networks, of which two were significantly associated with population, two were associated with both population and meat weight, and five were associated with oxygen treatment. Together, these findings provide insight into both the population-specific and generalized responses of *O. lurida* to two common west coast environmental stressors and lay a foundational framework for identifying climate-resilient phenotypes to inform future restoration breeding strategies.

IMMUNE PRIMING DEFENSE ACROSS DISTINCT LIFE STAGES IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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For decades, the aquaculture industry has suffered economic losses via unexplained oyster mortality. Although many stressors have been implicated, perhaps the most historically significant are infectious diseases. Yet, current disease management practices suffer from many issues. For instance, economically and ecologically valuable eastern oysters suffer from distinct pathogens during each critical period of development, hampering shellfish production. To assuage these concerns, there is great potential to leverage a phenomenon across distinct life stages called "immune priming," which improves resistance/tolerance to infection prior to disease onset. Under the hypothesis that prior pathogenic experience affects resistance and tolerance to secondary exposure, life stage-specific activation of oyster immune defense was performed by priming with heat-inactivated, cultured stocks of *Vibrio coralliilyticus*, *Vibrio alginolyticus*, *Tenacibaculum ascidiaceicola*, and *Roseovarius crassostreae*. Subsequently live secondary pathogen treatments were administered to larvae or seed representing all possible priming by secondary treatment combinations, with the prediction that homologous challenges will lower infection intensities and increase survival. When monitoring survival to secondary pathogen exposures, preliminary work has revealed immune priming specificity at the larval stage of development, where not only is survival improved by homologous challenges, but protection is pathogen species-specific. Additionally, immune priming may provide non-specific protection against pathogens known to affect seed. Although work is still ongoing to reveal how responses differ across hatchery sources and into adulthood, exploring and exploiting the efficacy of this evolved phenomenon in eastern oysters has great potential to benefit aquaculture disease management practices at both regional and national scales.

CHARACTERIZING OSHV-1INFECTION IN MIDORI AND MIYAGI PACIFIC OYSTERS USING LINEAGE-SPECIFIC TRANSCRIPTOMICS

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The OsHV-1 virus, in particular the highly virulent microvariants (μVars), have caused significant mortalities in Pacific oysters around the world, heavily impacting aquaculture production. Although OsHV1μVars outbreaks have been limited in the U.S., there is the potential for a devastating emergence. A proactive preventive approach includes a better understanding of the nature and dynamics of the oyster-virus interaction specifically in oyster populations that are grown in the U.S. West coast.

In this study, the early (48 h after infection) response of juvenile oysters from two different lineages of Pacific oysters (Midori and Miyagi) were comprehensively characterized to OsHV-1 μVars using RNA sequencing. Two different OsHV-1 μVar strains were also used for comparisons, one that was originally isolated in the U.S. (the "San Diego" microvariant) and one from Australia.

To increase the specificity of the study to U.S. Pacific oyster populations, the sequencing reads were used to assemble *de novo* oyster transcriptome, independently of publicly available reference genomes assembled which are based on oysters from Europe and/or Asia. Findings on oyster differentially expressed genes and pathways between populations and viral strains used will be presented.

SECOND HARVEST: BIOFOULING MACROALGAL YIELD IN CALIFORNIA OYSTER FARMS

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Macroalgal recruits in shellfish aquaculture are considered fouling organisms; however, several of these estuarine seaweed species can have significant ecological or commercial value. Increasing commercial demands for seaweeds coupled with the high costs and permitting barriers for new aquaculture sites in California call for cooperative research to identify the potential benefits of harvesting wild seaweed from existing aquaculture production gear. This study describes the community structure, yield, and quality of macroalgae associated with the three primary gear types for Pacific oyster (*Crassostrea gigas*) culture in California. These metrics are assessed across the three main growing areas for oyster aquaculture in California (Humboldt, Tomales, and Morro Bays) to inform shellfish growers who may want to consider harvesting seaweed. Monthly harvests over a year show distinct seasonal and regional algal communities associated with culture gear and allow identification of peak conditions for dominant species with commercial potential: *Pyropia* spp., *Ulva* spp., and *Gracilaria* spp. Analyses of harvest quality and elemental composition of these main species give insight into opportunities for food and agricultural markets. Finally, preliminary labor models indicate potential economic profitability for farmers. This research will support important management decisions from the individual farm level to sustainable aquaculture policy in California and beyond.

CIRCASEMILUNAR FORAGING ACTIVITY OF A PREDATORY WHELK: CUES AND CONSEQUENCES REVEALED BY TIDAL EMERSION EXPERIMENTS

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Predatory gastropods can have a controlling influence on community dynamics, including survival and size distributions of prey populations in both wild and farmed settings. For intertidal species like the dogwhelk *Nucella ostrina*, foraging on barnacle prey generally requires movement higher on the shore and, due to its slow mobility and prey handling time, increases thermal risk. Motivated by observations of whelk activity at field sites and studies of biological rhythms in other marine taxa, we examined whelk foraging activity in outdoor mesocosms with manipulated tidal conditions in Friday Harbor, Washington, a regional 'hot spot' known for extended daytime low tides in summer. Foraging activity followed a biweekly pattern; snails emerged from shelter to feed for ~4 days then retreated for the remaining ~10 days of each spring-neap cycle. Peak foraging activity coincided with the onset of spring tides, on days with reduced thermal risk due to early morning aerial exposure. A shift in the timing of the tidal cycle by 7 days caused a corresponding shift in foraging activity, while a shift of 12 hours resulted in aperiodic foraging. Under tidal regimes that provided cool foraging opportunities for longer durations snails foraged more and growth increased. These results suggest *N. ostrina* relies on environmental cues beyond solar and lunar illumination to tune its foraging behavior and underscores the importance of understanding the temporal patterns of microhabitat usage in assessing the thermal exposure of mobile organisms and potential cascading impacts to their prey.

DOMESTICATION AND SELECTIVE BREEDING DRIVE INTESTINAL MICROBIOTA STABILIZATION IN THE SHRIMP, *PENAEUS VANNAMEI*

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Domestication, selective breeding, and improved culture practices have driven the successful expansion of shrimp aquaculture in Mexico. The intestinal microbiota (IM) is a critical component of shrimp health, contributing to digestion, immunity, and protection against pathogens, and recent studies emphasize the importance of the IM for the development of more sustainable aquaculture practices; however, the effect of aquaculture-induced domestication on the shrimp IM and its implications for the shrimp industry remain poorly understood.

This study characterized the host genetics and IM of wild-type (WT) and domesticated (AQ) shrimp from Sinaloa, Mexico, across three production cycles (2015, 2016, and 2018). Genomic analysis using single-nucleotide polymorphisms (SNP) revealed genetic differentiation (FST = 0.02), confirming that AQ lines have diverged from their wild counterparts. Analysis of 16S rRNA gene sequences demonstrated significant differences in IM composition between WT and AQ shrimp (ANOSIM $R = 0.85$, $p = 0.001$), with WT shrimp exhibiting higher community dispersion. Notably, AQ shrimp developed a core microbiota consisting of 23 genera that persisted across years, whereas WT shrimp presented only two core genera. AQ shrimp also exhibited a broader niche breadth, dominated by resilient generalist taxa and enriched in beneficial genera, including Bacillus, Pseudoalteromonas, and Ruegeria.

These findings demonstrate that domestication promotes genetic divergence and that aquaculture environments favor more stable, specialized, and beneficial microbial communities. Understanding these changes is essential for developing sustainable management practices and monitoring tools that ensure the continued efficiency and health of the shrimp farming industry.

MANILA CLAM AQUACULTURE IN PUGET SOUND: ESTIMATING NUTRIENT REMOVAL FROM HARVESTS

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Bivalves are a significant economic, cultural, and biological resource for the Pacific Northwest with the region providing 36% of the United States marine aquaculture value in 2022. Manila clams (*Ruditapes philippinarum*), for example, are harvested extensively around Puget Sound and Hood Canal. This pilot project is intended to quantify the amount of nutrients extracted during shellfish harvest at various farming locations in this region. By calculating how much nitrogen and phosphorus are extracted via clam harvests, there may be ecological services farmers may observe from harvesting bivalves in nutrient-varied marine environments. During the study, pilot methods for collecting morphometric and nutrient data for Pacific coast shellfish, similar to the methods used for eastern oysters (*Crassostrea virginica*) as part of a nutrient removal calculator specific to the U.S. mid-Atlantic and Northeast regions. Puget Sound was divided into four main ecoregions to analyze the difference in Manila clam and Pacific oyster (*Crassostrea gigas*) morphometric and N, C, and P content. These data will provide the foundation for a nutrient removal calculator specific to the Puget Sound region, which will aid both growers and regulators in the permitting process. Preliminary results of the pilot study indicate clam tissue contains 10.5% nitrogen by weight. Variations in weight and body size relationships among regions may suggest differences in growth rates and nutrient dynamics across regions. Preliminary conclusions suggest the relationships between the Manila clam size and nutrient removal are not as variable as that of Pacific oysters in the same harvest area.

COMPARATIVE TRANSCRIPTOMIC RESPONSES OF FULL-SIBLINGS DIPLOID AND TRIPLOID PACIFIC OYSTERS UNDER EXTREME SALINITY STRESS

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Farming triploid Pacific oysters has become an industry standard globally because of their reduced reproductive potential and associated superior growth and quality; however, oysters face dynamic and harsh environmental conditions, such as heavy rainfall and subsequent low salinity events, which affect organism fitness and result in substantial economic and social damages. Triploid vulnerability, relative to diploids, to low salinity stress and molecular mechanisms underpinning tolerance remains poorly understood. The effects of varying exposure times (3d, 6d, 9d) to salinity levels of 0 on the survival, reproductive status, and transcriptome of biparental families of reciprocal diploid and triploid oysters was tested and determined the influence of ploidy on these phenotypes. It was found that oysters could survive well after 3 days of freshwater exposure, while 6 days resulted in family-specific responses, and 9 days of freshwater exposure was lethal for most oysters. Overall, limited advantage of triploidy was found after 6 days, with similar survival rates for both diploids and triploids in response to acute low-salinity challenge. Quantitative assessment of reproductive condition of diploids and triploids after 6 days showed higher overall gonadal maturation in diploids, but varying levels of gonad coverage in triploids suggested a positive influence of gametogenesis on survival. Transcriptome analyses indicated that diploids and triploids have comparable responses to low salinity, both undergoing a metabolic shift towards gluconeogenesis and experiencing immune suppression. These findings will inform growers about potential risk factors associated with farming triploids in unfavourable environments and contribute to improved selective breeding for complex traits in Pacific oysters.

WIDESPREAD DEMOGRAPHIC SUPPLEMENTATION OF CONNECTICUT WILD OYSTERS BY AQUACULTURE FARMS

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Large populations of eastern oyster (*Crassostrea virginica*) can be ecological keystones, but their historical decline has severely curtailed potential ecosystem services. More recently, a growing oyster aquaculture industry is sustainably enhancing food production and local economies. Farm oysters can provide many of the same ecosystem services – water filtration, nutrient cycling, and habitat provisioning. An underexplored ecosystem service of farms includes recruitment supplementation of wild populations by farm-source larvae as a result of spawning before harvest.

Based on the discovery that early oyster domestication generates repeatable differentiation at a genomically broad set of markers, the goal of this project is to quantify the spatial and temporal patterns of farm-derived spat recruitment in wild populations along the Connecticut coast. Both wild oysters and gear-based aquaculture are geographically extensive in Connecticut. Using 905 informative markers to study Connecticut oyster spat settled in 2022, admixture (mix of ancestry) analyses revealed few immigrants from farm oyster parents, but farm oyster ancestry averaged 20% across Connecticut 'wild' spat individuals. Co-occurring mixed-age adults had similar levels of aquaculture marker introgression. This pattern is consistent with a low annual level of realized immigration from farms, probably spanning decades. The findings suggest that farmed oysters in Connecticut demographically bolster wild recruitment at low levels. Further work is assessing temporal admixture variation across additional cohorts and inferring potential fitness impacts based on genomic patterns of variation.

PHYSIOLOGICAL RESPONSES OF *MYTILUS EDULIS* TO SINGLE AND RECURRENT HEATWAVE EVENTS

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Blue mussels (*Mytilus edulis*), valued as a sustainable, protein-rich food, were the most farmed Canadian shellfish in 2023. Farming triploid bivalves has gained attention for their functional sterility, higher growth rate, higher year-round meat yields, and increased byssal thread production. However, triploids have been shown to have a lower upper thermal tolerance limit. As marine heatwaves intensify in the North Atlantic, concerns are growing over the survival and performance of both diploid and triploid blue mussels, and consequently for mussel farming. Previous studies show that long-term exposure to 25°C water can be deadly for diploid mussels, but how short-term or recurrent heatwaves affect triploids remains unknown. This study investigates how recurrent marine heatwaves affect the energy balance of diploid and triploid blue mussels. Diploid and triploid mussels with the same genetic background experienced one of two temperature treatments: (1) a "naïve" group kept at 20°C for 16 days and then exposed to a 5-day heatwave at 25°C, or (2) a "recurrent" group cycled through three 5-day heatwave events interspersed with 2-day recovery periods. Respiration and feeding rates were measured to gain an understanding on how diploid and triploid mussels use energy under environmentally relevant thermally stressful events. Preliminary results show that mussels under repeated heatwave conditions experience physiological signs of stress through a reduction of byssus produced and increased respiration rates. This research will improve the understanding of how heatwaves affect mussel performance and could help the aquaculture industry develop more resilient and heat-tolerant mussel stocks.

SHELLFISH AQUACULTURE EDUCATION IN THE CLASSROOM AND ON THE TIDE FLATS

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Pacific Shellfish Institute (PSI) has conducted outreach and education to K-12 students for decades. In response to teacher demand for Career and Technical Education (CTE) materials, PSI has shifted its focus to introducing middle and high school students to careers in marine science. In this session, the PSI will showcase two new Shellfish Aquaculture curricula available to the public via Open Educational Resources (OER) Commons. The curricula include activities (microscopy, population surveys, farm practices, and stewardship) that highlight skills utilized in shellfish-related careers ranging from working on-the-farm to regulatory agencies such as Fish and Wildlife and Department of Health. PSI will also demonstrate how activities can be incorporated into fun and competitive relay-style learning opportunities for audiences of all ages.

HIGH RESOLUTION ENVIRONMENTAL SURVEILLANCE CONTEXTUALIZES MOLECULAR SIGNALS TO REVEAL MICROBIAL DYNAMICS DURING OYSTER DISEASE OUTBREAK

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Disease outbreaks and resulting mortality events have detrimentally affected the growth of the oyster aquaculture industry in North Carolina. Due to the complexity of marine systems, etiology and onset of disease remains largely unexplained. To improve the understanding of disease dynamics at play in the environment, a longitudinal study over 60 consecutive days was undertaken at an oyster lease with a history of severe mortality. On a daily basis, a subset of oysters (*Crassostrea virginica*), water samples, and environmental parameters daily were collected to interpret the status of the oysters and identify key fluctuations in the environment. A suite of molecular assays for droplet digital PCR (ddPCR) was employed to quantify multiple *Vibrio* spp. in both the visceral mass and surrounding water column. Additionally, a panel of oyster-specific immune markers was included to monitor the stress response of oysters to putative pathogens by taking advantage of environmental RNA (eRNA) to track cytokine production. Prior to the first observations of mortality on the lease, there was a strong oscillatory microbial signal in the water column followed by an accumulation of *Vibrio* belonging to the Harveyi clade in the oyster tissue. Both cytokine and *Vibrio* spp. DNA concentrations reached their maximum before oysters began to present with pathology suggesting a possible sentinel signal that offers predictive capacity for disease onset. For the molecular signatures, a pattern began to emerge with peaks in concentration occurring every four days which would be missed with weekly assessments making more regular sampling critical for optimal surveillance.

OYSTER MICROBIOME INSIGHTS: EXPLORING RELATIONSHIPS BETWEEN BACTERIAL COMMUNITIES AND HOST HEALTH METRICS

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Microbiomes have the potential to provide beneficial services to bivalve hosts through antimicrobial and probiotic activity, immune defense, and response to environmental stressors which can impact host performance. Ongoing work aims to classify core members of oyster microbiomes to better establish bacterial symbionts that serve as markers of oyster health. This talk will synthesize two 16S metabarcoding field studies of oyster gills - a survey and a reciprocal transplant - to provide insight into microbial members contributing to *Crassostrea virginica* health and performance in Chesapeake Bay. Oyster gills surveyed in the field maintained distinct bacterial communities from the water, varied by site, and revealed an association between *Endozoicomonas* and the absence of *Perkinsus* spp. infection. No ASV were shared by all oysters, but 103 ASV were shared across surveyed sites spanning 4 tributaries. During transplant experiments, oyster condition depended on disease status and recovery location rather than deployment/source location. Oyster gills shared 4 core ASV and bacterial community composition clustered by source location with shifts in composition for oysters transplanted between rivers. These results indicate the current environment and infection status are more important for oyster health than oyster source, but shifts in microbial community vary based on both source and current environment. Further synthesis across studies will explore shifts in gill microbiomes with ploidy, site-specific features, and oyster health metrics.

SIZE-BASED INGESTION OF MICROSPHERES AND MICROFIBERS BY TWO FRESHWATER MUSSEL SPECIES (*DREISSENA BUGENSIS* AND *ELLIPTIO COMPLANATA*): IMPLICATIONS FOR REMOVAL OF MICROPLASTIC POLLUTION

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Quagga mussels (*Dreissena bugensis*) and eastern elliptio (*Elliptio complanata*) are two freshwater bivalve species in the United States. The ability of these species to process large volumes of water may have applications for water clarification in freshwater systems, including wastewater treatment plants. Degradation of MP pollution could be furthered by co-concentrating MP and plastic-degrading bacteria in the biodeposits of mussels. Lacking are data on the way in which *D. bugensis* and *E. complanata* handle MP, including whether large microfibers and microspheres are ingested or rejected in pseudofeces, which are diffuse and may be more easily resuspended than denser feces. To examine this issue mussels were exposed to MP spheres and fibers, ranging from 20µm to 1mm in length or diameter in individual assays. The number of MP rejected in pseudofeces and egested in feces was quantified to determine the proportion of each type that was rejected vs. ingested. Large microfibers and spheres (250 µm, 500 µm, 1mm) were rejected in high proportions up to 100%, whereas the smallest particles (50µm and 75µm fibers, 20µm and 50µm spheres) were rejected in lower proportions (ca. 20 to 75%). The eastern elliptio overall rejected MP in lower proportions than the quagga mussel, indicating that this species may be better at removing MP from freshwater systems. Follow-up feeding assays were conducted with *E. complanata* to examine processing of MP and bacteria. Data indicate that suspension-feeding represents a potential avenue to co-concentrate MP and plastic-degrading bacteria to increase the elimination of plastic particles.

HARNESSING NORTHERN QUAHOG (= HARD CLAM) (*MERCENARIA MERCENARIA*) BURIAL BEHAVIOR FOR EELGRASS (*ZOSTERA MARINA*) RESTORATION: PRELIMINARY EVIDENCE FOR EFFECTIVENESS

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Seagrass beds are nursery habitat for fish, crustaceans, and bivalves. Beds provide foraging grounds for migratory fish and birds. Seagrass ecosystems are declining globally due to eutrophication, pollution, overfishing, habitat degradation, and climate change. While seagrass research and restoration projects have a long history, the underlying anthropogenic pressures (shoreline development, pollution, climate change, etc.) that cause seagrass loss continue to persist. Current seagrass restoration methods are laborious, expensive, and have low success rates.

In this preliminary study, the feasibility of using natural northern quahog (= hard clam) *Mercenaria mercenaria* burial behavior and gelatin-based hydrated glue to plant eelgrass (*Zostera marina*) seeds was tested. The 9% gelatine glue is easy to prepare, sprayable, and generates a protective hydration layer. When coupled with hard clams, this allows for seeds to be planted at 1-3 cm depth. Gelatin adhered seeds on clams remained attached at least 17-fold longer than the hour plus time it takes most clams to rebury once dislodged. In well-oxygenated, low turbulent flow laboratory experiments, hand broadcast seeds and clam-planted seeds in the same substrate sprouted at similar rates. Hard clams in a range of sizes reached similar burial depths. Clam drop experiments in a seawater tank were used to determine the area of planted seeds. Clam planted seeds had greater above- and below-ground biomass than broadcast seeds, but germination rates were approximately equal. Results show that using two foundational species and taking advantage of predictable configurations and their facilitative relationship could be an effective approach to restoration.

PHYSIOLOGICAL RESPONSES TO EXTENDED WINTER HOLDING PERIODS AND SUBSEQUENT WARM-UP IN EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) SEED

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Shellfish hatcheries continually seek ways to augment production to meet industry demand. Oyster Seed Holdings, Inc. (OSH), a commercial oyster hatchery in Virginia, “overproduces” seed early in the season from mid-January through mid-February, principally because of prime water quality. This early seed cannot be transferred to outdoor nursery systems until late-March to early-April, requiring storage inside the hatchery during an early holding period (EHP). During the EHP, temperatures are lowered to 17°C and food is restricted to limit growth. Because of this extended period of torpor, up to 50% of seed experience mortality or “stunting” post EHP, rendering them non-viable for sale. These losses likely result from physiological stress accumulated during the EHP followed by rapid warm-up. OSH collaborated with VIMS to (1) examine physiological parameters during EHP durations of 8, 6, and 4 weeks and (2) test fast vs slow warm-up after EHP. Oxygen consumption rates declined across all treatments relative to the start of EHP; however, duration of EHP had no significant effect on oxygen consumption at the end of cold holding. At the end of EHP, seed were split into slow warming and fast warming groups (15-27°C). Fast-warming groups showed signs of acute stress. Additional analyses of energy stores, biomass, oxidative stress, and carbonate chemistry will be discussed. Overall, results highlight opportunities to refine holding and warming protocols to reduce mortality and improve seed health.

GRANT WRITING TRAINING WORKSHOP

Clifford T. Cosgrove

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NOAA Fisheries is offering a FREE grant applicant training workshop that is open to anyone interested in applying to NOAA (or other federal agencies) for federal grants. During this 3-hour workshop subject matter experts from NOAA Fisheries will cover everything you will need to know about the new registration process for all federal grants, how to write a competitive grant application, submit a federal grant application, the do’s and don’ts preparing a proposal and the best practices to incorporate when applying.

GENOME-WIDE ASSOCIATION STUDY FOR HEAT STRESS TOLERANCE IN NORTHERN QUAHOGS (= HARD CLAMS), *MERCENARIA MERCENARIA*

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In any aquaculture endeavor, field mortality is addressed either through avoidance or alleviation. Avoidance is achieved through site selection or harvesting stocks prior to cumulative mortality rendering the stock unprofitable; however, when growing conditions are unfavorable, alleviation techniques, such as selective breeding, may be required. As is the case with hard clams and resistance to a prevalent mass-mortality stressor, summer heat waves. Traditional breeding has proved beneficial for many species; however, utilization of genome-wide association studies (GWAS) in conjunction with genetic selection (GS) of one's stock hastens the process and captures performance that could otherwise not be measured. To understand the genetic architecture of heat tolerance and lay the ground for GS, GWAS was conducted using hard clams produced at the Haskin Shellfish Research Laboratory (HSRL). Clams (n = 1250) from an intertidal site were harvested post-summer and utilized for a heat stress experiment, where animals were exposed to gradually increasing water temperatures reflecting summer heat wave conditions. Individuals that died, had their time of death recorded and their tissue fixed for genotyping, along with individuals that survived the exposure, to serve as the training population. An additional 500 individuals from the same population were non-lethally sampled to serve as a breeding population. All samples were genotyped with a 66K SNP array. From the phenotypic and genotypic data from the training population, multiple markers that confer heat tolerance were identified by GWAS, and prediction models were evaluated and used to estimate the breeding values of the breeding population for GS.

MULTIGENERATIONAL GENOME-WIDE ASSOCIATION STUDY FOR DERMO RESISTANCE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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The eastern oyster, *Crassostrea virginica*, has a long history of selective breeding amongst shellfish species. The most common traits targeted have included growth, survival, and disease resistance. Selection for resistance to some diseases, such as MSX (Multinucleated Sphere Unknown) and ROD (Roseovarius Oyster Disease), has been highly effective; however, selection against Dermo, a disease caused by the protist *Perkinsus marinus*, has had limited success, possibly because the trait is polygenic. For polygenic traits, determined by many small-effect genes, genomic selection, which uses all genetic variation in the genome, is expected to be more effective. In a previous study, genomic selection (GS) was performed in a wild population of oysters from Florida (P), where oysters were challenged with *P. marinus*, and then separated based on survival. Individuals were then genotyped using a 66K SNP array to serve as the training population for GS. This was performed again in the F1 and F2 of the population. In this study, genome-wide association studies (GWAS) were conducted using the combined training data from the three generations. A common difficulty in GWAS is the requirement of a sufficient number of individuals to properly develop relationships between markers and phenotypes. The combination of datasets greatly increased the sample size (n = 2423) and detection power. Further, multiple datasets provided an opportunity to validate markers by examining how their genotypic frequencies were distributed across three generations. Through this process, markers with significant association with Dermo resistance were identified, including those from genes involved in mucus production.

NETWORK ANALYSIS OF OYSTER RESTORATION AND MANAGEMENT AT THE ELKHORN SLOUGH NATIONAL ESTUARINE RESEARCH RESERVE IN CALIFORNIA

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International, national, State, research, and local conservation networks have played a key role in the success of oyster restoration efforts at the Elkhorn Slough National Estuarine Research Reserve (ESNERR) in California, which is part of a network of 30 NOAA affiliated National Estuarine Research Reserves. After over a decade without signs of recruitment, native Olympia oyster populations in the Elkhorn Slough showed signs of recovery in 2024 when juvenile oysters were discovered after implementation of the State's first oyster conservation aquaculture project. Olympia oyster conservation on the west coast and at ESNERR is an example of collaborative governance in conservation, with multiple agencies involved throughout implementation and planning processes. This study analyzed native Olympia oyster restoration networks in the State's second largest estuary to investigate 1) who stakeholders are in oyster conservation, 2) how they interact with and influence restoration processes through formal agreements and informal participation, and 3) the role that local, national, and international networks play in oyster conservation, and the importance of funding and support for coordination at multiple scales.

OYSTER RESTORATION AND BLUE CARBON: LEVERAGING OYSTER REEF ECOSYSTEM SERVICES FOR SALT MARSH CONSERVATION

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Salt marshes are highly productive intertidal ecosystems, capturing carbon through biomass and sediment burial for long-term carbon sequestration. Ongoing threats of erosion and displacement of these blue carbon ecosystems from accelerated sea-level rise rates and increased development necessitate effective conservation strategies for coastal land managers. Georgia supports nearly 150,000 hectares of salt marshes, and one commonly used nature-based strategy aimed at their conservation has been the restoration of fringing oyster reefs through bagged oyster shell deployment. These shell-bags provide hard substrate for oyster spat recruitment and enhance wave attenuation and sediment capture, supporting nearby salt marsh ecosystems and facilitating carbon sequestration. Using aerial imagery and elevation data collected by the Georgia DNR Coastal Resources Division through UAV surveying before and in the months following shell-bag deployment, this study assesses the change in salt marsh vegetation coverage and coastal geomorphology to determine the effectiveness of oyster reef restoration as a salt marsh conservation strategy. Preliminary results at three areas where shell-bags were deployed suggest there was a gradual net seaward shift of vegetation after 5, 8, and 13 months, with greater vegetation growth rates than nearby control sites. Further analysis will be done to determine the impact factors like hydrodynamics, tidal creeks, and tidal regime position has on shell-bag oyster reef restoration for salt marsh conservation.

CHARACTERIZING THE DISTRIBUTION, ABUNDANCE, AND HABITAT ASSOCIATIONS OF TIDEFLAT SHELLFISH POPULATIONS IN TILLAMOOK BAY, OREGON, USA: IMPLICATIONS FOR RESOURCE MANAGEMENT

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Shellfish communities in Pacific Northwest estuaries utilize several different habitat types. These habitats are heterogeneous in Oregon estuaries and vary greatly from bay to bay creating challenges for management of shellfish resources. The Oregon Department of Fish and Wildlife Shellfish Program conducts decadal assessments using paired shellfish population surveys and habitat assessments in several Oregon estuaries using a stratified-random sampling design. These surveys have identified three key intertidal habitat types which differ in shellfish species composition, abundance, and relative biomass: eelgrass (*Zostera marina*) beds, unvegetated regions with coarse sediments (e.g., gravel and cobble), and unvegetated areas with finer sediments (e.g., sand and silt). The purpose of this study was two-fold: 1) to compare the shellfish community composition and distribution among these habitat types from a recent survey (2022-2024) in Tillamook Bay; and 2) evaluate shellfish-habitat associations and identify potential driving factors to estimate distribution for recreationally and commercially important bay clams: cockles (*Clinocardium nuttallii*), gaper clams (*Tresus capax*), butter clams (*Saxidomus gigantea*), and littleneck clams (*Leukoma staminea*). A combination of spatial analysis techniques and multivariate approaches were used to evaluate a suite of habitat and environmental variables (e.g. vegetation, grain size variables, substrate composition, temperature, tidal elevation, distance from mouth) to identify variables that can be used to predict the distribution and presence of managed clam species within Oregon estuaries. Bay clams are managed as a unit, and these results will inform management decisions and policy pertaining to shellfish fisheries, critical habitats, shellfish mariculture, and estuarine development.

QUANTITATIVE RISK ASSESSMENT OF INDIVIDUAL OYSTER HARVESTS USING INDUSTRY OBSERVATIONS CAN EXPAND *VIBRIO* RISK MANAGEMENT OPTIONS

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Quantitative risk assessment (QRA) for *V. vulnificus* (Vv) in raw oysters was released by the Food and Agriculture Organization/World Health Organization in 2005. Water temperature determined Vv levels in oyster at harvest and post-harvest growth on ambient air temperature and cooldown time to minimum growth temperature (< 13°C). The U.S. Food and Drug Administration developed an Excel risk calculator based on this QRA to facilitate scenario analysis by state authorities. The National Shellfish Sanitation Program (NSSP) adopted a Vv Control Plan based on this risk calculator in 2009. States can use average monthly maximum water temperature in the previous five years to implement controls that will minimize risk to: (< 3/100,000 when > 80°F; < 2.5/100,000 when 75-80°F; and < 1.75/100,000 when 70-75°F).

The NSSP allows states other risk management options: "may implement alternative controls that will reduce the risk to a level comparable to the risk per serving identified above". States have generally adopted plans based on a single scenario analysis with rigid maximum harvest and cooling times. This "one size fits all" policy can result in excessive risk during heat anomalies and also restricts industry risk management options that could extent harvest periods by harvesting at cooler times or rapid cooling.

A paradigm shift using observed harvest condition instead or relying on average historical temperatures is a more granular alternative control that improves QRA accuracy and expands compliance options. QRA could support other Vv policy changes to permit serving oysters during farm tours or to support a variance from re-mergence requirements during winter.

ENHANCING MARINE AND FRESHWATER ECOSYSTEMS AND PROMOTING SUSTAINABLE AQUACULTURE: THE ESRAG COMMITMENT TO A HEALTHIER PLANET

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The ESRAG has been engaged in various initiatives to conserve fish, shellfish, and mangroves, and to support aquaculture businesses. These efforts align with the ESRAG broader environmental sustainability goals, particularly in promoting healthy ecosystems and sustainable resource management. The ESRAG has been involved in projects that focus on mangrove conservation and restoration. Mangroves are vital ecosystems that protect coastal regions, support biodiversity, and provide nurseries for fish and shellfish. Through educational initiatives, ESRAG encourages the adoption of best practices in fishing and aquaculture that reduce overfishing, bycatch, and habitat destruction. Projects often focus on community-driven efforts to manage marine resources in ways that support biodiversity while providing economic benefits. Networking and collaboration on a global scale enable partnerships with local communities, businesses, and governments to advance initiatives that integrate environmental advocacy with practical, on-the-ground conservation efforts.

This presentation explores the ESRAG framework, emphasizing its role in promoting sustainable practices within the aquaculture sector. The framework focuses on biodiversity preservation, supporting the transition to a circular economy, and improving food systems. These elements are crucial for minimizing environmental impacts, enhancing resource efficiency, and mitigating climate change. By integrating sustainability into aquaculture, the ESRAG framework also addresses the pressing challenges of pollution in aquatic ecosystems, fostering innovation in sustainable production. The presentation will highlight practical strategies to protect biodiversity, reduce waste, and promote responsible aquaculture practices, ensuring long-term resilience against climate change and environmental degradation. Through collaboration and education, this framework paves the way for a sustainable future, aligning with global efforts to promote a healthier and more resilient planet.

THE ENVIRONMENTAL SUSTAINABILITY ROTARY ACTION GROUP (ESRAG): HELPING TO IMPLEMENT SUSTAINABLE PRACTICES ON BIODIVERSITY, CIRCULAR ECONOMY, FOOD SYSTEMS, SUSTAINABILITY, CLIMATE, AND POLLUTION

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The ESRAG has been engaged in various initiatives to conserve fish, shellfish, and mangroves, and to support aquaculture businesses. These efforts align with the ESRAG broader environmental sustainability goals, particularly in promoting healthy ecosystems and sustainable resource management. By promoting practices such as responsible fish and shellfish farming, the ESRAG helps reduce pressure on wild fish populations and supports the circular economy by promoting more efficient, sustainable food systems. Through educational initiatives, the ESRAG encourages the adoption of best practices in fishing and aquaculture that reduce overfishing, bycatch, and habitat destruction. Projects often focus on community-driven efforts to manage marine resources in ways that support biodiversity while providing economic benefits. The ESRAG actively advocates for reducing pollution that affects marine ecosystems, including plastic pollution and chemical runoff that harms fish and shellfish habitats.

HOW TO WRITE EFFECTIVE GLOBAL GRANTS TO APPLY FOR FUNDING FOR YOUR PROJECT BY ROTARY INTERNATIONAL

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Rotary International is a global network of 1.4 million neighbors, friends, leaders, and problem-solvers from 36,000 local communities and 46,000+ clubs around the world. Rotarians see a world where people unite and take action to create lasting change – across the globe, in our communities and in ourselves. Rotary clubs work together to promote peace, fight disease, provide clean water, sanitation, and hygiene, save mothers and children, support education, grow local economies, and protect the environment (https://www.rotary.org/en/about-rotary). The Rotary mission is to provide service to others, promote integrity, and advance world understanding, goodwill, and peace through our fellowship of business, professional, and community leaders. Rotary provides service wherever there is a recognized need with humanitarian and now Environmental Projects. The Rotary Foundation has spent more than $24 million on Environmental Projects worldwide since 2014 and would like to increase the amount spent on shellfish restoration projects. To learn more about how to develop projects and write effective global grants for funding by Rotary International go to: https://my.rotary.org/en/take-action/develop-projects/developing-effective-projects.

THE TROPHIC RELATIONSHIPS OF INVASIVE GREEN CRABS IN THE COOS BAY ESTUARY ARE REVEALED USING FATTY ACIDS AS BIOMARKERS

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A consistent increase in abundance of five-spine green crab (*Carcinus maenas*) has been observed in the Coos Bay estuary, Oregon, where the South Slough National Estuarine Research Reserve (SSNERR) has been monitoring the invasion since 2002. The effects of the growing population of green crab on the Coos Bay estuary food web and significant local fishery species are still unknown. Green crabs are known to have a variable and omnivorous diet, with other shellfish species as the most common prey items; however, it is difficult to make direct feeding observations and physical stomach content analysis is biased against soft bodied organisms. Fatty acids can be used as trophic biomarkers to infer trophic relationships in marine invertebrates, particularly when paired with experimental feeding trials aimed at measuring consumer assimilation of dietary fatty acids. To investigate their diet and trophic relationships, green crabs were collected from ten SSNERR monitoring sites around the Coos Bay estuary. Fifty-three crabs were fed *ad libidum* single species diets (shore crabs, Dungeness crabs, Pacific oysters, or butter clams) for eight weeks in lab experiments. These were compared to green crabs collected in the field (n = 69). Muscle tissue samples were dissected from their claws for fatty acids analysis. Single species diets influenced the fatty acid composition of green crabs, such that the proportions of fatty acids were significantly different between green crabs fed different diets, demonstrating variable diet-dependent assimilation. Wild green crabs from different locations around the Coos Bay estuary exhibit similarity in fatty acid signature, indicating similar diet throughout the estuary.

NEW INSIGHTS INTO POPULATION STRUCTURE AND PHENOTYPIC VARIATION IN SALISH SEA DUNGENESS CRAB

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The Dungeness crab is the most valuable fishery species along the U.S. Pacific coast. In Washington State, the Salish Sea Dungeness crab fishery is managed independently from the open coast fishery and accounts for nearly half of the statewide catch. It has long been thought that the Salish Sea represents a mixed-stock fishery, in which fishery yields vary according to the relative strength of genetically distinct populations. This hypothesis was evaluated by analyzing genome-wide variation among both larval and adult crab throughout Washington, leveraging established regional collaborations of the Pacific Northwest Crab Research Group.

Genomic analysis revealed strong connectivity between the outer coast and the Strait of Juan de Fuca that quickly dissipated north of the San Juan Islands and south of Admiralty Inlet, leading to weaker connectivity between the coast and both Puget Sound and the Strait of Georgia. This pattern is consistent with seasonal variation in larval catches throughout the region and can be explained by regional variation in hatch timing and predominant estuarine circulation patterns within the Salish Sea.

Widely-reported phenotypic variation in body size among megalopae was also addressed. Coastal-origin megalopae typically arrive in the Salish Sea in April and May and are consistently larger than later cohorts that originate within the Salish Sea. A suite of genomic and environmental analyses, as well as earlier laboratory studies, suggest that these size differences may reflect temperature-driven phenotypic plasticity. Potential demographic and fishery consequences arising from the combined effects of connectivity patterns and phenotypic plasticity will be discussed.

MAXIMIZING NITROGEN BIOEXTRACTION THROUGH THE CO-CULTIVATION OF SEAWEED WITH OYSTERS

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Like bivalves, seaweeds are non-fed, extractive aquaculture crops that sequester nutrients from surrounding waters. These nutrients are removed from marine systems when bivalves and seaweed are harvested, a process known as bioextraction. This study sought to directly quantify and compare nitrogen (N) removal rates obtainable through the year-round co-cultivation of oysters and seaweed across a eutrophication gradient in Long Island Sound, NY, ranging from eutrophic urban waters near New York City (East River), to a mesotrophic, suburban bay ~40 miles away (Mt. Sinai Harbor). Sugar kelp, *Saccharina latissima*, was cultivated during the colder months (December-May) along horizontal long-lines, and *Ulva* sp. was co-cultivated with oysters in floating bags during the warmer months (May-November). Based on the biomass yields and N content of each species, along with realistic farm design assumptions, it was estimated that a one-hectare kelp-*Ulva*-oyster farm would be capable of removing 438 kg N yr^{-1} in eutrophic waters, and 304 kg N yr^{-1} in mesotrophic waters, with the relative contribution of each aquaculture species differing among the sites. Seaweed, and kelp in particular, was more effective at extracting nitrogen in the more nitrogen-rich waters, owing to significantly higher tissue N content (kelp and *Ulva*) and significantly higher growth rates (kelp). Oysters, conversely, had significantly higher growth and extracted more nitrogen in the less nitrogen-impacted waters, potentially due to better water quality for oyster growth. The results demonstrate that the co-cultivation of seaweed and bivalves can maximize nitrogen bioextraction across a range of estuarine conditions and water qualities.

CAN PACIFIC OYSTER CONDITION BE RELATED TO ENVIRONMENTAL SHIFTS, REPRODUCTIVE STATE, AND MORTALITY EVENTS IN A U.S. PACIFIC COAST ESTUARY?

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Pacific oysters (*Crassostrea* [*Magallana*] *gigas*) were introduced from Japan to the U.S. Pacific coast beginning in the early 1900s and have become the predominant cultivated shellfish species on this coast contributing substantially to U.S. domestic production. These oysters became naturalized in several locations including Willapa Bay where a monitoring program was established to track both larval set and the condition of adult oysters during the mid-1950s and maintained since that time. The gametogenic cycle for oysters is well studied and previously correlated with environmental triggers like temperature, salinity, and food which influence oyster condition, but can also act as stressors and are linked to summer mortality events. Broad decadal temporal scale and Pacific Ocean basin spatial scale environmental forcing factors have been shown to influence oyster condition in Willapa Bay and can also be linked to seasonal shifts and reported summer mortality events that have occurred in this estuary. Results from a joint U.S.-Japan study conducted in 2019 when one such mortality event occurred and similar data was collected from the Seto Inland Sea suggest that multiple stressors are likely involved and differ by location, but the response of oysters to local growing conditions like the presence of seagrass or where oysters were cultured was similar. A framework to further examine metabolic or energetic characteristics that could be used to breed oysters for resilience to such stressors and/or provide growers the ability to adapt to and mitigate for the effects of an uncertain future climate is proposed.

ASSESSING THE THERMAL TOLERANCE OF ATLANTIC SEA SCALLOP (*PLACOPECTEN MAGELLANICUS*) EARLY LIFE STAGES

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Ocean warming affects numerous traits in early life history stages of invertebrates and fishes, which may reduce recruitment and harvestable biomass. A prime example is the Atlantic sea scallop (*Placopecten magellanicus*), which supports one of the most valuable fisheries in the northwest Atlantic with annual landings over $350 million USD. This fishery may be at risk due to its high sensitivity to projected future ocean conditions; prior studies have quantified decreases in recruitment, growth, biomass and population distribution shifts across the Mid-Atlantic Bight (MAB). Few studies, however, examine the response of planktonic larvae to future conditions, resulting in a critical knowledge gap on the thermal tolerance for larvae. To address this, fully factorial experiments were conducted to evaluate the physiological response of larvae across a range of current and future environmentally relevant temperatures. This study provides empirical physiological data which can be incorporated into bio-physical model parameterizations and used to improve predictions of future population dynamics in the MAB under expected temperature escalations. The results of this study will help sustain stock biomass and aid in adaptive fisheries management under future temperature projections.

EXPLORING GROWER PERCEPTIONS OF STRESSORS IN THE NORTH CAROLINA OYSTER FARMING INDUSTRY

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

The purpose of this study was to establish a framework for both individual growers and the industry that identifies and defines the most important stressors affecting oyster farming in NC. The framework contextualized these stressors over different temporal scales at the individual and industry level through qualitative interviews with individual growers, industry stakeholders, and regulatory groups. Lastly, the authors investigated grower perceptions of the various stressors they face daily and seasonally. The authors accomplish this through quantitative surveys developed from analyzing the preceding interviews and identifying commonalities. As the oyster farming industry continues to grow, this work is essential for assessing and identifying strategies to improve adaptive capacity, especially in the face of climate change. Unlike commercial fisheries that are often top heavy and favor capital, the NC oyster farming industry is currently flush with small-scale operations. Through collaboration across stakeholders, regulatory bodies, and farmers, the industry has the potential to increase its value and create enabling industries.

MANSIONS IN THE MARSH: MONITORING THE PERFORMANCE OF OYSTER CASTLES® IN COASTAL SOUTH CAROLINA, USA

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For over 20 years, researchers and natural resource managers at the South Carolina Department of Natural Resources (SCDNR) have used oyster shell substrate for eastern oyster (*Crassostrea virginica*) habitat restoration and enhancement in the substrate-limited, intertidal estuarine environments of coastal South Carolina (SC). As natural oyster shell is limited, often requiring importation from other states, and is increasingly expensive, habitat restoration and enhancement efforts have shifted to investigating the potential of alternative substrates, such as 3-dimensional concrete- and wire-based materials, that do not depend on oyster shell for the successful creation of new reef habitat. Since 2009, restoration practitioners at The Nature Conservancy (TNC) have installed tiered interlocking concrete Oyster Castles® (Allied Concrete, Inc.) to combat shoreline erosion and to provide substrate for oyster settlement at multiple sites in SC. From 2024 - 2025, researchers from the SCDNR Marine Resources Research Institute monitored the performance of these materials at a selection of sites using on-the-ground metrics, such as quadrat-based percent oyster coverage, real time kinematic (RTK) global navigation satellite system (GNSS) positioning, and aerial imagery-based GIS products collected using unoccupied aerial vehicles (UAV) or drones. This presentation will discuss: 1) key methodologies used to monitor the progress of Oyster Castle® installations; and 2) initial observations on long-term performance of these materials in coastal SC.

COMPARATIVE ANALYSIS OF MITOCHONDRIAL ACTIVITY IN TRIPLOID AND DIPLOID OYSTERS

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A growing number of studies report disproportionate mortality in triploid oysters, particularly when exposed to multiple environmental stressors such as temperature and salinity fluctuations. While research into organismal-scale energy differences has yielded limited insights, a significant gap remains in understanding stress response differences between diploid and triploid oysters at the cellular and sub-cellular levels. Building on recent findings that intracellular mitochondrial concentrations in hemocytes (i.e., blood cells) differ significantly between diploid and triploid oysters, a comparative analysis of cellular respiration metrics was conducted. Simultaneous measurements of oxygen consumption and extracellular acidification rates following exposure to mitochondrial inhibitors revealed a three- to four-fold increase in both maximum and reserve respiratory capacity in triploid hemocytes compared to diploid counterparts, highlighting substantial differences in cellular energy metabolism between both groups. Ongoing work focuses on comparing cellular respiration in diploid and triploid oysters under environmental stress conditions to assess whether heightened respiratory metrics observed in triploids under ambient conditions influences their long-term responses to complex stressors (i.e., trade-offs), potentially offering a mechanistic explanation for differential mortality observed in the field.

INVASIVE EUROPEAN GREEN CRAB (*CARCINUS MAENAS*) PREDATION IN A WASHINGTON STATE ESTUARY REVEALED WITH DNA METABARCODING

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In the U.S. Pacific northwest, European green crab (*Carcinus maenas*) has recently experienced increases in abundance and expanding distributions; however, regionally-specific information on the trophic impacts of invasive green crab is highly limited. The stomach contents of green crabs collected on aquaculture beds versus natural intertidal sloughs in Willapa Bay, Washington, were compared to provide the first in-depth description of European green crab diet at a particularly crucial time for regional management. Putative prey items were identified using DNA metabarcoding. From the stomach contents of 62 green crabs, 56 unique taxa belonging to nine phyla were identified. The stomach contents of crabs collected from aquaculture beds were significantly different from the stomach contents of crabs collected at natural intertidal sloughs. Across all sites, arthropods were the most frequently detected prey, with the native hairy shore crab (*Hemigrapsus oregonensis*), the single most common prey item. Since DNA metabarcoding provides only presence/absence and relative abundance data, for eight key prey species a quantitative model was used to calculate the absolute abundance of each species' DNA in crab stomach contents. When present, the DNA from two ecologically-important native species – the sand shrimp (*Crangon franciscorum*) and the Pacific staghorn sculpin (*Leptocottus armatus*) – were the most abundant in crab stomach contents. In addition to providing timely information on green crab diet, this research demonstrates the novel application of a recently developed model for quantitative DNA metabarcoding. This represents another step towards producing the quantitative data necessary for modeling invasive species impacts.

EXPLORING UNINTENDED OUTCOMES FROM CLIMATE ADAPTATION FOR THE WELL-BEING OF FISHERS

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Shellfisheries face extreme events of increasing frequency and intensity. Efforts to address the short-term impacts of extreme events can have trade-offs and unintended consequences for fishers' well-being. Qualitative network models (QNM) can be a useful tool to explore how adaptation to extreme events may amplify or dampen climate change impacts. Drawing on the dynamics of the U.S. West Coast Dungeness crab fishery, we simulate a harmful algal bloom in a model fishing community and compare outcomes for human well-being, with and without climate adaptation. A range of adaptations that were drawn from regionally-focused climate change scenario planning, peer-reviewed literature, and expert knowledge were considered. Results demonstrate how QNM can (1) reveal shared trade-offs across diverse adaptation strategies, (2) explore how diversity in a social-ecological system may contribute to inequitable outcomes, and (3) help to identify future research and monitoring priorities.

MATSUSHIMA BAY: REVISITING THE ANCESTRAL HOME OF (NEARLY) ALL PACIFIC OYSTERS IN THE WORLD

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Beginning in 1919, seed oysters (spat on shell) began moving from Miyagi Prefecture in northern Japan to the Salish Sea region. Over the next 70 years the great diaspora of Miyagi *Crassostrea gigas* continued, and Pacific oysters came to dominate the American west coast, Australia, and eventually Europe. Nearly all these animals trace their roots back to two very special embayments in Miyagi - Matsushima and Watanoha.

Why were these two tiny embayments the source of the seed oysters worldwide for nearly 70 years? This presentation will share photos, stories from contemporary shellfish farmers, and some interesting historical data uncovered during a trip to the region in November 2025. The current state of oyster farming in the region today will be discussed - citing challenges and prospects for the future.

MARINE BIOTOXIN DEPURATION RATES: MANAGEMENT APPLICATIONS, RESEARCH PRIORITIES, AND PREDICTIONS FOR UNSTUDIED SPECIES

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Monitoring and managing the public health risk posed by marine biotoxins is a daunting challenge. With expansive coastlines, numerous seafood species, and dozens of biotoxins, monitoring cannot occur everywhere at once. Improving the cost-effectiveness of biotoxin monitoring is thus critical to expanding coverage to include more species, toxins, and locations. Notably, understanding the rate at which seafood species depurate biotoxins can be used to optimize the cadence of monitoring. A systematic review was conducted to collate marine biotoxin depuration rates and synthesize the factors that influence them; identify knowledge gaps, best practices, and research priorities; and generate predictions of depuration rates for unstudied species. It was found that only 85 marine species have been studied for their biotoxin depuration rates. Depuration rates for non-bivalves and for toxins besides paralytic shellfish toxins (PST) are especially understudied. Depuration half-lives varied from 0.03 to 693 days based on species, toxin, tissue, and environmental conditions. In general, depuration accelerates with increased temperature and food availability, with implications for aquaculture siting, depuration enhancement, and biotoxin monitoring. Unstudied bivalve species that are highly produced and vulnerable to HAB that are high priorities for future research were identified. Finally, a Bayesian regression model was used to predict PST depuration rates for 102 unstudied bivalve species, the only clade-syndrome with sufficient training data. These predictions can guide efficient monitoring and management until lab- or field-based depuration rates become available. It is recommended that future studies directly estimate depuration rates to ensure their comparability across studies and utility to managers.

CLIMATE-ADAPTIVE MANAGEMENT OF THE U.S. WEST COAST DUNGENESS CRAB FISHERY USING PROJECTIONS OF DISTRIBUTION SHIFTS AND CATCH FORECASTS

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The Dungeness crab (*Metacarcinus magister*) fishery is arguably the most commercially important fishery on the U.S. west coast. Understanding the vulnerability of the fishery the rising threats of ocean warming, hypoxia, and acidification is important to designing management that is adaptive to these impacts. The NOAA bottom trawl survey data and high-resolution (2 km) down-scaled oceanographic climate projections were used to model Dungeness crab abundance as a function of bottom temperature, dissolved oxygen, and carbonate chemistry. The model was used to hindcast distributions from 1993-2020 and assess the impacts of changing availability on port-level revenues. Distribution shifts were then projected under a moderate climate change scenario (RCP 4.5) and assess changes in availability to fishing ports coastwide. Finally, lagged indices of relative abundance derived from the NOAA bottom trawl survey were used to generate 1- to 2-year forecasts of state-specific catch. The utility of these forecasts to business planning and to ensuring adequate head start for tribal fishers in Washington, where treaty tribes are guaranteed 50% of seasonal harvests will be discussed. Overall, this talk will discuss the value of these tools in promoting climate-adaptive management in the west coast Dungeness crab fishery.

MOLECULAR SIGNATURES OF RESILIENCE: EVALUATING STRESS PRIMING IN JUVENILE EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) USING HEAT SHOCK PROTEIN 70 EXPRESSION

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While oysters are well-adapted to dynamic environments, extreme fluctuations in environmental conditions cause mass mortality, reduce growth, and limit reproductive success. Stress priming is a tactic that leverages the molecular 'memory' formed during a primary stress to protect an organism during a secondary exposure. One way to assess this molecular response is through a biomarker such as heat shock protein 70 (HSP70), a common molecular chaperone that is upregulated during periods of stress. To better understand whether stress priming enhances resilience in juvenile oysters, independent experiments were conducted under low-salinity and hypoxia conditions, and samples for transcriptomic analyses were collected throughout the experiment. For the salinity experiments, primed oysters had lower HSP70 expression (avg fold change: 3.06) and less mortality (8.8-11.2%) than unprimed oysters (FC: 12.41, 24%) during the secondary exposure; however, these primed groups had variable mortality rates during repeated experiments and potential long-term reductions in growth. Experiments honing a hypoxia prime were conducted, and HSP70 gene expression analyses are underway. Preliminary results indicate low mortality under three-week hypoxia exposures with small differences between some prime and unprimed treatments. Thus far, these experiments suggest that short, intense primes may induce a tolerance protecting them during a subsequent exposure, but inconsistent mortality rates and long-term costs could reduce the utility of stress priming. To move beyond single-gene indicators, next steps for this work include evaluating transcriptomic and epigenomic (miRNA) profiles of primed and unprimed oysters to more broadly assess molecular mechanisms underpinning the stress response.

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

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

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

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

A COLLABORATIVE DUNGENESS CRAB LARVAL MONITORING NETWORK IN THE PACIFIC NORTHWEST PROVIDES LONG-TERM, FISHERY-RELEVANT DATA

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The Pacific Northwest Crab Research Group (PCRG) leads a collaborative, stakeholder-driven effort to generate essential biological information for the data-poor, co-managed Dungeness crab (*Metacarcinus magister*) fishery. Formed to address critical knowledge gaps surrounding this high-value, climate-sensitive resource, the group unites State and Federal agencies, tribes, nongovernmental organizations, academic institutions, and local communities under a shared research framework that is strategically aligned with fisheries management priorities.

The PCRG core program, the larval crab monitoring network, is producing the first standardized, long-term dataset on Dungeness crab larval dynamics in the region. Seven years of monitoring allow for broad evaluation of spatial and temporal patterns in larval flux, phenology, and size, offering new insights into early-life variability that influences recruitment. Though not yet integrated into co-management decision-making, these data provide a foundation for future fisheries applications, such as refining indices of larval supply, evaluating environmental drivers of recruitment, contextualizing interannual harvest variability, and ultimately, informing future forecasting of adult crab abundance. By leveraging strong cross-sector partnerships, the network expands access to educational opportunities, accelerates new research, and builds trust among stakeholders. The success of the PCRG larval crab monitoring program illustrates how a cooperative, network-based approach can effectively fill key research gaps and support resilient management, offering a viable model for other data-limited fisheries.

PRESENCE-ABSENCE VARIATION (PAV) SHAPES GENOMIC SIGNATURES IN BIVALVES: A COMPARATIVE STUDY

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Presence/absence variation (PAV) is a well-known phenomenon in prokaryotes, first described in bivalves in 2020 in the Mediterranean mussel. The objective of the present study was to further our understanding of the PAV phenomenon by exploring the genomic signatures in two bivalve species, *Ostrea chilensis* and *Mytilus chilensis*. The distribution of PAV was studied in a chromosome-level genome context, combining transcriptome and methylation data from wild populations of oyster and mussel. A widespread distribution, with hotspots of dispensability, was observed, and statistical analysis reveals molecular signatures related to the local populations. Special attention was given to the effect of PAV on gene expression and methylation, since dispensable genes are inherently subject to distortion due to their sparse distribution across individuals. Notably, high transcription levels were associated with PAV, suggesting that those dispensable genes shape the genomic signatures in bivalves. Population specificity of some dispensable genes, such as immune-related genes, strongly supported their biological relevance. The significant differences in the repertoire of dispensable genes associated with geographically distinct populations suggest that PAV is involved in local adaptation. Overall, the PAV phenomenon would provide a key selective advantage at the population level.

DISRUPTION OF THE GILL-GUT-HEMOLYMPH AXIS IN THICK-SHELLED MUSSELS (*MYTILUS CORUSCUS*) INDUCED BY CO-EXPOSURE TO POLYSTYRENE MICROPLASTICS AND DI(2-ETHYLHEXYL) PHTHALATE

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Polystyrene microplastics (PS-MP) and di(2-ethylhexyl) phthalate (DEHP) are widespread contaminants in marine ecosystems that pose significant risks to marine life. To study the combined effects of these pollutants on physiological and immune responses, we exposed thick-shelled mussels, *Mytilus coruscus*, to vary PS-MP concentrations alone or combined with DEHP for 30 days. It was found that significant morphological changes in gill structures, including reduced lamella dimensions and thinner stromal tissue, impaired pulmonary gas exchange. Co-exposure to PS-MP and DEHP led to altered respiratory metabolism, with suppressed lactate dehydrogenase (LDH) and succinate dehydrogenase (SDH) activities, increased pyruvate kinase (PK) activity, and decreased ATPase activity, indicating a shift in energy regulation toward glycolysis. Notably, immune functions were disrupted, evidenced by decreased total hemocyte counts (THC) and esterase activity (EA), while oxidative stress markers such as reactive oxygen species (ROS) and malondialdehyde (MDA) were elevated. Furthermore, high pollutant concentrations caused gut microbiota dysbiosis, specifically the depletion of beneficial Lactobacillus and the proliferation of opportunistic pathogens like Vibrio and Pseudomonas. Thus, PS-MP and DEHP disrupt mussel health via a pollutant cascade mechanism linking tissue damage, metabolic reprogramming, and microbial imbalance along the "gill-intestine-hemolymph" axis. Therefore, the mixture of microplastics and DEHP poses a significant synergistic risk to marine organisms.

PREDICTORS OF THE HABITAT VALUE OF OYSTERS – A GLOBAL META-ANALYSIS

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Structured habitats provided by oysters augment the abundance and diversity of associated species, yet the magnitude of this effect could reflect oyster attributes, environmental characteristics, non-oyster habitat type, or which response variables are considered. From an initial screen of 2684 publications, almost 200 provided data from field studies comparing abundance or diversity of associated species on and off live oysters. Because one study could provide many effect sizes (Hedges g), the publication was considered a random effect in analyses. Total abundance and diversity overall increased on live oysters, whereas particular species responded with more variability. The degree of enhancement in abundance or diversity was modified by the off-oyster comparison, with the effect size greatest in comparison to soft sediment and declining as the off-oyster habitat for comparison became more structured. Fish and birds were generally studied at larger spatial scales than infauna, epifauna, or algae; differences among these responding taxa also emerged in terms of which habitat comparisons were tested and generated the largest effect sizes. A weaker modifying effect was provided by the on-oyster habitat factor and whether these consisted of wild, restored, or cultivated oysters.

SAFEGUARDING A RESILIENT TRIBAL DUNGENESS CRAB FISHERY THROUGH IMPROVED BIOLOGICAL MONITORING AND ADAPTIVE MANAGEMENT

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The sustainability of the Dungeness crab (*Metacarcinus magister*) fishery in Puget Sound Washington is increasingly jeopardized by data gaps in population demographics and timing of the annual reproductive molt cycle. Conservation of the fishery is reliant on a "3-S" (sex, size, season) management framework which must be periodically re-evaluated to support adaptive management in a changing marine environment. This study, led by the Jamestown S'Klallam Tribe in partnership with the Pacific Northwest Crab Research Group, establishes a new fishery-independent survey designed to acquire baseline data on Dungeness crab population demographics and shell condition within the Eastern Strait of Juan de Fuca management area of the Puget Sound fishery. The survey methodology involves monthly sampling over a year to track seasonal patterns. Sampling is spatially stratified by depth, targeting 12 randomly selected index stations within fisher-informed crab habitat using modified (ventless) commercial crab traps to sample adult crab (females, sublegal-size and legal-size males). The primary objective is to quantify key demographic parameters: carapace width, sex ratio, and use an established shell condition index to identify the peak molting period. Data loggers affixed to gear collect temperature and dissolved oxygen at depth to establish measurements of relevant environmental covariates. The results will be essential for evaluating the effectiveness of the current seasonal fishing closure period in preserving mating potential and reducing handling-related mortality of soft crab. This work will provide Puget Sound crab co-managers with the necessary biological and environmental metrics to enhance stock resiliency and implement data-driven management strategies.

ADVANCING THE DEVELOPMENT OF A NOVEL STERILITY METHOD IN SHELLFISH

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Reproductively sterile shellfish are a market-driven need and 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 (future gamete) formation and development. Before this approach can be applied in bivalves, however, two significant challenges must be overcome: 1) characterization of genes involved in bivalve germ cell formation ('primordial germ cell (PGC) specification'), and 2) optimization of robust, cost-effective methods to temporarily suppress expression of PGC genes via delivery of gene silencing molecules (e.g., morpholinos) to bivalve embryos - a particularly challenging step for shellfish aquaculture because bivalve embryos are extremely small, the window for molecule delivery is brief and the molecule delivery approach must be scalable for use in hatchery

settings. To address these challenges, single-cell RNA-sequencing was performed to assess PGC formation during *Crassostrea gigas* embryonic development and identify PGC-specific genes. The data suggest that PGC are sequestered during gastrulation and uniquely express a suite of genes that are potential targets for disruption of germ cell formation. Using these gene candidates, assays (e.g., hybridization chain reaction) are being optimized, and a variety of gene-silencing methods are being explored to assess whether disruption of PGC development can yield oysters that do not produce gametes. Together, these efforts will generate foundational biological insights and practical biotechnological tools for reproductive management in shellfish aquaculture.

MOVING BEYOND THE BASELINE: OYSTERS AS A PERFORMANCE METRIC FOR THE COMPREHENSIVE EVERGLADES RESTORATION PLAN

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Eastern oysters (*Crassostrea virginica*) have been monitored as an important biological indicator informing Everglades Restoration status reports since 2000 (Caloosahatchee River) and 2005 (St. Lucie Estuary, Loxahatchee River, and Lake Worth Lagoon). The principal metric, or performance measure, for oysters is acres of oyster habitat, but comprehensive surveys are time consuming and costly. Interim metrics that are monitored include monthly assessment of water quality, disease, settlement and reproduction, growth and mortality, and semi-annual surveys for abundance and size.

System Status Reports that provide updates to congress consider 2005-2017 to be the baseline for monitoring projects, and 2017-2024 to be a period when changes to water flow throughout the system began. In 2025 the first major water storage area was opened. The region is also subject to patterns of weather variability and climate change. The target estuaries had slightly drier conditions in the most recent observation period, yet one estuary had more days of freshwater flow exceeding desired conditions. A warming trend, especially in fall and winter, has also been observed. Recent trends in abundance and settlement of oysters, and a comparison of four estuaries, will be discussed.

CLIMATE-DRIVEN RECRUITMENT DYNAMICS IN THE WASHINGTON COASTAL RAZOR CLAM FISHERY

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The Washington coastal recreational razor clam (*Siliqua patula*) fishery is a culturally and economically vital resource, providing an average of 70 harvest days and $36.2 million in economic value annually over the past decade. Using nearly three decades of stock assessment and harvest data (1997–2025), this study evaluates long-term recruitment trends, population cyclicity, beach-specific stability, and fishery performance across Washington's five managed coastal beaches. Recruitment has increased substantially over the history of the fishery, rising by more than 80% to approximately 35 million clams (2014-2025), with all beaches except Kalaloch exhibiting significant positive long-term trends. Spectral analysis identified strong cyclical structure, with a dominant 6-year recruitment cycle and secondary 7.5- and 10-year cycles consistent with Pacific Decadal Oscillation (PDO) and El Niño-Southern Oscillation (ENSO) forcing. Pre-recruit abundance demonstrated moderate predictive value for subsequent recruitment, although high interannual variability indicates strong environmental influence on juvenile survival. Beach-specific analyses revealed that Twin Harbors exhibited the most stable recruitment (CV = 40.3%), whereas Kalaloch displayed extreme variability (CV = 98%). Razor clam condition index was not correlated with recruitment. Management actions closely tracked underlying stock status, with higher exploitation rates applied during strong recruitment years. These results underscore the importance of continued integration of environmental monitoring, refinement of recruitment forecasting tools, and incorporation of climate-linked variability into beach-specific management thresholds for sustainable harvest.

HIGH-SPEED IMAGING MICROSCOPY IN SHELLFISH HATCHERY RESEARCH

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Flow imaging microscopy (FIM) has been used in biological oceanography for over two decades to image, count, measure, and classify plankton. More recently, FIM has also been applied to shellfish hatchery research to increase throughput and enrich data collection, enabling researchers to collect more data on every larva than previously possible; however, protocols for how to use FIM in a hatchery context are not yet common knowledge. This presentation will describe FIM protocols being developed using FlowCam and explore how imaging data supports the enumeration and evaluation of shellfish larvae. Adjacent applications like phytoplankton monitoring will also be discussed.

INGESTION AND EGESTION OF CRYO-MILLED TIRE TREAD PARTICLES BY OYSTERS (*CRASSOSTREA VIRGINICA*) AND MUSSELS (*MYTILUS EDULIS*)

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Tire wear particles (TWP) are recognized as significant anthropogenic contaminants in estuaries adjacent to human-built environments; however, few studies have examined their interactions with estuarine animals. Suspension feeders could be particularly impacted as they process large volumes of water and capture small particles (3 µm) with high efficiency. Using the eastern oyster (*Crassostrea virginica*) and blue mussel (*Mytilus edulis*), this study evaluated selective rejection, ingestion, and egestion of particles (= TWP; 20-211 µm) over 96 h. Animals were fed TWP directly with a similar-sized diatom over a 2 h period. Pseudofeces and feces were collected at < 3 h, 24 h, 48 h, 72 h, and 96 h, digested in 1M sodium hydroxide, and TWP counted. At 48 h and 96 h, a subset of bivalves were sacrificed, the gut isolated, digested in 1M sodium hydroxide, and residual TWP counted. Results demonstrated that both species rejected the highest proportion of TWP in < 3 h, and oysters rejected a higher proportion (29.9%) than mussels (3.1%). Small amounts of rejected TWP were noted up to 48 h post-exposure in both oysters (1.9%) and mussels (2.3%). The proportion of TWP egested by oysters in intestinal feces (< 3 h) was higher (48.4%) than mussels (10.9%). Overall, 96.7-98.3% of egested material was eliminated within 72 h, with gut tissue confirming < 1% at 48 and 96 h for both species. This research provides vital information for adverse outcome pathways of TWP exposure by identifying the proportion actually ingested and the time-course for elimination in oysters and mussels.

THE HALO EFFECT: THE ABILITY OF SEAWEEDS TO TRANSFORM BIVALVE AQUACULTURE IN THE ANTHROPOCENE

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Bivalve aquaculture currently faces an "existential quartet" of threats: hypoxia, ocean acidification (OA), harmful algal blooms (HAB), and seasonal food limitation. As climate change exacerbates these stressors, traditional reactive mitigation strategies prove insufficient for monocultures. This manuscript synthesizes evidence for a proactive, nature-based engineering solution: the "Halo Effect" of co-culturing macroalgae. Halo is defined not merely as a general ecosystem service, but as a spatially distinct, actionable gradient of improved water quality surrounding seaweed infrastructure. This review delineates four protective mechanisms within this zone: (1) macroalgae act as biological aerators, generating dissolved oxygen reserves that aid bivalve metabolic survival during thermal stratification; (2) photosynthetic CO_2extraction elevates local pH and saturation states, safeguarding calcification in vulnerable larvae and adults; (3) seaweed allelopathy chemically suppresses HAB densities and facilitates faster toxin depuration in bivalve tissue; and (4) macroalgal detritus provides essential trophic subsidies, bridging nutritional gaps when phytoplankton is scarce. Optimizing this "Halo" requires balancing farm density with hydrodynamic flow to maximize chemical benefits without causing stagnation. Ultimately, this review argues for a paradigm shift: viewing macroalgae not solely as a secondary crop, but as essential "living infrastructure" - a restorative shield capable of rendering bivalve aquaculture resilient in the Anthropocene.

WRANGLING, TANGLING, AND FOLLOWING INVASIVE GREEN MONSTERS IN COASTAL MAINE WATERS

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European green crabs (*Carcinus maenas*) have been ubiquitous invaders of the shallow coastal waters of the Gulf of Maine for over 125 years and have been implicated in a wide range of adverse effects on economically important species and sensitive ecological habitats. Over the last several years, work in the western Gulf of Maine (USA) has explored green crab movement ecology, behavior, and physiology to further the understanding of this species and inform potential mitigation strategies. An acoustic telemetry study quantified green crab movements in an estuarine system and demonstrated how their behaviors vary with reproductive status and environmental covariates at scales ranging from diel to seasonal. Complementary to the telemetry study, trapping surveys in the same area have illustrated how green crab distribution and abundance vary across an estuary. Additionally, research conducted in tandem with local harvesters sought to develop a diagnostic molt prediction tool using crab hemolymph color and biochemistry to bolster the development of a soft-shell crab market. Collectively, this portfolio serves to inform a variety of stakeholders including those considering intervention strategies as well as those seeking to capitalize on this abundant resource in a way that simultaneously mitigates their population growth.

PARTNERSHIP FOR RESEARCH EXCELLENCE IN SUSTAINABLE SEAFOOD (PRESS): LESSONS LEARNED

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Seafood consumption in the United States is increasing, with demand expected to grow 60% by 2050. Yet seafood production is threatened by a myriad of challenges from disease and environmental stress to gaps in processing and distribution chains. The Partnership for Research Excellence in Sustainable Seafood (PRESS) is a $1 million, 4-year funding program designed to address challenges experienced by the seafood system in Rhode Island through collaborative research. Program objectives are to: 1) identify emerging issues affecting seafood production in Rhode Island, 2) complement existing sources of federal, state, or private funding for sustainable seafood efforts, and 3) develop a process for research innovation and workforce development incubator driven by stakeholder input. Each proposal is reviewed by an interdisciplinary advisory board of stakeholders from the seafood system and funding is distributed rapidly to respond to pressing issues. Launched in 2023, the PRESS has funded 15 proposals so far from teams of industry members and researchers, on subjects as diverse as a train the trainer workshop in the use of ikejime to add value to underutilized fish species, assessing seafood safety issues due to birds roosting on floating aquaculture gear, evaluating the impact of gear and water quality on oyster growth, a shell waste valorization study, evaluating the value of fisheries to the economy of Rhode Island, shell disease impact on lobster growth, and fostering the use of automatic squid jigging. Lessons learned through the PRESS will be discussed so others may use this model to improve local seafood food security.

CAN SUBMERGED AQUATIC VEGETATION AND SHELLFISH AQUACULTURE CO-EXIST IN MARYLAND? A CASE STUDY OF INTERACTIONS AT CHOPTANK OYSTER CO.

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The expansion of oyster aquaculture in the Chesapeake Bay in Maryland has intensified concerns about potential interactions with submerged aquatic vegetation (SAV), a foundational habitat that provides critical ecosystem services. Maryland regulations prohibit aquaculture activities over SAV without written authorization, and temporary exemptions to this rule (HB 841) are scheduled to expire in 2026. To support evidence-based management, we collaborated with the Maryland Department of Natural Resources and Choptank Oyster Co. to implement a before–after–control–impact (BACI) monitoring study evaluating ecological interactions between surface oyster culture and SAV within and adjacent to an active lease in the Choptank River.

From 2023 to 2025, coordinated field surveys and environmental monitoring were conducted across restricted lease areas, exempted aquaculture zones, and a nearby natural SAV meadow. Monthly assessments of SAV abundance and species composition were paired with high-frequency measurements of light intensity and sediment analysis. Biogeochemical incubation from select locations were also conducted, but at lower frequency. Light loggers were deployed beneath oyster gear, in non-gear reference areas, and within SAV beds to quantify shading and light attenuation. Sediment cores were analyzed for grain size, organic matter content, and the short-lived radionuclide ^{7}Be to assess deposition dynamics and sediment provenance.

Preliminary results will be unveiled, and their implications will be discussed. This ongoing partnership builds upon the growing body of work seeking to assess aquaculture–SAV interactions and will inform future permitting, policy decisions, and sustainable aquaculture practices in Chesapeake Bay and beyond.

THE IMPACT OF FEEDING AND FEEDING DELAY ON LARVAL EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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The cultivation of eastern oysters represents a fast-growing industry within the U.S. The demand for high-quality products, however, outweighs US production capacity. Nearly half of oysters consumed within the U.S. are imported from out-of-country. To expand production and be less reliant upon imports, local hatchery-based production needs to be expanded. Early-life stages represent a substantial bottleneck and are sensitive to culture conditions, food abundance, food composition, and other environmental factors (e.g., salinity, oxygen, and temperature) during early development. A better understanding of early-larval husbandry and the biochemical basis underlying fast growth may facilitate increased production and diversify product sources. Currently, there is limited information regarding early-biochemical and metabolic development among eastern oysters, and how feeding and feeding-delay impact early metabolic development, growth, and survival. Identifying how early-life stages respond physiologically to feeding and feeding-delays may reveal unique life-history strategies applicable for aquaculture. The purpose of the study was to provide biological context of feeding and feeding delay through quantification of biochemical growth and metabolic rate during starvation and after feeding delay. Specifically, oyster larvae delayed food during the initial 10-days development and then fed, exhibited more rapid metabolic and biochemical growth relative to larvae fed 2-days post-fertilization. Feeding-delayed larvae, as feeding initiated, reached later-developmental stages more quickly than larvae fed earlier and at a relatively lower metabolic burden. Future studies should seek to determine if this is a result of early environment or an interaction between environment and genotype and whether strategies can be utilized to enhance shellfish aquaculture.

BODY CONDITION INDEX OF A PANDALID SHRIMP, A NOVEL METHOD FOR ASSESSING OCEAN SHRIMP POPULATIONS

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Assessing stocks of short-lived marine invertebrates is complex, yet highly valuable to fishery management. Knowledge of stock abundance prior to fishing has obvious advantages but is less attainable for shorter lived “recruitment fisheries.” The U.S. west coast ocean shrimp (*Pandalus jordani*) fishery relies on back calculation to understand stock abundance. Using 23 years of dockside biological sampling data (2001-2023), there was a strong relationship between Body Condition Index (BCI) of ocean shrimp and fishery catch per unit effort. For predicting seasonal abundance, several factors (fishery CPUE, environmental conditions, predator levels) were considered; however, BCI showed the strongest correlation. BCI at season onset (April) was the best predictor of annual catch. The strong connection of ocean shrimp population abundance to BCI may allow the variable’s use in predicting contemporaneous abundance. The potential uses of BCI include, 1) a simple preseason population abundance metric to aid seasonal catch expectations and, 2) developing new harvest control rules, both of which may be used to improve the sustainability of the ocean shrimp fishery.

FLAT ABALONE: FROM ROBUST FISHERY TO RISK OF EXTIRPATION

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Flat abalone (*Haliotis walallensis*), once a modest component of rocky reef ecosystems from Baja California to Oregon, is now among the most imperiled marine molluscs on the U.S. west coast. Historically abundant in northern California and southern Oregon, the species supported localized fisheries, including the artisanal commercial fishery of Oregon (2001–2008), which removed nearly 30,000 individuals under limited-entry quotas. Despite its small scale, this fishery triggered sharp population declines, with densities at key sites (e.g., Nellies Cove) dropping by > 80% within seven years. Following closure, populations faced additional stressors: illegal harvest, ecosystem shifts, and an unprecedented marine heatwave (2014–2016) that caused > 90% kelp canopy loss and explosive sea urchin proliferation. Surveys before and after these events reveal near-total collapse: Oregon densities fell from $0.013/m^2$ in 2015 to $0.002/m^2$ by 2019, while long-term monitoring in California shows densities and recruitment plummeting to near-zero post-2015. No evidence of recovery has emerged; recruitment modules and transects indicate functional reproductive failure. Combined anthropogenic and climate-driven stressors - serial depletion, habitat loss, warming, and food scarcity - suggest flat abalone may be undergoing a "neoextinction."

FIRST MAROSPORIDA NUCLEAR GENOME: A DRAFT GENOME ASSEMBLY OF BAY SCALLOP MAROSPORIDA (BSM) ASSOCIATED WITH BAY SCALLOP MORTALITY IN NEW YORK

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Bay scallop Marosporida (BSM) is an apicomplexan parasite associated with severe mortality in bay scallops in New York. BSM belongs to the recently recognized lineage Marosporida, which has lacked nuclear reference genomes. This has left Marosporida largely absent from genome-scale comparisons across Apicomplexa. This study presents a draft nuclear genome assembly for BSM, representing the first nuclear genome for Marosporida and establishing a new reference point for apicomplexan comparative genomics. The assembly totals 41.0 Mb in 6700 scaffolds (N_{50} = 9,041 bp; GC 33.7%). Repeat masking indicates 45.4% of bases are repetitive, dominated by simple repeats (34.6%) and additional interspersed repeats (10.7%), a landscape consistent with the observed assembly fragmentation. BUSCO (n = 446) estimates 78.9% completeness, with 9.6% fragmented and 11.4% missing genes Organelle genomes were also recovered, including an apicoplast genome of ~18.5 kb and a highly reduced mitochondrial genome of < 6 kb. This enables comparative analyses of organelle reduction versus nuclear genome architecture. Phylogenomic analyses place BSM within Marosporida as a distinct lineage within Apicomplexa. This provides a long-missing genomic anchor for resolving deep relationships and inferring lineage-specific gene content. Functional profiling using KEGG modules supports central carbon metabolism (glycolysis and gluconeogenesis), nucleotide biosynthesis, lipid metabolism, the shikimate pathway, and the non-mevalonate isoprenoid pathway, generating testable hypotheses about metabolic capability and host dependence. These resources enable targeted marker design, genome-wide surveys of parasite diversity, and hypothesis-driven studies of gene families and candidate interaction factors potentially linked to intracellular parasitism and disease outcomes in scallops.

A CHROMOSOME-LEVEL GENOME ASSEMBLY AND ORGAN TRANSCRIPTOMES OF THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA*

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The Atlantic surfclam, *Spisula solidissima,* is a major fishery species as well as a promising aquaculture species in the United States. It occurs in large biomasses and plays a crucial role in benthic ecology. Despite its economic and ecological significance, genomic resources for the surfclam are scarce. This study presents a chromosome-level genome assembly of the surfclam along with organ transcriptomes and a mitogenome. A wild surfclam from offshore New Jersey was collected and used in this study. DNA from the adductor muscle was used to generate PacBio long reads and Hi-C short reads. The assembled genome consisted of 1,036 Mb in 207 scaffolds, with a N50 of 55.1 Mb and a GC content of 35.27%. Using the Hi-C data, 99.04% of the genome was assembled into 19 chromosomes, consistent with the haploid number. Repetitive sequences accounted for 47.26% of the assembly. A total of 26,333 protein-coding genes were identified based on *de novo* prediction, homology and transcriptome evidence, with 98.01% of them functionally annotated. Benchmarking universal single-copy ortholog (BUSCO) analysis revealed that 94.8% of the conserved single-copy genes were present and complete, indicating the completeness of the assembly. Transcriptome profiles were generated for mantle, gill, foot, digestive gland, kidney (nephridia) and adductor muscle. A complete mitochondrial genome was also assembled. The genome assembly, organ transcriptomes, and the mitogenome provide valuable resources for comparative genomics as well as studies on the biology and genetics of the Atlantic surfclam, an ecologically and economically important species.

AN IMPROVED GENOME ASSEMBLY AND TRANSCRIPTOMIC RESOURCES FOR THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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The eastern oyster is one of the most important fisheries and aquaculture species in the United States, and it is also a popular model for ecological research. A genome assembly of the eastern oyster has been published and has contributed significantly to oyster genetics and breeding; however, the old assembly contains considerable redundancy and errors in chromosome assembly, which are problematic for some applications. This study presents an improved genome assembly and transcriptomic datasets for the eastern oyster. The new assembly consisted of 586 Mb in 294 scaffolds with a N50 of 52 Mb, 90.1% of which were anchored to 10 chromosomes. The new assembly was 100 Mb shorter and much closer to the expected genome size of 578 Mb than the old assembly of 686 Mb. A total of 28,538 protein-coding genes were identified based on *de novo* prediction, homology and mRNA evidence, with 97.4% of them functionally annotated. The gene number was similar to that of other oyster species and 21% smaller than the 34,596 of the old assembly. Benchmarking universal single-copy ortholog (BUSCO) analysis revealed that 95.0% of the conserved single-copy orthologs were present and complete, indicating the completeness of the assembly. The redundancy was reduced and known chromosome assembly errors were corrected. Transcriptomic datasets were generated for 9 organs and 16 developmental stages, which can be used to infer gene function. The improved genome assembly and transcriptomic datasets provide valuable resources for comparative genomics as well as studies on the biology and genetics of oysters.

THE MULTIPLE STRESSORS OF A MULTIPLE-STRESSOR SYSTEM: ENGINEERING A BUDGET-CONSCIOUS EXPERIMENTAL SYSTEM

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Building low-cost experimental systems capable of manipulating biologically relevant combinations of temperature, oxygen, salinity, food availability, and microbial stressors requires balancing precision and stability against budget limitations, component compatibility, reliability, and the practical constraints of day-to-day operation. With these concerns in mind, the authors designed and implemented a budget-conscious, flow-through culture platform capable of tightly controlling multiple environmental parameters for marine invertebrate experiments, the Hatfield Aquatic Dynamic Environmental System (HADES).

At the center of this work is a modular, flow-through design that couples header tanks, distribution manifolds, pumps, and experimental vessels with networked sensors, and automated controls. The build is less expensive than prefabricated commercial systems or industrial options, yet supports precise, independent manipulation of temperature, pH, oxygen concentration, salinity, flow rate, microalgal dosing, and microbial control, with redundancy and bypass options for emergency alterations and reconfiguration. This apparatus supports long-term, high-density rearing under complex multi-stressor scenarios utilizing marine invertebrates, including oyster larvae and juveniles, Dungeness crab megalopae and instars, purple urchin larvae, and krill.

This presentation will describe schematics, component choices, and some operational protocols including target setpoints, realized environmental stability (with associated challenges), costs, and planned upgrades as a template for labs seeking to implement similar budget-conscious, multi-stressor systems. Emphasizing the successes across multiple taxa and life stages, the authors demonstrate how the HADES may serve as a prototype or 'backbone' for developing customized, flexible, low-cost experimental systems applicable to a diversity of marine experimental programs, from larval ecology and climate-change biology to aquaculture-oriented husbandry and method development.

ESTABLISHING BASELINE IMMUNE PARAMETERS TO INVESTIGATE SUDDEN UNUSUAL MORTALITY SYNDROME (SUMS) IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*)

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Sudden Unusual Mortality Syndrome (SUMS) in eastern oysters (*Crassostrea virginica*) is characterized by rapid, large-scale mortalities in market or near-market size oysters, yet its underlying causes remain unknown. In a preliminary laboratory experiment, rapid mortality was associated with injection of 0.2 µm–filtered homogenate from moribund oysters collected during a suspected SUMS event, motivating further investigation of immune responses following exposure to filtered oyster homogenates.

A controlled experiment was conducted to characterize oyster immune function before and after injection with artificial seawater (ASW; control), 0.2 µm–filtered homogenate from healthy oysters, or 0.2 µm–filtered homogenate from moribund oysters. Approximately 280 adult oysters were cleaned, measured, anesthetized, and injected, then maintained in flow-through raceways. Six individuals per treatment were sampled weekly to document morphology and collect hemolymph and gill tissue for immune parameter analyses. Mantle tissue was collected to quantify *Perkinsus marinus* prevalence and intensity to identify immune variation resulting from parasitic infection.

A SUMS-like mortality event did not occur, and survival remained high across all treatments. Immune responses were evaluated under these sublethal conditions, allowing immune function to be compared before and after injection and tracked over time. The resulting data establishes baseline ranges and variation of immune metrics in eastern oysters. These baselines will support future studies aimed at interpreting immune responses associated with SUMS events and distinguishing normal immune variation from early indicators of mortality.

USING TRIBAL COMMERCIAL FISHERS TO SURVEY DUNGENESS CRAB BIOMASS IN PUGET SOUND, WASHINGTON STATE

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Crustacean fisheries are the fastest developing wild stock fisheries in the world, with total global landings nearly doubling over the past three decades. In the inland waters of Washington State (WA), the harvest of Dungeness crab (*Metacarcinus magister*) provides critical commercial, recreational, and subsistence opportunities. The 1994 Rafeedie decision (US v. Washington, 873 F. Supp. 1422) reaffirmed the tribal treaty right to half of all state shellfish resources which are co-managed by the Treaty Tribes and the State of Washington. Without a stock assessment for Dungeness crab, the co-managers rely on a "3-S" system of management, which regulates harvest by sex, size, and season. This crab fishery is managed with little to no contemporary biological data, leaving Washington comanagers unable to develop adaptable management strategies. Together with the Pacific Northwest Crab Research Group and WA crustacean managers, the Port Gamble S'Klallam Tribe designed and tested the feasibility of using a random stratified sampling regime to determine crab biomass within a discrete management area. Tribal fishers were employed and used ventless commercial pots to sample during the winter and spring of 2025. Local weather and currents precluded us from hitting 100% of targeted trapping sites and commercial openers presented scheduling challenges. Nonethless, survey efforts showed a large increase in biomass of male crabs at all depths in as little as three months. Continuing to develop the tools and capacity to better understand the harvestable abundance of crab will allow co-managers to adapt management and harvest practices ensuring the resilience of this species for generations.

BIAS ENHANCED ELECTRO PHOTOCATALYSIS: NOVEL THERAPY FOR *VIBRIO PARAHAEMOLYTICUS* INFECTIONS IN SHRIMP AQUACULTURE

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Acute Hepatopancreatic Necrosis Disease (AHPND) in shrimp is caused by a strain of *Vibrio parahaemolyticus* (Vp) that emerged from China in 2009. AHPND causes approximately $6 billion in crop losses annually and existing technologies have been ineffective as AHPND has spread globally.

Bias enhanced electro-photocatalysis (BEEP) degrades organic compounds in seawater including forever chemicals (PFAS). Triplicate Studies conducted at the University of Arizona Aquaculture Pathology Lab (APL), a USDA reference laboratory, evaluated efficacy of BEEP against AHPND. Experimental shrimp were exposed in aquaria to lethal concentrations of Vp (10^6/mL). Initial challenge trials indicated BEEP treatment ~ 50% survival compared to controls that had no survival in 72 hours. Histopathology confirmed recovery from infection in remaining shrimp ~ 20% at 7 days. A subsequent study of Vp without shrimp showed no reduction of CFU using BEEP treatment versus controls over 48 hours. A challenge was designed to reduce re-infection from residual bacteria from the APL protocol high concentration of inoculant over the course of a 7-day trial by introducing UVC sterilization of the water column at 4 hours. The UVC control tanks at 72 hours, had ~70% mortality. At 7 days, the combination of BEEP and UVC resulted in 100% survival.

The mechanism of BEEP resolving AHPND infections in shrimp is under active investigation. The working hypothesis is BEEP degrades compounds called auto-inducers that bacteria release to communicate in quorum sensing (QS). With population density and auto-inducer concentration, coordination occurs. Auto-inducers regulate swarming, biofilm, defense, virulence, motility, and appearance.

CAUSES OF TRIPLOID OYSTER MORTALITY IN THE U.S. PACIFIC NORTHWEST

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Mass summer mortality of the Pacific oyster, *Crassostrea gigas,* is a well-known phenomenon attributed to a complex interaction of seasonal reproductive effort, stressful thermal and chemical environments, and opportunistic pathogens. More recently, summer mortality of triploid oysters has been widely reported, including for Pacific oysters on the U.S. West Coast, which is paradoxical supposing that triploids are sterile, with greatly reduced reproductive effort.

A field study was designed to influence the likelihood of summer mortality at sites with high productivity, by growing single oysters at high or low densities and tidal elevations and in suspended flip-bags or bottom bags. To assess the effect of ploidy, diploid, chemically induced triploid, and mated triploid Pacific oysters were produced from a common parent pool and distributed in replicate bags across levels of the nested experiment. Mortality and live weights of subsampled individuals were recorded for each bag, at each low tide cycle, during the summers of 2023 and 2024. Reproductive condition was assessed histologically.

In 2024, at sites and in treatments where summer mortality was observed (i.e. at higher-than-typical levels of ≈30% or less), mated triploids suffered from 43% to 93% mortality (average, 68%), significantly higher than mortality of diploids and even induced triploids, in most cases. Consequently, average yield per bag of mated triploids was lower, despite greater individual size, than average yields of diploids or induced triploids. Mated triploids are vulnerable to summer mortality because of substantial reproductive effort, likely reflecting derivation of tetraploids from ripe triploids and their subsequent propagation.

EVALUATING NOVEL *VIBRIO* ASSAYS AGAINST APPROVED METHODS

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The bacterial pathogens, *Vibrio vulnificus* (*Vv*) and *V. parahaemolyticus* (*Vp*), are abundant in coastal waters around the United States and are common causes of illnesses that arise from raw oyster consumption. While testing exists, the current FDA approved methods are laborious and expensive and therefore do not allow for testing to understand pathogenic *Vibrio* dynamics at the farm level. To increase testing capabilities, biphasic assays were developed for *V. vulnificus* (*Vv*) and *V. parahaemolyticus* (*Vp*) that are simple to use and provide overnight enumeration of these bacteria.

The goals of this project were to evaluate the 1) accuracy of the assays using qPCR, 2) ruggedness to reagent lot changes, and 3) specificity using qPCR and known isolates. Biphasic *Vv* assay results (MPN/g) are comparable to those from qPCR ($p = 0.523$) and the assays also provide similar results when using separate reagent lots ($p = 0.275$). *Vv* assays were highly specific, with false negative and false positive rates below 0.1%. On the other hand, *Vp* assays have significantly different MPN/g results when compared to qPCR ($p < 0.001$) and report different concentrations based on reagent lot ($p = 0.009$). They have a high false negative rate (14.4%), but a low false positive rate (0.11%).

Results indicate that biphasic *Vv* assays are accurate to established methods whereas *Vp* assays may need optimization and/or formulation changes to increase accuracy. This presentation will also discuss the potential for these assays to be incorporated into oyster farming practices to improve seafood safety.

WORKSHOP: ART AND DESIGN OF EFFECTIVE SCIENCE PRESENTATIONS

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As scientists and researchers, we all have two jobs – do the science and communicate the science. We receive a great deal of training (and build experience) to conduct research and innovate, but - except for journal publications - little to no training in communicating our science. Designing aesthetically pleasing presentations or producing quality audio and video, especially to effectively reach divergent groups of stakeholders or audiences are all full time pursuits taking years to master, but there are a number of core ideas and techniques that can help all of us create more engaging presentations using free or with low cost tools (many that you probably already have) that will in turn help us communicate more effectively to all audiences. Join Eric (a scientist and scientific illustrator/communicator) for tips on becoming a more effective visual communicator followed by an "Ask Me Anything" session.

INTEGRATING GENOMICS INTO PACIFIC OYSTER BREEDING: DEVELOPMENT AND DEPLOYMENT OF AN OPERATIONAL SELECTION FRAMEWORK

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Genomic selection has become the dominant method for accelerating genetic gain in terrestrial livestock, yet its routine application in molluscan aquaculture is only now becoming feasible due to advances in genotyping platforms, statistical methods, and integration into commercial breeding operations. Oysters present both opportunities and challenges for genomic breeding: high fecundity and strong selection differentials enable rapid response, while lethal phenotyping, multi-site environmental variation, and complex disease pressures require robust reference populations and efficient genomic workflows. Early work in oysters has demonstrated that genomic prediction can substantially increase accuracy for key traits, positioning the technology as a logical next step for modern oyster breeding programs.

Within this context, the Australian Seafood Industries (ASI) Pacific oyster breeding program has initiated its operational transition to genomic selection. During the first year, the program has established the core components required for routine genomic evaluations, including a multi-year reference population with matched phenotypes and genotypes, and genomically characterised broodstock populations to support within-family selection. Genotype datasets have been quality-assured, pedigree-verified, and imputed to a common marker set, enabling the integration of genomic information into existing trait models through single-step GBLUP.

Operational pipelines for tissue sampling, tagging, genotyping, and GEBV computation have been implemented across both breeding hubs and aligned with strict breeding timelines. Hatchery processes have been adapted to enable individual-based rather than family-based spawning, supporting the expected increase in selection accuracy.

This presentation will outline the technical progress achieved in the first year, discuss the operational lessons learned, and describe the next steps toward fully validated genomic gains in the ASI breeding program.

UNRAVELING THE MYSTERY OF THE MECHANISM BY WHICH FEEDING BENEFICIAL MICROORGANISMS TO SHRIMP REDUCES MORTALITY FROM MICROBIAL INFECTIONS

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Invertebrates lack an adaptive immune system, which makes developing disease management and prevention strategies for shrimp difficult. This project investigated whether administering beneficial microorganisms enhances disease resistance in shrimp by activating innate immunity or trained immunity. The shrimp, *Penaeus vannamei*, was fed a diet supplemented with certain lactic acid bacteria (LAB) and conducted a comprehensive analysis of gene expression. Gene expression profiling identified genes whose expression changed with LAB administration. Differences in circular RNA expression were also investigated. Administering disease-resistant LAB improved survival rates against infection by *Vibrio parahaemolyticus*, the causative agent of acute hepatopancreatic necrosis disease (AHPND) and white spot syndrome virus (WSSV). Transcriptome analysis revealed that LAB supplementation induced changes in gene expression related to pathogen recognition, antimicrobial peptides, transcriptional regulation, and immune memory. These results suggest that shrimp resistance mechanisms against these two pathogens differ. This study demonstrates that LAB administration influences both innate and trained immunity against bacterial and viral pathogens in shrimp. Furthermore, LAB has been found to activate and regulate the immune system including the formation of extracellular traps. Specific beneficial bacteria were enriched in the gills, stomach, and intestine after feeding LAB. Interestingly, despite these specific changes, the overall structure of the microbiota was not significantly altered based on diversity indices. Moreover, these results emphasize that, despite the absence of adaptive immunity in shrimp, feeding them beneficial microorganisms can induce sustained immune enhancement against infection. Research using photosynthetic bacteria and *Bacillus* was also conducted and will be discussed.

EXPANDING ENGAGEMENT OF UNDERREPRESENTED COMMUNITIES AND ALTERNATIVE LEARNING INSTITUTIONS IN COASTAL HABITAT RESTORATION AND RECREATIONAL FISHING IN SOUTH CAROLINA

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In 2022, the South Carolina Department of Natural Resources Oyster Recycling and Enhancement Program and South Carolina Sea Grant Consortium coordinated with the Southeast Aquatic Resources Partnership (SARP) to secure funding from the NOAA National Fish Habitat Partnership to support the development of a comprehensive curriculum that focuses on engagement with Title 1 schools and alternative learning institutions. The objective of this project is using the framework from the South Carolina Sea Grant ‘From Seeds to Shoreline®’ program to develop a model for implementation of lessons that focus on salt marsh education, oyster reef restoration, and recreational angling activities.

This project provides students with direct hands-on opportunities to understand and recognize the ecological importance of coastal habitat restoration to recreational and commercial fisheries, while also fostering a love for the salt marsh. Many underrepresented communities in South Carolina struggle with barriers to entry to our natural resources, whether it is access to the resource, positive experiences in the salt marsh, or lack of understanding how to experience the salt marsh. At projects end, a transferable curriculum will be developed that can be shared with other entities that can implement this same type of work. By empowering the next generation of South Carolina anglers with not only the knowledge of their fishery, but also a passion to see their fishery flourish, will ideally lead to more youth enjoying their estuaries and fostering environmental stewardship for future generations.

THINKING OUTSIDE THE SHELL: ALTERNATIVE METHODS AND MATERIALS TO ACCELERATE AND EXPAND OYSTER RESTORATION IN SOUTH CAROLINA

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The South Carolina Department of Natural Resources (SCDNR) manages and restores oysters on state-managed shellfish grounds. Historically, restoration has relied on two primary approaches: a community-based program using bagged shell and manufactured wire reef structures, and a large-scale program that plants shucked and cured oyster shell using barges and heavy equipment. While both methods are effective, each faces growing logistical and financial constraints.

Although South Carolina operates a successful oyster shell recycling program, recycled shell alone no longer meets restoration demand. To supplement supply, the state must purchase shell from out-of-state sources. As oyster shell becomes increasingly scarce nationwide, costs continue to rise, making large-scale and living shoreline projects more difficult to implement solely with shell-based materials. The large-scale restoration program is further limited by its reliance on barges and heavy equipment, which restricts work to sites with sufficient creek width, appropriate bank conditions, and favorable seasonal windows. These constraints reduce flexibility, limit suitable project locations, and slow restoration progress.

To increase the pace and scale of oyster restoration, the SCDNR is exploring alternative approaches. These include methods traditionally used by commercial oyster harvesters, as well as emerging cement- and concrete-based products designed for living shorelines. This presentation highlights these alternative techniques, summarizes ongoing research, and compares costs to help inform future restoration strategies.

DRONES FOR SUSTAINABLE SHELLFISH FARM MANAGEMENT

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Drone technologies for precision agriculture are advancing rapidly and successfully used in terrestrial settings. To investigate applications for commercial aquaculture, drone flights were completed during low tides May – August from 2023- 2025 to collect imagery (≤ 1 cm/px) of intertidal shellfish farms in Washington state. Drone imagery was collected on farms with on-bottom Pacific oysters (*Crassostrea gigas*), aquaculture gear (clam nets, oyster containers), eelgrass (*Zostera marina*), and ghost shrimp (*Neotrypaea californiensis*) burrows. Imagery was collected with a DJI Mavic 3 drone with a RGB 20 MP camera. Images were post-processed into orthomosaics, then imported into ArcGIS Pro. Benthic features visible in the raster imagery were either digitized or classified using object-based image analysis (OBIA). For the process of OBIA, raster images were segmented using groups of neighboring pixels (objects) that share similar attributes. Following image segmentation, training data was created for each benthic feature to be classified. Using the Support Vector Machine (SVM) algorithm, images were classified with inputs from the training data. Classified features were converted from raster to vector polygon layers and summary statistics were calculated to determine total areal cover (m^2) of each feature. Shellfish biomass estimates were calculated by multiplying average commercial planting densities by total areal cover. Benthic surveys in mapped areas were completed to estimate live oyster densities (counts) and average size (shell length) within 0.25 m^2 quadrats. This study demonstrated the use of drones and classified orthoimagery as a tool for sustainable shellfish farm management.

FECAL COLIFORM MEASURES ELUCIDATE INCONSEQUENTIAL RISK FROM RESIDENT AND MIGRATING BIRDS ON SURFACE CULTURE IN WILLAPA BAY, WASHINGTON, USA

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The potential risk of bacterial contamination at two oyster farms in Willapa Bay, Washington was evaluated through seasonal observation of migratory and resident birds perching on the floating gear, and enumeration of fecal coliform in water within the floating arrays. Visual and remote camera observations estimated bird presence during seasonal migrations in spring 2024 through fall 2025. When birds were present, water samples were collected from at least three locations within the culture arrays. Collections followed standard protocols for shellfish growing waters and were transferred to an accredited lab within 24 hours. Results demonstrate that both aquaculture sites meet water quality standards, as specified by the National Shellfish Sanitation Plan (NSSP). Excluding reference samples, the median most probable number (MPN) during bird presence was 1 MPN (4 samples > 43) at one farm site, and 2 MPN (never > 43) at the second site. Therefore, both sites did not exceed the fecal coliform standard (median > 14 MPN per 100 mL, and ≤ 10% samples > 43 MPN per 100 mL) when sampling targeted periods of substantial bird presence on surface culture oyster farms. These results suggest that fecal coliform contamination from birds on surface gear is not a significant risk at these sites. Furthermore, although larger birds, such as gulls and pelicans, may produce greater amounts of guano in a single defecation than a much smaller shorebird, the difference in bird density/cage between the two suggests that overall oyster exposure to bird fecal matter may not necessarily be greater in the presence of larger birds.

U.S. OYSTER PRODUCTION: RECENT TRENDS AND MARKET POTENTIAL

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The U.S. oyster industry has experienced significant developments in production, market dynamics, and economic impact. A new NOAA Technical Memo explores trends in oyster production, market potential, and growth opportunities. The report also identifies challenges such as price declines, market disruptions, and highlights the need for improved data collection and reporting. The analysis aims to provide a foundation for strategic decisions toward a sustainable and thriving oyster industry in the coming decade.

Oyster production and farm-gate value information was gathered from every U.S. coastal state engaged in private and public oyster harvest. The best available data indicates that U.S. production peaked in 2017 but declined due to environmental events and the COVID-19 pandemic. Production rebounded post-pandemic but has not fully recovered to pre-pandemic levels, however, data quality issues are apparent and restrict the ability to perform a robust evaluation.

Interviews with experts in the oyster production, processing, and distribution sectors were also conducted, and revealed varied growth trajectories across regions, with some producers facing market ceilings. Experts believe that demand drivers include price, quality, food safety, consumer preferences, and storytelling about origin and sustainability. Experts state that consumer preference favors smaller oysters for raw consumption, with growing interest in value-added products. Seasonal demand fluctuations and the dominance of restaurant consumption channels create vulnerabilities. Furthermore, press coverage of food safety issues can severely impact demand, even when human health risk is minimal. Marketing and education efforts are limited by resource constraints but are critical for growth.

PROTECTING SUBSISTENCE RESOURCES: MANAGEMENT OF EUROPEAN GREEN CRAB ON THE ANNETTE ISLANDS RESERVE IN SOUTHEAST ALASKA AND BEYOND

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Since the detection of the European green crab (EGC) in southeast Alaska in 2022, the Metlakatla Indian Community Department of Fish and Wildlife (MIC DFW) has been working extensively to manage and monitor EGC populations on Annette Islands Reserve (AIR) and beyond. The community of Metlakatla is located on the AIR, 15 miles south of the city of Ketchikan, and has a population of roughly 1,500.

With the goal of achieving functional eradication of the EGC population on the AIR, the MIC DFW Crab Team has prioritized important cultural and economic subsistence areas to limit the environmental degradation caused by the EGC. Data from the 2025 trapping season show that the 2023-2024 El Niño event likely contributed to higher recruitment and a broader distribution of European green crab on the AIR and throughout southern southeast Alaska. In 2025, the MIC DFW saw a seven-fold increase in the number of crabs removed compared to all other years combined, removing over 42,000 live EGC. The MIC DFW has also been a key organization in understanding the extent of the EGC in southeast Alaska, identifying at least nine new locations that have EGC around Gravina and Prince of Wales Islands.

With four years of intensive trapping efforts, the MIC DFW Crab Team has on-the-ground experience in identifying potential EGC habitat, and locations for trapping in the intertidal zone. As the range of the EGC expands northward, the MIC DFW knowledge of EGC will be vital for managing the invasion into the future.

BEYOND THE BASICS FOR BUSINESSES AND PRACTITIONERS

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Aquaculture is a growing and vital part of the Rhode Island and regional maritime seascape. In January 2025, Rhode Island Sea Grant launched “Professional Aquaculture Training: Beyond the Basics for Businesses and Practitioners.” This course is a hybrid (live, in-person and virtual) 12-week course that aims to provide an advanced understanding of aquaculture in five main topic areas: 1) Economics of Shellfish Farming, 2) Staying Healthy in Aquaculture, 3) Keeping the Peace in Aquaculture, 4) Effective Communication in Aquaculture, and 5) 21st Century Farming Principles, Practices and Considerations.

This course provides participants with information to competently and confidently improve farm businesses and operations, minimize conflict with coastal residents and other users, and take advantage of state and federal resources. There are no official prerequisites for the course, but it is highly recommended to have taken an aquaculture course available to the public. Weekly guest presentations by topical experts are available by a pre-recorded video(s) or during a hybrid class. It is clear from recent, contentious lease applications in Rhode Island that the State’s aquaculture industry will have to make some changes if it is to contribute to a more favorable future. This includes ensuring the use of best management practices, more effective communication strategies when engaging with the public, and participating meaningfully in research and outreach, all of which are covered in this course. In this presentation, lessons learned from teaching the course in 2025 and anticipated updates for the 2026 course offering will be discussed.

THE STATUS OF BIVALVE SHELLFISH HATCHERIES ON THE ATLANTIC COAST OF THE UNITED STATES: A REPORT FROM THE BIVALVE HATCHERY HEALTH CONSORTIUM

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Bivalve hatcheries are essential as a source of larvae and seed/spat. Several hatcheries in the USA have reported experiencing slow larval growth or high mortality events due to unknown causes. With a limited number of shellfish hatcheries supplying seed to a growing seafood industry and restoration efforts, it is important to develop management protocols to minimize these issues. To address larval crashes on the Atlantic coast of the USA, the Bivalve Hatchery Health Consortium (BHHC) was formed. Using a collaborative, stakeholder-driven, comprehensive, reiterative approach, the BHHC developed a process for: (1) stakeholder enrollment; (2) collection of information on hatchery operations; and (3) collection of samples and metadata for good and bad production runs. Information is collected following a process that ensures hatchery privacy and confidentiality, and data is anonymized and aggregated before dissemination.

The participating hatcheries in the BHHC complete an Enrollment Survey whose responses provide baseline information for the individual facilities as well as an understanding of the status of the hatcheries along the east coast. An almost even representation from public (breeding, research, or restoration) and private (commercial) hatcheries is found in the BHHC. This presentation will provide a broad overview of BHHC hatcheries, including type of hatchery (public or private), species produced, technology used, general production methods, production levels and reported issues that have been impacting their facilities. This information is being used to identify which management practices and hatchery conditions may be associated with low larval performance and develop protocols to minimize losses.

THE BIVALVE HATCHERY HEALTH CONSORTIUM: A COLLABORATIVE WORKSHOP TO IDENTIFY AND MANAGE CAUSES OF DECREASED LARVAL PERFORMANCE IN HATCHERIES

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Disease remains an impediment to reliable larval production of bivalves, with periodic outbreaks in hatcheries affecting the availability of seed for grow-out. The Bivalve Hatchery Health Consortium (BHHC) was established in 2023 to identify causes leading to reduced larval performance and develop management tools. A process was developed for enrollment of hatcheries into the BHHC that protects confidentiality of their data and production practices. The BHHC also developed protocols for the proactive collection of samples of water, algae, and larvae from good and bad larval production runs, from broodstock conditioning to post-set. High levels of interest from the industry demonstrated that hatchery crashes are widespread and severely impacting larval production throughout the U.S. As of September 2025, 37 hatcheries from the Atlantic coast of the USA have enrolled in the BHHC, providing samples and data for more than 60 production runs in 2024 and 2025. In 2024 and 2025, 55% of the production runs were crashes or showed low larval performance. The objectives of this interactive workshop are to: 1) share lessons learned from the BHHC enrollment and sampling process; 2) report findings from the 2024 sampling season, 3) engage participants in interpreting the data collected so far, and 4) discuss further steps. Members of the BHHC coordinating team, including pathologists, ecologists, hatchery managers, and extension specialists, will answer questions and gather feedback from those interested in the program on how to address this critical issue of larval crashes.

SPAWNING, LARVAE REARING, AND JUVENILE NURSERY CULTURING OF WARTY SEA CUCUMBER, *APOSTICHOPUS PARVIMENSIS*

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The warty sea cucumber (*Apostichopus parvimensis*) is an important commercial species along the Pacific coast of the United States. Developing reliable aquaculture techniques is essential to reduce pressure on wild populations and to support stock-enhancement efforts through the out-planting of cultured juveniles. This study reports advances in spawning induction, larval rearing, and juvenile nursery culture for this species.

Among four spawning induction methods tested, peptide (NGLWYamide) injection proved most effective, consistently producing healthy gametes. Larval development progressed through five stages, reaching the pentactula stage in 17 days at 20°C with a survival rate of 26.67 ± 2.89%. A mixed microalgal diet of *Rhodomonas* sp. and *Tisochrysis lutea* supported the best larval performance, and 24°C was identified as the upper thermal limit for normal development and acceptable survival (25.00 ± 2.50%). *Doliolaria* larvae showed comparable settlement rates across multiple settlement inducers, including cultured *Navicula* sp., wild cultured benthic diatoms, *Spirulina* coatings, and AlgaMac products.

Juveniles (5.67 ± 0.93 g wet weight) were fed four diet types to evaluate growth and nutrient assimilation. Juveniles fed exclusively *Sargassum* powder achieved the highest daily growth in dry weight (0.90 ± 0.53% d^{-1}) and condition index (0.0045 ± 0.0011% d^{-1}). The lowest crude protein content of *Sargassum* powder was low (12.20% DW) resulted in the highest fecal output yet exhibited comparable apparent protein digestibility to other diets (14.90–33.60% DW).

These findings provide a foundational framework for hatchery development and juvenile nursery culture of *A. parvimensis* along the U.S. Pacific coast.

OPTIMUM MICROALGAL COMBINATION DIETS FOR LARVAE AND SPAT OF THE PACIFIC CALICO SCALLOP, *ARGOPECTEN VENTRICOSUS*

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In this study, six microalgae species, *Nannochloropsis oculata* (NANNO), *Tisochrysis lutea* (CISO), *Diacronema lutheri* (MONO), *Chaetoceros calcitrans* (CC), *Tetraselmis suecica* (TET), and *Rhodomonas* sp. (RHODO), along with their bi-, tri-, tetra-, and penta-algal combination diets, were evaluated for larvae and spat of the Pacific calico scallop (PCS, *Argopecten ventricosus*) to refine hatchery-based seed production technology.

PCS larvae reared on single species showed highest survival in CISO (13.8%) and MONO (11.7%), while all larvae in CC died at 10 days' post-fertilization. Among combinations, larvae in CISO+MONO+CC (18.96%) and CISO+MONO+NANNO+CC (16.67%) had the highest survival, with the fastest growth in CISO+MONO+CC (5%/d). A 1:1:1 ratio of CISO+MONO+CC produced the highest survival and growth compared with other ratios of this combination.

For PCS spat, the MONO+CC at a 1:1 ratio resulted in a shell-height growth rate of 0.26 mm/d, similar to several CISO+MONO+CC treatments; however, growth in ash-free dry weight (AFDW) (14.95%/day) was significantly higher than in all other treatments. When TET and RHODO were added, spat growth in shell height was significantly lower than in the 2:2:1 MONO+CC+RHODO treatment and showed significantly lower AFDW growth than in several tri- and tetra-algal MONO+CC+TET+RHODO combinations. Cornstarch additions at 0.5%, 1.5%, and 3.0% of total live weight/d did not improve growth.

Overall, results indicate that the optimal larval diet is CISO+MONO at an equal ratio during the first week, followed by adding CC. For spat, the optimal diet is MONO+CC at an equal ratio, with optional additions of TET, RHODO, or TET+RHODO at varying ratios.

PILOT TESTING THE TIMING AND EFFECTIVENESS OF TIDAL EXPOSURE AND TWO DIP TREATMENTS FOR CONTROL OF SHELL PESTS IN CULTURED OYSTERS

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Cultured eastern oysters (*Crassostrea virginica*) are a highly valuable Massachusetts seafood product, but their growth and markertability is challenged by shell pests: mud blister worms (*Polydora websteri*) and boring sponge (*Cliona celata*). This study investigated the impact of tidal exposure on oyster performance at two sites in Wellfleet Harbor. One-year-old wild and hatchery oysters were grown for one summer across five distinct tidal elevations. Key indicators monitored included viability (survival) and growth (shell, weight, condition index); biofouling biomass (e.g., sponge, mud blisters, tunicates); and shell pest presence.

Performance varied significantly with tidal height. Biofouling was minimal at the high exposure level. Analysis is underway to relate tidal height to mud blister and boring sponge presence. Preliminary data suggests a critical trade-off between maximizing growth and minimizing fouling/pest pressure, driven by tidal elevation. Separately, growers expressed interest in evaluating super-saturated brine and freshwater ice dip treatments for these pests, as well as the optimal timing of treatment. Pilot testing was conducted in summer 2025 on three Massachusetts oyster farms. Treatment efficacy and pest reproductive periods will be discussed.

EVALUATION OF THE COMBINED EFFECTS OF AMMONIA AND NITRITE ON THE SURVIVAL AND GROWTH OF JUVENILE PACIFIC WHITE SHRIMP, *PENAEUS VANNAMEI*

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Pacific white shrimp (*Penaeus vannamei*) dominates global shrimp aquaculture, making up the largest share of farmed shrimp, and its rapid expansion has been driven by the increasing global market and the development of high-density intensive culture systems; however, intensification has led to major water-quality challenges, particularly the buildup of total ammonia nitrogen (TAN-N) and nitrite (NO_2-N), both of which are highly toxic to shrimp. Although toxicity thresholds have been established for ammonia and nitrogen individually, shrimp in commercial systems are often exposed to both compounds simultaneously, and their potential interactive and combined effects remain poorly defined. Therefore, the present study aimed to quantify the combined effects of TAN and nitrite on the survival and growth performance of *P. vannamei* to develop more practical and relevant water quality thresholds for intensive shrimp aquaculture.

A 30-day trial was conducted on juvenile *P. vannamei* (initial average weight 1.94 ± 0.2 g). A total of 360 shrimp were placed in 18 aquaria (60 L each, 20 shrimp per aquarium), and six different treatments applied: T1 control; T2 nitrite only (10 mg/L); T3 (2 mg/L) and T5 (5 mg/L) ammonia only; T4 (2,10) and T6 (5,10) mg/L for ammonia and nitrite, respectively. Water parameters were measured, such as temperature 24-27°C, pH 7.5-8.2, dissolved oxygen 5.5-6.5 mg/L, and salinity of 20. Ammonia-N, nitrite-N, and nitrate-N were measured twice a week. Nitrite levels were raised to 20 mg/L and subsequently to 30 mg/L after mortality was not observed at 10 mg/L. After 30 days, survival and growth of *P. vannamei* shrimp differed significantly across treatments ($p < 0.05$). The lowest survival and growth occurred in treatments combining ammonia and nitrite.

THE PECULIAR CASE OF THE VIRGINIA "CONCH": CHALLENGES CONFRONTING A SMALL-SCALE COMMERCIAL FISHERY

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Channeled whelk (*Busycotypus canaliculatus*) and knobbed whelk (*Busycon carica*) are two species of marine gastropod commonly fished in Virginia waters. These fisheries often provide watermen with supplemental income. Despite this economic value, considerable uncertainty surrounds whelk stock status. This presentation explores trends in landings data and highlights key unanswered questions, emphasizing the challenges common to small-scale, understudied fisheries. It concludes with steps currently underway to address these knowledge gaps.

MOVEMENT ECOLOGY OF THE CHANNELED WHELK (*BUSYCOTYPUS CANALICULATUS*) DURING THE DEVELOPMENT OF AN OFFSHORE WIND LEASE SITE

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Offshore wind development often overlaps with existing ocean uses, including commercial fisheries. Along coastal Virginia, the development of the Coastal Virginia Offshore Wind (CVOW) lease area may impact commercial fishers targeting the marine gastropod, channeled whelk (*Busycotypus canaliculatus*). Channeled whelk is a commercially valuable yet relatively understudied species in the region, and the impacts of industrial development on this organism remain unknown. This species is presumed to have limited mobility and may be susceptible to anthropogenic disturbances. Understanding the drivers - whether anthropogenic or abiotic - of whelk behavior could inform future marine spatial planning decisions that seek to balance ocean development with sustainable fisheries. To investigate these dynamics, 15 channeled whelks were tagged with acoustic transmitters and released into a fine-scale receiver array at the CVOW pilot turbines. The movements of these tagged individuals were monitored from April to early October 2024, which encompassed a period of active construction (of the adjacent CVOW Commercial project) and varying environmental conditions. A hidden Markov model was then applied to examine how anthropogenic factors (i.e., pile driving) and abiotic factors (i.e., temperature, wave height, time of day, and lunar phase) influenced whelk movement and behavioral states. This presentation explores the findings of this research and demonstrates the utility of acoustic telemetry for tracking a commercially important marine gastropod in the context of offshore energy development.

COORDINATED MULTI-ESTUARY FARM TRIALS TO FURTHER UNDERSTANDING OF PACIFIC OYSTER PERFORMANCE AND SURVIVAL IN CALIFORNIA AND WASHINGTON

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In 1919, *Crassostrea gigas* was first imported from the Miyagi Prefecture in norther Japan to the U.S. West Coast and proved to be a valuable commercial product. In 1996, with a goal of selectively breeding for growth and survivorship, The Molluscan Broodstock Program (MBP) been breeding *C. gigas*, and oyster growers across the California Current use its primary "Miyagi" lineage extensively. In 2004, the MBP imported a new lineage of *C. gigas* from Southern Japan (the "Midori") which should potential increased resilience to thermal stress and disease in field trials in 2016. The introduction of the Midori lineage has garnered significant interest from industry members seeking to enhance their operations. This has led to wide-spread cultivation of both Miyagi and Midori lineages. This study evaluated how *C. gigas* from these different lineages, as well as triploid individuals, performed in both laboratory challenge experiments and on-farm trials over the last two years. Findings highlight how repeated observations across years increase the understanding of factors likely impacting production. Finally, results show that mortality trends that expand beyond a single estuary may be linked to the presence of shellfish-specific harmful algal blooms that may be impacting *C. gigas* performance even at low densities.

COMPARATIVE THERMAL RESPONSES OF *PERKINSUS MARINUS* ISOLATES FROM THE GULF OF SAINT LAWRENCE, CANADA, AND THE GULF OF MEXICO, USA

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Eastern oysters (*Crassostrea virginica*) are a primary aquaculture species in Atlantic Canada and are threatened by the protistan parasite *Perkinsus marinus*, which is known to cause mass mortality in both wild and cultured oysters in the US. The detection of *P. marinus* in the northern Atlantic off New Brunswick, Canada, in late 2024 may be linked to progressively warming water; nevertheless, it also raises concerns about potential adaptation to lower temperatures, because *P. marinus* tends to proliferate at temperatures above ~ 20°C, which are generally confined to summer months in this region. This study aims to compare the in vitro performance of isolates of *P. marinus*, via the measurements of cell viability, size, proliferation, and metabolic activity across a range of temperatures. Isolates were obtained from eastern oysters sourced from the southern range in Grand Isle, Louisiana, USA, and were established for the first time from the newly expanded northern range in Nova Scotia, Canada. The hypothesis is that Nova Scotia isolates will exhibit better performance at lower temperatures, while Louisiana isolates will exhibit better performance at higher temperatures. Isolates were held at four different temperatures, and performance was measured periodically over 40 days at 5 and 15°C, and 16 days at 25 and 35°C. The lower temperatures reflect seawater temperatures in Canada for most of the year, whereas the higher temperatures represent the southern thermal range of *P. marinus*. This information will help inform the level of threat to the local aquaculture industry and establish a baseline for management strategies.

BUILDING A SKILLED, CONNECTED, AND RESILIENT MARICULTURE WORKFORCE: AN INTEGRATED OUTREACH MODEL FOR SHELLFISH FARMING IN ALASKA

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Alaska Sea Grant and the Alaska Mariculture Research & Training Center (AMRTC) are implementing a comprehensive workforce development initiative that combines hands-on training, technical assistance, public outreach, and interstate knowledge exchange to advance sustainable shellfish farming. In 2025, the program delivered targeted workshops - including oyster farm operations, HAB monitoring, kelp nursery management, and business-practice skills such as forklift and HACCP training - engaging rural residents and Alaska Native communities statewide. New outreach tools, such as the 'AMRTC Salty Interview Sessions' video series and expanded farmer-to-farmer exchanges with Washington State, have strengthened peer learning and industry visibility.

Parallel curriculum development in marine safety, hatchery best practices, updated oyster farming guidance, and oyster cultivation manual are building a scalable training ecosystem. Public-facing engagement including the Mariculture Conference of Alaska, undergraduate internships, and support for Indigenous communities exploring aquaculture technologies, has broadened participation in shellfish farming. This presentation shares lessons learned, early impacts on industry capacity and safety, and outreach strategies that help cultivate a skilled, resilient workforce for shellfish mariculture in Alaska.

LONG-TERM SEASONAL ECOLOGY OF *VIBRIO* SPP. POPULATION ECOLOGY IN NEW HAMPSHIRE OYSTERS

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Over the past two decades, shellfish-borne infections from pathogenic *Vibrio* bacteria have increased significantly in the northeastern United States. Monitoring and predicting the population trends of *Vibrio* pathogens provides important knowledge for shellfish producers and managers to anticipate and mitigate public health risks. Since 2007, three *Vibrio* species at two natural oyster reefs in New Hampshire Great Bay Estuary, a significant oyster farming location in the northeast have been monitored. Previous studies have focused primarily on the population dynamics of *V. parahaemolyticus*, while the ecology of *V. vulnificus* and *V. cholerae* remains largely unknown despite posing public health concerns, especially considering the high mortality rate associated with *V. vulnificus* infections. The population trends of all three *Vibrio* species in oyster tissue in Great Bay from 2007 to 2024 were examined. Concentrations of *Vibrio* exhibited seasonal fluctuations and interannual variability, with higher abundances from June through August, and a notable spike in 2017. Populations of *V. parahaemolyticus* were higher and more persistent than the other two species. To understand the ecological drivers of these trends, environmental parameters over the same period were analyzed and found a strong relationship with temperature for populations of all three species, with lesser influence by other factors. Continued monitoring is underway to inform public health risk assessments and develop more robust predictive models of *Vibrio* population trends.

DIFFERENTIATION OF MICROBIAL COMMUNITIES IN COASTAL WATERS DURING HARMFUL ALGAL BLOOMS IN CHILE

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Harmful algal blooms (HAB) are a recurrent phenomenon in coastal waters worldwide, and particularly relevant for society, economy and aquatic ecosystems of southern Chile where aquaculture and fisheries industries are mainly concentrated. As consequent, public and private HAB monitoring programs have been established which are mainly based on physicochemical, toxicological, and microscopical parameters; however, their occurrence and spatiotemporal distribution is still difficult to predict, which is pivotal to take appropriated countermeasures to mitigate their impact. In this study, rRNA genes amplicon sequencing and bioinformatic analysis were applied to explore the changes in HAB-associated microbial communities in Chilean coastal waters. In northern Chile (Atacama Desert), results revealed differences in microbial communities before and during a *Akashiwo sanguinea* bloom. The bacterial communities were dominated by Flavobacteriaceae and Rhodobacteraceae families and members of Pseudomonadota and Bacteroidota were suggested as keystone taxa. Results also highlighted the positive relationships within microbial communities during the *A. sanguinea* bloom. In southern Chile (Patagonian fjords), differentiation between studied microbial communities were also detected during *Heterosigma akashiwo* and *Alexandrium catenella* blooms. The bacterial communities in *H. akashiwo* and *A. catenella* blooms were dominated by Proteobacteria, Bacteroidota and Cyanobacteria and they also accompanied by abundant diatoms and dinoflagellates. In *A. catenella* bloom, the bacteria Blastopirellula and the dinoflagellate Dino-Group-I-Clade-1 were suggested as keystone taxa. Finally, the potential use of microbial data coupled with empirical dynamic modeling and machine learning algorithms to predict HAB events will be presented and discussed in aquaculture, particularly in mangroves/shellfish ecosystems.

SOME ADVANCES ON THE CHARACTERIZATION OF MICROBIAL COMMUNITIES IN AQUATIC ECOSYSTEMS OF SOUTHERN CHILE

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Chile currently is the second and third largest global producer of salmon and mussels, respectively. As result, aquaculture is important for the society, economy and ecosystems of southern Chile. In this context, the impact of anthropogenic activities on aquatic ecosystems, such as freshwater lakes, estuaries, and coastal waters is controversial, and programs of monitoring and environmental protection have been adopted by Chilean government. Despite that microbiomes are essential for fitness of aquatic organisms and considered as sentinels (or bioindicators) of environmental health and ecological risks by their rapid and sensitive responses, changes in microbial communities are rarely considered in these programs. Under this scenario, culture-dependent and culture-independent approaches were used to characterize the microbial communities in aquatic ecosystems influenced by aquaculture activities in southern Chile. By using rRNA gene amplicon sequencing and bioinformatic analysis, not only the composition and potential microbial functions of bacterial communities in sediments of the freshwater and coastal lakes (Villarrica and Budi Lakes, respectively) were differentiated, but also bacterial genes involved in phosphorus and nitrogen cycling were detected and quantified. In addition, multiple antibiotic resistance (amoxicillin, chloramphenicol, and oxytetracycline) and herbicide (atrazine and glyphosate) degrading culturable bacteria were isolated and characterized from Villarrica Lake sediments. Differentiation in the composition and putative microbial functions of bacterial community in tissues (digestive gland and intestine) of the mussel *Choromytilus chorus* were also revealed between extensive (estuary) and intensive (bay) long-line systems in southern Chile, which are managed by artisan fishermen and aquaculturists, respectively.

A NEEDLE IN A HAYSTACK - RECOGNIZING YESSOTOXINS AND THEIR ROLE IN SHELLFISH MORTALITY

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For nearly a century, shellfish in Washington State have experienced ‘summer’ mortality events. Phytoplankton have been noted but not implicated in these mortality events. A bloom of *Protoceratium reticulatum* associated with a massive shellfish mortality event opened the door to earnestly evaluating the role of phytoplankton in summer mortality events in Washington State.

The SoundToxins partnership had been documenting increasing numbers of *P. reticulatum* and *Akashiwo sanguinea* in summer months, which had been associated with declining shellfish health or mortality at various sites in Puget Sound. In July 2019, a dramatic scene of surfacing stressed, gaping Manila clams signaled that something was wrong. Pathology reports, observations of the bay, and analytical testing suggested that yessotoxins (YTX) could be the cause. Subsequent YTX concentrations in clam tissues were measured at a maximum of 0.28 mg/kg and their histology demonstrated damage to digestive glands. A culture of *P. reticulatum*, isolated from North Bay during this massive bloom and shellfish mortality event, showed YTX reaching 26.6 pg/cell, the highest recorded toxin quota measured in the U.S. This mortality event led to previously collected data which further demonstrated YTX and other phytoplankton involvement in shellfish mortality events in Washington State over the last century. Why the needle in the haystack? YTX produced by *P. reticulatum* were first isolated from scallops in Japan in 1986, so it is a relatively ‘new’ toxin and something not commonly on the radar of researchers.

WASHINGTON AND OREGON SHELLFISH AQUACULTURE PERMITTING GUIDES

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NOAA Fisheries has developed guides for individuals, companies, and organizations interested in understanding the aquaculture permitting processes for growing oysters, mussels, clams, geoduck, and other shellfish in Washington and Oregon. These guides apply to commercial, subsistence, and restoration projects.

Washington and Oregon differ in several key aspects of shellfish aquaculture permitting. For example, Washington does not allow the use of the U.S. Army Corps of Engineers (USACE) Nationwide Permit 48, while Oregon does. The two states also differ in which agency oversees seafood safety: the Oregon Department of Agriculture in Oregon and the Washington State Department of Health in Washington.

Each guide outlines the application steps and identifies the relevant permitting agencies, required forms, and appropriate links specific to each state. The guides also include a flowchart that illustrates the permitting process and the recommended order for submitting applications. A Washington seaweed permitting guide will be released soon.

OYSTER REEF BUILDING SUCCESS ON ALTERNATIVE RESTORATION SUBSTRATE IN A HIGH SALINITY ESTUARY

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Settlement of larval eastern oysters (*Crassostrea virginica*) varies based on available hard substrate types. Their long-term restoration success may not equate to settlement rate, but it is vital to producing healthy oyster reefs. Many estuaries in Florida have experienced increases in salinity due to a lack of freshwater input. This has resulted in oyster reefs being diminished or vanishing completely in areas where they once thrived. With changing salinity placement of costly restoration substrate needs to be thoroughly planned.

Due to a limited supply of oyster shell, the optimal restoration substrate, other objects are often used for substrate to enhance restoration. In Lake Worth Lagoon rocks were chosen as an alternate restoration substrate. Initially rocks showed promise with high pioneer *C. virginica* settlement, but years after restoration, *C. virginica* spat were not thriving past initial recruitment. This is likely due to a multitude of environmental issues, some of which are associated with the high salinity environment. Settlement on rocks and oyster shell was compared by placing growth cages in the subtidal and intertidal range at the inner and outer edges of the restoration reef.

Replicate cages were planted in May 2024 prior to the peak settlement period and remained in place until January 2025. Monthly settlement to clean oyster shell with settlement stringers was also measured. The combined observations allow for comparison of background settlement rates and seasonal recruitment to two types of reef substrate in both subtidal and intertidal zones.

INCREASING COASTAL RESILIENCY AROUND SOUTH FENWICK ISLAND, SOUTH CAROLINA, USA: A CASE STUDY OF EASTERN OYSTER REEF RESTORATION

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Since 2011, oyster reef restoration biologists at the South Carolina Department of Natural Resources have used three-dimensional wire mesh structures to restore eastern oyster (*Crassostrea virginica*) reef habitat in the substrate-limited, intertidal estuarine environments of coastal South Carolina, USA. The early years (2011-2016) of these alternative material-base approaches to oyster restoration efforts focused on the repurposing of abandoned crab traps to create oyster reefs and reduce ghost fishing mortality of both target and non-target species. Beginning in 2016, however, recognizing that cement-coated wire mesh frames provide a large surface area that supports high rates of oyster recruitment, survival and growth, researchers began to deploy pre-fabricated wire mesh units in the form of manufactured wire reefs (MWR).

Multiple research projects have since demonstrated that these highly customizable MWR are successful at both creating new oyster reefs and reducing the erosional loss of salt marsh habitat, thereby increasing the resiliency of estuarine shorelines. This presentation will focus on restoration efforts conducted within the ACE Basin National Estuarine Research Reserve (NERR) and funded by the Bipartisan Infrastructure Law. Restoration efforts for this project included the installation of over 800 ft of MWR on South Fenwick Island as well as the loose shell planting on approximately two acres of fringing intertidal habitat. Details will be presented on both the deployments of these two forms of restoration approaches as well as the on-the-ground (e.g., quadrat-based percent cover) and drone-based (e.g., footprints, volume estimated and elevation mapping) monitoring conducted approximately one year after installation.

GYOTAKU WORKSHOP

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This hands-on workshop introduces the Japanese art of *Gyotaku* as a pathway to community engagement. All materials and supplies are provided for this 3-hour session that focuses on finfish as the printing subject. Cost: $115 for professionals and $95 for students. Enrollment is limited to 12 individuals, thus ensuring 1:1 interaction with the instructor. Instructor, Bruce Koike, has been practicing *Gyotaku* since the early 1990s. Like Lewis and Clark's expedition, register with a "*esprit de corps*". Contact the instructor if you have questions.

COLLABORATIVE MODELING AND ORAL HISTORY TO SUPPORT RESILIENT SHELLFISH AQUACULTURE

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Shellfish aquaculture is core to the social-ecological system in Willapa Bay and Grays Harbor, the southwest estuaries of Washington. This 125-year-old industry produces a substantial percentage of the cultivated shellfish of the nation, yet its future is threatened by ocean acidification, rising temperatures, invasive species, water quality threats, workforce shortages, and regulatory constraints. The Willapa-Grays Harbor Estuary Collaborative - a group of shellfish growers, Tribes, and local, State, and Federal organizations - launched in 2022 with a mission to strengthen the resilience of local communities and ecosystems. This project advances that mission using two strategies: collaborative modeling and oral histories. Focus groups were convened across diverse stakeholders to capture values, priorities, and trade-offs within the system. Participants generated conceptual maps of the social-ecological systems of the region which were synthesized within stakeholder groups as a first step toward confronting differences in understanding and attempting consensus. These maps will be aggregated and formalized into a fuzzy cognitive map to explicitly evaluate trade-offs during scenario planning and evaluation of alternative management strategies. In parallel, the project team conducted oral history interviews with shellfish growers, community members, researchers, and regulators to document experiences of environmental change and community resilience. Together, these approaches will integrate diverse knowledge sources and produce tools to evaluate and communicate potential outcomes and trade-offs for shellfish aquaculture in these rural communities. Beyond the tools themselves, the process of working toward consensus requires stakeholders to explicitly evaluate conflicting priorities, generating more common understandings and enhancing the perceived legitimacy of ecosystem-based management in the region.

TAMING THE PACIFIC OYSTER IN THE “WILD WEST”

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The Pacific oyster, *Crassostrea gigas,* has been farmed on the U.S. West Coast for over 100 years. First introduced from the Miyagi Prefecture in Japan in 1918, this species has proven to be highly adaptable to West Coast conditions. Efforts to domesticate or “tame” this species began in the mid-1900s with the identification of suitable algal diets and the application of hatchery and husbandry techniques. Despite extensive subsequent research efforts, it has not been possible to replace living algal diets with biochemically defined microparticulate artificial diets, resulting in only a partial understanding of the oyster’s nutritional requirements.

A family-based selection program (Molluscan Broodstock Program; MBP) was initiated at the Hatfield Marine Science Center (HMSC), Oregon State University, in 1996. Over a period of 27 years and eight generations of selection, efforts of the MBP resulted in improvements of approximately 67% in yields, potentially resulting in enhanced annual harvests worth >$90 million (USD). Application of marker-assisted selection against the oyster herpes virus OsHV-1 resulted in additional improvements in yield. At the HMSC, the application of probiotics to modulate the oyster larval innate immune system to improve disease resistance have also been explored. Overall, the Pacific oyster is only partially tamed in the “wild” West, with much more corralling to be done!

MARKER-ASSISTED SELECTION FOR RESISTANCE TO OsHV-1 IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*

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A collaborative project has focused on preparing oyster hatcheries and farmers for a more challenging future due to the possible spread of OsHV-1 along the Pacific Coast by improving broodstock resistance through selection. The Oregon State University Molluscan Broodstock Program (MBP) improved survival of oysters exposed to the Tomales Bay (TB) OsHV-1 variant in Tomales Bay, California, through both pedigree and marker-assisted selection (MAS), using a SNP marker on chromosome 8 (CHR8). It was determined that the effect of the presence of this CHR8 marker on the survival of families exposed to the TB variant in field plantings as well as laboratory exposures to both a more pathogenic UK variant of OsHV-1 and the bacterial pathogens *Vibrio coralliilyticus* (RE22) and *Vibrio aestuarianus*. Further, genetic analysis of families exposed to these OsHV-1 variants identified additional SNP markers for OsHV-1 resistance that could be useful in MAS and genomic selection programs. Broodstock families have been created that should be homozygous for the protective allele of the CHR8 marker, ensuring that this marker will be inherited by progeny in crosses with other breeding populations.

ASSESSING THE INFLUENCE OF BIRDS AND SITE-SPECIFIC CHARACTERISTICS OF OYSTER FARMS ON FECAL COLIFORM LEVELS IN SOUTHERN NEW ENGLAND

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Floating oyster aquaculture gear provides roosting habitat for coastal waterbirds, which may increase the risk of fecal contamination and trigger regulatory closures when fecal coliform (FC) levels exceed risk thresholds. A preliminary study conducted in 2021–2022 in Rhode Island identified terns, gulls, and cormorants as the most abundant species during the post-breeding season (mid-July through mid-October) and their abundance was especially high while roosting on floating oyster cages.

A follow-up study in 2024 evaluated waterbird deterrent effectiveness, FC concentrations in water and oysters, and pathogenic *Campylobacter* spp. in oysters at six floating oyster farms in Massachusetts and Rhode Island from August through November. Deterrents effectively reduced roosting bird abundance on all farms; however, Kruskal–Wallis tests indicated no significant differences in FC concentrations among deterrent treatments, and site-level variation in FC was not explained by bird density. Fecal coliform concentrations were also not significantly related to water temperature, precipitation, tide, or proximity to shore. No pathogenic *Campylobacter* spp. were detected in water or oyster samples.

Building on these results, further modeling will incorporate different precipitation measures, land use patterns, distances to watershed outlets, vertical mixing, site depth, and flow velocity at the sites. The goal is to better understand how bird presence and environmental factors together affect water FC. These findings are expected to help shellfish growers and regulators by enhancing site selection, guiding bird management strategies, and supporting risk-based decisions that reduce closures while protecting public health.

REDUCED WATER FLOW AND INCREASED STOCKING DENSITY EXACERBATE HYPOXIA RISK IN OYSTERS

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Low dissolved oxygen (DO) availability, or hypoxia, poses physiological challenges to oysters globally, and oyster respiration in dense aggregations can further reduce DO in their local microenvironment; however, high water flow can potentially "rescue" oysters from hypoxia by enhancing DO circulation. Thus, understanding the relationship between water flow speed, oyster density, and in-bed DO is critical for accurately assessing risk of hypoxia at aquaculture and restoration sites.

Two lab experiments were conducted to build a model of hypoxia risk in bag-cultured Pacific oysters (*Crassostrea gigas*). A water tunnel was used to evaluate the effect of oyster density and water flow speed on DO concentration within an oyster aggregation. The first experiment varied flow speed (1-20 cm/s) at a set density (250 oysters/bag, half full, 2.5 oyster layers), and another varied density (50-500 oysters/bag) at two different field-relevant flow speeds (1 and 6 cm/s).

Statistical models of DO based on the experimental data parameterized a nonlinear omnibus model of hypoxia risk based on density, flow speed, and temperature (using published Q_{10} values). Risk of hypoxia increases sharply at flow speeds below 10 cm/s and densities greater than half a bag, reducing in-bag DO down to 1.5 mg/L below ambient DO. For hypoxia prone areas, densities > 1 oyster layer/bag coupled with flow speeds < 10 cm/s will drive in-bed DO below the hypoxia threshold (2 mg/L) during the summer. Overall, this hypoxia risk framework provides an efficient way to fine-tune husbandry practices based on site-specific water flow, temperatures, and farm practices.

DEVELOPMENT OF A HABITAT SUITABILITY MODEL FOR THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) IN FLORIDA ESTUARIES

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Habitat suitability models (HSM) are widely used to relate species distribution spatially to abiotic and biotic environmental factors, and to evaluate the relative suitability of a habitat for a given species. In marine systems, HSM have been applied to assess habitat quality and water management practices, guide aquaculture and restoration efforts, and evaluate the effects of changing conditions in estuaries. Numerous HSM have been developed for the eastern oyster (*Crassostrea virginica*) across estuaries from Texas to Florida and along the northeastern coast of the United States. These models commonly incorporate salinity, temperature, indicators of current or historical oyster presence, water depth, and substrate type. Additional parameters are often used, but vary widely across studies. Differences in data application methods and parameter specificity often limit the ability to compare models across regions.

To support broader geographic comparison, a standardized HSM for *C. virginica* has been developed. The proposed model incorporates salinity, temperature, mapped oyster habitat from the previous four years, and navigation channels as primary parameters, and freshwater input and seagrass habitat as secondary parameters. The model was applied to two common examples of oyster habitat in Florida: the flow-managed St. Lucie Estuary and Suwannee Sound, which experiences natural flow. Model outputs from each system were compared to evaluate performance across varied oyster habitats and to assess the feasibility of region-wide comparisons.

HABITAT USE OF ARTIFICIAL OYSTER REEFS BY CRABS, FISH, AND DIAMONDBACK TERRAPIN: PERFORMANCE AND ANALYSIS OF A NOVEL VIDEO TECHNIQUE IN TURBID WATERS

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The Lynnhaven River system (LRS) in lower Chesapeake Bay has experienced major oyster restoration efforts. Subtidal restoration reefs have been constructed of oyster shell and alternative reef substrates including rock, concrete and reef balls across 50 ha. In Lynnhaven Bay of LRS, a 3.24 ha restoration site houses a network of 28,045 reef balls (0.3 m high, 0.46 m diam). Habitat use of the reefs by fish and invertebrates has been difficult to assess because of turbid waters. In summer 2024, we developed a novel video technique to quantify utilization of oyster reefs in turbid waters, by modifying a Baited Remote Underwater Video (BRUV) system using a GoPro camera housed inside of a large glass container filled with freshwater (Clearview Camera System, CCS). In the network and control marsh and unvegetated bottom sites, the CCS produced clear images of fish and invertebrates, allowing us to identify and measure individuals within 0.5 m, including juvenile black seabass (*Centropristis striata*), silver perch (*Bairdiella chrysoura*), silverside (*Menidia menidia*), pigfish (*Orthopristis chrysoptera*), blue crab (*Callinectes sapidus*), common spider crab (*Libinia emarginata*), and diamondback terrapin (*Malaclemys terrapin*) among others. Video analysis using MaxN demonstrated species-specific and general habitat use, such as species-specific use of the network as a nursery by black sea bass, and generalized use of the network, marsh and soft bottom as a foraging ground by blue crab. This is one of the few investigations to document comprehensive habitat use of subtidal, artificial oyster reefs by fish, turtles and crabs in turbid waters.

ASSESSING THE ROLE OF PLASTICITY IN DETERMINING THERMAL RISK ACROSS THE LIFE CYCLE OF AN INTERTIDAL GASTROPOD

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A key challenge to predicting the impacts of climate change on coastal marine mollusks is determining which life stages face the highest thermal risk. Most organismal thermal risk assessments are based on unchanging physiological threshold values, yet organisms can buffer themselves from temperature variation via plasticity in both thermal tolerance and behavior. The predominant view is that plasticity in thermotolerance is not sufficient to buffer organisms from overheating risk, but most estimates do not incorporate behavioral plasticity. Therefore, the relative importance of thermal tolerance versus behavioral plasticity in buffering organisms from thermal risk remains underexplored.

This study used the intertidal gastropod, *Haminoea vesicula,* in a Pacific Northwest tidal flat as a model system to quantify thermal risk in two life stages and the roles of physiological and behavioral plasticity in determining risk. Adult snails have highly plastic thermotolerances, adjusting T_{opt} (the temperature that maximizes aerobic scope) by 8°C from spring to summer. By contrast, embryos have high thermal tolerance compared to adults (8°C warmer T_{opt}), with no seasonal plasticity in thermal tolerance; however, adult snails deposit embryos in sync with tidal rhythms, with ~90% of egg deposition occurring at the beginning of the spring tidal phase. Consequently, favorable developmental temperatures increase embryo performance compared to random or constant egg deposition behavior. Overall, adult snails depend on physiological plasticity, while embryos depend on behavioral plasticity of adults (well-timed reproduction) in order to persist in thermally dynamic environments.

INVESTIGATING RIVER OTTER PREDATION ON INVASIVE EUROPEAN GREEN CRAB WITHIN THE ESTUARIES OF MAKAH BAY, WASHINGTON

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European green crab (*Carcinus maenas*) populations have increased substantially in the estuaries of Makah Bay, Washington since early monitoring started in 2017, raising important questions about whether native predators may exert biotic resistance. North American river otters (*Lontra canadensis*) are highly opportunistic mesopredators whose latrine sites in the Wa'atch and Tsoo-Yess River estuaries directly overlap with areas of high green crab density, making them strong candidates for influencing the population trajectory of the invasive crab.

This study quantified the presence of green crab in river otter diet using a combined molecular and hard-parts approach applied to scat collected across 2023–2025. DNA metabarcoding assays targeting mitochondrial 16S markers are used to characterize prey assemblages, complemented by morphological identification of crustacean fragments. Sex identification, site-level environmental factors, seasonality, and local green crab catch-per-unit-effort were incorporated to evaluate ecological and demographic drivers of predation. Results will be compared to a 2019 dataset, when green crab density was much lower, providing a before-and-after framework for assessing whether otter prey use has shifted in response to the rapid expansion of this invasive species.

Using estimated diet proportions, otter energetic requirements, and green crab biomass values, a consumption estimate is being developed to assess whether otter foraging pressure could meaningfully influence green crab abundance at the estuary scale. Findings will help clarify the role of a native predator within an altered food web and evaluate whether river otters contribute biologically relevant top-down pressure on a species of major ecological and cultural concern.

IDENTIFYING NATIVE AND INTRODUCED OYSTERS IN HAWAI‘I

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Hawai‘i is home to two native species of pearl oyster (family Pteriidae) and four known native species of true oysters (family Ostreidae). Oyster aquaculture in the state is primarily focused on the Pacific oyster, *Crassostrea gigas*, which was introduced in the early 1900s and has become established in Pearl Harbor and Kaneohe Bay. One species of native Hawaiian oyster, *Dendostrea sandvicensis*, has been cultured in fishponds (loko i‘a) across the state as well as at University of Hawai‘i at Hilo's Pacific Aquaculture and Coastal Resources Center (PACRC). *Dendostrea sandvicensis* has been previously identified in Pearl Harbor and is the only known species of native Hawaiian oyster in its genus. An unknown species of *Dendostrea* has been established in Nōmilu Loko i‘a on Kaua‘i. This study compares the unidentified *Dendostrea* from Nōmilu Loko i‘a, specimens collected from Pearl Harbor, and the *D. sandvichensis* that are cultured at PACRC. DNA barcoding using 5 standard loci was used to compare tissue samples of specimens from each location with the sequences available on GenBank. The results of this study will determine the identity of the unknown *Dendostrea* at Nōmilu Loko i‘a and identify oysters which have become established at Pearl Harbor which could be candidates for aquaculture applications.

ESTABLISHING A RELIABLE MILK CONCH, *MACROSTROMBUS COSTATUS*, CAPTIVE BREEDING PROGRAM

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A breakthrough at Florida Atlantic University has the potential to accelerate conch aquaculture by eliminating the reliance on collection of wild-sourced egg masses to supply hatcheries. Eighteen adult milk conch (*Macrostrombus costatus*), consisting of eleven females and seven males, were provided with a sand substrate, flow through seawater, and diatom-rich algal turf as their primary diet. This algal turf was cultured using nutrient-rich wastewater from an Integrated Multi-Trophic Aquaculture system. This diet has resulted in reliable and prolific spawning, compared to previous studies that used formulated feeds. This population has produced an average of 5.14 egg masses per week with a total of 442 egg masses from April 2024 to November 2025 (86 weeks) of which 82% were fertilized. This study showed that algal turf, as the primary nutrition source, is one of the key components, along with system design and management, for a reliable captive conch breeding program. As a Strombidae, the milk conch has a similar ecological role to the queen conch, *Aliger gigas.* This similarity allows milk conch to be used as a proxy species to test the concept of having a reliable queen conch captive breeding population, thereby eliminating the need to collect wild egg masses for restoration hatcheries.

ADAPTIVE MANAGEMENT IN THE FACE OF UNCERTAINTY: LESSONS LEARNED FROM A NATIVE OYSTER, *OSTREA LURIDA*, RESTORATION PROJECT IN THE SALISH SEA

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Overexploitation and water quality degradation nearly eliminated the population of Olympia oyster (*Ostrea lurida*) in Puget Sound by the early 1900s. In response, the Swinomish Tribe initiated a restoration effort to reestablish cultural connections to this traditional resource. The project also aimed to create self-sustaining oyster populations at two sites within a target region of Puget Sound. A primary objective of this study was to evaluate biological successes and failures to inform evidence-based, site-specific restoration strategies. Temporal changes in oyster shell length and density were measured as proxies for growth, recruitment, and survival over a six-year monitoring period. Significant oyster growth was observed annually at both lagoon sites, indicating favorable conditions for individual performance. Despite the documented presence of brooding adults and competent larvae in the region, no recruitment was detected at either site during the study. Survival declined significantly over time and differed between sites. Although evidence of growth and reproductive activity was observed, the absence of recruitment and declining survival suggest that current conditions limit the potential for long-term population persistence. Several factors are hypothesized to constrain restoration success, including small restored population sizes, limited availability of suitable surrounding habitat, and low water residence times that may reduce larval retention. These findings highlight the importance of long-term, site-specific monitoring to evaluate restoration outcomes and to identify potential local failures. Poor survival or recruitment alone should not necessitate project termination; rather, such outcomes underscore the need for adaptive management.

STRUCTURAL ELEMENTS AND NEIGHBORHOOD MOSAIC INFLUENCE NEKTON COMMUNITY SIMILARITY ACROSS EELGRASS AND OYSTER-CULTURE HABITATS

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Mobile organisms use habitat in response to structure at multiple spatial scales, from local structural complexity to habitat composition of the surrounding neighborhood. For nekton (mobile fish and decapods) occupying > 100 m^2 habitat patches on intertidal flats, multivariate community analysis was used to test how dissimilarity changed across gradients of structural complexity and presence of structural elements. The habitat mosaic included a gradient of native eelgrass (*Zostera marina*) densities in the presence and absence of structural elements contributed by Pacific oysters (*Crassostrea gigas*) cultured on-bottom as clusters or off-bottom on lines. These intertidal habitats were sampled with seine nets in spring and summer at 11 sites in Washington State (USA). In comparison to unstructured habitats, communities were increasingly dissimilar with more eelgrass, while the structural elements provided by aquaculture also resulted in dissimilarities, and these were not additive. For dissimilarity relative to communities in dense eelgrass, statistical interactions were also common: adding structural elements of oyster culture to otherwise bare areas moderated dissimilarity in comparison to communities in eelgrass. Overall, while the habitats provided by eelgrass and aquaculture were not redundant, nekton communities typical of structured habitats arose when eelgrass was interspersed with oyster culture. At a neighborhood (50-m radius) scale, nekton communities sampled across habitats at six of the 11 sites were most similar when eelgrass cover in the neighborhood was moderate (~ 40%). These results demonstrated that the nekton community-level response to structural complexity depends on structural elements, and a more uniform neighborhood can enhance patch-level habitat use distinctions.

ECOLOGICAL INTERACTIONS OF SHELLFISH AQUACULTURE IN PUGET SOUND NEARSHORE HABITATS AND A REVIEW OF RELEVANT TOOLS, MODELS, AND CALCULATORS

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In Washington State there are over 250 shellfish farms across more than 700 sites, the majority of which are in Puget Sound. Expanding shellfish aquaculture in Puget Sound could increase interactions with the surrounding ecosystem and local protected species such as salmon. These interactions could be positive, negative, or neutral. In Puget Sound juvenile Chinook salmon (*Oncorhynchus tshawytscha*), which are listed as threatened under the Endangered Species Act, depend on nearshore habitat and likely interact with shellfish farms, but to what extent and effect is unknown. Potential positive impacts of shellfish farms may include an increase in habitat structure and nutrient removal associated with harvest in eutrophic areas. Negative impacts may include reduced primary production related to nutrient removal at times when pelagic forage is limited for juvenile salmonids, reduced light affecting productivity, and disturbance of eelgrass beds and eelgrass-associated invertebrates and fish. Considerations of interactions at local and seascape scales are also important. Changing climatic conditions may shift the type, intensity, and outcome of aquaculture-environment interactions. Managers are keenly interested in understanding these interactions and the available approaches to assess them. A comprehensive literature review was conducted to synthesize shellfish aquaculture-environment interactions and a review of the tools, models, and calculators used to assess these interactions. This synthesis will inform plans to incorporate information about shellfish aquaculture-environment interactions into approaches for assessing the effects of anthropogenic change in nearshore habitats on Chinook salmon.

EVALUATING AN ACOUSTIC DETERRENT FOR BIRDS ON FLOATING OYSTER AQUACULTURE GEAR

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Bird presence on floating oyster aquaculture gear remains a concern as illnesses linked to raw oyster consumption increase, particularly those associated with *Campylobacter* found in bird fecal matter. In Virginia and in accordance with Federal regulations, leaseholders are required to have an operational bird deterrent plan; however, there is no clear guidance on which technology is most effective. Therefore, Cherrystone Aqua-Farms tested the effectiveness of the Guardian Technologies Acoustic Deterrence Technology system for deterring cormorants, seagulls, and terns from the open water floating aquaculture farm.

The deterrent system was mounted in a Carolina Skiff and centrally deployed within our floating oyster farm in Cherrystone Creek for two months during spring bird migration. Trail cameras mounted on the boat captured bird presence every 30 minutes during deployment. Generalized additive models (GAMS) were run to test the effect of wind direction, wind speed, distance from sound (close, middle, far), and time of day (hour) on bird counts. Bird presence during the experiment was dominated by seagulls, with terns appearing toward the end. Although the experiment had limitations, results showed the system deterred birds close to the sound source (0-40 m); however, complex wind dynamics (speed, direction, waves absorbing sound) greatly impacted the effectiveness of this deterrent method. Wind direction significantly impacted roosting location, with birds preferring to roost downwind of the sound. Bird presence was also higher at low to moderate wind speeds. While preliminary, this sound system warrants further testing as a deterrent method for shellfish aquaculture in the Chesapeake Bay.

AQUACULTURE FEASIBILITY IN FORT BRAGG, CALIFORNIA, USA

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The Mendocino Coast is a rural region overlooking the Pacific Ocean on the north coast of California. Beginning in the mid-19th century, the regional economy centered on logging and fishing. Over time, these natural resource industries declined, and the compounding effects of climate related stressors (e.g., drought, fire, kelp forest loss), demographic shifts, and the COVID-19 pandemic further exposed both a vulnerable environment and economy.

The City of Fort Bragg and Noyo Harbor District partnered with California Sea Grant to develop a blue economy planning initiative, providing an opportunity to gather technical baseline information about current conditions in Noyo Harbor as well as develop a shared community vision for coastal resiliency. In light of fisheries closures, there are emergent opportunities in aquaculture to create jobs, supplement incomes, produce local seafood, and support restoration.

The Aquaculture Feasibility Study was a proof-of-concept analysis to determine whether Pacific oysters (*Crassostrea gigas*), red abalone (*Haliotis rufescens*), purple sea urchin (*Strongylocentrotus purpuratus*), dulse seaweed (*Palmaria mollis*), and bull kelp (*Nereocystis luetkeana*) survive and grow in Noyo Harbor. The objectives included: 1) locate appropriate sites and species for aquaculture operations in Noyo Harbor, for both in-water and land-based operations; 2) examine water quality for compatibility with species production; and 3) analyze the restorative and commercial opportunities of rearing these species in this region. This presentation outlines shellfish survival and growth data from Noyo Harbor and recommendations for future aquaculture opportunities in the area, with the goal of sharing new scientific knowledge and ideas.

DESCRIBING THE IDENTITY AND IMPACTS OF SHELL BLISTER IN ATLANTIC SEA SCALLOPS

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Occurrence of shell blister in the Atlantic sea scallop (*Placopecten magellanicus*) in the Mid-Atlantic and Georges Bank regions poses a challenge to the fishery by impacting growth and marketability of affected individuals. This condition is typically associated with boring polychaetes penetrating the shell, leading to the scallop secreting a nacreous blister over the opening. These blisters may become filled with detritus and can increase in size and severity over time. When shucked, the blister can also foul the adductor muscle directly.

Despite persistent prevalence in commercial landings, the identity of the boring parasite responsible for shell blister across this region, as well as its quantitative effects on the infected scallop growth and health, remains poorly characterized. Visual morphological identification, Sanger sequencing and environmental DNA assays were used to determine the identity of the blister associated polychaetes across the Mid-Atlantic and Georges Bank. Morphometric and statistical analyses were conducted to quantify the relationship between blister presence and severity and scallop health metrics. Patterns in blister impacts were evaluated across spatial gradients with consideration of environmental conditions. Preliminary results indicate a potential multispecies contribution to blister severity, involving both boring and non-boring polychaetes. These findings provide insight into the drivers and consequences of shell blister in Atlantic sea scallops.

RECRUITMENT RHYTHMS: UNDERSTANDING SPATIAL AND TEMPORAL VARIABILITY IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA,* RECRUITMENT IN SOUTH CAROLINA, USA

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Understanding the spatial and temporal variability of larval recruitment is critical for the effective management and restoration of the eastern oyster, *Crassostrea virginica*. In 2015, the Shellfish Research Section of the Marine Resources Research Institute initiated a statewide monitoring program to gain a better understanding of baseline levels of natural mortality and recruitment in the wild oyster population in South Carolina (SC). This program annually samples oysters at 34 coastal reference sites and has improved our understanding of spatial and temporal fluctuations in wild oyster recruitment by allowing biologists to estimate relative recruitment rates across the coast. To better inform the timing of the field deployment of oyster reef settlement substrate during the recruitment season, biologists are interested in better understanding the ecological processes that drive the onset, cessation, and variability of recruitment each year, and how these phenological differences vary among reference sites. In 2025, a standardized recruitment study was conducted throughout the course of the recruitment season (April-October), at three estuaries near Charleston, SC. Biweekly trays were deployed and utilized to estimate the rate of recruitment for each 2-week period, and cumulative trays were deployed and utilized to estimate recruitment success and growth over the course of the study. This presentation will discuss: 1) overall trends in recruitment rates among reference sites from 2015-2025; and 2) results from the 2025 recruitment study and the ecological processes driving recruitment dynamics in SC.

BEYOND PREDATION: GREEN CRABS (*CARCINUS MAENAS*) DISRUPT JUVENILE PACIFIC OYSTER (*CRASSOSTREA GIGAS*) FUNCTION THROUGH BOTH CONSUMPTIVE AND NON-CONSUMPTIVE PATHWAYS

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The establishment of the introduced green crab, *Carcinus maenas,* creates ecological and economic impacts in estuaries, particularly through predation on bivalves. This study evaluates the direct (predation) and non-consumptive (presence) effects of *C. maenas* on juvenile Pacific oysters, *Crassostrea gigas*, under varying conditions. Clearance rates of the Pacific oyster were measured over 72 hours across different temperatures (14°C and 18°C) and predator identities, green crab, Pacific rock crab (*Romaleon antennarium*), both predators together, and a predator-free control. Predator contact was tested at three phases: acclimation (to temperature and chemical cue) phase, non-consumptive (banded) phase, and consumptive phase. Oyster clearance rates were influenced by both predator presence and phase, with green crab treatments suppressing clearance the most, even when crabs lacked access to direct predation. Green crabs consumed more oysters than both the native Pacific rock crabs and mixed treatments, indicating stronger predation pressure and greater potential competition with native species. Unlike Pacific rock crabs, which showed a positive foraging association with size, green crabs consumed oysters indiscriminately, suggesting less size selectivity and more opportunistic feeding within our sample of juvenile oyster spat (< 40 mm). Green crab alters estuarine function through both its trophic and non-trophic effects, with implications for invasive species management and oyster cultivation.

BIOINDICATORS OF MICROPLASTICS: ARE BIVALVES THE BEST CHOICE? (SPOILER, THEY ARE NOT)

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Microplastics are an emerging contaminant distributed worldwide. Many studies have suggested that suspension-feeding bivalves would be good bioindicators for microplastics as they are known to consume plastic particles in the environment, are widely distributed, sessile, and easy to collect; however, bivalves are selective feeders and do not consume all particles that they capture. This study investigated how other suspension feeders interact with microfibers of different sizes and polymer types to assess their suitability as bioindicator species, including: the Atlantic slippersnail *Crepidula fornicata* (gastropod), sea grape *Molgula manhattensis* (tunicate), and rough sea squirt *Styela clava* (tunicate). Animals were offered aged polyester or nylon microfibers of different lengths, or nylon and polyester microfibers of similar lengths during 2-h exposure periods. Pseudofeces and feces were collected during and after exposure and the microfibers within enumerated. Bivalves exhibited size-based selection of microplastics, with rejection of up to 60% of captured fibers and rapid egestion of up to 40% of ingested fibers within 3 h. Slippersnails exhibited selective rejection of fibers similar to bivalves but rapidly egested over 50% of some fiber lengths. Tunicates rejected a lower proportion of microfibers compared to molluscs with *S. clava* being the least selective, rejecting less than 4% of captured fibers regardless of size. Both tunicate species, however, egested between 20% and 75% of ingested fibers within 3 h. Polymer type did not influence ingestion or egestion of fibers by any species. These data demonstrate that certain species of tunicates should be investigated further as candidates for biomonitoring purposes.

MOLECULAR CLONING AND PROTEIN MODELLING OF THIOREDOXIN GLUTATHIONE REDUCTASE FROM THE SHRIMP, *PENAEUS VANNAMEI*

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Glutathione plays a major role in cellular homeostasis. In terrestrial invertebrates, the enzyme thioredoxin glutathione reductase (TGR) reduces oxidized glutathione; however, little is known about TGR in penaeid shrimp. This study aimed to characterize the TGR gene in the shrimp, *Penaeus vannamei*. The coding sequences of TGR were amplified from hepatopancreas cDNA by PCR, cloned in pGEM-T Easy Vector and sequenced. The conserved domains and motifs were identified using the NCBI CD database and Expasy Protparam. Phylogenetic evaluation was done with MEGA-12, and protein modelling with AlphaFold3. Putative transcription factor (TF) recognition sites were identified using JASPAR and PROMO, and CpG islands with MethPrimer. The CDS of TGR is 1989 bp with 596 amino acids. The conserved motifs for selenocysteine extension, GSH binding and FAD/NADPH binding pockets are present, classifying this enzyme as a TGR. The promoter region of TGR in *P. vannamei* has three possible CpG islands and conserved recognition sites for the TFs Nrf2 and Ahr. This could indicate a likely methylation target for epigenetic expression regulation. The identification and characterization of the TGR is key to future studies on the effects of stress on the response of GHS-related enzymes in *P. vannamei,* and the beginning of a better understanding of its regulation *via* epigenetics.

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

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The National Phytoplankton Monitoring Network (PMN) is a community-based network of volunteers monitoring marine and freshwater phytoplankton and harmful algal blooms (HAB). Formed in 2001, the PMN enhances the ability of the United States to respond to and manage the growing threat posed by HAB by collecting important data such as phytoplankton species composition, distribution, and environmental conditions. HAB have been observed in every State resulting in over $1 billion in losses to communities that rely on recreation, tourism, and seafood harvesting. In the aquaculture industry, both shellfish and finfish, have experienced direct adverse effects of harmful algal blooms, both toxin-producing species and non-toxin-producing species. For the individual aquaculture farm, blooms of certain non-toxic phytoplankton are of paramount concern because they are known to cause the mortality of shellfish and finfish worldwide. Since these species do not cause human health concerns, most are usually not included in state-wide monitoring programs.

The Aquaculture Phytoplankton Monitoring Network (AQPMN) project expands the scope of the participatory science approach of the PMN to include the partnership of aquaculture farms. The AQPMN will catalog existing and new phytoplankton species responsible for finfish and shellfish injury and establish a national monitoring platform operated by aquaculture farms, empowering farms to take action to protect or harvest. This presentation will cover the methods used to monitor aquaculture sites and progress made by the AQPMN to establish a national participatory science approach to monitor ichthyotoxic HAB, co-developed by the shellfish industries.

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

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

The NOAA National Phytoplankton Monitoring Network is a community-based volunteer science approach to monitor harmful algal blooms and their associated toxins. Founded in 2001, the network has trained over 600 volunteers across 36 U.S. states and 4 countries including Costa Rica. The network includes coastal tribes from California to Arctic Alaska which serves as an early warning system for HAB and their toxins and protects tribal communities that rely on subsistence harvesting. The tribal partnership empowers tribes through training and co-management, enabling them to integrate Indigenous knowledge with scientific monitoring and take greater control over marine resource decisions. This model has been used since 2022 with a partnership with Innoceana, a global marine conservation organization that works to preserve the ocean for future generations by empowering coastal communities through access to education and innovative tools, to monitor potential harmful algae along Isla Violin. This project will expand the initial sampling conducted by increasing the number of sites and involve local schools and community groups to monitor the entire coast of Costa Rica.

THE ARCHAEOLOGY OF INDIGENOUS SHELLFISHERIES ON THE NORTHWEST COAST OF NORTH AMERICA

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Modern humans and our Neanderthal ancestors have been using shellfish for at least 150,000 years. On the northwest coast of North America (Alaska south to Oregon), humans have been using shellfish ever since they first occupied the coastline, roughly 15,000 years ago. Molluscs, crustaceans, and echinoderms have been key Indigenous resources since time immemorial. Most of the archaeological sites of the region contain the remains of clams, cockles, mussels, sea urchins, chitons, and barnacles. These and other shellfish played a range of dietary and social roles ranging from feast foods to emergency rations. Some Indigenous groups even intensified their use of shellfish by creating "clam gardens," a type of mariculture. Shell itself was used to make tools, jewelry and in site engineering. In this talk, the author will survey what archaeologists have learned about Indigenous shellfisheries on the northwest coast.

HIDDEN HEARTS: SCREENING ASSAYS SUGGEST INVOLVEMENT OF TOXINS, POLLUTANTS, OR VIRUSES IN SOME BIVALVE HATCHERY LARVAL CRASHES IN THE ATLANTIC COAST

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Widespread recent increases in larval crashes in bivalve hatcheries along the Atlantic Coast of the United States showcase the need for cross-institution collaboration, standardized sampling, high throughput sample processing, and the use of a comprehensive set of diagnostic assays to identify potential causes and develop targeted management tools. The Bivalve Hatchery Health Consortium (BHHC) has developed a screening assay using healthy larvae exposed to hatchery-collected samples to identify the type of disease-causing agents that could be present in the water or larvae from hatcheries experiencing low larval performance. In 2024 and 2025, more than 30 BHHC hatcheries collected incoming water (before hatchery treatment), larval tank water, and larval samples from more than 60 production runs experiencing unusual losses, as well as from normal runs (control samples). Preliminary results from the screening of whole and size-fractionated water samples from a subset of 21 hatcheries experiencing poor larval performance indicate that causes and factors leading to the low larval performance are heterogeneous. A portion of these 21 samples of incoming and tank water caused mortality in healthy larvae after filtration through 0.22-micron filters, indicating the presence of toxin/s and/or viral agents. Results also indicate that mortality in water-exposed larvae was affected by salinity. Additional samples are in the process of being tested using the larval screening assay. Results from these assays will be used by the BHHC pathology working group to develop more specific diagnostic tests and make management recommendations.

MICROBIOMES UNDER STRESS – TOLERANCE OF THE BLUE MUSSEL (*MYTILUS EDULIS*) AND ITS GUT MICROBIOME TO TOXIC PHARMACEUTICAL EXPOSURE

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Pharmaceutically active compounds in wastewater discharge can create toxic conditions for marine life. Suspension-feeding animals are especially vulnerable as they filter large volumes of water per unit time, bringing their internal tissues into constant contact with these evolutionarily foreign compounds. Carbamazepine (CBZ), an anti-epilepsy medication, exhibits < 10% removal efficiency following traditional sewage treatment techniques, causing several sublethal toxic effects in suspension-feeding bivalves. CBZ exposure can disrupt the gut microbiomes of zebrafish and frog larvae, but in bivalves, these effects are not known. The gut microbiome plays crucial functional roles across the animal kingdom, including detoxification of ingested toxins in several terrestrial herbivores and insects; however, functional roles of bivalve microbiomes, especially under toxic stress, are poorly understood. Here, the effect of CBZ on the blue mussel (*Mytilus edulis*) "holobiont" was assessed, encompassing effects on both the mussel and its microbiome. Mussels were maintained in a system of sterilized glass microcosms, fed sterilized microalgal diets, and exposed to CBZ at concentrations ranging from environmentally relevant (1 µg/L) to highly polluted (10 and 40 µg/L). Toxic effects on mussels were evaluated by measuring biochemical markers of oxidative stress and biotransformation enzyme activity. The composition and activity of bacterial communities in the gut microbiomes were assessed using differential mRNA expression patterns derived from metatranscriptomics sequencing. By correlating host and microbiome tolerance to CBZ, this study sets up a framework for future experiments directly targeting host-microbiome tradeoffs involved in biotransformation of CBZ by the blue mussel.

MASS MORTALITY OF CULTURED JUVENILE YESSO SCALLOPS CAUSED BY EXTREME SUMMER WATER TEMPERATURES AND EFFECTS OF DEEP-WATER CULTURE ON SURVIVAL

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Yesso scallop (*Mizuhopecten yessoensis*) culture in southwestern Hokkaido produces an average annual harvest of approximately 70,000 tons. Beginning in 2023, northward intrusion of the warm Kuroshio Current elevated coastal surface water temperatures in northern Japan by approximately 6°C above normal. As a result, summer water temperatures at juvenile culture depths increased by 2-3°C or more from 2023 onward, consistently exceeding 24°C. Following reports of mass juvenile mortality in some areas, field surveys at seven sites collected 36 baskets from different producers, with culture depths estimated at 5.7-18.5 m based on producer interviews. Mortality rates ranged from 3-91% and were negatively correlated with basket suspension depth ($r = -0.64$, $p < 0.001$, $n = 36$), indicating temperature-related mortality. To isolate depth effects on temperature, growth, and survival, controlled experiments using 60 baskets compared culture at 6.7-18.8 m depths at two adjacent sites in summer 2025. Results showed that 10 m deeper culture reduced mean summer temperature by 3°C and mortality by 20 percentage points; however, after two months of culture, shell length at greater depth was 2.3 mm smaller. These results demonstrate that deeper culture can reduce temperature-related mortality but at the cost of reduced growth during optimal temperature periods. Successful implementation requires precise depth management to balance survival benefits against growth reduction from decreased food availability.

FINE-TUNING BREEDING STRATEGIES: FIELD PERFORMANCE AND DISEASE ACQUISITION OF SELECTIVELY BRED EASTERN OYSTER FAMILIES IN A BREEDING PROGRAM

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Aquaculture of the eastern oyster, *Crassostrea virginica*, continues to expand on the U.S. East Coast with sales exceeding $90 million in 2023. Despite continued industry growth, epizootics of protozoan parasites, *Haplosporidium nelsoni* and *Perkinsus marinus,* threaten production in growing areas such as the Chesapeake Bay. Twenty oyster families from the Aquaculture Genetics and Breeding Technology Center (ABC) at the Virginia Institute of Marine Science, spawned in Spring 2024, were deployed in March 2025 in triplicate at two sites, Cappahosic Oyster Company farm and the ABC research farm, at distant locations on the York River. Replicates were sampled at peak disease seasons of May, and September/October as well as July 2025. Survival was assessed, with basic morphometric data collected and tissues preserved for downstream qPCR and histological analyses from a subset of oysters within each replicate. DNA from tissue samples was analyzed with a pathogen-specific qPCR and histopathology to bolster qPCR data in determination of parasite prevalence, intensity and host response.

Family survival varied between sites and families, and average cumulative survival in Autumn 2025 for all families was higher at the site in the upper York River than in the lower York River. Survival data will be correlated to qPCR and histopathology data to better understand the relationship between field survival and infection by each pathogen. Confirming the association between these metrics may help improve current strategies for breeding for disease resistance by identifying the best approach to use to improve MSX and Dermo- resistant stocks for the commercial oyster industry.

GENOTYPE X ENVIRONMENT X PLOIDY INTERACTIONS IMPACT THE PERFORMANCE OF PACIFIC OYSTERS IN AQUACULTURE

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Triploid (individuals with three sets of chromosomes) Pacific oysters (*Crassostrea gigas*) provide substantial benefits to growers due to rapid growth and sterility which increases marketability; however, they show higher mortality than diploids. Mortality often coincides with periods of high temperature, low pH, and low oxygen, suggesting environmental stress interacts with chromosome number to reduce survival. Physiological mechanisms behind differences in mortality, remain unclear. Understanding drivers of triploid mortality is key to enhancing production and profitability of aquaculture. Thus, this study examined the impact of multiple interacting environmental stressors on diploids and triploids produced through tetraploid crossbreeding and chemical induction.

Oysters were outplanted at four shellfish farms throughout Puget Sound, Washington; mortality, growth, and respiration were monitored, and temperature, oxygen, and pH data were collected in summer 2023 and 2024. Mortality was similar in closely related diploids and induced triploids, while genetically distinct mated triploids showed higher mortality across sites. Intertidal sites showed higher mortality than subtidal sites, consistent with greater exposure to environmental extremes. Growth responded more strongly to spatial structure than to ploidy, with genetically similar oysters showing comparable growth at nearby sites, and no consistent growth pattern at more distant locations. Respiration varied across sites and years but did not align with growth and survival. Findings suggest reduced survival in triploids arises from specific genetic backgrounds, or production methods (chemical induction vs tetraploid crossbreeding), and interactions with the environment rather than triploidy alone, with implications for broodstock selection and climate resilience in oyster aquaculture.

SHELLFISH SENSITIVITY INDEX: A SUSTAINABILITY TOOL FOR ESTUARIES FACING LOW OXYGEN AND WARMING

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Estuaries support economically important shellfish species but experience varying levels of low dissolved oxygen (DO) and high temperature impairment. In the mid-Atlantic, four species—the eastern oyster (*Crassostrea virginica*), bay scallop (*Argopecten irradians*), northern quahog (= hard clam) (*Mercenaria mercenaria*), and blue crab (*Callinectes sapidus*)—face varying degrees of risk associated with warming and hypoxia, but their sensitivities and the impacts on suitable habitats remain unclear. To address this, a mid-Atlantic Shellfish Sensitivity Index, a database synthesizing negative effects of each stressor on each species' development, performance, and immunity, was developed for integration with geospatial temperature and DO data. A systematic literature review collated 465 experimental comparisons of species' tolerances to temperature and DO stress across life stages and exposure durations. Hypoxia comprised most comparisons (64%), followed by temperature (22%) and combined stress (14%). Across taxa, negative responses to temperature stress occurred at mean exposures of 28-35°C, with *A. irradians* eliciting responses at the lowest values (larval: 28.0°C; post-larval: 28.2°C). Separately, under hypoxic conditions, taxa exhibited negative responses at minimum and maximum DO concentrations of 0.003 mg L^{-1} and 4.54 mg L^{-1}, respectively. Using New York estuaries as a case study, variations in species sensitivities were assessed spatiotemporally. Across six estuaries, 20 years of temperature and 10 years of DO data were synthesized. This revealed significant summer warming of up to ~0.2°C $year^{-1}$ and spatially variable hypoxia (< 3 mg L^{-1}), identifying optimal and suboptimal habitat for *A. irradians* and other species. This versatile sustainability tool can support sustainable shellfisheries under changing environmental conditions.

SHELL COLOR AND PATTERN VARIATION IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*: INSIGHTS FOR SELECTIVE BREEDING

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Shell coloration in the eastern oyster, *Crassostrea virginica*, is a genetically, environmentally, and economically relevant trait for selective breeding, yet its relationship with growth, parental background, and shell patterning remains insufficiently characterized. Multiple datasets were integrated to evaluate drivers of shell color variation across genetically distinct oyster groups. Associations between purple shell color score and oyster size were assessed using multivariate analyses. Although statistically significant associations with height and weight emerged when groups were analyzed collectively, color score exhibited only weak negative relationships with size within individual groups. Color outcomes among color-selected polyploid crosses were then examined. Two tetraploid (4n) groups and one diploid (2n) group derived from red parents but originating from different broodstock lines exhibited similar color distributions. Triploid oysters produced from red 2n x red 4n displayed significantly more red color than triploids produced from white 2n x red 4n, demonstrating that parental color composition strongly influences offspring pigmentation. Shell pigmentation intensity quantified using ImageJ revealed significant differences among regionally separated wild populations. The southern stock (SC/NC/VA; 24SS) uniquely exhibited a significant number of light-colored top shells. Notably, the wild stock derived from New Jersey (Barnegat Bay; 24JJ) contained a significantly higher frequency of pin-striped shells. Collectively, these results indicate that shell coloration and patterning are primarily governed by genetic background and regional influences. These findings provide actionable insight for oyster breeding programs by enabling targeted selection of broodstock to enhance desirable shell color and pattern traits in cultured populations.

INFLUENCE OF ALASKAN OYSTER FARMS ON BENTHIC COMMUNITIES

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In South-east and South-central Alaska, oyster farms are a common occurrence in the coastal habitat, and these farms interact with many aspects of the surrounding ecosystem including the benthos. Oyster farms likely increase bio-deposition and organic nutrient flux to the benthos which may increase the amount of food available for benthic inhabitants. Oyster farms have the potential to support an abundant and diverse benthic community; however, it is debated if and how oyster farms influence those communities. Alaskan mariculture is a growing industry with plans to significantly expand though the effects of such expansions on the surrounding environment are unknown.

In this study, epibenthic and infaunal (abundance and biomass) communities were sampled underneath three oyster farms and respective control sites in Kachemak Bay, Alaska over three years. The central question of this study is if and how do Alaskan oyster farms influence benthic communities. Results show no overall significant differences between farm and control sites. Geographical area, even at a small scale, seems to be the most significant factor for differences in both epibenthic and infaunal biomass and abundance. Next steps will be to look at under-farm, benthic community change over a four-month time scale and compare local bivalve growth in and out of farms.

VARIABILITY IN SOMATIC GROWTH OVER TIME AND SPACE DETERMINES OPTIMAL SEASON-OPENING DATE IN THE OREGON OCEAN SHRIMP (*PANDALUS JORDANI*) FISHERY

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Growth variability is a key contributor to the dynamic productivity of populations. Thus, better understanding and accounting for variation in growth can improve both tactical and strategic management. Using ocean shrimp (*Pandalus jordani*) from the U.S. West Coast as a case study, interactions between growth and optimal fishery opening dates will be demonstrated. While the fishery opens on 1 April, industry often delays fishing to minimize catches of small shrimp. Understanding drivers of size-at-recruitment can help managers optimize opening dates and shrimpers plan their participation in this and other fisheries. Using three decades of fishery-dependent sampling, a spatially, temporally, and environmentally explicit Bayesian state-space model for shrimp size-at-age was developed. Model outputs were then used to parameterize a revenue-per-recruit model and explore how variability in size-at-recruitment impacted optimal opening dates. Shrimp recruited at smaller sizes farther north. Delaying opening would likely benefit shrimpers in areas and years with smaller shrimp and higher fishing mortality. Broadly, choosing when to open the fishery is a complex decision requiring understanding of growth, but also recruitment, economic incentives, and life history.

ARE *CREPIDULA FORNICATA* LARVAE PHENOTYICALLY PLASTIC?

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Development of many marine invertebrates is influenced by environmental factors, including food availability. Phenotypic plasticity, an organism's ability to adjust its morphology or behavior in response to local conditions, can provide valuable insight into how species respond to environmental change. For echinoderm larvae, it is well documented that food limitation can induce morphological change that enhances feeding efficiency, but such phenotypic plasticity has rarely been examined in molluscs. Gastropod veliger larvae use large ciliated lobes to capture microalgal food. If veligers are phenotypically plastic, larvae reared at lower food concentrations would be expected to have larger velar lobes relative to their shell size than those reared at higher food concentrations. To test this, larvae of the slipper snail (*Crepidula fornicata*) were reared under both high and low food conditions, and the size of the velum relative to size of the shell was measured across development. Mixed responses were found: one experiment found a significant increase in velum size relative to shell size with lower-food concentrations, others showed no response to food concentration, and one experiment revealed a significant decrease in velar size relative to shell size at lower food concentrations. These variable outcomes suggest that the expression of phenotypic plasticity in marine gastropod larvae can be complex and may be influenced by other factors including environmental conditions experienced during the mother's lifetime or genetic differences among maternal lineages. These results highlight the need for further research to determine how, and which, marine invertebrate species can respond quickly to changing environments.

TIMING IS EVERYTHING: ENERGETIC TRADEOFF WITH EARLY GONAD DEVELOPMENT WITH OCEAN ACIDIFICATION

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Most ocean acidification (OA) research with bivalves examines a single life stage in short-term experiments. It is difficult to extrapolate the results of these short-term experiments to lifetime responses of an organism, or to understand long-term population responses to OA. The northern bay scallop, *Argopecten irradians*, has a short generation time (< 1 year), and is economically important; previous studies have suggested that the larval stage is sensitive to OA. The bay scallop was selected to investigate capacity to respond and adapt to continuous exposure to OA over the entire lifespan. Bay scallops were grown from embryogenesis to sexual maturity under one of two OA conditions ($p\mathrm{CO}_2 = 400$ and 800 µatm). Survival, growth, and maturity were measured from 48 hours post-fertilization to adulthood. Survival after metamorphosis was similar between the two OA conditions, but differences in growth were observed at the time of gonad development and maturation. At 800 µatm gonad mass index occurred 28 days earlier and was 24% greater than for the 400 µatm treatment. The moderate treatment also had a 6% reduction in the adductor muscle index. For the moderate treatment, there was an apparent tradeoff, between gonad and adductor tissue weight. Post reproduction, this tradeoff disappeared, and adductor mass was similar between the two treatments.

WORKFORCE TRAINING IN SHELLFISH AQUACULTURE AT BELLINGHAM TECHNICAL COLLEGE - CURRICULUM AND HATCHERY UPDATES

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Since 1978, the Fisheries & Aquaculture Sciences Department at Bellingham Technical College (BTC) has produced highly skilled graduates for various “blue” industries, including shellfish aquaculture, salmon and trout hatcheries, and aquatic resource management. The program operates two hatchery facilities and cultures shellfish, finfish, and algae for various community projects. In 2024, the program was named one of the top 10 two-year USA college programs for student-led community-based projects in aquatic conservation.

The BTC mission is to provide student-centered, high-quality professional technical education with a focus on serving our community’s non-traditional students. While in the training program, BTC students gain valuable skills that range from technical to interpersonal to support the local economy with a highly skilled workforce. For the BTC training cohorts from 2018-2024, 96 percent of graduates found employment within nine months, with 84 percent working specifically in “blue” industries.

To expand training opportunities for remote students and early career professionals, the program recently adopted a “flipped classroom” where the lecture materials are offered fully online. For in-person students, the online materials compliment the hands-on training and for remote students, the courses can be taken independently to further professional development in any setting. Course topics range from “Principles of Aquaculture” (entry) to more advanced topics, such as “Seaweed Culturing”, “Microalgae Culturing”, and “Shellfish Hatchery Production”. Prospective students are encouraged to contact BTC instructors to learn more about online training opportunities.

EFFECTS OF ANTIFOULANT IRGAROL 1051 AND MICROPLASTICS ON THE ATTACHMENT PERFORMANCE OF THICK-SHELLED MUSSELS (*MYTILUS CORUSCUS*)

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Irgarol 1051 is a widely used antifouling biocide that, owing to its long half-life, persists in coastal waters. Microplastics can adsorb dissolved contaminants and modify their bioavailability, raising concern about combined exposures in benthic organisms. The thick-shelled mussel (*Mytilus coruscus*) was used to examine how a 14-day co-exposure to Irgarol and polystyrene microplastics (PS-MP) affects byssal attachment performance. Co-exposure significantly weakened the byssus, with the greatest damage at high Irgarol concentrations, indicating that Irgarol was the primary toxicant. The reduction in attachment strength coincided with increased plaque surface roughness and decreased polyphenol oxidase activity, consistent with disrupted byssal biosynthesis. Histological and ultrastructural analyses revealed oxidative stress and structural damage in the byssal gland, including perturbed mitochondria and endoplasmic reticulum. Biochemical assays showed inhibited Ca^{2+}–Mg^{2+}-ATPase activity and reduced ATP content, indicating compromised energy metabolism, while collagen synthesis displayed compensatory upregulation. At the molecular level, key genes involved in byssal secretion were downregulated and an apoptosis-related gene was upregulated, collectively undermining byssus structural stability. Overall, Irgarol and PS-MP jointly impair the functional integrity of mussel byssus, primarily through Irgarol-driven interference with biosynthetic and energetic pathways. These findings provide mechanistic evidence for the risks posed by composite antifouling-chemical and microplastic pollution to habitat-forming mussels and offer a basis for ecological risk assessment and the management of mussel aquaculture in contaminated coastal environments.

EUROPEAN GREEN CRAB MANAGEMENT PLAN FOR WASHINGTON: LESSONS LEARNED AND LOOKING FORWARD

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The Washington European Green Crab (EGC) Management Plan represents an unprecedented, multi-agency response to one of the region's most urgent aquatic invasive species threats. Led by the Washington Department of Fish and Wildlife in close coordination with over 50 tribal co-managers, federal and local agencies, shellfish growers, conservation districts, and community partners, the program integrates early-detection monitoring, rapid response, and large-scale removal across the state. Since January 2022, over 2.5 million EGC have been removed from Washington State marine waters which was brought together in large part by the 2022 emergency proclamation which is still in place today.

This presentation will discuss trends in detections and the effectiveness of unified management. Detection maps will show how EGC have spread along the coastlines of Washington. Monthly statewide reporting has enabled us to look at trends both locally and regionally. These lessons inform the evolving management plan, which emphasizes continued collaboration, adaptive response strategies, and investment in monitoring necessary to protect the Washington coastal ecosystems and dependent fisheries moving forward.

BIOPROSPECTING MANGROVE MICROBIOMES: IDENTIFICATION OF BACTERIAL STRAINS CAPABLE OF TUMOR CELL INHIBITION AND BIOREMEDIATION

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The Environmental Microbiology Laboratory at the State University of Ponta Grossa, Brazil, conducts research on ecological hotspots - specific environments that preferentially harbor bacterial communities with advanced response mechanisms and potential biotechnological applications in medicine and environmental remediation. Recent investigations have concentrated on mangrove ecosystems, situated at the interface between saline and freshwater habitats, which are characterized by diurnal fluctuations in physicochemical parameters and the presence of toxic xenobiotics. The microbiomes within these ecosystems are increasingly threatened by anthropogenic activities, including urban expansion, pollution, deforestation, river dredging, and unsustainable fishing and shellfish harvesting. The introduction of pesticides and microplastics, often containing toxic additives, results in their accumulation in sediments, imposing selective pressures that alter biodiversity and disrupt established ecological interactions. Consequently, mangroves may select for more competitive and potentially more aggressive microbial genomes that exhibit adaptive responses with promising applications, such as inhibiting tumor cell growth and degrading xenobiotics like glyphosate. This potential was explored through metagenomic data analysis, isolation and selection of bacterial strains, genomic characterization, and gene expression studies utilizing RT-PCR protocols. Our assessments included mangroves subjected to varying degrees of environmental impact and located at different proximities to the international port of Paranaguá. Preliminary results demonstrate that certain bacterial isolates can reduce the viability and proliferation of human lung carcinoma and breast adenocarcinoma cell lines and can also grow in culture media using glyphosate as the sole nutrient source. Future developments of this project aim to obtain probiotic strains to enhance the microbiomes of the fiddler crab, a shellfish species widely consumed locally, to confer glyphosate tolerance.

GROWTH OF ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA SOLIDISSIMA,* POPULATIONS AT INTERTIDAL SITES AROUND MASSACHUSETTS, USA

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Atlantic surfclam, *Spisula solidissima solidissima*, grow in nearshore waters around Massachusetts (MA). Two locations with large populations are Provincetown and Westport, MA. These populations were recently determined to be genetically distinct. To gain a better understanding of the growth rates of these populations, several transplant experiments were conducted at sites around MA. Seed clams were transplanted to cylindrical cages (20 cm diameter, 30.5 cm length), constructed from rigid polypropylene netting and driven ~25 cm into sandy sediment. During the 2022-2023 experiments, seed were stocked at 9 per cage (278 clams m^{-2}); whereas, they were stocked at 6 per cage (185 clams m^{-2}) for the 2024-2025 experiment. Individual cages were covered with netting to prevent predation. From May to September 2022, wild Provincetown seed (11-20 mm) exhibited average growth rates of 0.24, 0.17, and 0.16 mm/day at the Dennis, Provincetown, and East Falmouth sites, respectively. From September 2022 to June 2023, a second planting of wild Provincetown seed (8-16 mm) exhibited average growth rates of 0.13 and 0.09 mm/day at Provincetown and East Falmouth sites, respectively. From September 2024 to June 2025, wild Provincetown seed (12-20 mm) and hatchery-produced Westport seed (15-22mm), exhibited growth rates of 0.10 and 0.09 mm/day, respectively, at Provincetown and 0.06 and 0.05 mm/day, respectively, at Westport. While there were site differences in growth, the two distinct populations exhibited similar growth rates at Provincetown and Westport. Temperature, pH, and site disturbance all appeared to affect growth.

TRACKING SEASONAL OYSTER MORTALITY AND MSX DISEASE PREVALENCE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA,* IN THE MARYLAND PORTION OF THE CHESAPEAKE BAY FROM 2023 TO 2025

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Multinucleated sphere unknown (MSX) is a disease of eastern oysters (*Crassostrea virginica*) caused by the spore-forming parasitic protozoan, *Haplosporidium nelsoni* which needs a salinity of 15 or greater to infect oysters. At a salinity of 10 or lower though, oysters can expel *H. nelsoni* from their tissues. Using this information, salinity can thus be used as an indicator of whether MSX prevalences are likely increasing or decreasing in areas where salinity fluctuates around 15. The amount of mortality that results from MSX, however, is difficult to predict as there are many factors that influence this. To better understand the relationship between MSX and oyster mortality as well as the details of the impact of salinity on MSX, oysters were sampled from three sites in the Maryland portion of the Chesapeake Bay. The sites were the Choptank River (Lighthouse bar), Choptank River (Royston bar), and Tangier Sound (Piney Island bar). They were sampled for MSX (n = 30 per site) multiple times each year from 2023 to 2025 so the seasonal cycle of MSX could be captured, and effects of salinity could be seen. These sites were also tested for Dermo disease so this could be taken into account as a possible source of mortality.

BIRD-RELATED PATHOGEN CONTAMINATION IN SHELLFISH AQUACULTURE: A COMPREHENSIVE LITERATURE REVIEW

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The Food and Drug Administration conducted a comprehensive literature review of bird-related pathogen risks in shellfish aquaculture including shellfish illnesses, pathogen prevalence in bird feces, water, and shellfish, correlations to water quality indicators, seasonal and regional variations in prevalence, pathogen survival, shellfish purge rates, pathogenicity, and bird mitigation techniques. From 2000-2024, the CDC documented 11 *Campylobacter* outbreaks and 7 *Salmonella* outbreaks from shellfish consumption, with estimated actual burdens of 3,400 and 3,000 illnesses respectively when accounting for underreporting and underdiagnosis. Five documented *Campylobacter* and *Salmonella* outbreak investigations found the most likely cause of contamination to be bird feces in shellfish growing areas, especially those with floating aquaculture gear. There is an overall prevalence rate of 27%, 6.4%, and 20% for *Campylobacter, Salmonella,* and pathogenic *E. coli* in wild birds, respectfully, with *Campylobacter* having the most variable prevalence (0-88%) and other human pathogens rarely detected. Other studies found these pathogens in shellfish harvested from approved growing areas and isolated the pathogens from sediment and water. Traditional fecal indicator organisms showed poor correlation with *Campylobacter* and *Salmonella* presence. Prevalence of *Campylobacter* showed a clear seasonal pattern, with higher prevalence rates found in colder months. Physical deterrents like bird spikes and zip ties demonstrated highest efficacy for bird mitigation (74-99% reduction in bird interactions), while auditory and visual methods showed limited success. Critical knowledge gaps, such as limited research on pathogen survival in water and shellfish and insufficient data on purge rates, require additional targeted studies to support evidence-based risk assessment and management strategies.

SUPPORTING SUSTAINABLE OYSTER RESTORATION AND RESOURCE MANAGEMENT IN MISSISSIPPI USING STRUCTURED DECISION MAKING

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The eastern oyster is an integral part of the heritage, economy and ecology of the northern Gulf of Mexico. In Mississippi, oyster populations have suffered several mass mortality events post-*Deepwater Horizon* because of climate change-related precipitation events altering water quality conditions. Oyster reef restoration and revitalization of the oyster industry are top priorities for the State of Mississippi, but project planning and implementation require a better understanding of the complex interactions between management decisions and the factors that affect oyster abundance, health, and survival. The Mississippi Based RESTORE Act Center of Excellence (MBRACE) is a consortium of the four main research universities of Mississippi with the mission of supporting the sustainable use of State resources through a comprehensive understanding of the dynamic Mississippi Sound ecosystem. Using a structured decision-making approach, the decision context surrounding oyster restoration in Mississippi to inform research and management priorities for the recovery of a sustainable oyster resource was characterized. The activities the State has implemented, or is considering, to reach its oyster restoration goals of increasing oyster harvest, creating new jobs and business opportunities, and improving the environment through species recovery, habitat creation, and cleaner water were also reviewed. The potential consequences of these decision alternatives are being considered to evaluate the trade-off between oyster production for harvest and ecological benefits. Yet, climate change impacts on environmental variability are a key source of uncertainty for future oyster restoration and management and applied research is needed to inform the decision-making process.

RESTORING CLEAN WATER TO THE CHESAPEAKE BAY 2012-2025: ROTARY OYSTER REEF AT ST. MARY'S RIVER, MARYLAND

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This presentation documents the design, implementation, and outcomes of a long-term oyster reef restoration effort in the St. Mary's River, Maryland, initiated by a Rotary District 7620 environmental grant (2012–2014) and continues by the local community. The initiative aimed to improve water quality in the Chesapeake Bay by restoring oyster (*Crassostrea virginica*) populations, which are critical for biogenic filtration and habitat structure.

The restoration strategy involved constructing three-dimensional reef structures using over 2600 concrete reef balls and 250 metric tons of cleaned concrete rubble, distributed across more than 2 hectares. These substrates were seeded with approximately 8000 bushels of spat-on-shell, sourced in partnership with the University of Maryland Chesapeake Bay Program and local restaurants. Site selection prioritized areas with optimal water flow and substrate stability, avoiding silty bottoms to maximize spat survival and reef longevity.

Quantitative monitoring, following the 2011 Oyster Metrics Working Group protocols, assessed metrics including percentage cover, oyster density, biomass, and multi-year class presence. Results from 122 quadrat samples indicated a mean oyster density of 204.7 oysters/m^2 (60.7% coverage), with a mean dry biomass of 107 g/m^2 (53.3% coverage), and the presence of multiple year classes - exceeding restoration targets ($\geq$ 50 oysters/m^2, $\geq$ 50 g/m^2, 30% coverage, and $\geq$ 2 year classes). The success of the project was further validated by independent studies funded by NFWF and EPA.

The project demonstrates the effectiveness of community-driven, science-based reef restoration in enhancing oyster populations and water quality. The model has been replicated and expanded through partnerships with local watershed associations, academic institutions, and Rotary clubs, contributing to broader regional and international artificial reef and habitat restoration initiatives.

BORING INTO BENTHIC FLUXES: IN SITU MEASUREMENTS OF PUMPING AND ORGANIC MATTER PROCESSING BY A ROCK-BORING BIVALVE

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Sessile benthic suspension feeders strongly influence organic matter processing and nutrient regeneration in coastal ecosystems yet estimates of their subtidal contributions to resource transport and transformation remain sparse. Rock-boring bivalves (Pholadidae) dominate many hard-substrate communities along the Santa Barbara coast, where their feeding and biogenic outputs may shape coastal benthic-pelagic coupling and local biogeochemical cycling.

Direct, field-based approaches for resolving suspension feeder-mediated fluxes are rare. Here, pumping, filtration, excretion and fecal production by the pholad, *Parapholas californica*, were measured for individuals within a temperate kelp forest alongside concurrent characterization of dissolved and particulate organic carbon and nitrogen pools. Pairing organismal rate estimates with ambient resource availability reveals how a sessile filter feeder processes seston under natural conditions. The resulting rate estimates provide empirical constraints for scaling individual physiological activity to rocky reef populations within long-term monitoring sites of the Santa Barbara Coastal Long Term Monitoring program. These observations support ongoing efforts to characterize biological influences on coastal carbon and nutrient dynamics by providing direct, field-based estimates of suspension feeder activity.

ASSESSING RESTORATION OF THE OLYMPIA OYSTER IN SEQUIM BAY, WASHINGTON

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The Jamestown S'Klallam Tribe (JST) has partnered with the Clallam County Marine Resources Committee (CMRC) to reestablish a historic native Olympia oyster (*Ostrea lurida*) population in Sequim Bay, Washington. Sequim Bay historically supported a healthy population of Olympia oysters which served as an important food and cultural source to the S'Klallam people. Archeological data confirms the S'Klallam use of Olympia oysters dating back at least 1,100 years. Sequim Bay tidelands were negatively impacted by land use modification and altered sedimentation processes beginning in the 1870s. As a result of extensive estuary restoration in the early 2000s, suitable habitat for shellfish returned to the bay. This prompted JST and CMRC to reestablish the native Olympia oyster population. Beach enhancement of Olympia oyster seed from Sequim Bay broodstock and unseeded cultch (Pacific oyster shell) to bolster settlement substrate have occurred since 2012. Restoration activities have been evaluated annually since 2014 using standard metrics of assessment: density, estimated abundance and size-frequency distribution. Results show years of heightened recruitment and population growth and years without. Population survey results have informed the effectiveness of each round of restoration efforts and built a baseline for anticipated growth and recruitment. The team envisions restoration actions in 2023-2024 (informed by over a decade of monitoring) will be the final push needed to bolster a stable population. This effort shows that long-term monitoring is needed to understand the long-term success of restoration efforts.

ENVIRONMENTAL QUALITY OF MANGROVES IN THE NORTHERN ECUADORIAN COAST

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Multiple stressors with undetermined effects affect tropical wetlands that integrate hydrographic basins with deltaic and estuarine systems with mangroves in the northern Ecuadorian coast. Factors such as the growth of populated centers and untreated wastewater, the felling of forests and mangroves for forestry use, the conversion from mangroves and shorelines to shrimp ponds, the emergence of extensive monocultures dependent on agrochemicals such as bananas and palm oil, port development and mining activity, among others, have generated a mosaic of different conditions that require being described in their current quality and retrospectively to subsequently suggest improvements in the management of the same.

Information about analysis of water, sediment, and biota samples, with emphasis in nutrients and metals, will be presented from the following areas of the Esmeraldas province of Ecuador: Chamanga-Cojimíes, Esmeraldas River, and San Lorenzo-Reserva Ecológica Manglares Cayapas-Mataje (REMACAM).

BIRD-RELATED PATHOGEN RISK IN SHELLFISH AQUACULTURE

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The use of floating gear in oyster farming has gained popularity because it reduces mortality rates, improves product quality, and facilitates the management of fouling. Birds see floating gear as an attractive place to roost and have been implicated in 12 outbreaks of Campylobacteriosis related to shellfish consumption nationwide since 2009.

The National Shellfish Sanitation Program (NSSP) describes the regulations for shellfish harvest, handling and distribution. The FDA, working with Industry and state regulators through the Interstate Shellfish Sanitation Conference, has devised regulations and guidance designed to ensure that commercially harvested shellfish are safe and wholesome. The NSSP requires that if aquaculture gear may attract birds or mammals, operators must provide a written operational plan that describes how to address possible contamination of shellstock and potential adverse impacts on water quality.

The 2023 revision of the NSSP provides guidance on how States can address these concerns and outlines the various approaches States can consider to minimize health risks to consumers. State authorities can consider tidal dilution and mandate resubmergence of impacted shellfish prior to harvest. Bird deterrents are mandated in many States, and a variety of novel deterrent approaches are being tested.

The ISSC has established an Aquatic Bird Risk Assessment Committee to evaluate the research needs to develop a risk assessment that will help inform regulators on how to mitigate the risk of closures and illnesses.

SHELLFISH FARMING, OBSTACLES, AND OPPORTUNITIES

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While shellfish have been farmed for centuries, the intensive farming of hatchery-reared shellfish in bags and cages is a relatively recent development. Regulatory hurdles and advances in materials science have shaped the rapid evolution of growing methods. The proven benefits of ecosystem services, nutritional qualities, and a low carbon footprint have blunted the opposition to farms from coastal homeowners to some degree. It is the innovation and persistence of growers that have sparked a renaissance in production and demand, despite facing challenges such as disease, climate change, and economic pressures.

The industry is now at a crossroads, where inflation effects are curtailing demand, and the economics of production threatens the economic sustainability of farms. Imports are vying for market share, and the future direction of production trends is uncertain. It will be up to the next generation to develop solutions that shape the future of shellfish farming. Addressing the many obstacles facing the industry today will require innovative efforts from biologists, engineers, and economists to support ongoing growth. The field promises job security for those who are creative and persistent.

COMMUNITY ACTION FOR FRESH WATER (CAFW): A ROTARY INTERNATIONAL AND UNITED NATIONS ENVIRONMENT PROGRAM (UNEP) INITIATIVE TO RESTORE, PROTECT, AND SUSTAIN FRESHWATER ECOSYSTEMS

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Healthy freshwater systems are vital for sustaining all life, they are vital for flourishing and vibrant societies, but these systems are severely threatened by pollution, nature and biodiversity loss, and climate change. CAFW is the flagship initiative of the strategic partnership between Rotary International and the UNEP. Announced in January 2024, the initiative focuses on restoring, protecting, and monitoring freshwater ecosystems globally in response to escalating challenges such as pollution, climate change, and habitat degradation.

The CAFW initiative incorporates, learns from, and expands upon the success of Rotary members who have been protecting and restoring freshwater ecosystems under the pilot program “Adopt a River for Sustainable Development” which began with the UNEP and Rotary District 9212 (Eritrea, Ethiopia, Kenya, and South Sudan) in 2020 and since January of 2024 has expanded worldwide. The partnership connects the Rotary member resources and expertise in mobilizing volunteers with the technical expertise from the UNEP to develop a more sustainable, long-term environmental impact. The UNEP is the leading organization within the United Nations system in the field of the environment with the global mandate for the conservation, protection, enhancement, and support of nature and natural resources, including biological diversity (shellfish, fish).

Projects can focus on improving water quality, mitigating pollution, addressing water scarcity, removing invasive species, and conserving and rehabilitating ecosystems. Your plan can include activities that need different levels of expertise and engagement. Projects can start at any size, scope, and frequency. After you’ve developed a plan, register your project with ‘Community Action for Fresh Water’, or reach out to cafw@rotary.org with any questions.

ASSESSING DEPURATION OF *CAMPYLOBACTER* SPP. FROM OYSTERS

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The depuration dynamics of *Campylobacter* spp. in oysters were evaluated in three controlled laboratory studies using strains of *Campylobacter coli*, *C. jejuni*, and *C. lari*. Oysters were held in 4.6-gallon tanks containing filtered, UV-treated seawater with aeration and daily feeding. In all studies, oysters were artificially inoculated during a 16-hour static period in which water flow was stopped while aeration was maintained.

In the first study, oysters were inoculated with either individual strains or a cocktail of all three strains. Samples (N = 3) were collected immediately following inoculation, after which water flow was restored (19.6 ± 0.2 °C; 1000 mL/min). Additional samples were collected up to 11 days post-inoculation. *Campylobacter* spp. was detectable in oyster tissues through day 5 but was not detected by day 9.

In the second study, smaller oysters (~2”) were inoculated with two concentrations of a *Campylobacter* cocktail. Following inoculation, oysters were transferred to fresh seawater (20.9 ± 0.5 °C; 1000 mL/min), and samples (N = 4) were collected through day 6. *Campylobacter* spp. was detected in all oysters at 24 hours, in one low-concentration sample at 48 hours, and was undetectable by day 4. This experiment was repeated using larger oysters (~3”) held at a lower water temperature (12.8 ± 1.3°C; 1150 mL/min). In this trial, *Campylobacter* spp. persisted longer, with detection in some samples through day 4 but not by day 7. No *Campylobacter* was detected in control oysters. These results indicate that oyster size and water temperature influence *Campylobacter* depuration rates.

HOW TO PRODUCE HEALTHY SHRIMP FREE OF THE CONTAMINATED GLYPHOSATE-BASED FEEDS (SOYBEANS, CORN) USED TO PRODUCE BALANCED SHRIMP FOODS - RECOMMENDATIONS FROM THE WORLD ECONOMIC FORUM, ROTARY INTERNATIONAL-ESRAG, AND THE FOUNDATION FOR CONSERVATION OF BIODIVERSITY OF ECUADOR

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Shrimp is a popular seafood worldwide, but concerns are increasing about: the safety of shrimp and other shellfish we consume, the health of mangroves and wetlands where these species live in, and the water quality from aquatic and freshwater ecosystems, food security, and food safety issues.

This presentation will summarize the goals of (a) the annual meeting of the World Economic Forum in Blue Davos (https://www.weforum.org/stories/2026/01/what-is-blue-davos-everything-you-need-to-know/); (b) the 'Community Action For Fresh Water (CAFW): A Rotary International (RI) and United Nations Environment Program (UNEP) Initiative to restore, protect, and sustain freshwater ecosystems' (https://www.unep.org/topics/fresh-water/nature-based-solutions/working-nature/community-action-fresh-water); (c) the 'ONE HEALTH Epigenomes and Microbiomes Program' of the Foundation for Conservation of Aquatic and Terrestrial Biodiversity (FUCOBI) of Ecuador (www.fucobi.org); (d) the 'Environmental Sustainability Rotary Action Group (ESRAG) (https://esrag.org/blog/2024/09/06/why-community-freshwater/); and (e) Rotary International focus on waterways (https://www.rotary.org/en/rotary-partnership-united-nations-puts-focus-waterways). The CAFW Initiative was launched in 2024 to mobilize community-led action for protecting, restoring, and sustaining freshwater ecosystems globally, leveraging the volunteer network of the Rotary with the technical expertise of the UNEP for local river/lake cleanups, data collection (citizen science), and long-term management plans. This initiative expands on successful pilot projects, empowering Rotary clubs to work with local groups, governments, and experts to tackle pollution and degradation, contributing to global sustainability goals. The ESRAG is helping to implement sustainable practices on biodiversity, circular economy, food systems, sustainability, climate and pollution. Suggestions and recommendations will be provided about the steps we should follow to produce healthy shrimp free of the contaminated glyphosate-based feeds (soybeans, corn) used to produce balanced foods for shrimp.

DEVELOPMENT OF A GRTS SURVEY APPROACH FOR THE VIMS SEA SCALLOP DREDGE SURVEY

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Several approaches for constructing survey designs exist to estimate population abundance, including random and stratified random sampling theory. Generalized Random Tessellation Stratified sampling (GRTS) is a contemporary sampling approach that aims to ensure spatially balanced sampling for large survey areas and is being applied to fishery surveys across the United States.

The sea scallop (*Placopecten magellanicus*) dredge survey by the National Oceanic and Atmospheric Association transitioned to a GRTS sampling approach in 2025. The Virginia Institute of Marine Science (VIMS) conducts a complementary sea scallop dredge survey of the Mid-Atlantic Bight and portions of Georges Bank in the northwest Atlantic, using a stratified random sampling approach. For 2026, the VIMS is evaluating the application of a GRTS for its future dredge surveys.

Several decision points need to be considered for the VIMS survey when developing a GRTS. The time series of prior data to use for estimating biomass for station allocation is one consideration. A similar issue related to biomass estimation is the treatment of biomass in weight and number of animals (i.e., transformation of these values in modeling efforts). Another concern is how to potentially combine strata to ensure that all portions of the sea scallop resource receive a sufficient number of stations. The use of a minimum distance constraint between allocated stations also needs to be considered. How to communicate the new sampling design to stakeholders, as well as the time allocated for the VIMS staff to investigate this approach, also needs to be taken into consideration.

THE GALAPAGOS MANGROVES OF ECUADOR ARE IN DANGER DESPITE CONSERVATION EFFORTS

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Despite strong protection, the mangroves of the Galápagos Islands are considered "vulnerable" by the International Union for Conservation of Nature (IUCN). The major threats are: *Natural Disasters*: volcanic eruptions (Sierra Negra 2018) and tsunamis (2011) that cause rapid, large-scale damage; *Climate Change*: rising sea levels could submerge up to 25% of mangroves by 2060, while intensified El Niño events disrupt nutrient cycles; *Pollution:* plastic debris carried by currents gets trapped, breaking down into microplastics that enter the food web, harming wildlife; *Human Activity:* boat damage, urban expansion, tourism, invasive species, and fishing pressure disrupt ecosystems, challenging conservation efforts focused on "blue carbon" and biodiversity.

This talk will review Galapagos mangrove conservation efforts and challenges. *Protected Status*: the mangroves are within a protected area, but events show their fragility. *Blue Carbon:* crucial for storing "blue carbon," but climate change threatens this function. *Research & Management*: the Charles Darwin Foundation and other groups monitoring threats identify key areas and support management, but face challenges like insufficient funding and staffing. *Community Involvement:* local initiatives and international NGO support cleanups, reforestation, and sustainable practices, highlighting the need for broader systemic change. It's clear that while localized actions help, global issues like climate change and plastic pollution require worldwide solutions to truly protect these vital ecosystems and the unique species they support such as shrimp, clams, crabs, and the rare canchalagua (a black-shelled mollusc). On behalf of the FUCOBI Foundation of Ecuador (fucobi.org) we invite the Charles Darwin Foundation to join us in a project with ESRAG-Rotary International for funding of community activities through a global grant funded by Rotary International.

EPIGENETIC MECHANISMS OF CRUSTACEANS AND MOLLUSCS FROM MARINE AND FRESHWATER ECOSYSTEMS UNDER ENVIRONMENTAL STRESS: A ONE HEALTH APPROACH

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Crustaceans and bivalve molluscs inhabit marine and freshwater habitats that are increasingly affected by climate change, pollution, and the intensification of aquaculture. Despite their ecological and economic implications, epigenetic processes that govern gene expression and phenotypic adaptability to environmental stresses remain comparatively understudied in many marine invertebrates. This talk presents the current evidence on major epigenetic regulators in shellfish DNA methylation (5mC), RNA methylation (N6mA), histone modifications, and non-coding RNA and examines how they shape physiological and adaptive responses to climate-related stressors. Evidence from key aquaculture and model taxa, including penaeid shrimp (e.g., *Penaeus vannamei*, *P. monodon*, *P. japonicus*), decapod crustaceans (e.g., *Portunus trituberculatus*, *Eriocheir sinensis*, *Procambarus clarkii*, *Homarus americanus*), and bivalves (e.g., *Crassostrea* spp., *Mytilus* spp., razor and hard clams), complemented by insights from the crustaceans *Artemia franciscana*, *Daphnia magna*, and *Gammarus fossarum*.

Framed within a One Health perspective, how epigenetic responses to stressors and pollutants can link animal, environmental, and human health will be discussed. Integrating mechanistic, ecological, and applied viewpoints, the promise and limits of epigenetic signatures as indicators of environmental change will be assessed as tools for aquaculture health management, emphasizing the need for transdisciplinary research that combines genomics and epigenomics, standardized experimental ecology, and field validation. The priorities for advanced sequencing and integrative omics to clarify the inheritance of complex traits and support breeding and management strategies that enhance resilience and sustainability in global shrimp and shellfish aquaculture will be outlined.

RIBBED MUSSELS AT THE EDGE: SURVIVING (BUT NOT THRIVING) IN LIVING SHORELINES

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Nature-based strategies for shoreline protection, such as living shorelines, are increasingly implemented as coastal communities face erosion and sea level rise. Modeled after natural salt marsh systems, marsh-sill living shorelines along the Atlantic east coast provide critical habitat for marsh fauna and flora; however, the ribbed mussel (*Geukensia demissa*), a key marsh bivalve and secondary foundation species, is often absent from or present in low densities in the low marsh of living shorelines in Chesapeake Bay. Ribbed mussels provide ecosystem services such as water filtration, nutrient removal, and shoreline stabilization, and form a key mutualism with smooth cordgrass, *Spartina alterniflora,* that enhances primary productivity and marsh resiliency. This research aims to investigate biotic and abiotic factors affecting ribbed mussel populations in living shoreline marshes through a combination of lab and field studies, with a specific focus on early juvenile stages. Potential influential factors include construction materials (rock, coir, oyster structures), marsh grass planting densities, predation, and/or sediment composition. Preliminary results suggest that ribbed mussel settlement varies across living shoreline habitats, such as the rock sill and the low marsh, but habitat effects are variable between sites, suggesting other factors at play. Previous restoration efforts have relied on translocating animals from donor marsh populations, but we are exploring hatchery cultivation of ribbed mussels for incorporation into living shorelines. Understanding the drivers of mussel settlement, survival, and distribution within living shorelines will inform design to enhance natural recruitment and boost resiliency and adaptability of restoration projects.

MULTI-STRAIN PROBIOTIC COCKTAIL IMPROVES BIVALVE LARVAL SURVIVAL AGAINST PATHOGENS

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Hatchery crashes are a significant challenge in bivalve aquaculture, yet their causes remain poorly understood and difficult to predict. These crashes limit productivity, particularly during the vulnerable larval stage, highlighting the need for effective interventions. This study aimed to isolate and characterize bacterial strains from bivalve (eastern oyster, *Crassostrea virginica,* and northern quahog, *Mercenaria mercenaria*) larvae with diverse probiotic traits to evaluate their safety and efficacy, ultimately developing a multi-strain probiotic cocktail to improve larval survival.

A total of 168 bacterial strains were isolated and identified from larval samples across different hatcheries along the Atlantic coast of the U.S. The isolates were screened for antimicrobial activity, hemolytic activity, biofilm formation, and quorum quenching potential. Four potential probiotic candidates (*Algoriphagus yeomjeoni* DEN5, *Glutamicibacter soli* CLAM16, *Pseudooceanicola nitratireducens* NEH7, and *Marinomonas gallaica* CLAM9) were selected for their combined probiotic properties. Safety assessments of these strains showed no pathogenic effects on the larvae. Individual probiotic treatments improved larval survival when challenged with the pathogens *Vibrio coralliilyticus* RE22 and *Aliiroseovarius crassostreae* CV919-312. Multi-strain probiotic cocktails significantly increased larval survival compared to controls, with the complete consortium outperforming *Phaeobacter inhibens* S4 alone. Furthermore, the cocktail improved the survival of larvae challenged with diverse marine pathogens recently isolated from hatchery crashes.

This study showed the importance of comprehensive screening to identify probiotic candidates with broad functional traits, thereby providing a basis for practical multi-strain probiotic applications in bivalve hatcheries to enhance larval survival.

SINGLE-CELL TRANSCRIPTOMICS REVEALS IMMUNE EVASION AND GROWTH REPROGRAMMING IN TRANSMISSIBLE CANCER OF NORTHERN QUAHOG (= HARD CLAM) (*MERCENARIA MERCENARIA*)

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Disseminated neoplasia is a transmissible cancer that affects bivalves and poses a significant threat to both wild and aquaculture populations. To investigate the molecular mechanisms behind this disease in northern quahogs (= hard clams) (*Mercenaria mercenaria*), single-cell RNA sequencing of hemocytes from healthy and neoplastic clams was performed. Cohabitation experiments, in which healthy clams were exposed to neoplastic individuals, were conducted to confirm disease transmission. Hemocytes were then collected from these samples and processed using the 10x Genomics Chromium platform.

Clustering of hemocytes revealed nine distinct cell populations, with one cluster predominantly composed of neoplastic cells. Gene set enrichment analysis showed that this cluster exhibited downregulation of pathways including phagosome, endocytosis, ubiquitin-mediated proteolysis, and FoxO signaling, suggesting potential mechanisms of immune evasion and resistance to apoptosis. Gene co-expression network analysis identified six gene modules within this cluster, three of which were highly expressed in neoplastic cells and appear to be involved in metabolic reprogramming as well as the activation of growth and survival pathways. These modules were enriched for genes associated with DNA replication, Wnt, TGF-β, Notch signaling, and various metabolism-related pathways.

Additionally, alterations in gene copy number across multiple chromosomal regions, indicating genomic instability and potential oncogene amplification were observed. Together, these findings suggest that neoplastic cells in hard clams undergo significant molecular changes that support uncontrolled growth and survival. This study provides new insights into disseminated neoplasia pathogenesis and identifies candidate molecular targets for future research and management efforts in both wild and cultured hard clam populations.

OXYLIPINS, PUA, AND LARVAE: BIOACTIVE BYPRODUCTS OF PHYTOPLANKTON ARE AN EMERGING CONCERN FOR THE SHELLFISH AQUACULTURE INDUSTRY

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The success of shellfish aquaculture production on the U.S. East Coast is highly dependent on successful hatchery production. In 2020, a troublesome new syndrome presented in young oyster larvae at a hatchery in Maine, resulting in production failures which decreased seed output. Affected larvae were delayed in development and exhibited signs of digestive obstruction. Preliminary larval bioassays, coupled with lipidomic analyses, demonstrated a link between the pathological signs and bioactive phytoplankton byproducts, oxylipins, in hatchery water. Similar signs have since been observed in hatcheries across a wider geography of the East Coast and are reoccurring yearly, demonstrating the syndrome's persistence. Understanding the cause of hatchery failures is critical to identify solutions and ensure shellfish aquaculture sustainability.

Phytoplankton are rich in polyunsaturated fatty acids (PUFA), which make them a good food source; however, some phytoplankton release PUFA into the environment in response to stress, such as grazing. A wounding activated enzyme is also released which leads to an oxidative reaction that transforms PUFA to polyunsaturated aldehydes (PUA) which are further oxidized into oxylipins. New research on the effects of one PUA, decadienal (DDA), and two oxylipins, hydroxy eicosapentaenoic acid (HEPE) and hydroperoxy hexadecatrienoic acid (HpHTrE), on oyster larval fertilization and development will be presented. Through partnerships between industry and academia, this research strives to characterize and increase awareness on this new but persistent hatchery production issue and to identify effective mitigation technology with the goal of enhancing overall hatchery production.

SUSPENSION-FEEDERS TO CLEAR THE WATERS IN URBAN ESTUARIES

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Urban estuaries are often highly eutrophic and suffer the familiar consequences of algae blooms and low dissolved oxygen. To meet regulatory requirements for nutrient reduction, cities can turn to enhanced nitrogen removal by wastewater treatment plants and divert sediment from stormwater; however, there is a need for additional nutrient removal approaches, especially by nature-based means. One is to culture bivalves to reduce nutrients through suspension feeding and biomass accumulation. For example, in Chesapeake Bay, oyster culture is a best practice to remove seston and nutrients. Lack of substrate and pollution often make urban waters poor oyster habitat, so alternative non-food bivalves have been explored for this function. Helpful qualities for suspension feeders would be resilience to water quality changes and the ability to self-recruit. Along the Gulf coast and east coast of North America, the dark false mussel (DFM), *Mytilopsis leucophaeata*, often grows abundantly in low salinity estuaries. To assess the potential for this and other native suspension feeders improve water quality in Baltimore Harbor, studies are underway to address three kinds of knowledge gaps: 1) What is the phytoplankton clearance rate of DFM? 2) How many DFM live in Baltimore Harbor now? 3) How can the number of DFM be increased in a sustainable or economical manner? This report will provide an overview of related studies to measure the ability of DFM to consume phytoplankton blooms, estimate how many suspension feeders live in the Inner Harbor, and a design for recruiting DFM to re-usable artificial substrates.

DIRECT SETTING OF EASTERN OYSTER LARVAE (*CRASSOSTREA VIRGINICA*) IN MISSISSIPPI COASTAL WATERS

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Oyster populations in the Gulf of Mexico (GOM) have declined by 85%, prompting innovative restoration approaches. Direct setting - releasing competent larvae directly onto reef substrates - offers potential advantages over traditional remote setting by eliminating hatchery grow-out phases, reducing handling stress, and decreasing costs. While successful in Chesapeake Bay, this technique had not been tested in the GOM. The first direct setting trial in Mississippi Sound was conducted over a 2-month period, deploying *Crassostrea virginica* larvae at two density treatments on constructed reef sites. Despite challenging environmental conditions including suboptimal salinity levels and significant biofouling, direct setting demonstrated significant spat settlement success at both low and high larval density treatments ($p < 0.0001$). Importantly, no statistically significant difference was observed between density treatments ($p = 0.754$), indicating that lower, more cost-effective larval concentrations can potentially achieve comparable settlement success. This study provides the first proof-of-concept demonstration that direct setting is viable under GOM conditions. Results indicate that direct setting may offer a more efficient alternative to traditional remote setting in the Gulf, potentially reducing restoration costs while maintaining effectiveness.

INVESTIGATING DRIVERS OF NORTHERN QUAHOG (*MERCENARIA MERCENARIA*) GROWTH FOLLOWING COASTAL LIMESTONE APPLICATION IN A RHODE ISLAND ESTUARY

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Limestone ($CaCO_3$) application on coastal land has the potential to foster marine carbon dioxide removal by raising alkalinity, but it is unclear how this process may impact marine ecosystems in estuaries with high seasonal and diel variability in carbonate chemistry. This study examined the response of bivalves to potential carbonate system changes associated with the terrestrial spreading of 21 tons of limestone by a golf course on the coast of Winnapaug Pond, a coastal lagoon in Westerly, Rhode Island, in May 2024 and 2025. Juvenile northern quahogs (*Mercenaria mercenaria*) were placed in two locations in the pond: an eastern cove next to the golf course and a western site one mile from the golf course and farther from the ocean inlet. Each year, quahogs were placed in the pond just before limestone application and were subsampled every two weeks from spring to summer. Survival, shell length, tissue weight, and shell weight over time were compared across sites. Assessment of biological responses in relation to temperature, chlorophyll, and carbonate chemistry data from the same sites and time periods suggests that temperature is the primary driver of differences in growth, with higher temperatures and growth (up to 135% larger shells) at the western site. Results show that any possible quahog responses to changes in carbonate chemistry from the limestone application are outweighed by the effects of naturally variable conditions in the pond. They also highlight bivalve sensitivity to differences in environmental conditions and thus their importance as ecological indicators.

BEHAVIORAL CHANGES IN LARVAL EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) WHEN EXPOSED TO THE DINOFLAGELLATE, *MARGALEFIDINIUM POLYKRIKOIDES*

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Over recent decades, coastal waters of the northeastern United States have experienced outbreaks of “rust tide”, a harmful algal bloom caused by the dinoflagellate, *Margalefidinium polykrikoides*. These reddish-brown blooms can reach high cell densities ($>10^6$ cells/L) and produce toxic compounds that are stressful or lethal to a wide range of marine organisms including the eastern oyster, *Crassostrea virginica*. While adult oysters generally withstand these events, the sensitivity of early life stages is less known.

This study evaluated the response of D-stage oyster larvae to three bloom-level concentrations of *M. polykrikoides* (5,000; 10,000; and 15,000 cells/mL). Larval oysters were exposed over a three-day period under three treatments: *M. polykrikoides* (Mp), Mp combined with *Tisochrysis lutea* (TMp), and no Mp (control). The TMp treatments were designed to simulate natural conditions by including a food source. Each treatment containing Mp was tested at the three concentrations listed above in six replicate beakers.

Larval behavior was assessed twice daily using 10-minute video recordings at 4x magnification. Live counts were taken and behaviors such as time spent swimming and velum exposure were recorded. Larvae from three beakers per treatment were collected after 24 hours of exposure, and the remaining beakers were collected after 48 hours. Preliminary results indicate that time spent swimming, often in a helical motion, declined with exposure to TMp and Mp compared to the control, with oysters exposed to TMp spending more time swimming than Mp treatments alone. These experiments suggest that larval oysters are susceptible to various concentrations of rust tide.

PERFORMANCE OF SUBTIDAL AND INTERTIDAL ALTERNATIVE REEFS AT NAVAL WEAPONS STATION YORKTOWN, VIRGINIA

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As eastern oyster, *Crassostrea virginica*, populations declined, and natural oyster shell became scarce, alternative settlement substrates have been used for restoration. Concrete structures are promising settlement substrates, but their performance requires further assessment. Subtidal reefs can provide habitat for diverse ecosystems, and intertidal reefs created as "living shorelines" can protect uplands from erosion. This project aimed to construct: (1) living shorelines at the Naval Weapons Station Yorktown (NWSY) pier; (2) living shorelines at Penniman Spit; and (3) intertidal and subtidal oyster reefs at both locations. Fish, crabs, and benthos in habitats surrounding NWSY pier and Penniman Spit were sampled prior to reef construction. Then, intertidal and subtidal reefs were constructed with engineered oyster structures (granite, castles, diamonds, C-domes, X-reefs). These locations are enforced military installations and training grounds and serve as de facto protected areas. This ensures that land restoration will be left intact, and intertidal and subtidal oyster restoration will not be poached, aiding in restoration success. Intertidal oyster structures trapped sediment, supported high densities of oysters and other organisms, and enhanced protection of the shoreline marsh. Oyster densities on subtidal concrete reefs were extremely high (1,000-5,000 indiv. m^{-2}), with C-domes and X-reefs significantly higher than Diamonds. Mussel density was similarly high. Intertidal and subtidal oyster settlement was enhanced by alternative oyster reef structures. These alternative substrates serve as a protected area and are extremely effective at augmenting natural resources and improving marsh resilience to sea-level rise.

SEAWEEDS AS A SUPPLEMENTAL FOOD SOURCE FOR EASTERN OYSTERS GROWN IN AN AQUACULTURE SETTING

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The co-cultivation of seaweeds with bivalve shellfish is a potential strategy for protecting bivalve crops against anthropogenic coastal acidification and hypoxia. Seaweeds and bivalves were co-cultivated using a succession of seaweed species according to season (*Saccharina latissima* in winter, *Ulva* spp. in summer) together with eastern oysters (*Crassostrea virginica*). Bivalves and seaweeds were deployed in two estuaries that contrasted in trophic state, one mesotrophic and one eutrophic. In all five experiments in the mesotrophic system, co-cultivation with seaweeds significantly increased tissue- and/or shell-based growth of bivalves ($p < 0.05$). Seaweed cultivation significantly improved water quality metrics (increased pH and dissolved oxygen (DO); $p < 0.05$ in all cases) in and around the seaweed sites at both locations although increases in pH and DO were modest, and even in control treatments, there were not prolonged periods of harmful pH or DO levels. An abundance of macroalgal detritus may have bolstered the diets of co-cultivated bivalves in the mesotrophic estuary, a hypothesis supported by lower chlorophyll *a* concentration, and therefore lower planktonic food levels, at that site. To evaluate the nutritional subsidy provided by macroalgae, eastern oysters (*Crassostrea virginica*) were deployed in replicated cages both directly within *Ulva* or kelp arrays (co-culture) and at sites devoid of seaweed. Oyster tissue, macroalgal tissue, and background particulate organic matter (POM) was collected monthly, analyzing dried samples for stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) ratios via mass spectrometry. Relative dietary contributions were subsequently estimated using Bayesian stable isotope mixing models, which differentiated the isotopic signatures of macroalgal detritus from those of phytoplankton-dominated seston.

MICROPLASTICS AND MOLLUSCS – A BRIEF OVERVIEW OF A FLAWED FIELD

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Microplastics are a contaminant of global concern and, as such, there has been a rush to action and publication. Over the past decade, this haste has resulted in a chaotic and cluttered literature that is rife with inappropriate methodologies, unrealistic experimental protocols, misinterpreted results, and overstated significance. A comprehensive critical assessment of the current literature on interactions between particle-feeding molluscs and microplastics and their purported impacts (> 600 publications) has been published. It is not surprising that microplastics have been noted in shellfish globally. What is surprising is the extremely low level of particles routinely recorded. The literature on interactions and impacts of microplastics on bivalves is seriously flawed, and there are no unequivocal data demonstrating that their presence in bivalve molluscs is a serious risk to human health, and few data to demonstrate negative impacts on the shellfish. Editors of scientific journals must make a stronger effort to engage qualified peer-reviewers and stop the flow of poorly done studies and superficial reviews that do nothing more than confuse the literature and reinforce prior inadequate studies and potential reviews.

ENHANCEMENT OF POLYPLOID BREEDING STRATEGIES FOR THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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The Aquaculture Genetics and Breeding Technology Center (ABC) at the Virginia Institute of Marine Science (VIMS) provides diploid and tetraploid brood stock oysters to hatcheries along the U.S. east coast for commercial production. For more than a decade, the ABC has focused largely on family-based selection to advance gains in economically important traits of diploid lines. As triploid oysters have gained popularity in the mid-Atlantic and southern regions, the ABC has expanded its primary focus on diploid oyster breeding to include the genetic improvement of tetraploids, transitioning to family selection of tetraploids in 2015.

Tetraploid oyster breeding remains relatively novel due to challenges associated with their production and propagation. Over the past decade, the ABC has developed and evaluated tetraploid families across diverse environments, generating extensive data on chromosome stability, survival, and growth. These efforts have led to production of new families exhibiting improved performance across these three traits. In parallel, triploid families produced using sires genetically linked to tetraploid families have provided valuable insight into trait correlations between tetraploids and triploids, improving our understanding of how genetic gains in tetraploids translate into commercial triploid performance. To date, shell shape traits such as roundness and cup depth, a “hook” hinge trait, and meat yield have not been incorporated into the tetraploid selection index, despite the availability of a substantial dataset for these characteristics. Genetic parameters associated with this suite of traits in triploid and tetraploid oysters, and future strategies for refining tetraploid breeding to align with industry performance needs, will be presented.

RED ABALONE IN OREGON: SEASCAPE GENOMICS, SURVEY METHODS, AND MANAGEMENT APPLICATIONS

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Characterizing patterns of genetic diversity including evidence of local adaptation is relevant for predicting and managing species recovering from overexploitation in the face of climate change. Red abalone (*Haliotis rufescens*) is a species of conservation concern due to recent declines from overharvesting, disease and climate change, resulting in the closure of commercial and recreational fisheries. Using whole-genome resequencing data from 23 populations spanning their entire range (southern Oregon, USA, to Baja California, MEX) patterns of population connectivity and genotype-environment associations that would reveal local adaptation across the mosaic of coastal environments that define the California Current System (CCS) were investigated. High genetic diversity that is shared within and among populations was discovered, suggesting high historical range-wide gene flow. Little evidence was found for large selective sweeps between populations that occupy local habitats that vary by pH, strength of upwelling, chlorophyll, salinity and sea surface temperature. This is consistent with a broad range of species with similar life histories that show limited neutral or adaptive genetic variation across the same region and the same environments, suggesting that the mosaic of environmental variation across the CCS is insufficient to drive local adaptation in the face of high gene flow for some broad-cast spawning species. Given the high genetic connectivity across their range, state-mandated regulatory actions would be most effective if aligned across jurisdictional boundaries (i.e., Mexico, California and Oregon).

PROTECTIVE *VIBRIO MEDITERRANEI* LINEAGES RESCUE OYSTER LARVAE FROM PATHOGEN-INDUCED MORTALITY

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The previous genomic survey of *Vibrio* communities during eastern oyster (*Crassostrea virginica*) mortality events revealed that *Vibrio mediterranei* consistently colonized healthy oysters, but disappeared prior to mortality, coinciding with the proliferation of pathogenic *V. harveyi*. This pattern suggested *V. mediterranei* may function as a protective symbiont rather than an opportunistic colonizer in oysters.

Here, this hypothesis was tested using controlled larval challenge experiments and comparative genomics. Pre-colonizing oyster larvae with *V. mediterranei* Vm02, isolated from a healthy adult oyster, increased larval survival from 10-19% (pathogen-only controls) to 94-97% when challenged with pathogenic *V. harveyi* or *V. coralliilyticus*. Protection was effective at 28°C and 32°C, rapid (effective from co-inoculation), and durable (maintained > 96 hours). Fluorescence microscopy confirmed stable colonization of larval digestive tissues.

Challenge experiments with eleven *V. mediterranei* strains revealed three distinct phenotypes – protective, pathogenic, and intermediate – corresponding to monophyletic clades with 97.1-97.8% average nucleotide identity between lineages. Pangenome analysis identified 230 protective-specific orthogroups encoding regulatory systems, stress tolerance mechanisms, and a putative bacteriocin operon. In contrast, pathogenic strains harbored Type I and Type VI secretion systems absent from protective lineages. Based on these clade-specific markers, a multiplexed ddPCR assay was developed that differentiates protective versus pathogenic *V. mediterranei* lineages alongside *V. harveyi*. These findings establish *V. mediterranei* as a candidate probiotic and oyster health indicator, offering practical tools for monitoring beneficial microbiome populations and implementing biological control strategies in shellfish hatcheries.

ENGAGING COMMERCIAL FISHERMEN TO ADVANCE KNOWLEDGE OF ATLANTIC SEA SCALLOP PHYSIOLOGY AND RECRUITMENT EVENTS

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The Atlantic sea scallop supports the second most lucrative commercial fishery in the United States. As ocean conditions change and competition for marine resources intensifies, there is a growing need to better understand trends in scallop health, reproduction, and overall population dynamics. The Commercial Fisheries Research Foundation (CFRF), a non-profit organization established by commercial fishermen empowers the industry to collect data that improves our understanding of this crucial food and ecosystem resource.

The CFRF took an iterative approach to develop fishery-dependent data collection methods to track scallop health and fecundity through space and time. Commercial fishermen were originally asked to record scallop meat weights and reproductive stage, but participants were concerned with the time consumptive aspects, the inaccuracy of weighing small tissues at-sea on a moving platform, and the difficulty of classifying reproductive stage. To address these concerns, the CFRF developed protocols utilizing an image-based sampling method to extract biological data, including shell height, meat size and quality, and reproductive stage. This approach has been implemented across both the CFRF day-trips and multi-day trip scallop fleets. Additionally, the CFRF created a mobile phone application to collect biological data in a noncommittal fashion, using reward incentives to expand spatiotemporal coverage.

The evolution of these projects highlights the adaptability needed to overcome challenges and the successes of cooperative research, including issues related to data quality, standardization and validation, trust, and communication barriers. This presentation will summarize the ongoing scallop research initiatives of the CFRF and the opportunities and challenges inherent in cooperative research.

STRENGTHENING PARTNERSHIPS TO EXPAND OYSTER SHELL RECYCLING IN THE SOUTH CAROLINA SCORE PROGRAM

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The South Carolina Department of Natural Resources (SCDNR) oyster shell recycling program is among the largest oyster shell recyclers in the, yet it continues to recover less shell than needed to meet statewide annual planting requirements. As a result, the SCDNR must purchase out-of-state shell, a practice that creates increasing financial and logistical challenges and highlights the need to expand in-state shell recovery.

Program success now relies heavily on community engagement, education, and strong partner involvement. Before behavioral change in shell recycling can occur, residents, restaurants, and event organizers must understand the ecological importance of returning shell to state waters and how recycled shell supports healthy oyster habitat. The South Carolina Oyster Recycling and Enhancement (SCORE) program, a SCDNR initiative, plays a central role in cultivating this understanding by providing accessible education, facilitating hands-on volunteer experiences, and inspiring public enthusiasm for habitat restoration.

Equally critical is fostering partner buy-in and ownership of the need to recycle shell. The SCDNR works with counties, waste authorities, local organizations, and restaurants to expand infrastructure, improve collection efficiency, and ensure partners recognize their role in sustaining oyster populations. Partner commitment to infrastructure and strategic support, such as expanding drop-off access and optimizing collection systems, enhances the convenience of shell recycling and increases overall recovery.

Despite substantial progress, South Carolina continues to recover only a fraction of the shell consumed annually. Sustained emphasis on education, community engagement, and partner ownership remains critical to achieving a sustainable, shell-neutral future for the oyster resources of the State.

TERNSTROEMIA DENTISEPALA: A MEXICAN PLANT AS NOVEL RESOURCE OF METABOLITES AGAINST THE BACTERIUM, *VIBRIO PARAHAEMOLYTICUS*

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The present study evaluated, for the first time, the antibacterial activity of hydroalcoholic extracts (HAE) and total phenolic extracts (TPE) obtained from the leaves of *Ternstroemia dentisepala* and *T. lineata*, two species used in traditional Mexican medicine. The extracts were tested against clinically relevant Gram-positive and Gram-negative bacteria, including *Enterococcus faecalis*, *Streptococcus agalactiae*, *Streptococcus pyogenes*, *Salmonella typhi*, *Pseudomonas aeruginosa*, and *V. parahaemolyticus* strain 417, AHPND-positive.

The results showed that *T. dentisepala* exhibited superior antibacterial activity, as both its HAE and TPE were effective against all evaluated bacteria, with minimum inhibitory concentrations close to 1.0 mg/mL, the phenolic extract being the most active. The TPE from both species increased antibacterial activity by approximately 30% compared to the HAE.

The HAE of *T. dentisepala* showed a higher content of phenolic compounds and greater antioxidant activity, which correlated with lower IC$_{50}$ values. Chemical profiles obtained by TLC, HPLC, and ^{1}H NMR revealed significant differences between the two species, mainly associated with their phenolic composition. These findings suggest that *T. dentisepala* is a promising source of bioactive compounds with potential applications in the control of bacterial infections, particularly as a biotechnological alternative for the control of pathogenic bacteria such as *V. parahaemolyticus*, the causative agent of AHPND in shrimp farms, which leads to significant economic losses in aquaculture in eastern Mexico. An important advantage of this extract is that no toxic solvents are used during the extraction of the active compounds.

SIX DECADES OF OBSERVATIONS OF OYSTER RECRUITMENT IN THE CHESAPEAKE BAY: WHAT HAVE WE LEARNED?

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Long-term biological data collected in a consistent manner reflect the relative and combined impacts of attendant biological and physical influences. One such data set is the recruitment or "oyster shellstring" data series collected in three subestuaries of the Virginia Chesapeake Bay. A shellstring consists of twelve oyster shells generally similar in size (about 76 mm, (3-in) in length) drilled through the center and strung (inside of shell facing the substrate) on heavy gauge wire. These are suspended approximately 0.5 meters above the bottom and replaced weekly throughout the spawning season (late May through early October). Shellstrings provide substrate for the settlement of competent to metamorphose oyster larvae in the water column. Over the duration of one year the assembled data describe both temporal and spatial variation in settlement. Over a period of up to six decades, that is approximately the extent of continuous monitoring in some locations, the data record provides insight into variation driven by combinations of varying broodstock abundance, prolonged warm and cold periods, El Nino cycles, disease epizootics, varying fishery management strategies and replenishment actions, tropical storms, freshets, droughts, and more. Herein this talk will briefly examine this time series and pose the question "what have we learned and what does or does not drive temporal and spatial variation in oyster settlement on these monitoring tools?"

DECODING ENVIRONMENTAL STRESS TOLERANCE IN ALASKAN CRAB FISHERIES

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Wild crab fisheries in Alaska are among the most valuable in the world, yet many crab species are sensitive to climate stressors, including ocean acidification (OA). Experimental work conducted by the NOAA Alaska Fisheries Science Center at its Kodiak laboratory has shown that OA responses vary across life stages, exposure durations, and species. Notably, two closely related species, snow crab (*Chionoecetes opilio*) and Tanner crab (*Chionoecetes bairdi*), exhibit contrasting responses, with snow crab more resilient and Tanner crab more sensitive to acidified conditions. Despite these differences, the species overlap in distribution in the Bering Sea and are capable of hybridization.

Here, molecular approaches, including RNA sequencing and whole-genome sequencing, were used to compare acclimation mechanisms and longer-term consequences of OA exposure in snow and Tanner crab. Goals include identifying genomic and transcriptional differences underlying OA resilience, developing molecular stress markers to monitor wild stocks, and improving predictions of species-specific vulnerability and distributional shifts under future ocean conditions.

ECHINODERM AQUACULTURE, FISHERIES, AND THEIR INTERSECTIONS WITH BIVALVES

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This talk aims to discuss the current highlights of echinoderm aquaculture and fisheries in North America and worldwide. Echinoderms serve many roles in marine ecosystems and are vital parts of millions of people’s livelihood and sustenance. From responsibly managed to “boom and bust,” fisheries cover the globe. Occasional poaching empires spring up due to the desire and resultant high prices for key species.

Aquaculture of certain species can be billion-dollar industries leading to golden statues in the town square while most are still in the development stage. Echinoderm co-culture has been sought to reduce the nutrients and waste of species of other phylum and increase the growth of others. Of all the possible mixes and matches, bivalve shellfish and echinoderm co-culture may be the most promising and challenging.

SEEDING THE FUTURE OF AQUACULTURE: YOUTH ENGAGEMENT THROUGH THE NOAA SCIENCE CAMP AQUACULTURE SESSION

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Washington State is a major producer of farmed bivalves, with 2024 dockside values of $13.9 million in Pacific oysters and $12.2 million in Manila clams according to NOAA Fisheries, yet the aquaculture industry is experiencing significant challenges with workforce recruitment and retention. To address this gap, educators and experts from NOAA Fisheries Office of Aquaculture, NOAA Fisheries Northwest Fisheries Science Center, and Washington Sea Grant built upon the Seattle NOAA Science Camp to develop an aquaculture-focused pilot program. In partnership with Seattle MESA, UW GearUp Achievers, and the Puget Sound Skills Center, the team offered the inaugural NOAA Science Camp Aquaculture Session to 50 Seattle-area middle and high school students in a three-day program covering aquaculture science, careers, and ecosystem connections. Sessions included shellfish and seaweed biology, survey methods, links between aquaculture and water quality, and aquaculture ecosystem services. Students met local growers and observed organisms in their natural habitats during a tidepooling excursion. The camp culminated in a group project where students designed their own aquaculture farm - selecting a site, budgeting "fish bucks" for products and gear, and constructing a model of their operation. This pilot program demonstrated strong potential for aquaculture-focused experiential learning and youth engagement in marine career pathways. Lesson plans and materials will be made publicly available as part of ongoing curriculum development centered on shellfish aquaculture workforce development. Inspiring the next generation of aquaculture growers, researchers, and informed consumers is essential to strengthening a robust and resilient aquaculture industry in Washington and across the nation.

IMPROVED GENOMIC PREDICTION FOR DERMO RESISTANCE IN EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) USING MACHINE LEARNING AND RARE VARIANTS

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Dermo disease caused by the protist, *Perkinsus marinus,* severely impacts the aquaculture of the eastern oyster, *Crassostrea virginica*. Traditional phenotypic selective breeding approaches have been slow to develop dermo resistance in oysters, in part due to the highly polygenic nature of the trait. Previously, three generations of genomic selection for dermo resistance were conducted using oysters experimentally challenged with *P. marinus* and genotyped with a high-density 66K single-nucleotide polymorphism (SNP) array, which indicated that genomic selection was more effective than phenotypic selection for dermo resistance. Here, improved genomic predictions were made with new models and a combined dataset spanning three generations and over 2,400 oysters. A total of nine genomic prediction models were evaluated, including three supervised machine learning algorithms. Gradient-boosted machine learning models achieved the highest overall genomic prediction accuracy. Using data from all three generations instead of only the most recent F_2 generation, almost all models achieved equivalent or improved prediction accuracy, indicating that increased training samples may enable better capture of genome-wide resistance patterns. Similarly, across all modeling approaches, prediction accuracy increased when including SNP with a lower minor allele frequency threshold ($MAF > 0.01$), suggesting that rare variants can contribute significantly to dermo resistance. Taken together, these results highlight the potential of machine learning for improving genomic selection for dermo resistance and advancing eastern oyster aquaculture.

IMPACTS OF EUROPEAN GREEN CRAB (*CARCINUS MAENAS*) FORAGING AND TEMPERATURE ON EELGRASS, *ZOSTERA MARINA*

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Eelgrass meadows, comprised of *Zostera marina*, are a critical nearshore resource, serving as a foundation species and critical marine habitat for many organisms. Eelgrass is critical for its role in bay hydrology and as a nursery for numerous recreationally and commercially important fish and invertebrates. While protected by State and Federal laws, eelgrass has experienced historic losses due to anthropogenic modifications to the habitat, rising sea levels, and warming waters.

Another emerging threat to eelgrass resilience, and to how managers tackle eelgrass conservation, is the threat that invasive species may pose to vulnerable eelgrass beds. As the population of European green crabs (*Carcinus maenas*), a relatively recent invader to Oregon estuaries, increases, the destructive behaviors exhibited by the crab put additional pressure on already stressed eelgrass beds. Juvenile green crabs shred and consume eelgrass blades and adults uproot plants while foraging and occasionally shred rhizomes. This destruction appears to be correlated with green crab biomass, with crab-dense bays experiencing greater loss of eelgrass coverage.

When exposed to warmer temperatures green crabs have several plastic physiological mechanisms that allow them to rapidly respond to changes in their environment. Increases in temperature have been linked to higher foraging of bivalves and other nutrient-rich prey by green crabs, likely in response to the increased metabolic stress of physiological plasticity. The effect of this foraging for clams, dubbed feeding pits, is hypothesized to negatively impact eelgrass beds by destabilizing and resuspending sediment and directly damaging the belowground rhizome network of eelgrass.

THE MITIGATION OF HARMFUL ALGAL BLOOMS BY CULTIVABLE SEAWEEDS

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Harmful algal blooms (HAB) are a significant threat to ecosystems, economies, and human health. There is, therefore, great interest in the development of approaches that can effectively prevent, mitigate, and control (PCM) these events. Results from a collection of studies will be presented that demonstrate the HAB-mitigating effects of seaweeds that can be grown in an aquaculture setting– predominantly, the effects of *Ulva* spp. on warmer-water HAB species *Margalefidinium polykrikoides* and *Dinophysis acuminata*, and the effects of sugar kelp (*Saccharina latissima*) on cool-water HAB including *Alexandrium catenella* and *Pseudo-nitzschia* spp. Algicidal activity was present for all pairs of HAB and seaweeds; for example, in bloom water incubations, *Ulva* significantly reduced (92% reduction) bloom populations of wild *M. polykrikoides* compared to control ($p < 0.05$), *S. latissima* significantly reduced bloom populations of *A. catenella* (73-95% reduction, $p < 0.005$) and bloom populations of *Pseudo-nitzschia* species assemblies (69-75% reduction, $p < 0.05$). Mitigation potential was also demonstrated in many of these pairs using multiple strains of each species in culture. The presence of sugar kelp in shellfish enclosures significantly decreased toxin accumulation in shellfish fed toxic HAB phytoplankton; kelp significantly lessened saxitoxin accumulation ($p < 0.05$) from *A. catenella* in blue mussels (*Mytilus edilus*) and domoic acid accumulation ($p < 0.05$) from *Pseudo-nitzschia multiseries* in razor clams (*Ensis* spp.), demonstrating the efficacy of seaweeds to inhibiting both HAB and the trophic transfer to HAB toxins. This talk will discuss the aquaculture of seaweeds as a revenue-generating approach for HAB mitigation.

AN UPDATE ON SUDDEN UNUSUAL MORTALITY SYNDROME (SUMS) ON THE U.S. GULF COAST

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Eastern oyster (*Crassostrea virginica*) aquaculture is a growing industry along the northern U.S. Gulf Coast (northern Gulf). Unfortunately, in recent years, farms have suffered substantial losses during events described as Sudden Unusual Mortality Syndrome (SUMS). During a SUMS event, rapid die-offs occur in oysters that are at or near market size. Initially occurring only in late spring and early summer, recent observations from the northern Gulf suggest that SUMS can occur from late winter through late fall. Mortality rates can reach nearly 100%; therefore, SUMS is a significant threat to the economic viability of oyster aquaculture in the region.

This presentation will give an overview of SUMS in the northern Gulf, drawing on information from various research efforts and monitoring activities. It will discuss current and future projects aimed at identifying the causes of SUMS and possible mitigation strategies for oyster farmers. This overview will highlight what is known about SUMS in the region and where knowledge gaps remain that need to be addressed to support industry sustainability.

DEVELOPMENT AND ASSESSMENT OF AN INDUSTRY-LED APPRENTICESHIP PROGRAM

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Access to a qualified workforce is a challenge in oyster aquaculture, and workforce development is listed as a priority in the U.S. National Aquaculture Development Plan. In 2023, an apprenticeship program was established in Alabama and Mississippi that provided funding for 10 apprenticeships across the two states. These positions were guided by the participating oyster farm, including choice of apprentice, wages, hours, and areas of training. Thus, this program was led by industry participants.

A total of four apprentices from Alabama and six from Mississippi were funded. The apprentices and their supervisors completed a questionnaire to assess the level of knowledge prior to and after completion of the program. There were no differences in the scoring between apprentices and their supervisors, and on average, ratings after the program were ~1.9 point higher (on a 5-point scale) than prior to training. Significantly improved ratings included areas such as spawning, seed maintenance, seed maintenance, gear maintenance, and desiccation, among others. No significant improvement was reported in larval rearing or nursery production, likely due to the participation of few hatcheries and nurseries.

Additional funding was obtained to continue this program using feedback from the first program cycle. In round 2, 12 apprentices (5 in Alabama, 7 in Mississippi) were funded. Apprentices will participate in local industry meetings, as well as complete an online oyster aquaculture course. Together, these results demonstrate that an industry-led apprenticeship program effectively builds practical skills for oyster aquaculture while remaining adaptable to workforce needs in the U.S. Gulf region.

CURRENT AND EMERGING DIAGNOSTIC TECHNIQUES FOR SHRIMP DISEASES

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Aquaculture is the fastest growing food production sector in the world, with its production growing at 7.5 percent per year since 1970. The most important aquaculture production from an economic standpoint is that of farmed marine shrimp. The annual value of production of marine shrimp is estimated at 40 billion USD on the world market with production reaching around 9.7 million tonnes (farmed 6.4 MMT + wild 3.3 MMT) in 2023. During the past three decades, infectious diseases have caused serious economic losses in intensive shrimp culture systems. Accurate disease diagnosis is critical for developing strategies to prevent or manage aquatic diseases.

First, basic diagnostic procedures (e.g., case history records, gross pathology, presumptive diagnostic methods and histopathology) are described. Furthermore, emerging molecular diagnostic technologies are discussed, these include PCR methods (conventional, quantitative, digital), isothermal amplification methods (LAMP, RPA), CRISPR-based detection, antibody-based assays and lateral flow immunoassays. In recent years, new diagnostic tools, such as next generation sequencing technologies, artificial intelligence, environmental DNA/RNA and point-of-care testing have also applied to diagnostics. The advantages and limitations of each diagnostic method are discussed. Developing and increasing diagnostic capabilities can help shrimp producers better prepare for disease outbreaks.

COMBATING CLIMATE-LINKED OYSTER MASS MORTALITY: GENOMIC AND HATCHERY SOLUTIONS FOR CHINA AND SOUTHEAST ASIA

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The Hong Kong (HK) oyster is a leading aquaculture species, comprising over 30% of global oyster production and supporting major livelihoods in southern China. Despite rising demand, the industry faces critical challenges from Winter Mass Mortality (WMM), driven by climate change and salinity stress, alongside declining product quality and food safety. These issues directly threaten grower incomes and downstream industries such as oyster sauce production. Coastal aquaculture ecosystems around the world are being threatened by climate change (ocean acidification, warming and their seasonal shift) and unsustainable farming practices (stressful salinity in cultivation areas) to meet increasing demand. First, the root cause of WMM has been identified. Surprisingly it is not primarily caused by known bacteria and viruses. By using previously identified thousands of stress response genes, proteins and associated networks of regulatory metabolic pathways, HK oysters tolerant to multiple climate change stressors and mass mortality have been selected. Simultaneously, grower-friendly hatchery technology has been developed to produce seeds with WMM tolerance traits. Results have identified the root cause of WMM, revealing it is not primarily pathogenic by well-known shellfish disease causing bacteria or viruses, but stems from physiological stress and opportunistic protozoans. Leveraging this insight, molecular tools have been used to select oysters tolerant to multiple climate stressors and have been developing a practical, grower-friendly hatchery technology to produce resilient seeds. This talk will outline the current challenges facing oyster aquaculture in South China and demonstrate how this cooperative model is linking university, industry, and growers - is successfully deploying this sustainable technology, offering an effective solution for growers in China and southeast Asia.

A QUANTITATIVE GENETIC EVALUATION OF MULTIPLE PACIFIC OYSTER POPULATIONS RESPONSE TO OsHV-1 MICROVARIANT (SAN DIEGO BAY) EXPOSURE IN LABORATORY TRIALS

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Ostreid Herpesvirus-1 microvariants (OsHV-1) are known to decimate Pacific oyster (*Crassostrea gigas*) aquaculture when the virus becomes established. Genetic selection programs in Europe and Oceania have been successful at improving survival against OsHV-1 exposure, but such programs are still in their early phases on the U.S. Pacific coast. Using juvenile Pacific oysters from the USDA ARS Pacific Oyster Genomic Selection (POGS) project a laboratory challenge was conducted using a recently identified OsHV-1microvariant from San Diego Bay (California). The oyster populations included two breeding populations and one naturally-recruited population from Southwestern Washington State. A common-garden approach was taken, with each replicate being exposed to an approximately 10e6 dose of OsHV-1 per oyster. Survival was monitored for 7 days, with mortalities removed and preserved daily. All survivors were sampled and tissues preserved for genetic parentage analysis. Animal models were used to analyze the data and produce estimates of population level responses, heritability and estimate breeding values. These parameters are crucial for understanding the relative performance of these populations as potential breeding program source groups for the POGS breeding project. Survival was moderately heritable, and variation in estimated breeding values is sufficient for conducting genetic selection for germplasm improvement. Utilizing all three populations evaluated in this study provides a strong foundation to improve survival against exposure to OsHV-1 microvariant (San Diego Bay) using genetic selection methods.

PROBIOTIC STRATEGIES TO MITIGATE BACTERIAL-INDUCED MORTALITIES OF PACIFIC OYSTER LARVAE: INSIGHTS FROM HATCHERY TRIALS

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Bacterial pathogens of shellfish larvae cause mass mortality events worldwide, leading to unpredictable hatchery supplies of healthy oyster larvae for shellfish farmers. Multiple studies have reported benefits from adding probiotics to shellfish larval cultures to reduce pathogen-induced mortalities. Previously, at the Oregon State University Hatfield Marine Science Center in Newport, Oregon, three marine bacterial isolates were identified as highly beneficial when added to Pacific oyster (*Crassostrea gigas*) larval cultures. A single dose of the probiotic combination administered to developing embryos reduced acute mortality when exposed to the pathogen *Vibrio coralliilyticus* RE22 compared to controls without probiotics.

In axenic larval culture, 80-90% of larvae treated with these probiotics within 24 hours of fertilization survived a lethal dose of *V. coralliilyticus* at 48 hours post-fertilization. In subsequent testing in multiple non-axenic seawater sources, larvae treated with probiotics had an average survival of 75-90% against *V. coralliilyticus*. Several of the tested seawater types were found to negatively impact larval survival (cause unknown), with an average larval survival of 38%, but treatment with probiotics improved survival to 91%.

This presentation highlights recent challenges, successes, and insights gained in developing strategies for using our probiotic mixture in a commercial hatchery. The authors present findings on the effects of probiotics on larval development and metamorphosis success, survival against pathogen challenges, and probiotic-associated changes in the *Vibrio* community of larval cultures.

MOTHERS KNOW BEST: MATERNAL SIGNALING BOOSTS LARVAL RESILIENCE UNDER OCEAN ACIDIFICATION CONDITIONS

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Ocean acidification (OA) has been problematic for shellfish hatcheries for years, prompting mitigation strategies such as production avoidance of low pH events and seawater buffering. Parental priming, whereby parental exposure to low pH confers resilience to OA in the offspring, offers another mitigation strategy. This concept has shown some promise in previous work, but the mechanisms of inheritance are unknown. It was hypothesized that maternal provisioning of eggs may be the key to understanding parental priming. Among the molecules passed from mother to offspring via the oocyte, lipids constitute the main nutritive source for developing larvae and mRNA contributes to baseline physiology of the zygote. To explore this hypothesis, adult Manila clams were maintained at low or ambient pH for 78 days, during the gametogenic period. Upon maturity, eggs were collected for lipidomics and mRNA transcriptomics and crosses were made to produce larvae. Larvae were exposed to ambient or low pH in a full factorial design for 14 days. Larvae from low pH-primed broodstock showed improved growth and survival at both pH, compared to larvae from unprimed broodstock. Adult physiology, including egg lipidomes, was remarkably unaffected, suggesting that all larvae received the same lipid resources from their mothers. Transcriptomic changes were subtle, encompassing 48 genes, but the categories of genes that changed expression suggest regulatory shifts that may have important downstream impacts on expression of the zygotic genome. This work points to a potential role of the maternal transcriptome in the mechanism of priming for OA resilience in hatchery-reared larvae.

UNDERSTANDING LONG-TERM CHANGE IN THE ATLANTIC BAY SCALLOP FISHERY

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The Atlantic bay scallop (*Argopecten irradians*) once supported a widespread and productive fishery along the U.S. east coast, yet over the past 75 years that fishery has contracted substantially in both magnitude and geographic extent. Using historical commercial landings records from high-resolution state archives and the Atlantic Cooperative Statistics Program, long-term changes in bay scallop fisheries were quantified, revealing a decline of > 94% in total landings since 1950, along with a northward shift of ~ 83 km in the center of the fishery over 5 decades. To interpret these trends, results from recent, prior, and emerging research were synthesized to evaluate the interacting roles of environmental stress. Recent findings indicate that heat (> ~28–30°C), hypoxia (< ~3 mg L^{-1}), disease, and habitat availability influence bay scallop survival and recruitment, helping explain divergent population trajectories along the coast. Mirroring patterns reported in New York, results from a 3-month field deployment in 2025 across the Maryland Coastal Bays indicated enhanced mortality (> 50% loss) at a high-stress site in the month immediately following broadcast spawning compared to a low-stress site (< 20% loss). Quantification of heat shock protein expression will be used to assess stress and reproductive tradeoffs.

Together, fishery trends and recent mechanistic insights can inform domestic bay scallop aquaculture. Despite strong demand, U.S. production remains under 100 metric tons annually, while imports of small, farmed scallops exceed 22,000 metric tons. As east coast aquaculture capacity expands, *A. irradians* offers a compelling opportunity to translate lessons from fishery collapse and persistence into a resilient aquaculture crop.

IMMOBILIZATION OF BURROWING SHRIMP (*NEOTRYPAEA CALIFORNIENSIS*) VIA SUBSURFACE SEDIMENT VIBRATION AS A PEST CONTROL STRATEGY FOR SHELLFISH FARMS

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Bioturbation by burrowing shrimp (*Neotrypaea californiensis* (Dana 1854)) has restricted oyster farming on intertidal flats of Washington State, USA. A novel mechanical control method – subsurface high-cycle vibration with commercial cement vibrators – was developed that immobilized shrimp *in situ*, where they then asphyxiated over several days. Subsurface vibration collapsed the burrow galleries, and surface pressure was applied concurrently that packed sediment and prevented new burrow creation. In initial trials delivered by hand while standing in shallow water, efficacy improved with closer insertion spacing until reaching 84% efficacy at a density of 12.5 insertions m^{-2} (0.3 m spacing), consistent with manufacturer specifications. This spacing was applied to treatment plots at four sites spanning 0.4-20% mud content, with vibration applied by lowering gang-mounted vibrating heads from a custom scow. Surface pressure of 34 kPa was applied adjacent to each insertion for coverage of ~one-third of the total plot area. Core sampling at these experimental sites one week after vibration treatment revealed that live shrimp densities were reduced 72-98% relative to adjacent reference plots, a target effect comparable to chemical control. Similarly spaced insertions to 0.5 m depth reduced shrimp densities by 87%. This experimental method was necessarily time-consuming due to manual operation but has high potential to be optimized and automated to control burrowing shrimp on multi-hectare shellfish farms.

ADVANCING RIBBED MUSSEL (*GEUKENSIA DEMISSA*) SPAWNING PROTOCOLS TO ACCELERATE COMMERCIALIZATION AND MEET GROWING DEMAND

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Demand for cultured ribbed mussels (*Geukensia demissa*) has grown exponentially in recent years due to their use in ecological engineering projects, such as bacterial remediation, bioextraction, ecosystem stabilization, living shoreline development, and coastal resiliency; however, unlike the well-established husbandry techniques for the eastern oyster (*Crassostrea virginica*) and the northern quahog (= hard clam) (*Mercenaria mercenaria*), culture techniques for ribbed mussels remain severely underdeveloped. To meet the growing demand for cultured ribbed mussels, the project team built upon preliminary work to develop consistent protocols for spawning ribbed mussels by improving upon the current standard, the “bin-silo” method. The project objective investigates the independent and interactive effects of thermal cycling and the presence of marsh cordgrass (*Spartina alterniflora*) on the induction and success of spawning in sexually mature ribbed mussels (*Geukensia demissa*) during their first season of maturity. Initial results suggest that 1) a change in temperature (ΔT) influences gamete release regardless of the presence or absence of marsh cordgrass (*Spartina alterniflora*), though observationally marsh cordgrass inclusion suggests promise in aiding hatchery production and early life-history development, and 2) yearling ribbed mussels can serve as viable broodstock for hatchery production. Although this research is still in its preliminary stages, continued investigations will inform hatchery practices and support the development of ribbed mussel aquaculture. Continued work will generate actionable insights for a wide range of stakeholders across New Jersey and beyond, including hatcheries, shellfish farmers, coastal restoration practitioners, non-governmental organizations, academic institutions, and government agencies.

TEMPERATURE-DEPENDENT ENERGY FLOW AND GROWTH IN PINTO ABALONE (*HALIOTIS KAMTSCHATKANA*) THROUGH A DYNAMIC ENERGY BUDGET FRAMEWORK

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Dynamic Energy Budget (DEB) models provide a mechanistic framework to quantify how organisms assimilate and allocate energy to growth, maintenance, and reproduction across variable environments. While DEB models have been developed for several abalone species, none exist for pinto abalone (*Haliotis kamtschatkana*), a cold-water species of ecological and cultural significance in the North Pacific. The absence of a species-specific bioenergetic model limits our ability to predict growth performance, metabolic trade-offs, and thermal sensitivity in this region.

The first DEB model for *H. kamtschatkana* was constructed by adapting parameterization methods from existing models for disk abalone (*H. discus hannai*). Laboratory experiments provided empirical data on pinto abalone juvenile growth and respiration at 6°C, 10°C, 13°C, and 15°C. Core DEB parameters, including volume-specific maintenance and structural costs, were calibrated using regressions and preliminarily evaluated against independent experimental datasets not used in model fitting. Comparative analysis with disk abalone highlighted species-specific deviations in energy allocation strategies and thermal tolerance.

The resulting model describes energy assimilation, allocation, and expenditure in juvenile pinto abalone (~ 2 years old) and predicts performance across environmentally relevant temperature scenarios. By quantifying metabolic constraints and energy trade-offs, this work advances understanding of cold-water abalone physiology and contributes to broader efforts to model bioenergetics in North Pacific shellfish. This framework also provides a foundation for evaluating responses to climate variability and supports future applications in aquaculture and restoration planning.

NASA AQUACULTURE WORKSHOP: INTRODUCTORY REMOTE SENSING - MONITORING HARMFUL ALGAL BLOOM INDICATORS FOR AQUACULTURE

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Satellites observations can detect harmful algal blooms, pollution, and changes in water temperature, salinity, and turbidity that can impact fishery and aquaculture operations. This introductory workshop will provide an overview of NASA remote sensing data for supporting shellfishery activities in marine and freshwater environments. The training will include an introduction to remote sensing of water quality, and how to access and visualize data for monitoring harmful algal blooms, total suspended solids, and water transparency. No prior knowledge or experience is required to attend the training.

BIOLOGICAL ASPECTS THAT ENHANCE THE GROWTH OF THE PATHOGEN BACTERIUM, *VIBRIO PARAHAEMOLYTICUS*

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The pathogenic bacterium, *Vibrio parahaemolyticus*, impacts the health and safety of shellfish and poses a significant risk to human health. According to the Centers for Disease Control and Prevention (CDC), at least one outbreak of *V. parahaemolyticus* infection is reported each year in the United States, typically associated with the consumption of raw or under-cooked shellfish such as oysters, shrimp, clams, and mussels. In addition, in 2013 a new pathogenic strain of *V. parahaemolyticus* carrying the Acute Hepatopancreatic Necrosis Disease (AHPND)-associated plasmid emerged, causing an estimated 60% reduction in shrimp production and leading to global economic losses of approximately US$43 billion for the shrimp farming industry. Therefore, gaining a deeper understanding of the biological factors that allow this bacterium to thrive in diverse environmental conditions is crucial for ensuring future food security and providing economic stability to aquaculture producers.

The goal of this talk is to present results of ongoing efforts to elucidate the biological mechanisms that enhance the environmental survival of *V. parahaemolyticus* using omics-based tools. This talk will share the most relevant findings from two research projects: (1) the molecular mechanisms that support the growth of *V. parahaemolyticus* in anaerobic sulfur-rich environments, and (2) the molecular mechanisms that support its growth in environments with limited carbon sources.

ANALYSIS OF NEW SIZE-LENGTH MODELS FOR THE SEA CUCUMBER, *APOSTICHOPUS CALIFORNICUS,* AND THEIR EFFECTIVENESS IN A MANAGEMENT CONTEXT

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Due to historical overharvesting, populations of *Apostichopus californicus* have been depleted in the Puget Sound. As such, new management tools that allow for more efficient and accurate stock assessment are critical to better monitor the recovery of these populations. This study explores the potential use of new metrics circumference and body shape at time of sampling to better inform the relationship between size and weight of specimens.

To examine the efficacy of these metrics, 1,246 cucumbers were sampled and measured from a specific management region within the central Puget Sound. These measurements were used to create a size index which was regressed against the whole wet weight of the specimens. The study also explores multiple regressions for this relationship, with some relying on the body shape of the specimen at time of processing while others do not. Analysis suggests that all models were effective at estimating the weight of specimens with body shape having minimal effects.

The temporal effect of the sampling procedure was also examined. While specimens were processed, they were stored in buckets of seawater on deck. Evaluation was conducted to see if specimens with the longest holding time showed any noteworthy difference in size or weight when compared to those sampled first. Neither size nor weight showed any trend upwards or downwards across sample processing.

MODELING OsHV-1μVAR TRANSMISSION RISK IN PACIFIC OYSTERS ON THE U.S. WEST COAST USING INNOVATIVE BIOLOGICAL MODELS

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In a NOAA Fisheries–commissioned co-development project, DHI Water & Environment, Inc. collaborated with the NOAA Northeast Fisheries Science Center, with input from a working group of experts, to develop dynamic spatiotemporal models assessing the risk of Ostreid herpesvirus-1 microvariant (OsHV-1μvar) transmission in Pacific oysters (*Crassostrea gigas*) on the U.S. West Coast. The study integrated hydrodynamic modeling (MIKE 3) with innovative biological transmission models (MIKE ECO Lab and ABM Lab) to simulate dispersal of free virus and infected larvae and evaluate infection risk at regional and local scales.

The phased approach included: (1) initial regional agent-based modeling and Automated Information System -based vessel movement analyses to identify Areas of Concern (AoC); (2) local modeling of virus and larval dynamics within AoC; and (3) refinement of regional connectivity risk using local AOC modeling output.

The regional modeling indicates that hydro-connectivity transmission risk of OsHV-1μvar is low, with dispersal largely confined to San Diego Bay (i.e., the original area of infection) and selected AoC. In contrast, local AoC modeling shows that high oyster densities – typified by areas of intense mariculture operations - and favorable hydrodynamics can result in cascading infections at the embayment scale. Key governing factors include oyster density, habitat proximity, hydrodynamics, and outbreak timing. Challenges arising from the unavailability of spatiotemporal empirical monitoring data of an OsHV-1μvar infection event; and the host-pathogen dynamics behind the conclusions drawn from regional and local modeling will be highlighted.

ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND): AN OUTCOME OF *VIBRIO PARAHAEMOLYTICUS* NICHE COLONIZATION

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Bacterial competition is a key process in microbial ecology and plays an important role in the regulation of virulence factors in the presence of competing species. In this study, the biological function of the PirB^{vp} toxin was investigated through competition assays involving a toxin-producing, a non-producing strain, and a phylogenetically distinct species sharing similar ecological niches. The producing strain exhibited a basal PirB^{vp} concentration of 134 ng/mL, which increased to 347 ng/mL during coculture with *Vibrio cholerae* and reached a maximum of 424 ng/mL when *V. parahaemolyticus* was inoculated into a *V. cholerae* culture, exceeding levels observed under non-competitive conditions. Immunological analyses confirmed the continuous presence of PirB^{vp} and its induction following coculture initiation. The antibacterial activity of the B subunit, which contains a jacalin-like domain, was assessed through agglutination, growth inhibition, and bacterial competition assays. PirB^{vp} induced agglutination of *V. cholerae*, *Aliivibrio fischeri*, and *Staphylococcus aureus* at low microgram concentrations. Growth inhibition assays demonstrated bactericidal effects against *V. cholerae* and *A. fischeri* and a bacteriostatic effect against *S. aureus*. Notably, bactericidal activity against *V. cholerae* was abolished in the presence of isopropyl-β-D-1-thiogalactopyranoside, suggesting the involvement of the jacalin-like domain. *In vitro* competition assays showed that *V. parahaemolyticus* remained viable while *V. cholerae* was eliminated, whereas coexistence occurred with the non-toxin-producing strain. These findings demonstrate that PirB^{vp} production is inducible, promotes competitive survival of *V. parahaemolyticus*, and mediates antibacterial activity through interactions with extracellular bacterial structures.

FROM PRODUCTIVITY TO RESILIENCE: AN INDUSTRY-ENGAGED MODEL FOR SHELLFISH BREEDING IN NEW ZEALAND

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The Cawthron Institute in New Zealand (NZ) has developed a unique, industry-engaged model for commercial-scale shellfish breeding that has delivered substantial productivity gains and is now enabling a transition toward climate resilience. Breeding programmes for Greenshell™ mussels (*Perna canaliculus*) and Pacific oysters (*Crassostrea gigas*) implemented in collaboration with BreedCo and Moana NZ respectively, have been built around strong industry involvement at every stage, from setting breeding objectives to providing broodstock, grow-out environments, and hatchery infrastructure for deployment of improved juveniles.

This applied breeding pipeline has generated significant genetic gains over more than two decades, particularly for growth, meat yield and condition, shell quality and disease resistance. For example, selectively-bred hatchery spat exhibit up to ~ 80% faster growth than wild-sourced spat, demonstrating realised gain has driven industry uptake, increased demand for selectively-bred spat, and supported ongoing investment in hatchery capacity. The success of the model stems from its integrated structure: industry identifies priority traits and provides commercial-scale test environments, while Cawthron deliver hatchery expertise, scalable family rearing technologies, quantitative genetics expertise, trait evaluation, and breeding value estimation.

With the increasing frequency of marine heatwaves and summer mortality events, the programmes have expanded their breeding objectives to include climate resilience. For Greenshell™ mussels, thermal tolerance assessed via controlled heat-challenge trials has shown high heritability ($h^2 \approx 0.5$), indicating substantial potential for genetic improvement. Similar progress is being made in Pacific oysters for resilience traits such as low-salinity tolerance. These new traits are being integrated into multi-trait selection indices to balance resilience with ongoing productivity goals.

SHRIMP SCAMPI: A CITIZEN SCIENCE PROJECT - EDUCATING PEOPLE ABOUT MICROBES AND ENDOCRINE DISRUPTING CHEMICALS (EDC) SUCH AS METALS AND GLYPHOSATE USING FOLDSCOPES

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Shrimp Scampi was initiated by Massachusetts (MA) high school students to assess the adverse health effects to the environment, wildlife, seafood (shrimp), and people, caused by endocrine disrupting chemicals (EDC) such as metals and the antimicrobial herbicide glyphosate. Some EDC are associated with diabetes, obesity, non-Hodgkin's lymphoma, non-alcoholic fatty liver disease, antimicrobial resistance, mental health, congenital malformations, and neural tube defects.

Shrimp is a popular seafood of Americans, most of it is imported, causing a yearly ~US$4.5 billion trade deficit. Shrimp viruses and metals have been detected in frozen shrimp sold at MA supermarkets, but no official compulsory testing of contaminants in imported seafood is being performed by government agencies. The goals of Shrimp Scampi are to (1) to examine EDC levels in muscle of frozen shrimp sold at MA supermarkets and in wild shrimp from Ecuador, (2) perform a review of the scientific literature about EDC like glyphosate, metals chelated by glyphosate, interactions of microbes and glyphosate, and trans-generational epigenetic inheritance after exposure to low levels of EDC, and (3) educate American and Ecuadorian mothers about contaminants in shrimp and potential human health effects. Preliminary results will be presented about metals in shrimp and the work being performed in Ecuador to educate about contaminants in shellfish by using foldscopes. Over 200 foldscopes have been distributed through the project 'Foldscopes: From Southborough to Ecuador' (https://fucobi-english.weebly.com/). We are making 'microscopy' available to schools in remote areas. Students and teachers have a wonderful time learning about microcosms, and teachers express their gratitude and enthusiasm for being able to have this new classroom tool since they currently do not have a science laboratory.

DULSE SEAWEED, *DEVALERAEA MOLLIS,* MITIGATES EFFECTS OF OCEAN ACIDIFICATION ON LARVAL PACIFIC OYSTERS, *CRASSOSTREA GIGAS*

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Ocean acidification (OA), driven by upwelling and climate change, interferes with calcification in marine organisms such as larval Pacific oysters (*Crassostrea gigas*). Seaweed photosynthesis has been shown to provide small-scale OA refuges for calcifiers, but previous research excludes the sensitive larval shellfish stage. This study examines the potential for Pacific dulse (*Devaleraea mollis*) to mitigate OA and its effects on Pacific oyster larvae.

Under continuous light for 23 days, the presence of dulse resulted in a consistent increase of 0.1-0.9 in aragonite saturation state and 0.1-0.5 in pH units. Oysters were fertilized and reared for 48 hours in the absence or presence of dulse under treatments corresponding to ambient (pH 7.8, 450 µatm CO_2), future OA (pH 7.6, 800 µatm CO_2), and future OA + upwelling (pH 7.4, 1200 µatm CO_2) seawater conditions. Dulse presence fully mitigated the 5-10% decrease in larval size due to OA. Under the future OA + upwelling treatment, dulse presence reduced the odds by over 50% of underdeveloped oyster larvae at 14 hours post fertilization (hpf), and larvae with hinge abnormalities at 24 hpf. Even when no effect of OA was observed, dulse was seen to decrease morphological abnormalities including underdevelopment, protruded tissue, and convex or rounded hinges. Dulse also induced minor changes to immune response gene expression at 48 hpf.

These findings highlight the benefits of seaweed presence for organisms sensitive to OA, and will be useful for shellfish farms and habitat restoration and stewardship efforts looking to mitigate climate change effects.

CONTRIBUTION OF DISTINCTIVE VPaI EFFECTORS ASSOCIATED *VIBRIO PARAHAEMOLYTICUS* LINEAGES THAT DOMINATE INFECTIONS IN THE U.S. NORTHEAST TO ENVIRONMENTAL FITNESS

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As in other areas with rising *Vibrio parahaemolyticus* disease in recent decades, the northeast U.S. has displayed a shift from sporadic shellfish-borne infections caused by diverse strains to infections repeatedly caused by the same lineage(s). Here, ST36, an invasive Pacific lineage, and ST631, an Atlantic lineage, have been responsible for > 70% of local-source infections. Although the two strains evolved from distinct populations, they each contain an evolutionarily related and horizontally-acquired pathogenicity island (VPaI-γ) harboring both *tdh* and *trh* and genes encoding a distinctive Type-3 Secretion System, specifically T3SS2-β. This VPaI is highly divergent from the VPaI-α (VPaI-7) found in pandemic strains that encodes an array of well-defined effectors. Whereas the effectors from pandemic strains promote environmental fitness by deterring protist grazing, many strains harboring T3SS2-β were relatively ineffective against protist grazing. The orthologous and unique effectors encoded by VPaI-γ were defined and demonstrated that toxin secretion does confer protection against protist predation. Furthermore, analysis of isogenic derivatives with and without toxin secretion varied in their survival in microcosms of water from the New Hampshire Great Bay Estuary revealing that strains defective in toxin secretion better survived in the absence of protists, and that strains capable of secreting toxins survived better in the presence of zooplankton, and in the absence of bacterial competitors. These studies alluded to the potential evolution of higher toxicity by some strains harboring T3SS2-β and reveal that some ecosystem conditions in northeastern coastal areas of the U.S. may promote pathogen dominance and uptake by oysters.

PERSISTENCE OF THE PATHOGEN, *VIBRIO PARAHAEMOLYTICUS,* ON MICROPLASTIC SURFACES AND TRANSMISSION INTO THE PACIFIC OYSTER

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Microplastics in the marine environment develop complex microbial biofilms, “the plastisphere” that can harbor opportunistic bacterial pathogens with implications for both environmental and human health. Closed microcosm systems were implemented to measure the persistence of *Vibrio parahaemolyticus* on polyethylene microplastics and the transmission potential to an oyster host. *V. parahaemolyticus* persisted within the plastisphere for ≥ 30 days, with early enrichment in the plastisphere relative to the surrounding seawater and temperature-dependent shifts in abundance as the biofilms matured. The next experiment measured the impact of microplastics on the uptake of *V. parahaemolyticus* by the Pacific oyster (*Crassostrea gigas*). Under simulated bloom conditions, microplastics did not elevate pathogen accumulation beyond waterborne exposure; however, in pathogen-free seawater, oysters exposed to microplastics with *V. parahaemolyticus* biofilms showed significant pathogen uptake, even when direct ingestion of particles was prevented, indicating indirect transfer of pathogens from surface to host through biofilm shedding. These findings demonstrate that microplastics can act as persistent reservoirs for marine pathogens and facilitate their introduction into filter-feeding organisms, with relevance to seafood safety, pathogen range expansion, and environmental monitoring.

GENETIC TRACKING OF OYSTER SPAT ON A RESTORATION SITE

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Because oysters are a vital part of many coastal ecosystems due to their influence on water quality, support of biodiversity, and habitat creation, oyster restoration has been undertaken around the world, including along the Atlantic and Gulf coasts of North America. Despite the successes and metrics related to oyster restoration, the proportion of oysters on a restoration site that are from a hatchery-raised cohort and how this proportion changes over time is not known. The objective of this project is to utilize a single nucleotide polymorphism (SNP) genotyping panel that can genetically differentiate wild and hatchery-reared oysters, and to track parentage or origin (hatchery vs. wild) of oysters on a restoration reef over time. Oyster spat from the LOLA broodstock line, known for disease resistance, were bred from select parents and planted onto a restoration site within the Manokin River oyster sanctuary in Maryland. Spat were collected and tissues were sampled before deployment and then six, twelve, and eighteen months after deployment. Preliminary results indicated that the SNP panel (3000 markers) is able to genetically differentiate between the wild and LOLA populations and thus will be a useful tool for tracking the genetic origin of oysters sampled on the restored reef and the survival of hatchery-reared spat over time. In addition, this technique could lay the groundwork for determining larval spillover from marine protected areas (MPA) utilizing a parentage-based tagging approach.

FIELD EVALUATION OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) GENOMICALLY SELECTED FOR ENHANCED DERMO RESILIENCE AND GROWTH

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Performance and resilience of living breakwater systems depend on strong colonization and stable populations of key foundation species such as oysters. Genomic selection was evaluated to develop Dermo disease resistant oyster lines with improved growth for deployment on a living shoreline in St. Andrew Bay, Florida. Wild broodstock from the study site were ranked using genomic estimated breeding values (GEBV) derived from SNP associations following laboratory Dermo challenges and used to produce four F1 lines: a high-GEBV Florida line selected for Dermo resistance (FLGS), a high-GEBV aquaculture line selected for resistance and growth (LAFTGS), a low-GEBV control (FLC), and a phenotypically selected line from challenge survivors (FLP). F1 lines were deployed in Alabama, Louisiana, and Florida. Growth varied among sites with LAFTGS growing fastest. Field survival differed widely despite clear laboratory evidence ranking dermo resistance in F1 lines as FLGS > FLP > FLC > LAFTGS.

F1 broodstock were then selected using GEBV weighted for whole oyster weight to improve both growth and disease resistance, producing four F2 lines: FLGS, FLC (average-GEBV control), FLP, and a wild control, FLWC. Laboratory challenges of F2 lines showed significantly higher survival in selected lines (FLGS 79% > FLP 51% = FLC 43% > FLWC 22%). In St. Andrew Bay, F2 FLGS line exhibited 25% greater growth and 72% higher survival than FLWC. Validated success of dermo resistance and increased growth led to the production of an F3 FLGS line that supplied ~54 million larvae and 80,000 seed oysters for deployment to the breakwater.

MULTIPLE LARVAL SOURCES FOR OREGON AND COASTAL WASHINGTON GREEN CRAB POPULATIONS

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The abundance of the green crab (*Carcinus maenas*) in Oregon estuaries falls into two phases: before and after the strong 2015-2016 El Niño. Prior to 2016, recruitment of 0-Age European green crabs to Oregon estuaries was sporadic, with many years of recruitment failure. Ocean indicators of warm surface water and strong north-flowing currents during the winter were followed by good year classes of young green crabs, indicating that larvae were transported from California to Oregon in the Davidson Current. This pattern changed after the 2015-2016 El Niño, when good recruitment occurred every year, and the adult populations in estuaries increased to averages of up to 7 crabs per trap per day. The presence of greater than predicted number of 0-Age crabs after cold winters indicates the existence of additional larval sources. Evidence will be presented for local reproduction and for larval transport from the north. Very early instar larvae were collected in Coos Bay during a mini El Niño from January to March 2010. These larvae had to be locally produced. Genetic evidence suggests that larvae from a genetically distinct population in the Salish Sea were transported south to Washington coastal and northern Oregon estuaries in the Shelf-break current during the summer. Now that the green crab breeding populations have built up along the coast, Oregon estuaries can receive larvae from the south in the winter, from the north in the summer and from local sources. The presence of these multiple larval sources complicates control efforts for this invader.

ANTIOXIDANT SYSTEM AND OXIDATIVE STRESS RESPONSES IN SHRIMP UNDER ENVIRONMENTAL CHANGES

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Global warming can provoke environmental stress to aquatic animals, as the oxygen content of water decreases (hypoxia) concurrently with higher temperatures. In the white shrimp Penaeus vannamei, one of the most important cultivated crustacean species worldwide, we have been studying the responses to hypoxia and higher temperatures of the first-line antioxidant system enzymes, two manganese superoxide dismutases MnSOD (mitochondrial and cytosolic) and two glutathione peroxidase (GPx) GPx2 and GPx4. Silencing using RNAi was employed to investigate the effects of one isozyme on the other in the corresponding pair and the impact of silencing the transcription factor p53. Additionally, carbonylated proteins and lipid peroxidation were evaluated as indicators of oxidative stress. Hypoxia and/or heat affected the expression of the analysed genes differentially. Oxidative damage, detected as lipid and/or protein oxidation, was also differentially detected. Current work focuses on analysing potential epigenetic regulation of antioxidant enzymes and transcription factors as responses to stress.

TRANSLATING OYSTER QUALITY ACROSS MARKETS AND FOOD CULTURES

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This paper examines how oyster quality and market value are defined, evaluated, and translated across different national and consumption contexts, with attention to size, taste, and consumer expectations. Drawing on ethnographic fieldwork at a nationwide oyster competition held at the Toyosu Fish Market in Japan - the largest fish market in the world - including interviews with intermediate wholesalers and firsthand experience as a judge, the study documents how criteria such as plumpness, flavor, and size shape quality assessment in the Japanese market. These standards are contrasted with responses from oyster producers, industry professionals, and consumers encountered at aquaculture-related events in Australia and the United Kingdom, revealing significant differences in size preference, sensory evaluation, and modes of consumption. In Europe and North America, oysters are predominantly consumed raw, favoring smaller shell sizes and consistent year-round supply. In Japan, by contrast, larger oysters have historically been preferred due to cooking practices that prioritize volume retention; however, recent growth in raw bars and platter-style dining has contributed to increasing demand for smaller oysters, particularly bioengineered triploid varieties that enable branding, standardization, and year-round availability. By tracing how oyster bodies are selectively bred, graded, and marketed to meet changing consumer and market demands, this presentation highlights the practical implications of shifting food cultures for oyster production, size grading, and product differentiation. The findings offer insights relevant to breeders, growers, and marketers navigating global shellfish markets, where biological traits, labor practices, and consumer expectations are increasingly aligned to optimize both sensory quality and economic value.

CONSEQUENCES OF DIFFERING MATURITY DEFINITIONS ON MANAGEMENT REGULATIONS FOR A GASTROPOD FISHERY

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The channeled whelk, *Busycotypus canaliculatus*, is the primary whelk species in the southern New England multi-species whelk fishery and is currently overfished. Here, the definition of maturity as it pertains to size-at-maturity (L_{50}) estimates were reassessed to update life history traits from a decades-old stock assessment. Whelk were sampled seasonally (2021, 2022, 2023) in three regions of southeastern Massachusetts: Buzzards Bay, Vineyard Sound, and Nantucket Sound. Specimens were dissected to assess size-at-maturity and life history traits. Data showed that reproductive development and maturity were conflated in previous literature definitions of maturity and was redefined based on biological principles. Literature definitions of female maturity resulted in an estimated L_{50} of ~89 to 105 mm shell width (SW) and ~154 – 175 mm shell length (SL), while the revised biological definition used here resulted in a 28 to 42% decrease in SW (61 to 66 mm) and 26 to 37% decrease SL (109 to 117 mm) L_{50}. In contrast, male L_{50} determinations remained similar, regardless of maturity definition. Throughout this study, there were more males than females collected (mean ± SD: 65 ± 10%), because the fishery has removed proportionally more females due to their larger size and higher likelihood to be above the harvestable size limit. The results presented here highlight the need for a more precise data-based definition of maturity, as maturity classifications can drastically alter size-at-maturity estimates and fishery management decisions.

POSTER PRESENTATIONS

ASSESSING THE REPRODUCTIVE PATTERNS OF THE OYSTER, *CRASSOSTREA GIGAS*, IN SOUTHERN CALIFORNIA

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The purpose of this project was to investigate the reproductive viability of Japanese oysters by integrating histological and ecological data. Monthly, oyster gonads were collected and processed to determine gamete development. Oocytes significantly increased in size ($p < 0.0001$) during the collection period, indicating actively developing oocytes and potential reproduction. Ecological assessments of population density, percent coverage, and size frequency provided data on population growth. No significant population growth was observed during the ecological surveys ($p > 0.05$). Although the population did not exhibit significant growth, the growth of oocytes suggests a potential for oyster reproduction. A key component of assessing the potential impact of non-native species lies in examining reproductive traits - specifically, the abilities and patterns that drive species establishment and spread.

DEVELOPMENT OF HEMOCYTE VIABILITY ASSAY FOR EARLY DETECTION OF MASS MORTALITY DRIVERS IN BIVALVE HATCHERIES

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Bivalve hatcheries have experienced larval crashes at unprecedented rates along the Atlantic Coast of the United States. Investigating the specific drivers of mass mortality events can reveal vulnerabilities affecting global shellfish populations and support the development of preventative and mitigation strategies. Current detection methods, including 1- to 7-day larval assays, can be too slow to allow hatchery managers to intervene before high levels of mortality occur. There is a critical need for rapid screening tools that can detect adverse environmental conditions before they can significantly impact seed production. This study aimed to develop a hemocyte-based viability assay as an early warning system for bivalve hatcheries. Adult oyster (*Crassostrea virginica*) hemocytes were challenged by 0.22-micron filtered tank water samples collected from participating hatcheries within the Bivalve Hatchery Health Consortium. Hemocyte viability was measured using a resazurin-based fluorometric assay, with results obtained in approximately 10-12 hours compared to the traditional 7-day larval assay. Hemocyte viability was correlated with larval survival rates from paired larval assays conducted on the same water samples. Assay optimization is ongoing, with preliminary data showing correlation trends between hemocyte mortality and larval survival outcomes. If validated, this rapid screening method would enable hatchery managers to identify potentially deadly conditions within hours rather than days, allowing for proactive interventions such as water source changes or husbandry adjustments. This assay methodology should be applicable across bivalve species, providing a valuable diagnostic tool for the broader shellfish aquaculture industry.

THE WRONG OYSTER, *OSTREA EQUESTRIS*

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The crested oyster, *Ostrea equestris* Say 1834, ranges from North Carolina in the United States to the southern Caribbean. It occurs with the commercially and ecologically important eastern oyster, *Crassostrea virginica* Gmelin 1791, in the U.S. Smaller than *C. virginica*, *O. equestris* is limited to salinities above 20, but the two overlap enough in both morphology and habitat that *O. equestris* is frequently confused as juvenile *C. virginica*. Also, *O. equestris* can be abundant, dominating some high-salinity habitats. There are diagnostic shell characters – chomata, or denticles on the shell margins of *O. equestris* – but these are small, internal, and require training. External shell differences are inconsistent. A researcher cannot simply look at a cluster of coastal oysters in a southern U.S. estuary and reliably distinguish the species.

The similarity of the two oysters is compounded by a widespread lack of awareness of *O. equestris*. Informal censusing of shellfish resource managers and aquaculturists suggests the majority do not know there is a second species of oyster, and fewer know how to tell the species apart. The result can be misinterpretation of oyster population data, confusing *O. equestris* for juvenile *C. virginica*. This is important because not only does *O. equestris* never grow to market size, but it also does not create oyster reefs, despite attaching to shells of other species. Oyster researchers, managers, and growers need to be aware of the two species and their diagnostic differences, and sample regularly to assess their relative frequency.

DEVELOPING INFRASTRUCTURE FOR LARVAL SHELLFISH OUTPLANTING

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Atlantic surfclams (*Spisula solidissima solidissima*) are economically important bivalves native to the northeastern United States. Like other calcifying organisms, they are highly vulnerable to climate change, especially the alterations in carbonate chemistry due to ocean acidification. Carbonate chemistry in the surfclam habitat has high spatial variability and seasonality, resulting in populations of surfclams at sites with distinct chemical differences. To assess the larval success of various surfclam populations in current environmental conditions, deployment containers are needed to ensure that the larvae being studied remain contained, adequately fed, and safe from predation. Containers of two volumes with cutaway 31-micron mesh windows were suspended at varying depths in Milford Harbor and stocked with four-hour-old surfclam embryos of two separate populations and one genetic hybrid, with a follow-up test stocking 21-day-old larval oysters. After 48 hours, the larvae were retrieved, and their survival and development were compared to those of identical indoor cultures. Results showed that containment units outdoors had sufficient water flow to deliver phytoplankton to the larvae, and that the size and depth of containers have little effect on survival. This means that by utilizing equipment such as the containers outlined in this study, deployed larval surfclams are exposed to an adequate food supply from the surrounding water column and can be utilized to study environmental conditions such as ocean acidification.

MANGROVES, CORALS, SALTMARSHES, AND SHELLFISH OF TANZANIA

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Mangroves are prime nesting and resting sites for hundreds of shorebirds and migratory bird species, including kingfishers, herons, and egrets. Mangrove roots provide support for filter- feeders like mussels, oysters, and barnacles. "A jet fuel spill in Ensenada Honda, Puerto Rico, was investigated to determine impacts on mangrove communities. The toxic oil spill pollution levels in black-lip pearl oyster (*Pinctada margaritifera*). An investigation on oil spill pollution was made at the National Environment Management Council from samples of sediments and biological indicators. Coral reefs are very important in Tanzania, both ecologically and socio-economically, as major fishing grounds. The Global Coral Reef Alliance (GCRA) has taken the lead in documenting coral bleaching events worldwide and relating them to climate and weather anomalies as well as locally derived environmental stresses. The goals of this project were to (1) examine metal/oil levels in oysters and saltmarsh, (2) assess the survival of oysters and saltmarsh using the Biorock method mineral accretion and (3) perform an economic analysis of innovative methods to enhance productivity in the cultivation of oysters, seaweed, mussels, and fish. Biorock method Accretion Technology increases shellfish settlement while reducing hydroid fouling, keeping oysters and saltmarsh alive and growing under conditions that would otherwise be toxic. This method stimulated a greater settlement of larvae of different marine species. Local funding can help Curtin University in Mauritius to partner with a local research group in Tanzania to see if Biorock speeds up healing.

ASSESSMENT OF HEAVY METALS AND HUMAN HEALTH RISK IN SHRIMP COLLECTED FROM DIFFERENT FARMS AT CITY OF MATI, DAVAO ORIENTAL, PHILIPPINES

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Heavy metals are natural constituents of the Earth's surface, but anthropogenic activities can increase their concentration, posing significant threats to the environment and living organisms. The concentrations of cadmium, chromium, iron, lead, manganese, and nickel in water, sediment, and shrimp (tissue and shell) samples from two farms in Barangays Dahican and Dawan, City of Mati, Davao Oriental were studied using Atomic Absorption Spectrometry. Potential non-carcinogenic health risks associated with their consumption were assessed using the Target Hazard Quotient (THQ) and Hazard Index (HI), in accordance with U.S. Environmental Protection Agency guidelines. Results showed that water samples from both Dahican and Dawan had chromium and nickel levels exceeding the allowable thresholds set by the Department of Environment and Natural Resources (DENR), while other metals remained within permissible limits. In sediment samples, chromium, iron, lead, and manganese levels in Dahican exceeded World Health Organization (WHO) limits, but Dawan samples showed elevated levels of chromium, iron, and manganese, with nickel levels surpassing the National Oceanic and Atmospheric Administration standards. In shrimp from Dahican, chromium concentration exceeded WHO limits but was not detected in either tissue or shell samples from Dawan. Manganese in shrimp tissue from Dawan exceeded WHO guidelines. Iron concentrations in both tissue and shell samples from both farms were within safe limits, while cadmium, lead, and nickel were either undetected or below detection limits. Despite these exceedances, the THQ and HI for all metals from both farms were below one, indicating that long-term, continuous intake is unlikely to pose any significant health hazards. Nonetheless, continuous monitoring and management of heavy metals in shrimp farming remain essential to prevent future contamination risks and safeguard environmental and public health.

STRAIN-SPECIFIC COLONIZATION AND VIRULENCE MODULES IDENTIFIED THROUGH INTEGRATED GENOME AND TRANSCRIPTOME PROFILING OF *VIBRIO PARAHAEMOLYTICUS* AHPND STRAINS

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Acute hepatopancreatic necrosis disease (AHPND), caused by *Vibrio parahaemolyticus* harboring a unique virulence plasmid that encodes and secretes the PirAB toxins, continues to threaten global shrimp aquaculture, resulting in major economic, welfare, and environmental impacts relevant to One Health and EcoHealth perspectives. Although *V. parahaemolyticus* is recognized by WOAH as one of the most virulent and economically significant aquatic pathogens, the molecular mechanisms underlying differences in strain-level pathogenicity remain insufficiently understood.

This study analyzed two AHPND-positive *V. parahaemolyticus* strains, TUMSAT_D06_S3 (D6) and TUMSAT_DE1_S1 (E1) isolated from *Penaeus vannamei* shrimp. Phenotypic assays confirmed that, despite being standardized to the same starting cell/mL, D6 reached higher cell densities during growth-curve analysis, whereas E1 consistently produced higher CFU counts and greater early-cell densities on TCBS agar plates.

Complete hybrid genome assemblies, detailed annotation, and multi-timepoint transcriptomics (4 h, 9 h, 16 h) enabled the identification of strain-specific genomic modules and regulatory signatures associated with virulence. Comparative genomics and ortholog mapping revealed that E1 carries unique gene clusters linked to adhesion, motility, secretion, and colonization, many displaying elevated transcription across timepoints. Integration of expression profiles with KEGG/COG functional categories further highlighted E1-specific enrichment in pathways associated with environmental sensing, stress response, and host interaction, consistent with previously observed higher virulence.

Overall, this work provides a detailed molecular comparison of two *V. parahaemolyticus* strains and identifies candidate virulence determinants, regulatory patterns, and colonization-associated genes that may explain differential pathogenicity. These findings contribute to improved understanding of *V. parahaemolyticus* adaptation to shrimp hosts and aquaculture environments, with implications for disease surveillance and shellfish health management.

OYSTER REEF PESTS: A STUDY OF THE ROCK SNAIL, *STRAMONITA BUCHECKI,* IN THE LOXAHATCHEE RIVER, FLORIDA

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Freshwater flow into estuarine environments varies seasonally with extended influxes or extreme salinity changes causing stress to eastern oysters, *Crassostrea virginica*. Natural variations in salinity benefit the reef by reducing predation and disease, however, drastic prolonged drops in salinity may promote the proliferation of certain oyster pests and parasites with the ability to withstand the dramatic change. One such pest, the predatory rock snail, *Stramonita buchecki*, has been observed on eastern oyster reefs year-round in southeast Florida yet limited knowledge exists of its basic life-history. This drill causes damage to the reef by boring holes through oyster shell, consuming the tissue and often laying eggs inside the emptied shell.

After largescale freshwater influxes following the annual wet season, compounded by hurricanes Helene and Milton in 2024, *S. buchecki* abundance increased on Loxahatchee River oyster reefs. Preceding the 2025-2026 wet season, samples were collected monthly and assigned categorical reproductive stages to compare seasonal patterns in stage frequency as part of an ongoing study. Within a year, *Stramonita buchecki* appears to experience multiple spawning events, peaking in the spring. A decline in salinity during the 2024-2025 and 2025-2026 wet seasons was followed by an aggregation period of snails during the winter. The ability to reproduce despite large freshwater events may allow the abundance of this predator to increase on southeast Florida oyster reefs. This project serves as a baseline study of the annual pattern of reproductive development of the recently identified rock snail species present on three northern Loxahatchee eastern oyster reefs.

EFFECTS OF MICROPLASTICS ON GILL LATERAL CELL CILIA OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Microplastics are abundant in oceans, affecting metabolic activities and survival of microbes, phytoplankton, zooplankton, and fauna. In aquatic invertebrates, microplastics can decrease feeding, fertility, larval growth, increase oxygen consumption, and stimulate production of reactive oxygen species. The eastern oyster, *Crassostrea virginica,* is a filter-feeding bivalve, providing a significant role in water filtration, and economic and ecological benefits to the marine aquaculture industry. Oyster gills are involved in respiration, feeding, and filtering. Gill lateral cell cilia (GLCC) create water currents for respiration and feeding. They are innervated by serotonin and dopamine nerves. It was investigated if microplastics impacted GLCC activity, hypothesizing microplastics would negatively affect GLCC activity, either at the GLCC or by affecting neuronal innervation. Acute experiments were conducted applying 2.3 million particles/mL of micropolystyrene monodisperse (MPM) to isolated gills and mantle rim sensory tentacles, while measuring GLCC beating. Short-term, 5-day experiments were also conducted incubating animals with 2.3 million particles/mL of MPM and accessing serotonin application to visceral ganglia (VG) on GLCC.

Acute MPM application to gill or sensory tentacles had no effect on GLCC beating. The short-term experiments also did not decrease the ability of serotonin application to the VG to increase beating rates of GLCC. The study did not confirm the hypothesis. There were no neurotoxic effects of MPM on the serotonergic system of *C. virginica.* It must be noted that there are many different microplastics accumulating in the ocean and MPM is just one type. Others may have damaging actions to *C. virginica* and other marine animals.

HUMAN HEALTH RISK ASSESSMENT OF MICROPLASTICS AND ORGANIC POLLUTANTS FROM SELECTED BIVALVE SPECIES IN NEGROS ORIENTAL, PHILIPPINES

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This study assessed the occurrence and potential health risks of microplastics and organic pollutants in three bivalve species from Negros Oriental, Philippines, collected between 2020 and 2022. Samples included *Polymesoda expansa* from three sites, *Anadara antiquata* from Bais Bay, and bottled *Perna viridis* from a local market. Microplastics were isolated through potassium hydroxide (KOH) digestion and identified using a combination of hot-needle tests, microscopy, and either Fourier-Transform Infrared (FTIR) spectroscopy or micro-FTIR for detailed analysis. Organic pollutants, including polyaromatic hydrocarbons (PAH), phthalates, polychlorinated biphenyls (PCB), and pesticides, were analyzed using gas chromatography-mass spectrometry (GC-MS). Risk assessments were conducted using U.S. EPA oral reference doses, average body weights, and estimated consumption rates. Results revealed that all analyzed bivalves contained microplastics, predominantly fragments and fibers. In *A. antiquata*, 134 microplastic particles were detected among 50 individuals, with fragments being dominant and most particles smaller than 250 µm, suggesting increased potential for pollutant adsorption. In *P. expansa*, phthalates and PAH exhibited the highest concentrations at one site (Bais City), with Benzo[ghi]perylene, Anthracene, and Indeno(1,2,3-cd)pyrene as major source of PAH. Pesticides, including Chloroneb and Fenitrothion, were consistently detected across sites. Regression analyses indicated possible bioaccumulation of PAH and pesticides with bivalve size. Risk characterization suggested that while average concentrations of detected pollutants did not exceed EPA action levels, some samples contained PCB and PAH concentrations surpassing precautionary thresholds, indicating potential long-term risks. These findings emphasize the importance of continuous monitoring and pollution management in coastal ecosystems of Negros Oriental.

QUANTIFYING NATIVE FRESHWATER MUSSEL BIOFILTRATION AND ITS APPLICATION FOR ENHANCING TRADITIONAL POLLUTION CONTROL MEASURES IN NOVEL URBAN HABITATS OF THE LOWER DELAWARE RIVER BASIN (PHILADELPHIA, PENNSYLVANIA)

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The ability of freshwater mussels to influence the biogeochemical properties of free-flowing and lentic systems, their sensitivity to anthropogenic stressors, and their fragile ecological status, have recently gained considerable attention. Still, most research and management interests focus on species protection and conservation, because of the high level of imperilment among North American unionids. Accordingly, little consideration has been directed towards the potential use of freshwater bivalves to augment traditional pollution control measures, improve degraded water quality, and restore crucial ecosystem functions.

The cultivation of shellfish for the purposes of nutrient removal has become increasingly acknowledged as a mechanism that may abate eutrophic conditions in coastal waterways throughout the world. While bioextraction techniques in marine ecosystems have garnered acceptance within scientific and regulatory communities, in-water nutrient reduction strategies using freshwater mussels remains conceptual, in part due to their lack of commercial value, infaunal lifestyle, complex life cycle and biodiversity-focused management emphasis. Bivalve-mediated pollution abatement programs in freshwater ecosystems are noticeably absent from primary research, understated in discussion points, and infrequently addressed in future areas of study.

Despite these confounding factors, current studies have shown that the biofiltration properties and assimilative capacities of freshwater mussels are comparable to their marine counterparts. Together, these findings, coupled with rising capital costs and performance limitations of conventional pollution control measures, indicate that freshwater mussels may represent a viable complementary investment for pollutant removal and broader urban water-management applications.

PRESENCE OF GLUTAMATE NEURONS AND GLUTAMATE RECEPTORS IN THE MANTLE RIM SENSORY TENTACLES AND LABIAL PALPS OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Mammals and various invertebrates have glutamate neurons in their nervous systems. Human neurodegenerative diseases associated with glutamate dysfunctions include Parkinson's, Alzheimer's, Huntington's, autism, depression, and schizophrenia. Glutamate NMDA receptors were found in and involved with regulating metamorphosis in *Crassostrea gigas, Mercenaria mercenaria,* and *Mya arenaria*. Glutamate neurons and glutamate GluR-1 receptors have been found in visceral and cerebral ganglia of *C. virginica,* having neurophysiological functions increasing gill lateral cell cilia beating rates. Mantle rim sensory tentacles, which transmits sensory information to visceral ganglia, are sensitive to light, various algae, as well as crab extract. Immunohistofluorescence showed serotonin, dopamine, histamine and GABA receptors present. Histamine is involved with the photoreception. Labial palps are responsible for food sorting, particle selection and transferring food to the mouth. Few neurophysiology studies have been conducted on labial palps.

Using immunohistofluorescence microscopy, it was hypothesized that glutamate receptors are present in mantle rim sensory tentacle and serotonin, dopamine, GABA, histamine, and glutamate receptors are present in labial palps. Tissues were excised, snap frozen, cryostat sectioned, fixed with EDAC (N-Ethyl-N′-(3-dimethyl-aminopropyl) carbodiimide hydrochloride), treated with blockers, incubated with conjugated FITC antibodies, sectioned and viewed on a Leica epilume fluorescence microscope with a Leica DFC400 camera, 50-watt mercury lamp and FITC excitation/emission filters. Glutamate receptors were found in the sensory tentacle, as well as serotonin, dopamine, GABA, histamine, and glutamate receptors in labial palps. The study complements previous neurophysiology studies of *C. virginica* and provides new information about the neurophysiology of the labial palps.

SPECIES COMPOSITION VARIES AMONG ARTIFICIAL AND NATURAL BENTHIC SUBSTRATES WITHIN ESTUARINE ENVIRONMENTS

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As the commercial development of aquaculture grows, assessing the impact of culture gear on local marine communities becomes increasingly imperative. Gear associated with off-bottom oyster aquaculture introduces artificial structure to areas that would otherwise be devoid of structural complexity and heterogeneity. In this study, the abundance, diversity, and composition of fish assemblages near oyster rack-and-bag cages and natural systems was compared. In Lewes, DE, from June to August 2024, stationary video cameras surveyed a natural oyster reef, a rack-and-bag oyster cage, and a flat, sandy bottom. Despite limited visibility (0.18 – 0.56 m), video-based methods were effective in monitoring habitat along oyster-based structures. Analyses revealed no significant differences in sightings, Shannon diversity index, and family richness between the treatments ($p = 0.074$, $p = 0.103$, $p = 0.451$, respectively, Kruskal-Wallis, $n = 12$); however, the reef site had greater abundance in terms of total MaxN ($p = 0.009$, Kruskal Wallis, $n = 12$), and the three sites had unique community compositions ($p < 0.001$, all, pairwise PERMANOVA). While abundance and diversity suggest similar habitat provisioning between natural reefs and rack-and-bag systems, changes in composition suggest that each structure provides different ecological functions. This relationship is often conserved in similar studies that offer multiple metrics for assessing the habitat function of aquaculture gear; however, there has been a lack of emphasis on the differences in composition and how that may influence habitat function among altered benthic substrates. This study provides evidence of variable functional impact associated with altered benthic landscapes.

DEVELOPING A NOVEL RESTORATION TECHNIQUE BY GLUING EELGRASS SEEDS TO LIVING NORTHERN QUAHOGS (= HARD CLAMS)

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Climate change and other anthropogenic disturbances are causing unprecedented changes in marine ecosystems. Foundational habitats critical to species survival have declined rapidly. An emerging technique to habitat restoration is the utilization of facilitative relationships between species. Co-restoration using primary foundation species and secondary foundation species together may help ecosystems recover more quickly than focusing on a single species.

Seagrass habitat is one example of an ecosystem that has rapidly declined, especially across the east coast of the United States. These ecosystems were once crucial carbon sinks, nurseries for juvenile fish, habitats for invertebrates, and more. Many past and current restoration efforts rely on outplanting techniques of shoots or hand broadcasting of seeds for species that reproduce sexually. Broadcasting seeds results in seed loss due to predation and displacement from currents. There is growing evidence for facilitative relationships between seagrass species and bivalves. This is due in part to the many ecosystem services that bivalves provide, such as water filtration, nutrient cycling, and more.

A novel technique was developed utilizing the relationship between clams and seagrass to achieve an optimal burial depth for germination. The seeds of *Zostera marina* can be adhered to the valve of *Mercenaria mercenaria* using a safe, protective, gelatin-based adhesive. Seeds can be planted by coupling the natural burial behavior of the clams with the biodegradable adhesive. Preliminary results show this technique was equally effective at germinating eelgrass as hand-broadcasting. This poster outlines the anticipated development and application of this technique to seagrass restoration.

BORING PROBLEMS: QUANTIFYING BIOEROSION PATTERNS IN OLYMPIA OYSTERS ACROSS SOUTHERN CALIFORNIA ESTUARIES

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Bioerosion by boring sponges (*Cliona* spp.) and polychaete worms can compromise shell integrity in the Olympia oyster (*Ostrea lurida*), yet regional patterns in southern California remain poorly quantified. This study examined bioerosion distribution across valve surfaces and between estuarine sites in southern California. Erosion was quantified using ImageJ analysis of macro-photography images from *O. lurida* shells collected at Anaheim Bay (n = 562 valves from 281 individuals). Boring sponge and polychaete worm prevalence was assessed by comparing percent cover and borehole abundance between upper and lower valves. Preliminary findings reveal distinct valve-specific bioerosion patterns. Bottom valves exhibited higher boring worm area coverage (approximately 26% versus 19% on top valves) and greater total internal shell erosion (approximately 26% versus 21%). In contrast, top valves showed higher boring sponge area coverage (approximately 3.5% versus 0.8% on bottom valves) and greater worm bore hole abundance (approximately 8.5 versus 5 holes per valve). These patterns provide critical baseline data for assessing oyster bed health and predicting shell degradation rates in restoration contexts. Understanding valve-specific bioerosion vulnerability will help restoration practitioners evaluate population health and assess site-specific threats to Olympia oyster habitat across the species' southern range.

DEVELOPING A LARVAL RECRUITMENT INDEX FOR DUNGENESS CRAB IN THE SALISH SEA

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The Dungeness crab supports one of the most valuable fisheries on the U.S. West Coast, yet it has never been subject to a formal stock assessment and management relies primarily on the '3s' framework of size, sex, and season. Although catch statistics are often treated as an index of abundance, the absence of fishery-independent monitoring limits insight into underlying population processes and recruitment variability. Proxy metrics from larval and juvenile stages offer an additional means of assessing population trends, but interpretation in the Salish Sea is complicated by complex hydrodynamics and potential larval subsidy from the California Current System, which together generate regionally distinct signals. This study uses the larval crab monitoring network of the Pacific Northwest Crab Research Group to quantify spatial and temporal patterns of late-stage larval delivery across the Salish Sea. Analyses will identify dominant modes of larval supply, the spatial scales at which they operate, and the relative contribution of locally produced versus coastal-derived larvae. These patterns will inform development of a larval recruitment index that integrates magnitude and timing of delivery and incorporates likely larval sources. The index will be compared with young-of-the-year crab abundance and size structure in nearby intertidal habitats to assess whether variation in larval supply corresponds with benthic-stage metrics. This work provides a quantitative assessment of basin-scale larval delivery dynamics for Dungeness crab in the Salish Sea and support development of transferable, fishery-independent indicators of larval recruitment.

EARLY WARNING HAB SYSTEM: INSIGHTS FROM NEARLY TWO DECADES MONITORING HARMFUL ALGAE ON THE OREGON COAST

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Harmful Algae Blooms (HAB) along the Oregon coast have been documented since the 1990s and are associated with detrimental impacts to human health, marine life and coastal economies. Toxins produced by the diatom *Pseudo-nitzschia* spp. and dinoflagellate *Alexandrium* spp. accumulate in shellfish tissue and can cause Amnesiac Shellfish Poisoning and Paralytic Shellfish Poising respectively, resulting in shellfish harvesting closures. In response to the serious risk blooms of these phytoplankton pose, the Oregon Department of Fish and Wildlife (ODFW), Oregon State University and the National Oceanic and Atmospheric Administration (NOAA) established Monitoring Oregon Coastal Harmful Algae (MOCHA) in 2007. Since 2007, surf zone HAB monitoring has been supported by Federal grants from NOAA and the Northwest Association of Networked Ocean Observing Systems and has grown through regional and tribal partnerships. Monitoring includes weekly enumeration and identification of phytoplankton in water samples collected from standardized sites along the Oregon Coast. The program offers timely information on the status of HAB and informs the Pacific Northwest HAB Bulletin which provides an early warning of HAB risk to coastal shellfish managers. Beginning July of 2025, ODFW received state funding for the first time to support a coast-wide HAB monitoring program in Oregon. Presented here are data spanning from 2006-2025 showing the spatial and temporal distribution of HAB along the Oregon coast, including preliminary results from expanded sampling efforts and future program plans to address current gaps in monitoring. This data demonstrates how long-term HAB monitoring continues to inform effective decision making for fisheries managers.

OUTLINING A LARGE-SCALE ALGAL PRODUCTION SYSTEM FOUNDATIONAL FOR USDA-ARS RESEARCH AND BREEDING

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The USDA-ARS Pacific Shellfish Research Unit (PSRU) houses the Pacific Oyster Genomic Selection (POGS) breeding project and shellfish researchers focused on improving stocks and enhancing shellfish production along the U.S. Pacific coast while ensuring that culture practices are sustainable and environmentally acceptable. The PSRU-led collaborative research portfolio requires substantial volumes of live microalgae to conduct breeding program operations, experimental research and animal maintenance, which are often occurring simultaneously. Further complexity is introduced via the requirements for multiple phytoplankton species that differ substantially in husbandry requirements for optimal growth. These include dietary microalgae (i.e., *Chaetoceros, Tisochrysis*), as well as HAB and other dinoflagellates. The utilization of large volume photobioreactors (Industrial Plankton™) has been essential for supplying POGS and experimental research studies that can be rearing multiple shellfish life stages and prolific numbers of individuals at any given time. This poster describes PSRU algal propagation from batch culture systems (10L carboys, flasks etc.) to continuous culture systems (photobioreactors) and automated algal delivery systems for shellfish feeding. Additionally, procedures and protocols are outlined, with critical steps and considerations necessary to operate a successful large-scale microalgal production system with a limited number of personnel.

ASSESSING THE IMPACT OF MICROPLASTICS AND CHEMICAL CONTAMINANTS ON FOOD SAFETY IN SUSTAINABLE AQUACULTURE SYSTEMS: A COMPREHENSIVE LITERATURE-BASED PROPOSAL

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Sustainable aquaculture plays a critical role in addressing the global demand for seafood while striving to minimize environmental impacts and promote ecological balance. Nevertheless, the accumulation of emerging contaminants including microplastics, heavy metals, pesticides, and other chemical residues pose considerable risks to aquatic organisms (shellfish, fish) and human health, potentially undermining the safety and sustainability of aquaculture products.

This study aims to conduct a comprehensive literature review to evaluate the prevalence, pathways, and potential impacts of microplastics and chemical contaminants in aquaculture systems (shellfish and fish), with a focus on practices in developing countries. A systematic review methodology was applied to analyze peer-reviewed studies published between 2010 and 2025, supplemented by relevant data on residues in the Rapid Alert System for Food and Feed (RASFF). Key objectives include identifying the most prevalent contaminants, elucidating mechanisms of bioaccumulation in cultured aquatic organisms (crustaceans and mollusks), and assessing associated human health risks through seafood consumption.

Outcomes of this study include actionable insights into strategies for mitigating contamination in aquaculture systems, providing evidence-based recommendations for improving food safety protocols, and informing policy interventions. Furthermore, this review will contribute to advancing knowledge within the One Health framework, emphasizing the interconnectedness of environmental health, animal health, and human health. Ultimately, the findings will support the development of safe and sustainable aquaculture practices, ensuring the production of high-quality seafood in the context of increasing environmental challenges and global food security concerns.

EVALUATION OF HEMOLYMPH MICROBIOME CONTAMINATION AS A FUNCTION OF SAMPLING METHOD USING 16S AMPLICON SEQUENCING APPROACHES

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With its increasingly clear role in driving health and disease, research into oyster microbiome composition is rapidly gaining relevance and urgency. Importantly, with microbiome research comes the need for standardized tissue extraction methods and understanding of the biases implicit with these methods. Due to its immunological functions and role as an indicator of oyster health, hemolymph is a valuable medium for microbial community analysis. Unfortunately, much of the current literature regarding oyster hemolymph microbiomes is opaque in its description of hemolymph extraction methods. When methods are clearly described, hemolymph is typically collected via a needle inserted into the adductor through a hole cut in the shell. Due to the needle movement through soft tissues and mucus membranes, this notch method carries significant risk of sample contamination. An alternative hemolymph sampling method, hereby referred to as the hole method, minimizes potential sources of contamination by drilling a hole through decontaminated shell surface above the adductor muscle allowing needle insertion directly into the internal tissue. To compare these two sampling methods, with a particular focus on potential for contamination, oysters had hemolymph collected through both a notch and hole with order differing based on oyster. Following bioinformatic analysis of the resultant 16s rRNA sequences, the presence of significant *Vibrio* contamination in notch samples was clear. Overall, this analysis clearly demonstrates both the utility of the hole method and the need for bivalve microbiome researchers to be aware of their sample collection methods and the associated risk of potential contamination.

APPLES TO ORANGES? TESTING WHETHER AN EQUATION USED TO ESTIMATE CONCENTRATIONS OF AQUATIC MICROORGANISMS CAN BE APPLIED TO MICROPLASTIC CONCENTRATIONS NEAR SHELLFISH BEDS

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A major challenge in marine microplastics (MP) research is the distribution and abundance of plastic particles in commercially important shellfish beds. Two recently published papers enumerated environmental MP in seawater by filtering water samples, counting a subset of MP on each filter, and extrapolating total MP abundance using an equation developed for the "epifluorescence enumeration of microorganisms". Microplastic particles and bacteria differ in density and morphology, leading to questions whether they can be similarly counted. To assess the validity of this approach, a laboratory study was conducted that reproduced the methodology using known concentrations of MP. Using 6 µm and 45 µm fluorescent polystyrene microspheres, two concentrations were evaluated: 30 particles L^{-1} and 1000 particles L^{-1}. Following the study methodology, comparisons were made between concentrations obtained from counting selected regions of interest (ROI) and applying the microorganism calculation, and full-filter counting. Several technical issues arose, including significant clumping of MP at the 1000 particles L^{-1} concentration, and long filtration time when using the suggested Anodisc™/nitrocellulose filter combination. Results demonstrated that MP concentrations calculated from ROI counts and microorganism calculation were several orders of magnitude lower than those on whole-filter. Although these studies attempt to estimate MP of smaller field size (~1–12 µm and ~1–43 µm, respectively), the method should apply to any MP size. Based on the current laboratory study, estimates of environmental MP concentrations obtained by counting ROI and extrapolating using the microorganism calculation are inconsistent and not recommended for further studies where MP concentration accuracy is a priority.

FIELD VALIDATION OF OYSTER LARVAL DISPERSAL PREDICTIONS IN HUDSON RIVER ESTUARY

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Sustainable restoration of oysters to provide ecosystem functions depends on re-establishing sufficient larval connectivity to make a self-sustaining metapopulation. This not only requires water quality and productivity that can promote larval survival, but we also need a way to prioritize restoration sites most conducive to a network of larval exchange. To inform the scaling-up of oyster restoration in Hudson River Estuary, two approaches for field-validating connectivity predictions from a biophysical model are discussed. The model simulates larval dispersal based on known reproductive phenology, larval behavior and their interaction with estuarine hydrodynamics. First, oyster recruitment mapping since 2018 provides relative spatial trends that can be compared to model outputs. Second, genomics were used to distinguish spat with wild versus aquaculture strain parents because the largest wild population is near Tarrytown, north of New York City, while restoration sites in the city are all seeded with aquaculture strains. The model predicts spatially distinct patterns of recruitment, such as a spat abundance gradient from high in the north to low near the city. Also, no localized self-recruitment is predicted for Hudson River Park (HRP) where a large restoration population now contains 2–3-year-old breeders. Instead, the model predicts ~70% of HRP offspring settle on the New Jersey shore near the Palisades. Field recruitment data and genomic population assignments from thousands of spat will be presented that can falsify or validate model predictions. Biophysical models have been used to inform restoration planning in other systems, but rarely has this degree of field validation been possible.

EFFECTS OF SIZE ON SEX RATIOS AND SEXUAL MATURITY OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, IN THE LOXAHATCHEE RIVER ESTUARY, FLORIDA

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The eastern oyster, *Crassostrea virginica*, is a protandric species and capable of both hermaphroditism and secondary sex reversal. Age, size, nutrient availability, and environmental cues can contribute to the timing and occurrence of sex changes. Many studies have demonstrated that younger, smaller oysters are more likely to be male and older, larger oysters are more likely to be female. Fewer studies have noted how the proportion of males and females changes with increasing size and their consistency over time. Although the size of maturation has been researched, the characteristics used to define maturity appear to be inconsistent in literature.

To assess the influence of size on sex ratios and sexual maturity, oysters were collected monthly from 2020 to 2025 in the Loxahatchee River Estuary in southeast Florida. Maturity and sex ratios were compared across size classes by examining samples for the presence of reproductive structures and mature gametes. Samples collected between March and December 2025 were supplemented with oysters less than 50 mm in shell length to identify and compare the size at maturation between males and females. Throughout this study, females were more prevalent than males with slight fluctuations in sex ratios among years. While the expected trend of smaller males and larger females was observed, both males and females occurred in most size classes. Males were found to mature at a slightly smaller size than females and at a smaller size than most literature suggests. This study proposes a set of consistent characteristics used to define maturity.

PCR ASSAY FOR IDENTIFICATION OF ATLANTIC SURFCLAM (*SPISULA SOLIDISSIMA*) SUBSPECIES AND HYBRIDS

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The Atlantic surfclam (*Spisula solidissima*) is a prominent member of benthic shelf communities along the Atlantic coast of the United States and Canada and supports a valuable commercial fishery. The species is divided into two subspecies: the larger, more offshore *S. s. solidissima* and the smaller, more coastal *S. s. similis*; the ranges of which partially overlap. Hybridization between the subspecies has been observed in the laboratory and the field. As surfclam habitat responds to a changing climate, tracking the spatial patterns of the subspecies and their hybrids will provide insight into the mechanisms underlying population response to environmental change.

To enable fast and reliable discrimination of Atlantic surfclam subspecies and hybrids, a set of PCR markers was developed. Oligonucleotide primers were designed from whole genome re-sequencing data to amplify subspecies-specific nuclear and mitochondrial DNA fragments of different lengths. As expected, most of the nine nuclear and three mitochondrial markers tested reliably amplified fragments of different lengths. Five nuclear and two mitochondrial markers were most robust and are recommended for diagnosis. The assays provided positive identification of *S. s. solidissima*, *S. s. similis,* and their hybrids, including the maternal lineage of the hybrids, and will serve as a useful tool supporting future ecological and breeding studies.

SEABIRD USE OF OFF-BOTTOM OYSTER AQUACULTURE GEAR

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Oyster farms on the U.S. Gulf coast primarily use off-bottom culture techniques including floating cages and long-line systems. Oysters from aquaculture are frequently sold to the premium half-shell market; however, off-bottom gear provides roosting surfaces for seabirds which have the potential to carry human pathogens, so bird-gear interactions raise concerns about contamination from bird feces. Despite regulations that require an operational plan that addresses bird management, there is limited research regarding efficacy of deterrents on oyster gear.

The goal of this project was to evaluate the effectiveness of a bird deterrent at an oyster farming park. During this six-week experiment, two parallel cage lines, each containing three floating cages equipped with plastic deterrent spikes, were deployed. A long-line system with three baskets was also included to compare bird interaction across gear types. Cameras were placed at each cage to record bird presence. After two weeks, the deterrents were removed from one line of the floating cages and photographic monitoring continued. After an additional two weeks, deterrents were reattached to the floating cages. Water, oyster, and bird fecal samples were collected every two weeks for bacterial community characterization.

The results of this study evaluate how physical deterrents influence seabird activity and what, if any, influence bird feces have on the bacteria associated with oyster aquaculture. Understanding birds' responses to deterrents can inform practical operational plans for farms in the Gulf region, and whether certain gear types, such as long-line systems, provide reduced contamination risk.

ASSESSMENT OF NATURAL OYSTER POPULATION HEALTH AND DYNAMICS TO INFORM RESTORATION AND AQUACULTURE PLANNING IN LONG ISLAND SOUND

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Oysters provide essential economic and ecosystem services to coastal communities including Long Island Sound. Both regionally and nationally, shellfish restoration continues to increase and expand natural beds, presenting an opportunity to increase oyster-related ecosystem services. Little is known about how expansion may affect the proliferation and transmission of oyster parasites between restored and cultured populations. To better understand the host-parasite interactions in a changing environment, monthly disease (*Perkinsus marinus* (Dermo), *Haplosporidium nelsoni* (MSX), *Haplosporidium costale* (SSO)) and reproduction assessments were conducted at two unmanaged, self-sustaining natural oyster beds in Connecticut over three years. Continuous water monitoring, combined with oyster biometrics, provided a quantitative understanding of the seasonal dynamics and helped to identify relevant water quality variables.

Preliminary analysis shows Dermo disease following historic trends. Body condition and gonad development were correlated with temperature. Adult mortality rates of 24-34% were observed during summer months when Dermo infection was high, but overall population densities remained stable because of high natural recruitment in the late summer and early fall. Water variables deviated from historical trends, with temperatures frequently exceeding 25°C and pH ranging from 7.0 to 7.7. Further disease analysis using qPCR and histology will improve the understanding of how changing environmental factors are affecting oyster population health. This comprehensive approach will fill critical information gaps and help to develop a hazard analysis to guide restoration planning that promotes the success of natural, restored, and cultivated oysters and supports healthy, resilient ecosystems and coastal communities.

EVALUATING MANAGEMENT OPTIONS FOR HIGH-DENSITY RECRUITMENT EVENTS IN THE ATLANTIC SEA SCALLOP FISHERY: A DECISION TREE APPROACH

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A major challenge in managing wild capture fisheries is their dependence on natural recruitment, which can be highly variable. The Atlantic sea scallop, *Placopecten magellanicus,* supports one of the most valuable fisheries in the USA, with annual ex-vessel values of USD $360–600 million since 2010. Fishery managers utilize annual surveys to document recruitment events and rotational area management to protect juveniles from fishing pressure. While effective, recent high-density recruitment events have prompted consideration of a broader set of management options. The authors propose developing decision trees to aid in the management of future high-density recruitment events. To guide decision tree development, the authors asked resource managers, industry advisors, and researchers to rank their concerns associated with managing high-density recruitment events, evaluate the feasibility of proposed management measures, and rank the importance of management information in their decision-making process. Participants expressed high levels of trust in the results of annual population surveys used to delineate the abundance and distribution of the resource but were concerned about elevated fishing mortality due to poor fishing practices in high-density areas. Participant perceptions of the proposed management measures informed the development of two decision trees: 1) evaluating management options for new recruitment events and 2) evaluating management options for rotational areas currently closed. The decision trees developed here provide a structured framework to evaluate management considerations with the aim of streamlining the management process for future high-density recruitment events in the sea scallop fishery.

ECOLOGICAL INTERACTIONS OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*) AQUACULTURE IN THE PACIFIC NORTHWEST

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Washington State is the national leader in bivalve aquaculture, harvesting an estimated $107 million (USD) of product yearly. Pacific oysters (*Crassostrea gigas*) represent the largest share of bivalve production, accounting for 38% by value and biomass. Oyster aquaculture provides numerous ecosystem services including water filtration, habitat creation, and nutrient sequestration. In nutrient rich systems, including some regions of Puget Sound, the removal of excess nutrients via bivalve harvest may improve ecosystem function.

The projected growth of shellfish aquaculture in Washington solicits further analysis of these impacts on a subregional scale. A pilot study was conducted for the development of an interactive calculator that will enable shellfish growers to quantify the nutrient removal potential resulting from harvest. Procedures were developed for collecting, processing, and recording data based on accepted methods and previous studies. Using a subset of the pilot data, the relationship between oyster tissue weight and drying time was defined in order to optimize efficiency in future large-scale sampling efforts. Existing datasets that included Pacific oyster morphometrics (e.g., shell length) and nitrogen concentrations were compiled; these data are necessary for developing the calculator. Preliminary analysis suggests that a larger sample size will be needed to relate oyster size to weight than to relate weight to nitrogen concentration, indicating that morphometrics are variable between individuals. Further research will examine if there is a significant correlation between farm location and nutrient concentration, with oysters from eutrophic regions sequestering larger quantities of nitrogen.

EFFECTS OF PHYTO-FEED LEVELS AND BORING SPONGE PRESENCE ON THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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The eastern oyster (*Crassostrea virginica*) is an important economic shellfish for southeast Georgia. Boring sponge (*Cliona celata*) bore into the calcium carbonate shell typically leading to reduced conditions, and in severe conditions, damaging the mantle cavity. This project assessed the relationship between boring sponge presence and food availability on the condition index, shell weight, growth of the eastern oyster. It was expected that greater food availability would mitigate the negative impacts of boring sponge on oysters. Oysters with and without boring sponge were placed in three treatments of phytofeed levels: 500 µL, 1000 µL, and 2000 µL from Reed Mariculture (Shellfish Diet 1800) per day representing different feeding levels. Initial shell length and buoyant weight were measured before oysters were put into treatments. Condition indices for oysters were calculated by dividing the dry tissue weight by the difference between the wet weight and the dry shell weight. The presence of the boring sponge significantly reduced oyster condition, although there was not a relationship between sponge biomass presence and oyster condition index. Results found no significant effect of food availability on the condition index of oysters with or without boring sponge. There was also no difference in boring sponge biomass among the different food treatments. Overall, research did not support that increased food availability allowed oysters to compensate for sponge presence.

OYSTER HEALTH AND RESTORATION IN LONG ISLAND SOUND: TRENDS IN DISEASE AND REPRODUCTION OF UNMANAGED OYSTER POPULATIONS

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Expanding existing natural beds presents a desirable opportunity to increase oyster-related ecosystem services; however, little is known about how expansion may affect the proliferation and transmission of oyster pathogens between restored and harvested populations. Development of risk-based guidance for mitigating bivalve diseases is essential to the successful restoration and cultivation of oysters throughout Long Island Sound and may translate to other coastal regions in the United States. The goal is to establish a standard methodology for incorporating disease burden in oyster population health assessments for future evaluation on restoration projects.

To this end, diagnostic methods were employed to assess the progression of Dermo (*Perkinsus marinus*), MSX (*Haplosporidium nelsoni*), and SSO (*Haplosporidium costale*) diseases, including the implementation and validation of a triplex qPCR assay, histopathology, and Ray's Fluid Thioglycollate Medium (RFTM). Additionally, histology is used to evaluate reproductive success, gonad development, and gamete ratios. Chosen study sites represent unique environments and population sizes with both intertidal and subtidal reefs, as well as established and newly restored beds being monitored. Preliminary results of monthly monitoring from three study sites will be presented.

RISK ASSESSMENT AND INFRASTRUCTURE INVENTORY OF U.S. SHELLFISH HATCHERIES

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Shellfish hatcheries are a critical yet understudied form of coastal infrastructure, characterized by diverse ownership structures and complex operational models. They underpin commercial aquaculture, stock enhancement, and restoration efforts across the United States, yet few studies have conducted national-scale assessments of hatchery inventory, operational capacity, and perceived risk. This study presents a novel, survey-based assessment of U.S. shellfish hatcheries designed to document species production, facility characteristics, infrastructure and technological capacity, workforce conditions, and exposure to operational vulnerabilities. The survey further captures hatchery perceptions of risk related to funding stability, workforce retention, infrastructure condition, regulatory change, environmental variability, and supply-chain reliability, as well as confidence in long-term operational stability and resilience capacity. Planned analyses include descriptive summaries to establish a national hatchery inventory and characterize regional patterns. Additional analyses employ structural equation modeling to evaluate hypothesized relationships among perceived risk, operational stability, and resilience capacity. By integrating a national infrastructure inventory with a risk-assessment framework, this work provides new insight into how hatchery characteristics and perceived vulnerabilities shape confidence in long-term operations and preparedness for disruption. Findings are intended to inform future research, extension efforts, and policy discussions aimed at strengthening shellfish hatchery infrastructure and resilience nationwide.

PROFILE OF WOMEN MANGROVE PLANTERS THROUGH THEIR KNOWLEDGE, ATTITUDES, AND PRACTICES ON COMMUNITY-BASED MANGROVE CONSERVATION APPROACHES IN PUJADA BAY, CITY OF MATI, DAVAO ORIENTAL, PHILIPPINES

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This study assessed the knowledge, attitudes, and practices (KAP) of women mangrove planters in six barangays of Pujada Bay, examining demographic influences on their conservation efforts. Employing a mixed-methods design, it integrated quantitative surveys of planters - stakeholders, including barangay officials, women's association leaders, NGO representatives, Department of Environmental and Natural Resources (DENR) personnel, youth, fishermen, and gleaners. Quantitative results showed very high knowledge levels on mangrove ecology, economic value (e.g., coastal protection, habitat, flood control), and threats like population growth and land-use changes. Respondents strongly endorsed protective measures such as anti-dumping laws, polluter accountability, and clean-ups, rejecting misconceptions about mangroves as building materials or food sources. Attitudes were overwhelmingly positive towards environmental functions and legal safeguards. Practices were robust, encompassing waste management, restoration participation, policy consultation, expert advice-seeking, and cost willingness. Analyses linked knowledge to age, attitudes to age and livelihood dependency, and practices to experience, age, ethnicity, and education. Qualitative data underscored collaborative stewardship via partnerships among barangays, women's associations, DENR-City/Community Environment and Natural Resources Office (CENRO), NGO like Mama Earth Foundation, and community groups. Barangays enforced laws and monitored sites; women led projects, education, and outreach; DENR provided guidance; and NGO/youth delivered training and advocacy. Despite resource limits and youth retention challenges, these efforts planted hundreds of thousands of seedlings and integrated mangrove-coral rehabilitation. Findings emphasize community empowerment, inclusive governance, and capacity-building for sustainable conservation, cultivating resilient stewardship, ecosystem health, and coastal community viability in Pujada Bay.

DOES TIDAL ELEVATION INFLUENCE INTERACTIONS BETWEEN THE NATIVE OYSTER, *OSTREA LURIDA*, AND THE NON-NATIVE, *CRASSOSTREA GIGAS*?

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Olympia oysters, *Ostrea lurida*, were once prominent ecosystem engineers along the west coast of the United States before being overfished and replaced by the nonnative Pacific oyster, *Crassostrea gigas*. Remnant *O. lurida* populations now coexist with feral *C. gigas*, yet little research has studied how they interact where their tidal ranges overlap. Existing research has hinted at competition but *O. lurida* settle on *C. gigas* shells at tidal elevations above their typical distribution limit, suggesting *C. gigas* may facilitate a tidal range expansion. To confirm the nature of their relationship, *O lurida* and *C. gigas* were placed on concrete tiles in both mono and mixed cultures of varying densities. These tiles were then set at a low (+0 m MLLW) and high (+0.6 m MLLW) tidal elevation, along their shared tidal range. Over a one-year period, growth and survival will be measured monthly, with plans to assess body condition measured at the end. At low tidal elevation, *O. lurida* is expected to see low survival and growth when *C. gigas* is present relative to on its own. At high elevation, *O. lurida* is expected to see higher survival and growth when *C. gigas* is present relative to on its own as *C. gigas* shells may provide shade and relief from desiccation. Temperature loggers are placed at both elevations to confirm whether *C. gigas* provides temperature relief. With *O. lurida* restoration becoming more prominent in recent years, understanding this relationship could help inform management strategies for both species.

AN AFFORDABLE AND EFFICIENT MARKER PANEL TO ADVANCE SOUTHERN QUAHOG (= HARD CLAM) (*MERCENARIA CAMPECHIENSIS*) AQUACULTURE

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The southern quahod (= hard clam), *Mercenaria campechiensis*, is the native *Mercenaria* species found along the Florida Gulf Coast, however, the northern quahog (= hard clam) (*M. mercenaria*) was introduced to the region in the mid-to-late 20th century, resulting in hybridization. Recently, several *M. campechiensis* restoration projects have been funded, providing a novel economic opportunity for hatcheries and growers. Currently, there are no reliable methods to distinguish the two species or hybrids, resulting in a near total lack of verified broodstock. Preliminary work indicated that clams identified as *M. campechiensis* based on morphological features were often hybrids. An affordable, rapid genetic method for verifying broodstock integrity is being developed. Wild *M. campechiensis* samples were collected from sites across the Gulf Coast of Florida. Genomic DNA is being isolated from these clams for genotyping-by-sequencing. These data will be used to assess the population structure of *M. campechiensis* in Florida and establish a genetic baseline for single nucleotide polymorphism (SNP) marker development. A common SNP dataset will be identified by co-analyzing the *M campechiensis* SNP with those previously identified for *M. mercenaria*. A low-density SNP panel will be developed to allow discrimination between the two species and identification of hybrids. This panel will be made commercially available to the aquaculture industry so that *M campechiensis* broodstock can be genotyped rapidly and confidently at an affordable cost to verify genetic integrity.

STUDY OF THE NEUROTOXIC EFFECTS OF CADMIUM ON THE INNERVATION OF GILL LATERAL CELL CILIA OF THE BIVALVE, *CRASSOSTREA VIRGINICA*

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Cadmium can interfere with dopamine synthesis and receptor function causing motor impairments. It also can alter serotonin reuptake, and decrease serotonin levels in midbrain and frontal cortex, as well as affect GABA receptor function. The eastern oyster, *Crassostrea virginica,* has a serotonergic and dopaminergic innervation of its gill, controlling beating rates of gill lateral cell cilia (GLCC). Serotonin excites GLCC and dopamine inhibits GLCC. Glutamate neurons were found present in the ganglia as excitatory interneurons innervating serotonin neurons. It was hypothesized that acute and short-term cadmium treatment of *C. virginica* will have a damaging effect on the serotonergic and dopaminergic gill innervation. Acute experiments were conducted applying cadmium to gill and mantle rim sensory tentacles and accessed GLCC beating. Short-term, 5-day experiments were also conducted incubating animals with 500µM of cadmium and accessed serotonin application to visceral ganglia on GLCC. Beating rates of GLC cilia were measured by stroboscopic microscopy.

Acute cadmium application to gill and sensory tentacles had no effect on the GLCC beating; however, short-term cadmium treatment significantly decreased the ability of serotonin application to visceral ganglia to increase GLCC beating. The dose response of serotonin (10^{-5} – 10^{-3}M) increased beating rates from 2 to 8.2 beats/sec, compared to controls 16 to 24 beats/sec. The study thus far shows the neurotoxic effects of cadmium on the serotonergic system of the marine bivalve *C. virginica*, and demonstrates that *C. virginica* is a useful model to study neurophysiology of potentially toxic chemicals in the environment.

IMPROVEMENT OF THE PRODUCTION OF PACIFIC WHITE SHRIMP, *PENAEUS VANNAMEI*, IN SEMI-INTENSIVE CULTURE THROUGH THE SUPPLEMENTATION OF PROBIOTIC BACTERIA TO REDUCE THE MORTALITY RATE IN THE PALMERAS AQUACULTURE COMPANY IN THE TUMBES REGION, PERU

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This study evaluated the effect of the commercial probiotic BIOPRO 4000 (composed of three strains of bacteria of the genus *Bacillus* spp.) on the production of Pacific white shrimp, *Penaeus vannamei,* in semi-intensive culture. To this purpose, four ponds (control, 1, 2, and 3, respectively) belonging to the company Exportadora Acuícola Palmeras S.R.L. were used to reduce the mortality rate of shrimp. The experimental design consisted of supplying different doses of probiotic in the experimental ponds (5 kg/ha in pond 1, 9 kg/ha in pond 2, and 13 kg/ha in pond 3), except for the control pond without probiotic addition. The following parameters were evaluated: survival, organism health indicators, and microbiological quality of the culture water. Survival at the end of the *P. vannamei* culture cycle was 43.5% in the control pond, 46.3% in pond 1, 50.0% in pond 2, and 58.3% in pond 3, with the latter showing a higher survival rate and a 14.8% reduction in mortality rate compared to the control pond. The results suggest that the application of this commercial probiotic has a positive influence on *P. vannamei* production, improving water quality, reducing microalgae species harmful to cultivation such as cyanobacteria and dinoflagellates, and increasing beneficial algae species of Bacillariophyceae, such as: *Cymbella* spp., *Diploneis* spp., *Nitzschia* spp., and *Gyrosigma* spp.

THE THIOREDOXIN GLUTATHIONE REDUCTASE (TGR) GENE FROM THE WHITE SHRIMP, *PENAEUS VANNAMEI*

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Glutathione plays a major role in cellular homeostasis. In terrestrial invertebrates, the enzyme thioredoxin glutathione reductase (TGR) reduces oxidized glutathione. Despite numerous studies on GSH-associated enzymes in crustacea, little is known about the possible epigenetic regulation of their expression. This study aimed to characterize the TGR gene in the shrimp, *Penaeus vannamei,* and an *in silico* evaluation of its promoter region. The coding sequences of TGR were amplified from hepatopancreas cDNA by PCR, cloned in pGEM-T Easy and sequenced. The conserved domains and motifs were identified using the NCBI CD database and Expasy Protparam. Phylogenetic evaluation was done with MEGA-12, and protein modelling *in silico* was done with AlphaFold3. In the promoter region of the gene, putative transcription factor (TF) recognition sites were identified using JASPAR and PROMO, and CpG islands with MethPrimer. The CDS of TGR is 1989 bp with 596 amino acids. The conserved motifs for selenocysteine extension, GSH and FAD/NADPH binding pockets are present, classifying this enzyme as a TGR. The promoter region of TGR in *P. vannamei* has three possible CpG islands and conserved recognition sites for the TFs Nrf2 and Ahr. This could indicate a likely methylation target for epigenetic expression regulation. The identification and characterization of the TGR is key to future studies on the effects of stress on the response of GHS-associated enzymes in *P. vannamei,* and for a better understanding of its regulation via epigenetics.

THE RESPONSE OF THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) TO ELEVATED TEMPERATURE AND SALINITY

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Eastern oysters (*Crassostrea virginica*) are ecologically and economically vital foundation species, yet they face mounting stress from climate change, which drives shifts in water temperature and salinity. Understanding the physiological and molecular pathways underlying oyster stress responses is essential for predicting resilience and informing restoration and aquaculture strategies. This study explored the question: How do elevated salinity levels and temperatures influence oyster respiration, and are these effects reflected in the expression of genes associated with stress responses? Oysters were placed under experimental treatments with different salinity and temperature combinations over five days. Dual stressor experimental data revealed that neither elevated salinity nor temperature significantly affected oyster respiration, even when the stressors acted in combination; however, it was noted that peak physiological response in the form of elevated respiration rate occurred on day 3 of the five-day experiment. Gill tissue samples were taken from all experimental oysters, and RNA was extracted and preserved. Quantitative PCR was conducted to quantify the relative expression of HSP70, BAX, and HIF1α, genes that serve as established biomarkers of osmotic and thermal stress in marine invertebrates. By integrating organismal physiology with molecular stress responses, this study provides a better understanding of oyster resilience thresholds, which informs both ecological knowledge and aquaculture management.

STUDY OF THE NEUROTOXIC EFFECTS OF LEAD ON THE INNERVATION OF GILL LATERAL CELL CILIA OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

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Lead exposure is associated with neurotoxic actions. Lead interferes with dopamine synthesis and receptor function, leading to motor impairment. It also alters serotonin reuptake and decreases serotonin levels. The eastern oyster, *Crassostrea virginica,* has a serotonergic and dopaminergic gill innervation, controlling beating of gill lateral cell cilia (GLCC). Serotonin causes cilio-excitation and dopamine cilio-inhibition of GLCC. Glutamate neurons are present in the ganglia as excitatory interneurons innervating serotonin neurons. The neurotoxic effects of lead on the serotonin systems of *C. virginica* was studied. It was hypothesized that acute and short-term lead treatment would damage serotonergic gill innervation. Acute experiments were conducted applying 500µM of lead to gill and mantle rim sensory tentacles and accessed GLCC beating. Short-term, 5-day experiments were also conducted incubating animals with 500µM lead and accessed actions of serotonin and glutamate to visceral ganglia on GLCC.

Acute lead application to gill or sensory tentacles had no effect on GLCC beating; however, short-term lead treatments significantly decreased ability of serotonin and glutamate application to visceral ganglia to increase beating rates of GLCC. Dose response of serotonin (10^{-5} – 10^{-3}M) increased beating from 2.2 to 8.4 beats/sec, compared to 16 to 24 beats/sec of the control. Short-term lead treatment completely blocked glutamate (10^{-5} – 10^{-3}M) application to increase GLCC beating rates. The study shows the neurotoxic effects of lead on the serotonergic system of the marine bivalve *C. virginica* and demonstrates that *C. virginica* is a useful model to study neurophysiology of potentially toxic chemicals in the environment.

NEAREST-NEIGHBOR DISTANCE, CLUMPING, AND FERTILIZATION SUCCESS IN ATLANTIC SEA SCALLOPS FROM GEORGES BANK

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Atlantic sea scallops, *Placopecten magellanicus*, are broadcast spawners whose reproductive success depends on the interaction between population density, nearest-neighbor distance, and spawning synchrony. While large-scale declines in scallop density are often assumed to reduce fertilization success, fine-scale spatial structure may mitigate these effects. Field observations from Georges Bank indicate that scallops frequently occur in small, dense clumps, resulting in reduced nearest-neighbor distances even when overall population density is low. This study examines how fine-scale clumping influences fertilization success under controlled conditions designed to replicate densities characteristic of scallop aggregations with a focus on Habitat Area of Particular Concern within Closed Area II on Georges Bank.

Experimental trials will quantify fertilization success across a range of nearest-neighbor distances reflecting observed clump structure. In addition, the relationship between shell height and egg production will be evaluated to verify size-based fecundity estimates, and gonad volume will be measured to refine estimates of total gamete output. Together, these metrics will be used to improve understanding of reproductive potential at biologically relevant spatial scales.

By isolating the effects of nearest-neighbor distance while maintaining realistic aggregation patterns, this work aims to bridge the gap between classical fertilization models and field observations. Results are expected to improve predictions of reproductive output in managed scallop populations and contribute to a more mechanistic understanding of how fine-scale spatial structure supports population resilience.

EVALUATING GENE EXPRESSION DIFFERENCES BETWEEN FEMALE AND MALE EASTERN OYSTER TISSUES

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The eastern oyster aquaculture industry is increasingly reliant on seed produced in hatcheries. Protocols that improve hatchery production and reduce costs are essential. Because broodstock conditioning is expensive and sexual monomorphism necessitates caring for extra broodstock to achieve required sex ratios, a tool for predicting sex early in the gonadal maturation process would be beneficial. Global gene expression patterns were evaluated to identify genetic markers that differentiate female and male oysters. A total of 7,675 differentially expressed transcripts were detected (3,936 and 3,739 up-regulated in males and females, respectively) and include those associated with sex in other invertebrate and vertebrate species such as Dmrt1, SOX-30, bindin, dpy-30, and histone H4 in males and foxl2, vitellogenin, and Bystin in females. GO terms associated with transcripts up-regulated in male gonad include protein modification, reproductive process, and cell projection organization, while RNA metabolic process and amino acid metabolic process were associated with transcripts up-regulated in females. Because gonad tissues are difficult to sample non-destructively, gene expression patterns in mantle tissues collected from the same oysters were also compared. Far fewer transcripts were differentially expressed in this tissue; however, 41% of transcripts identified as differentially expressed between male and female mantle tissues were also differentially expressed between male and female gonads. This study represents the first characterization of differences between male and female eastern oyster transcriptomes and the results hold promise for the development of a non-destructive sex identification assay that can be applied to hatchery broodstock during the conditioning process.

TARGETED ISOLATION OF *VIBRIO FLUVIALIS* AND *V. MIMICUS* FROM OYSTERS AND SEDIMENT

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Although food safety efforts have focused on reducing *Vibrio parahaemolyticus* and *V. vulnificus* illnesses, other species are increasingly recognized as causes of foodborne vibriosis, especially associated with consumption of raw bivalve molluscan shellfish. The top emerging causes of vibriosis include *V. fluvialis, V. cholerae* (non-O1/non-O139), and *V. mimicus,* which are naturally occurring in estuarine waters where shellfish are grown. To better understand their prevalence, distribution, and environmental drivers, appropriate methods are needed to detect, isolate, and identify these species from shellfish, water, and sediment. This study aimed to isolate *V. fluvialis* and *V. mimicus* from oysters and sediment. Oyster homogenate or sediment was enriched overnight in Alkaline Peptone Water (APW) at 35° or 41° C, then streaked to chromogenic agars. Typical colonies were purified and characterized by streaking on chromogenic agars and TCBS to determine phenotypic profiles. Isolates with typical *V. fluvialis* and *V. mimicus* profiles were analyzed with newly developed real-time PCR assays. Select PCR-positive isolates were confirmed by whole genome sequencing (WGS). Of the 32 *V. fluvialis*-typical colonies, 20 were PCR-positive. Four isolates were sequenced, and all were confirmed as *V. fluvialis.* Of the 39 *V. mimicus*-typical isolates, 28 were PCR-positive. Ten PCR-positive and 11 PCR-negative isolates were sequenced, with 100% agreement between PCR and WGS. The results demonstrate the utility of this approach for isolating and identifying *V. fluvialis* and *V. mimicus*. Future work will evaluate the real-time PCR assays for screening enrichments to aid in detection of emerging *Vibrio* spp.

TARGETED RNAi AGAINST WSV249 PROVIDES COMPLETE PROTECTION FROM WHITE SPOT SYNDROME VIRUS IN THE SHRIMP, *PENAEUS VANNAMEI*

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White spot syndrome virus (WSSV) remains one of the most dangerous pathogens affecting global shrimp aquaculture; however, several viral genes have been associated with pathogenesis; the functional roles of many genes remain unclear. This study investigated the in vivo role of WSV249, a putative E3-ubiquitin-ligase gene, during infection in *Penaeus vannamei* using targeted RNA interference (RNAi). Shrimp were injected with dsRNA-WSV249, dsRNA-EGFP, or PBS before WSSV challenge, and survival, viral load, viral gene expression, and transcriptomic responses were examined.

Silencing of WSV249 was performed from the infection challenge test, whereas both control groups exhibited 100% mortality by days 4 - 5. Viral load accumulation was markedly reduced in the WSV249 RNAi group, accompanied by suppressed expression of viral genes, including WSV249, VP28, and thymidylate kinase. Transcriptomic analysis indicated that WSSV infection led to significant disruption of host pathways related to cytoskeletal stability, immune signaling, metabolic activities, and stress responses. In contrast, WSV249-silenced shrimp displayed significantly fewer differentially expressed genes, indicating reduced transcriptional disruption. KEGG enrichment analysis further demonstrated restoration of structural, immune, and metabolic pathways, suggesting that WSV249 is a key factor in host transcriptome instability during infection.

These findings identify WSV249 as a critical virulence factor and demonstrate that RNAi targeting this gene stabilizes host cellular networks and prevents mortality. This work highlights a potential molecular interference for improving shrimp resistance against WSSV and contributes to advancing disease management strategies in aquaculture.

BLUE MUSSELS: A MODEL FOR AQUACULTURE GENETICS INSTRUCTION IN UNDERGRADUATE LABORATORY COURSES

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As coastal waters warm in New England, blue mussels are facing increased mortality from thermal stress negatively impacting the mussel culture industry in the state of Maine and raising strong interest in developing more thermotolerant stocks of mussels. This poster will illustrate how the blue mussel, *Mytilus edulis*, has been used as a model organism in undergraduate lab courses at the University of Maine exploring potential physiological genetic responses to environmental stressors including temperature stress. Mussels were collected from a single population in Eastport, Maine and acclimated to 16°C. A subset was then subjected to a three-day sub-lethal temperature shock while the remaining mussels were kept at 16°C throughout the experiment (control). Survival was monitored in both groups during a two-week recovery period. Subsequently, an impedance pneumography approach was used to track the change in heart rate during exposure to a separate, acute (~2 hr) temperature shock for both control mussels and those that survived the three-day heat shock treatment. The Arrhenius Break Temperature (ABT) and Q_{10} temperature coefficient was calculated for individual mussels from the resulting heart rate data. Estimates of Q_{10} indicates the sensitivity of cardiac activity to a rapid temperature increase while ABT provides a measure of the cardiac capacity of an individual to respond to stress. Students used these metrics to test the hypothesis that exposure to an extreme but sublethal temperature selected for mussels that were more tolerant of temperature stress.

ASSESSING THE EFFECTS OF HARMFUL ALGAL BLOOMS AND ASSOCIATED TOXINS ON THE EARLY LIFE STAGES OF GREEN-LIPPED MUSSELS IN NEW ZEALAND

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Harmful algal blooms (HAB) in New Zealand present significant ecological and economic challenges, particularly to the early life stages of the native and economically important, green-lipped mussel (*Perna canaliculus*). Spermiotoxicity and embryo-larval development assays for this bivalve species were done to assess the impacts of exposure to key HAB species and biotoxins commonly found in New Zealand waters.

Passive samplers, which adsorb commonly occurring HAB toxins, were deployed multiple times over two years, in the Marlborough Sounds - a major *P. canaliculus* aquaculture region experiencing massively reduced spat fall and unexplained summer mortalities of mussels. Samplers were extracted into methanol and the attained natural biotoxin 'cocktail' extracts were tested using the spermiotoxicity assay. Acute spermiotoxicity corresponded with peak biotoxin levels in 2022. Subsequent investigation of the involvement of pectenotoxins (PTX) and okadaic acid (OA), identified to be abundant during screening of the biotoxin cocktails, did not induce similar levels of toxicity in subsequent spermiotoxicity assays, suggesting that toxicity was likely caused by a combination of toxins and/or by unknown or uncharacterised toxins.

Further, environmentally relevant HAB exposures were carried out, exposing sperm and developing embryos of *P. canaliculus* to *Alexandrium* spp., a paralytic shellfish toxin producing dinoflagellate, which blooms annually in the Marlborough Sounds. Developmental disruptions and spermiotoxicity were recorded at environmentally relevant concentrations, with variation observed between algal species. These findings show that HAB and associated toxins can impact green-lipped mussels and underscore the need to consider sublethal and early life-stage effects of HAB in environmental and commercial risk assessments.

IMPACT OF WATER QUALITY AND GEAR TYPE ON EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) GROWTH IN NARRAGANSETT BAY, RHODE ISLAND

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Oyster aquaculture is expanding in Rhode Island, yet key farming regions in the lower West Passage of Narragansett Bay lack the *in-situ*, high-temporal resolution monitoring needed to evaluate emerging stressors and support production. Less is known about the impacts of emerging gear types on oyster physiology. This project established a 1.5-year continuous water quality time series and paired these observations with physiological assessments of eastern oysters (*Crassostrea virginica*) grown in three cultivation methods (e.g., gear types). Multiparameter sondes were installed at a 4-acre oyster farm, positioned one meter below the surface and one meter above the sediment, to measure temperature, salinity, dissolved oxygen, and pH. Discrete bottle samples were used to validate the sondes and calculate carbonate saturation state (Ω) and an ocean acidification exposure metric that quantifies the magnitude and duration of undersaturated conditions ($\Omega < 1$). Early life-stage oysters (13-19 mm) were deployed in traditional surface, traditional bottom, and a recently-developed alternative surface gear. Oyster survival, shell morphometrics, and scope for growth (SFG) were evaluated to characterize growth and metabolic performance across gear types from June to December 2025. Results provide physiological and biological context for oyster production among three cultivation methods in different water conditions. Ultimately, this research will support the growing aquaculture industry of Rhode Island by optimizing cultivation strategies to meet the growing demand for sustainable seafood.

EPIGENETIC AND METABOLIC REGULATION OF THE GAPDH GENE IN THE SHRIMP, *PENAEUS VANNAMEI*, UNDER HYPOXIC AND REOXYGENATION STRESS

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Hypoxia and reoxygenation are environmental stressors for the whiteleg shrimp *Penaeus vannamei*. Under these conditions, shrimp activate biochemical and possibly epigenetic pathways associated with genes encoding essential enzymes such as glyceraldehyde-3-phosphate dehydrogenase (GAPDH). This study quantified epigenetic and metabolic changes in the gills of P. *vannamei* during hypoxia and reoxygenation. Samples were collected at 6 h, 12 h, and 24 h, and alterations in GAPDH enzymatic activity and gene expression were evaluated. Bioinformatic analyses were also performed on the promoter and flanking regions of the GAPDH gene in the P. *vannamei* genome. Three ~1000 bp fragments were PCR-amplified and sequenced to identify CpG islands susceptible to methylation. A bioassay exposed shrimp to hypoxia followed by reoxygenation. In gill tissue, global DNA methylation was quantified by ELISA, and changes in GAPDH gene expression were assessed by RT-qPCR. GAPDH activity and levels of glucose, lactate, and thiobarbituric acid reactive substances (TBARS) were evaluated spectrophotometrically. Consensus binding sequences for HIF-1α, p53, TBP, and five CpG islands were identified in the promoter. Global DNA methylation increased after 12 h of hypoxia and 24 h of reoxygenation. GAPDH transcript levels rose at 6 h and 12 h in both conditions. GAPDH activity exhibited condition-dependent variation. Glucose concentrations under hypoxia and reoxygenation differed from normoxia at 6, 12, and 24 h, whereas lactate levels decreased under both stressors and TBARS increased at 6 and 12 h. These findings indicate that hypoxia and reoxygenation induce epigenetic remodeling in gills of *P. vannamei*, accompanied by changes in GAPDH regulation and metabolic status, reflecting the impact of oxygen limitation at the biochemical level.

MANAGEMENT COLLABORATION LEADS TO DETECTION OF EUROPEAN GREEN CRABS IN AND NEAR PORT GAMBLE BAY, WASHINGTON

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The European green crab (EGC), *Carcinus maenas*, is an invasive species that poses a threat to the ecological, economic, and cultural resources of the Port Gamble S'Klallam Tribe (PGST). Originally native to Europe, the EGC has proliferated throughout coastal USA habitats, and was first detected in Washington waters in 1998. This high-risk invader can impact coastal marine ecosystems by displacing native species, degrading and disturbing native habitats, and altering food webs. In areas where EGC have established resident populations for extended periods, they may negatively impact other species, particularly smaller crabs and bivalves. For this reason, detecting and minimizing EGC in new areas while their numbers are still low is a crucial step in effective invasive species management. Over the past 7 years of collaborative trapping efforts with Washington Department of Fish and Wildlife and Washington Sea Grant, the PGST has set hundreds of traps in at least four areas identified as potential EGC habitat. Traps are baited and fished for 1-3 days and all data, including bycatch, were recorded using Survey123 and QuickCapture. No EGC were detected in any location from 2018-2024, however in 2025, 131 EGC were detected in Port Gamble Bay (404 trap sets), and two EGC were detected in Races Cove (233 trap sets). Going forward, the PGST is working to increase and optimize trapping capacity through continued partner collaboration.

FLOW IMAGING MICROSCOPY FOR SHELLFISH RESEARCH AND MONITORING

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Counting, measuring, and evaluating larval development via microscopy are routine tasks in shellfish research and husbandry. Routine microscopy tasks also include counting algae, identifying culture contaminants, and - in some cases - monitoring for harmful algae in environmental samples. Whether focused on algae and/or larvae, these routine microscopy tasks are essential but can demand hours of time on a daily or weekly basis. To help save time, some research programs and hatchery operations have incorporated technology like flow imaging microscopy (FIM) into their workflow; however, standardization of protocols is a critical step on that path towards successful implementation. To that end, this poster summarizes recent progress towards the standardization of FIM for key applications in shellfish research and monitoring. Key focus areas include sample preparation and handling, image acquisition, and particle analysis.

MORPHOLOGICAL DIFFERENCES IN LOWER DELAWARE RIVER FRESHWATER MUSSEL GLOCHIDIA AND IMPLICATIONS OF HOST-FISH SPECIFICITY

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Freshwater mussels (Unionidae) are among the most imperiled faunal groups in North America, and their complex life cycle, which includes an obligate parasitic larval stage (glochidia) that generally depends on specific fish hosts, makes accurate species identification essential for effective conservation. In the Delaware River watershed, more than a dozen native mussel species occur, many of which are rare, threatened, or endangered. Although accurate identification is essential, shell morphology is often ambiguous, and sacrificing live specimens for internal examination is neither ethical nor permissible.

Many mussel species exhibit species-specific variation in glochidia size and shape. For example, species that infest gill tissues typically produce smaller, rounded glochidia, whereas species that attach to fins or scales often have larger larvae equipped with well-developed hooks. Recognizing these subtle morphological differences allows accurate identification of glochidia recovered from wild-caught fishes. This in turn yields critical insight into natural host-fish interactions, clarifying which fish species function as ecological hosts *in situ* versus those identified as physiological hosts solely through laboratory trials.

Accurate understanding of host-fish specificity is central to mussel conservation and restoration in the lower Delaware River Basin. Knowing which species are required to complete successful metamorphosis (e.g., alewife, *Alosa pseudoharengus,* for alewife floater, *Utterbackiana implicata*) informs state and federal regulators and underscores the importance of maintaining fish passage and habitat connectivity. Without this knowledge, conservation measures are less effective, placing at risk the recovery of these ecologically critical organisms that filter millions of gallons of water from the river daily.

PLANT GROWTH-PROMOTING BACTERIA AND THEIR PERSPECTIVES FOR CONSERVATION AND RESTORATION OF COASTAL AQUATIC ECOSYSTEMS AND SHELLFISH RESOURCES

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Aquatic ecosystems, such as peatlands and mangroves, provide essential ecosystem services at global level, including carbon sequestration, biodiversity conservation, and nutrient cycling. Despite their ecological and socio-economic importance, these aquatic ecosystems are increasingly threatened by multiple environmental stressors, such as pesticide pollution, eutrophication, habitat degradation, and climate adverse events (e.g., intense precipitation, prolonged droughts, hot waves, frosts). These stressors also compromise their associated native vegetation which is essential for the long-term ecosystem stability. Currently, the relevance of microbiomes is widely recognized for growth and fitness of plants, particularly those named as plant growth-promoting bacteria (PGPB), which have emerged as key contributors to growth and stress tolerance of crops in agriculture. The PGPB has also being considered as an attractive tool for environmental conservation and restoration. PGPB improves plant performance through diverse direct and indirect mechanisms, including improved nutrient acquisition, modulation of phytohormone balance, stimulation of antioxidant defenses, and protection against emerging pathogens. Similarly, it has highlighted the functional diversity of PGPB and their capacity to alleviate abiotic stress (e.g., salinity, herbicides, and heavy metals) through the production of stress-related metabolites, activation of plant defense pathways, and detoxification of toxic compounds. As result, PGPB-based inoculants are commonly commercialized and applied as a nature-based solution for the restoration and management of stressed ecosystems. In this sense, the beneficial plant-microbe interactions and PGPB also represent a promising and attractive strategy to protect mangroves ecosystems against environmental stressors derived from shellfish aquaculture activity.

PHYSIOLOGICAL EFFECTS OF WATER TEMPERATURE ON RECOVERY AFTER LOW TIDE EXPOSURE IN PACIFIC BLUE MUSSELS (*MYTILUS TROSSULUS*)

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The rocky intertidal in the Gulf of Alaska is a highly dynamic and stressful habitat for marine taxa inhabiting it, often living at the edge of their physiological tolerances. Changes to environmental conditions can therefore have detrimental physiological impacts on these organisms. Specifically, marine heatwaves and climate warming are a growing concern. As such, there is a need to understand how anomalously warm waters affect recovery from the already stressful low tides in ecologically important intertidal taxa. Pacific blue mussels (*Mytilus trossulus*) are an ideal organism for this study, given their sedentary nature, ecological importance, and adaptations to intertidal life. An aquarium experiment was conducted to assess the effect of +3°C warmer than ambient water temperature, mimicking heatwave conditions, on the recovery after low tide exposure. Low tides were simulated for six hours every day at 24°C air temperature for both ambient and warm water treatments. Mussels were measured three hours after submersion for metabolic rate, energy content, and differential transcription of heat-shock proteins. Initial findings show mussels in the warm treatment had significantly higher metabolic rates than in ambient, indicating +3°C seawater warming can substantially increase mussel metabolism. The thermal sensitivity (Q10) across experimental time varied from 2.17 to 4.87 with increasing temperature as a result of air exposure. Findings from this study will help understand organismal response to warming waters from marine heatwaves or climate warming and have broader implications on energy flow and coastal food web structure.

eDNA METABARCODING-BASED ASSESSMENT OF RIVER ECOSYSTEM HEALTH AND PATHOGEN SCREENING IN MALAYSIA

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Freshwater rivers are essential for domestic use, agriculture and aquaculture, and early biological monitoring helps maintain environmental and public safety. This study assessed the ecological condition of the Perak River in Malaysia using environmental DNA (eDNA) metabarcoding. Water samples were analyzed through 16S and 18S rRNA sequencing to characterize microbial and microeukaryote communities.

A total of 4,045 bacterial OTU and 3,422 eukaryotic OTU were detected, indicating substantial taxonomic diversity within the river system. Several taxa showed unusually high relative abundance, including *Serratia marcescens* and *Strombidium*. These dominant groups provide useful biological signals that may reflect nutrient enrichment, organic load or other environmental pressures within the river. In addition, 35 potential pathogenic organisms were identified, including bacteria, fungi and parasites. Most were opportunistic and no major virulent pathogens were detected, indicating no immediate biological hazards under current conditions; however, their presence still warrants periodic monitoring to prevent potential exposure risks.

This work represents the first application of eDNA metabarcoding for environmental health assessment in Malaysia. The method enables community profiling and pathogen detection using a unified sequencing workflow and can be incorporated into baseline surveillance programs. The approach provides a practical foundation for developing systematic monitoring frameworks by environmental agencies, supporting long-term water management and One Health-oriented decision-making, particularly in shellfish from freshwater ecosystems.

EVALUATING SUBMERSION DURATION AND COOLING PRACTICES TO REDUCE *VIBRIO* RISK IN OYSTERS FROM COASTAL GEORGIA

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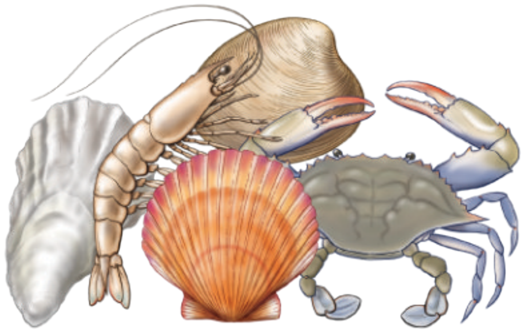
Pathogenic *Vibrio* species pose a persistent food-safety concern in oyster aquaculture. In Georgia, oysters can only be harvested after 14 days of submersion; however, growers are interested in whether shorter submersion durations could be implemented safely. Post-harvest cooling practices are permitted as mitigation strategies within two hours of harvest. This study evaluated the combined effects of submersion duration and post-harvest cooling method on *Vibrio* abundance in oysters. Therefore, two submersion durations – 10-day and 14-day, and three cooling methods – direct cooling (ice), indirect cooling (refrigeration) and no cooling – were compared.

Oysters were sampled monthly from July through September of 2025; for each time point, fifteen oysters per treatment were collected and characterized using a multiplex qPCR assay targeting *V. cholerae*, *V. parahaemolyticus*, and *V. vulnificus*. Across 270 oysters, overall detection was low (11%), and positive samples amplified at late cycle threshold values near the limit of detection. Statistical analyses based on presence/absence data indicated that oysters that were not chilled after harvest consistently exhibited the highest *Vibrio* detection, whereas direct cooling resulted in the fewest detections across months. Longer submersion tended to increase the presence of *Vibrio* in comparison to the 10-day treatment, which suggests that prolonged warm-water exposure may elevate the risk. Results indicate that direct cooling is the most effective post-harvest handling practice and a shorter submersion period may offer a safer alternative to the 14-day schedule. Ongoing analyses will incorporate quantitative estimates of bacterial load and statistical modeling to refine these preliminary results.



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