NATIONAL SHELLFISHERIES ASSOCIATION

Program and Abstracts of the 110th Annual Meeting

March 18 – 22, 2018

Seattle, Washington

Sea Grant Washington

Sea Grant California

Sea Grant Oregon

Fundación para la Conservación de Biodiversidad

FUCOBI

Sheridan

A CJK Group Company

NATIONAL OCEANIC AND ATMOSPHERIC ADMINISTRATION

NOAA

U.S. DEPARTMENT OF COMMERCE

Sweet Oysters

BAYWATER

REED MARICULTURE

USA

PCSGA

PACIFIC COAST SHELLFISH GROWERS ASSOCIATION

Bigelow | National Center for Marine Algae and Microbiota

NSA 110th ANNUAL MEETING
National Shellfisheries Association
Renaissance Hotel, SEATTLE, WASHINGTON
March 18 – March 22, 2018

SUNDAY, MARCH 18, 2018

6:30 PM	**STUDENT ORIENTATION (Foyer outside Courtyard Ballroom)**
7:00 PM	**PRESIDENT'S RECEPTION Courtyard Ballroom**

MONDAY, MARCH 19, 2018

6:30-8:00 AM	**STUDENT BREAKFAST (students only) South**
8:00-8:50 AM	**PLENARY LECTURE: Suzanne Williams (Natural History Museum, London) Courtyard Ballroom**

	Federal	Superior	Municipal	James	North
9:00-10:30 AM	OLYMPIA OYSTERS	GENETICS, GENOMICS, AND BREEDING	SHELLFISH LEASING AND PERMITTING WORKSHOP: CASE STUDIES FOR OVERCOMING COMMON LEGAL BARRIERS	THE SHRIMP EPIGENOME (ShrimpENCODE) PROJECT	SCALLOPS
10:30-11:00AM	MORNING BREAK				
11:00-12:30PM	OLYMPIA OYSTERS	GENETICS, GENOMICS, AND BREEDING	COLLABORATIVE RESEARCH AND ENGAGING FISHERMEN	THE SHRIMP EPIGENOME (ShrimpENCODE) PROJECT	SCALLOPS
12:30-1:30 PM	LUNCH BREAK				
1:30-2:15 PM	OLYMPIA OYSTERS	GENETICS, GENOMICS, AND BREEDING	COLLABORATIVE RESEARCH AND ENGAGING FISHERMEN	THE SHRIMP EPIGENOME (ShrimpENCODE) PROJECT	SCALLOPS
2:15-3:00 PM	OLYMPIA OYSTERS	GENETICS, GENOMICS, AND BREEDING	COLLABORATIVE RESEARCH AND ENGAGING FISHERMEN	THE SHRIMP EPIGENOME (ShrimpENCODE) PROJECT	GENERAL CONTRIBUTED I
3:00-3:30 PM	AFTERNOON BREAK				
3:30-6:00 PM	OLYMPIA OYSTERS	GENETICS, GENOMICS, AND BREEDING	COLLABORATIVE RESEARCH AND ENGAGING FISHERMEN	THE SHRIMP EPIGENOME (ShrimpENCODE) PROJECT	GENERAL CONTRIBUTED I

TUESDAY, MARCH 20, 2018

8:00-8:50 AM	**PLENARY LECTURE: Peter Beninger (Universite de Nantes) Courtyard Ballroom**				
	Federal	**Superior**	**Municipal**	**James**	**North**
9:00-10:30 AM	**SCIENCE, ART, AND COMMUNICATION**	***VIBRIO***	**HARMFUL ALGAL BLOOMS**	**GENOMICS: AN INTRODUCTORY PRIMER WORKSHOP**	**GENERAL CONTRIBUTED II**
10:30-11:00AM	**MORNING BREAK**				
11:00-12:30PM	**SEAGRASS-BIVALVE INTERACTIONS**	***VIBRIO***	**HARMFUL ALGAL BLOOMS**	**COMPARATIVE GENOMICS: A HANDS-ON WORKSHOP ON THE EASTERN OYSTER GENOME**	**GENERAL CONTRIBUTED II**
12:30-1:30 PM	**LUNCH BREAK**				
1:30-3:15 PM	**SEAGRASS-BIVALVE INTERACTIONS**	***VIBRIO***	**CLAMS**	**PREPARATION OF SHELLFISH FOR DISEASE DIAGNOSTICS WORKSHOP**	**NORTHWEST INDIAN TRIBES SHELLFISH MANAGEMENT AND FISHERIES**
3:15-4:30 PM	**SEAGRASS-BIVALVE INTERACTIONS**	***VIBRIO***	**PHYTOPLANKTON CULTURE: A TRIBUTE TO RRL GUILLARD**	**PREPARATION OF SHELLFISH FOR DISEASE DIAGNOSTICS WORKSHOP**	**NORTHWEST INDIAN TRIBES SHELLFISH MANAGEMENT AND FISHERIES**
4:00-6:00 PM	**POSTER SESSION AND HAPPY HOUR Madison Ballroom**				
7:00PM -???	**STUDENT ENDOWMENT FUND AUCTION Courtyard Ballroom**				

WEDNESDAY, MARCH 21, 2018

8:00-8:50 AM	**PLENARY LECTURE: Donal Manahan (University of Southern California) Courtyard Ballroom**				
	North	**West**	**James**	**South**	**East**
9:00-10:30 AM	**GREEN CRABS**	**UNDERGRADUATE RESEARCH COLLOQUIUM**	**CONTAMINANTS OF EMERGING CONCERN**	**OYSTERS: EAST MEETS SOUTH MEETS WEST**	**GENERAL CONTRIBUTED III**
10:30-11:00AM	**MORNING BREAK**				
11:00-11:45PM	**GREEN CRABS**	**RIBBED MUSSELS**	**CONTAMINANTS OF EMERGING CONCERN**	**OYSTERS: EAST MEETS SOUTH MEETS WEST**	**GENERAL CONTRIBUTED III**
11:45-12:30PM	**GREEN CRABS**	**RIBBED MUSSELS**	**SHELLS AND MATERIALS**	**OYSTERS: EAST MEETS SOUTH MEETS WEST**	**GENERAL CONTRIBUTED III**
12:30-2:00 PM	**NSA BUSINESS LUNCHEON Courtyard Ballroom**				
2:00-4:30 PM	**SCALLOP GALLOP EXPLORE SEATTLE!!**				
4:30-6:00 PM	**POSTER SESSION AND HAPPY HOUR Madison Ballroom**				
6:30 PM-???	**KEN CHEW CHINESE DINNER (Tickets MUST be purchased by 5 PM on Monday)**				

THURSDAY, MARCH 22, 2018

8:00-8:50 AM	**PLENARY LECTURE: Gary Wikfors (NOAA/NMFS, Northeast Fisheries Science Center) Courtyard Ballroom**				
	Federal	**Superior**	**Municipal**	**North**	**West**
9:00-10:15 AM	**GEODUCKS**	**OsHV-1**	**SHELLFISH AND CLIMATE CHANGE**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP**
10:15-10:45AM	**MORNING BREAK**				
10:45-12:00PM	**GEODUCKS**	**OsHV-1**	**SHELLFISH AND CLIMATE CHANGE**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP**
12:00-1:00 PM	**LUNCH BREAK**				
1:00- 3:30PM	**DOWN ON THE FARM**	**OsHV-1**	**SHELLFISH AND CLIMATE CHANGE**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP**
3:30-6:30PM	**CLOSING HAPPY HOUR Madison Ballroom**				

All BREAKS are in the MADISON BALLROOM with the POSTERS.

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

PLEASE REMOVE YOUR POSTERS BY NOON ON THURSDAY

MONDAY March 19, 2018					
6:30-8:00AM	STUDENT BREAKFAST (STUDENTS ONLY) South				
8:00-8:50AM	PLENARY: Suzanne Williams -*Colourful shells: the evolution of colour in mollusca* Courtyard Ballroom				
ROOM	**Federal**	**Superior**	**Municipal**	**James**	**North**
SESSION TITLE	**OLYMPIA OYSTERS** **Kay McGraw & Betsy Peabody**	**GENETICS, GENOMICS, AND BREEDING** **Louis Plough**	**SHELLFISH LEASING & PERMITTING WORKSHOP: CASE STUDIES FOR OVERCOMING COMMON LEGAL BARRIERS** **Lisa Schiavinato**	**THE SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia Alcivar-Warren**	**SCALLOPS** **Steve Geiger**
9:00AM	OLYMPIA OYSTERS – PAST, PRESENT, AND FUTURE **McGraw & Peabody**	IMPACTS OF OCEAN ACIDIFICATION ON THE SETTLEMENT OF *CRASSOSTREA GIGAS* **Burton*, Meyer, Durland, Langond**	LEGAL REQUIREMENTS FOR THE USE OF WATERFRONT INFRASTRUCTURE BY SHELLFISH GROWERS IN RHODE ISLAND: CHALLENGES FOR INDUSTRY SUSTAINABILITY **Porter**	SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT SESSION **Alcivar-Warren**	DEVELOPMENT OF AQUACULTURE PRODUCTION TECHNIQUES FOR PURPLE-HINGE ROCK SCALLOPS **Davis**
9:15AM	COAST-WIDE OLYMPIA OYSTER NETWORK: RESILIENT NATIVE OYSTERS FROM BRITISH COLUMBIA, CANADA TO BAJA CALIFORNIA, MEXICO **Wasson, Zacherl, Zabin**	STAGE-SPECIFIC EFFECTS OF ELEVATED SEAWATER pCO_2 ON THE GENETIC COMPOSITION OF LARVAL PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) **Durland, Meyer, De Wit, Langdon**	SHELLFISH LEASING AND PERMITTING: CASE STUDIES FOR OVERCOMING COMMON LEGAL BARRIERS **Andrews**	SHRIMPENCODE (2017-2027): TOWARDS UNDERSTANDING THE EPIGENETIC MECHANISMS AND TRANSGENERATIONAL INHERITANCE ASSOCIATED WITH EXPOSURE OF SPF SHRIMP, *PENAEUS (LITOPENAEUS) VANNAMEI*, TO ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) CAUSING *VIBRIO* SPP. AND MICROBIAL TRANSGENE INSECTICIDE, *BACILLUS THURINGIENSIS* **Alcivar-Warren, ShrimpENCODE collaborators**	GROWTH, MORTALITY, AND YIELD OF FARMED SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) IN MAINE USING THE EAR-HANGING METHOD, AND INFLUENCES OF SUBSTRATE AND DEPTH ON YIELD OF SCALLOP SPAT COLLECTORS **Morse, Britsch, Perry, Cowperthwaite**
9:30AM	UNDERSTANDING TOP-DOWN, BOTTOM-UP, AND SUPPLY SIDE INFLUENCES ON OLYMPIA OYSTER POPULATIONS FOR MORE SUCCESSFUL RESTORATION **Grosholz, Kimbro, White**	GENOME SEQUENCING AND POPULATION GENOMIC ANALYSES PROVIDE INSIGHTS INTO THERMAL ADAPTATION OF PACIFIC ABALONE **You, Huang, Luo, Ke**	NAVIGATING THE COMPLEXITY OF AQUACULTURE PERMITTING: UNDERSTANDING HOW THE PIECES FIT TOGETHER THROUGH TWO CASE STUDIES **Nichols & Janasie**	EPIGENETIC RE-PROGRAMMING UPON FOREIGN (VIRAL) DNA INVASION INTO CELLS **Doerfler**	VARIABLE SPATIAL AND TEMPORAL OCEAN CONDITIONS IMPACT PHYSIOLOGICAL PERFORMANCE OF BIVALVES IN PUGET SOUND, WASHINGTON, USA **Alma*, Fiamengo, Alin, Jackson, Padilla-Gamino**
9:45AM	TEMPORAL AND SPATIAL VARIABILITY IN OYSTER PERFORMANCE IN RESTORATION PROJECTS IN SAN FRANCISCO BAY, USA **Zabin, Ayala, Kiriakopolos, Latta, Grosholz**	DEVELOPING RESILIENCE TO OCEAN ACIDIFICATION IN RED ABALONE AQUACULTURE **Swezey, Boles, Aquilino, Stott, Bush, Hill, Gaylord, Catton, Rogers-Bennett, Whitehead, Sanford**	AQUACULTURE OFF THE CALIFORNIA COAST: BREAKING POLICY BARRIERS AND NEW GROUND AT THE STATE AND FEDERAL LEVELS **Schiavinato**		BAY SCALLOP LARVAL SWIMMING BEHAVIOR IN RESPONSE TO TEMPERATURE, SALINITY, AND LIGHT **Lynch* & Caracappa**
10:00AM	HOW LOW CAN THEY GO? DISTRIBUTIONS OF THE OLYMPIA OYSTER (*OSTREA LURIDA*) AND THE PACIFIC OYSTER (*CRASSOSTREA GIGAS*) AS A FUNCTION OF TIDAL ELEVATIONS AND IMPLICATIONS FOR RESTORATION **Zacherl, Torres, Jr., Parker, Henderson, Tronske**	USING NEXT GENERATION SEQUENCING TO IDENTIFY POTENTIAL LOCAL ADAPTATION TO SALINITY IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, ALONG THE LOUISIANA GULF COAST **Riley*, Kelly, La Peyre, La Peyre**	**Discussion**		RECREATIONAL HARVEST OF BAY SCALLOPS IN FLORIDA **Geiger, Granneman, Scharf**
10:15AM	OLYMPIA OYSTER RECRUITMENT DYNAMICS FROM SOUTHERN CALIFORNIA TO BRITISH COLUMBIA **Wasson, Hughes, Berriman, Chang, Deck, Dinnel, Endris, Espinoza, Dudas, Ferner, Grosholz, Kimbro, Ruesink, Trimble, Vander Schaaf, Zabin, Zacherl**	MOLECULAR ADAPTATIONS OF BIVALVE MOLLUSCS REVEALED BY GENOMIC ANALYSES **Guo**			A PRELIMINARY ASSESSMENT OF THE ECONOMIC IMPACT ASSOCIATED WITH THE RECREATIONAL SCALLOP SEASON IN HERNANDO COUNTRY, FLORIDA **Scharf, Adams, Geiger**
10:30-11:00AM	MORNING BREAK				
SESSION TITLE	**OLYMPIA OYSTERS** **Kay McGraw & Betsy Peabody**	**GENETICS, GENOMICS, AND BREEDING** **Louis Plough**	**EXTENSION AND OUTREACH INITIATIVES TO GROW SHELLFISH AND AQUACULTURE ACTIVITIES** **Tessa Getchis & Julie Decker**	**THE SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia Alcivar-Warren**	**SCALLOPS** **Steve Geiger**
11:00 AM	RECRUITMENT PATTERNS OF OLYMPIA OYSTER, *OSTREA LURIDA* (CARPENTER 1864), IN THE GORGE WATERWAY – ENHANCEMENT FROM NEW BRIDGE PILINGS **Pearse*, Kravac, Schroeder, Wright, Carolsfeld, Page**	MONITORING THE GENETIC DIVERSITY OF HATCHERY-PRODUCED COHORTS AND SUPPLEMENTED REEFS OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Hornick* & Plough**	NOAA AQUACULTURE – OPENING RUMARKS **Rubino**	UNDERSTANDING THE MOLECULAR BASIS OF SUSCEPTIBILITY OF PATHOGENESIS OF THE WHITE SPOT SYNDROME VIRUS (WSSV) USING COMPARATIVE TRANSCRIPTOMICS IN THE PACIFIC WHITELEG SHRIMP (*PENAEUS VANNAMEI*) AND EUROPEAN SHORE CRAB (*CARCINUS MAENAS*) **Millard*, Verbruggen, Bickley, Bateman, Stentiford, Tyler, van Aerle, Santos**	THE RAMIFICATIONS OF MISMATCHING SPATIAL ROTATIONAL MANAGEMENT WITH LIFE HISTORY AND POPULATION TRAITS: AN EXAMPLE IN THE SEA SCALLOP FISHERY **Stokesbury, Keiley, Georgianna, Bethoney, Inglis**
11:15 AM	INDEX SITE SURVEYS FOR OLYMPIA OYSTERS (*OSTREA LURIDA*) IN BRITISH COLUMBIA - 2009 TO 2017 **Norgard, Bigg, MacConnachie, Finney, Gillespie**	TESTING FITNESS CONSEQUENCES OF DOMESTICATION SELECTION AT THE LARVAL STAGE IN EASTERN OYSTERS **McFarland, Plough, Nguyen, Hare**	ALASKAN MARICULTURE INITIATIVE – TANGIBLE INDICATIONS OF PROGRESS AS A RESULT OF A THREE-YEAR COMPREHENSIVE PLANNING PROCESS **Decker & Cullenberg**		CHAIN REACTION? DEVELOPMENT AND TESTING OF A MODIFIED SEA SCALLOP DREDGE TO REDUCE FLATFISH BYCATCH **Nichols, Pol, Chosid, Gribbin**
11:30 AM	FACTORS THAT AFFECT THE VERTICAL DISTRIBUTION OF OLYMPIA OYSTER LARVAE IN FIDALGO BAY WASHINGTON, USA **McIntyre*, McPhee-Shaw, Hatch, Arellano**	A GENOMIC TEST FOR HYBRIDIZATION BETWEEN SELECTIVELY BRED EASTERN OYSTER AQUACULTURE STRAINS AND WILD NEW YORK POPULATIONS **Hare & Kutsumi**	IMPLEMENTING PHASE II OF THE WASHINGTON SHELLFISH INITIATIVE **Butler & Hoberecht**	WHITE SPOT SYNDROME VIRUS (WSSV)-LIKE ELEMENT, *DNA1-1_LIE*, IN ORIGINAL SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *LITOPENAEUS VANNAMEI*, DOMESTICATED IN THE UNITED STATES **Bao, Alcivar-Warren*, Bogden, Tao, Iyer, Mikhaylenko, Wittendorp, Mraz, Hart, Hatas, Kujawa, Wilson, Voss**	DISCARD MORTALITY OF SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) FOLLOWING CAPTURE AND HANDLING IN THE SEA SCALLOP DREDGE FISHERY **Rudders, Roman*, Knotek, Sulikowski, Mandleman, Benoit**
11:45 AM	RECOGNIZING HOW LNC VARIATIONS EXPOSE OLYMPIA OYSTER POPULATIONS TO THERMAL RISK **Adams**	EVERYTHING FROM SHELLS: GENETICS OF SHELL SHAPE AND COLOR IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Whiteside* & Guo**	THE GULF OF MEXICO SHELLFISH INITIATIVE: A REGIONAL APPROACH **Walton, Swann, Walton**		THE MISSING LINK: TRANSMISSION OF APICOMPLEXAN INFECTION IN GRAY MEAT ATLANTIC SEA SCALLOPS **Inglis, Koop, Kristmundsson, Freeman, Georgianna**
12:00 NOON	IDENTIFYING REGULATORY BARRIERS TO NATIVE OYSTER RESTORATION IN WASHINGTON, USA **Edelman***	COMPARISON OF GENETIC VARIATION AND INBREEDING AMONG THREE LINES OF HATCHERY-REARED *CRASSOSTREA VIRGINICA* BROODSTOCK **Varney & Wilbur**	AN UPDATE ON THE STATUS OF OYSTER AQUACULTURE (*CRASSOSTREA VIRGINICA*) IN GEORGIA **Bliss, Guadagnoli, Andrews, Risse**	POLYMORPHISMS IN *RTE-3_LE1* NON-LTR RETROTRANSPOSON OF SPF *PENAEUS VANNAMEI* FROM THE UNITED STATES: ITS ASSOCIATION WITH THE *PENAEUS MONODON* ENDOGENOUS VIRUS IHHNV (INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS) FROM AFRICA AND AUSTRALIA **Espinoza*, Alcivar-Warren, Primavera, De La Pena, Tang, Zuniga, Xu**	DEVELOPMENT OF DIAGNOSTIC PCR ASSAY TO DETECT APICOMPLEXAN PARASITE IN ATLANTIC SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) WITH GRAY MEAT DISEASE **Mastrostefano*, Scro, Jackson, Smolowitz**
12:15 PM	OLYMPIA OYSTER PRODUCTION AND RESEARCH AT THE KENNETH K. CHEW CENTER FOR SHELLFISH RESEARCH AND RESTORATION **Ryan, Crim, Allen, Peabody**	UNCOVERING THE GENETIC BASES OF GROWTH HETEROSIS IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS* **Yin* & Hedgecock**	LIVELIHOOD DIVERSIFICATION AND IMPLICATIONS IN EXTENSION PLANNING **Michaelis*, Webster, Shaffer**		INVESTIGATION OF THE SCALLOP NEMATODE, *SYLCASCARIS SQUAMATE*: DISTRIBUTION, SEASONALITY, SHEDDING, TRANSMISSION, THERMAL TOLERANCE, AND HOST IMPACT **Rudders, Roman, Fisher, Bushek, Munroe, Bochenek, McGurk**
12:30-1:30 PM	LUNCH BREAK				

* denotes student presenter P denotes non first-author presenter

MONDAY
March 19, 2018

ROOM	Federal	Superior	Municipal	James	North
SESSION TITLE	**OLYMPIA OYSTERS** **Kay McGraw & Betsy Peabody**	**GENETICS, GENOMICS, AND BREEDING** **Louis Plough**	**EXTENSION AND OUTREACH INITIATIVES TO GROW SHELLFISH AND AQUACULTURE ACTIVITIES** **Tessa Getchis & Julie Decker**	**THE SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia Alcivar-Warren**	**SCALLOPS** **Steve Geiger**
1:30 PM	GENETIC CHARACTERIZATION OF WILD AND HATCHERY-PRODUCED *OSTREA LURIDA* IN PUGET SOUND, WASHINGTON, USA **Spencer*, Vadopalas, Simchick, Crim, Goetz, Roberts**	FAMILY-BASED GENETIC PARAMETERS FOR TETRAPLOID *CRASSOSTREA VIRGINICA* AND BREEDING IMPLICATIONS **Allen, Jr., Small, Kube**	SHELLFISH AQUACULTURE IN THE COASTAL INLAND BAYS OF DELAWARE 2010: STATUS AND OUTLOOK **Ewart**	THE PIRAR TOXIN-PRODUCING GENES OF *VIBRIO* SPP. HAVE A FUNCTION SIMILAR TO THE *BACILLUS THURINGIENSIS* CRY PROTEINS **Gómez-Gil, Soto-Rodríguez**	ISOLATION AND CHARACTERIZATION OF *FRANCISELLA BOLOTOVOI* FROM ABSCESS LESIONS IN THE ADDUCTOR MUSCLE OF YESSO SCALLOP, *PATINOPECTEN YESSOENSIS* **Kawahara*, Kazamori, Yoshinaga, Itoh**
1:45 PM	POPULATION GENOMICS AND PHYLOGEOGRAPHY OF THE OLYMPIA OYSTER **Silliman* & Eernisse**	OBSERVATIONS ON TETRAPLOID EASTERN OYSTERS, *CRASSOSTREA VIRGINICA*, AND IMPLICATIONS IN GENETIC IMPROVEMENT OF TRIPLOIDS **Guo**	FACILITATING BETTER DECISION-MAKING IN SHELLFISHING RIGHT FOR YOUT **Clemetson, Ciaramella, Rivara**		UPDATE ON TWO ENZOOTIC DISEASES (*PERKINSUS JOHNSONI* AND *FRANCISELLA BOLOTOVOI*) AFFECTING THE HEALTH OF CULTURED YESSO SCALLOPS (*PATINOPECTEN YESSOENSIS*) IN BRITISH COLUMBIA, CANADA **Meyer, Itoh, Lowe, Kim**
2:00 PM	POTENTIAL TRANSGENERATIONAL EFFECTS OF OCEAN ACIDIFICATION ON THE OLYMPIA OYSTER, *OSTREA LURIDA*: A THREE-PHASE EXPERIMENTAL STUDY **Wippel, Friedman, Cresson, Roberts, Strenge, George, Carrington, White**	MOLECULAR EVOLUTION OF I84 PROTEASE INHIBITOR FAMILY IN CHINESE RAZOR CLAMS AND PHYLUM MOLLUSCA **Wang, Xue, Mao, Dong, Li, Lin**	LISTENING, LEARNING, AND LEADING TO SUPPORT RESPONSIBLE AQUACULTURE DEVELOPMENT IN CONNECTICUT **Getchis, De Guise, Balcom, Concepcion**		GROWTH RATE MEASUREMENTS IN SCALLOPS: REVISITING MORRIS AFTER 50 YEARS ON THE LIBRARY SHELF **Long*, Mann, Rudders, Roman, Chute, Cronin, Walker**
SESSION TITLE	**OLYMPIA OYSTERS** **Kay McGraw & Betsy Peabody**	**GENETICS, GENOMICS, AND BREEDING** **Louis Plough**	**EXTENSION AND OUTREACH INITIATIVES TO GROW SHELLFISH AND AQUACULTURE ACTIVITIES** **Tessa Getchis & Julie Decker**	**THE SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia Alcivar-Warren**	**GENERAL CONTRIBUTED I** **Paul Rawson & Sharon Lynch**
2:15 PM	VARIATION IN RESPONSE TO OCEAN ACIDIFICATION AMONG OLYMPIA OYSTER FROM CALIFORNIA, OREGON, AND BRITISH COLUMBIA **Silliman*, Bennett, Roberts**	TRANSCRIPTOMIC RESPONSES TO DERMO DISEASE IN SUSCEPTIBLE AND RESISTANT EASTERN OYSTERS **Proestou, Lundgren, Small, Allen, Jr.**	INTERACTIVE TALK: BUILDING A SHELLFISH HEALTH DATABASE TO FACILITATE SHELLFISH TRANSFERS **Bushek, Calvo, Marsen, Carnegie, Rheault, Gustafson**	TRANSPOSASE DDE DOMAINS AND N-6 DNA METHYLASE FAMILY PROTEINS AS POTENTIAL EPIGENETIC MARKS OF PATHOGENIC *VIBRIO* SPP. FROM ASIA (CHINA, VIETNAM, THAILAND) AND LATIN AMERICA (MEXICO, ECUADOR) THAT CAUSE ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) IN SHRIMP **Alcivar-Warren, Gómez-Gil, Soto-Rodríguez, Xu, Espinoza[P]**	BACTERIAL COMMUNITY DYNAMICS IN AN OYSTER HATCHERY IN RESPONSE TO PROBIOTIC TREATMENT **Stevick*, Soha, Modak, Nelson, Rowley, Smolowitz, Post, Gómez-Chiarri**
2:30 PM	QUANTIFYING PARAMETERS OF ECOLOGICAL CHANGE BEFORE AND AFTER OLYMPIA OYSTER RESTORATION **Barber, Grossman, Cordell, McArdle, Hunter, Greiner**	DIFFERENTIAL EXPRESSION OF APOPTOSIS PATHWAY GENE FAMILIES IN RESPONSE TO IMMUNE CHALLENGE IN *CRASSOSTREA GIGAS* AND *CRASSOSTREA VIRGINICA* **Roberts* & Gomez-Chiarri**	INTERACTIVE TALK: DEVELOPING A SHELLFISH HATCHERY BIOSECURITY CERTIFICATION PROGRAM **Rheault, Bushek, Calvo, Carnegie, Hudson, Gustafson**	THE CORE AND ACCESSORY GENOME OF *VIBRIO PARAHAEMOLYTICUS*, A PATHOGEN OF PENAEID SHRIMP **Penir*, Saloma**	MOLECULAR AND MORPHOLOGICAL ANALYSIS OF BIVALVE SHELL BORERS OF THE GENUS *POLYDORA* FROM THE EASTERN UNITED STATES **Rawson, Rice, Lindsay**
2:45 PM	SPATIALLY EXPLICIT ESTIMATES OF OLYMPIA OYSTER (*OSTREA LURIDA*) FILTRATION SERVICES: A MODEL-BASED APPROACH FOR AUGMENTING ECOSYSTEM SERVICES AND REDUCING RISK FOR HURING RESTORATION **Gray, zu Ermgassen, Gair, Langdon, Lemagie, Levezzik**	UNIQUE AND COMMON PATTERNS IN THE STRESS RESPONSE OF THE PACIFIC OYSTER, *CRASSOSTREA GIGAS* **Eirin-Lopez & Suarez-Ulloa**	MASSACHUSETTS SHELLFISH INITIATIVE **Kirk**		EXPERIMENTAL INFECTION TO ASSESS PATHOGENICITY OF *PERKINSUS BEURMANDI* AGAINST DOMESTIC BIVALVE SPECIES IN JAPAN **Kamatsu, Yoshinaga, Itoh[P]**
3:00 – 3:30 PM	**AFTERNOON BREAK**				
SESSION TITLE	**OLYMPIA OYSTERS** **Kay McGraw & Betsy Peabody**	**GENETICS, GENOMICS, AND BREEDING** **Louis Plough**	**EXTENSION AND OUTREACH INITIATIVES TO GROW SHELLFISH AND AQUACULTURE ACTIVITIES** **Tessa Getchis & Julie Decker**	**THE SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT** **Acacia Alcivar-Warren**	**SCALLOPS** **Steve Geiger**
3:30 PM	TRACE ELEMENTAL FINGERPRINTS: AN ECOLOGICAL DETECTIVE'S TOOL TO TRACE OLYMPIA OYSTERS (*OSTREA LURIDA*) **Hintz*, Becker, Carson, Rusk, Hatch, Allen, Vadopalas, Roberts**	IMMUNOLOGICAL RESPONSE OF *CRASSOSTREA GIGAS* LARVAE TO PROBIOTIC *BACILLUS PUMILUS* RI06-95 **Modak*, Nelson, Rowley, Gomez-Chiarri**	FROM PILOT EFFORT TO A REGIONAL MONITORING PROGRAM: THE COAST-WIDE VENTLESS LOBSTER TRAP SURVEY **Glenn & Pugh**	DEFINING THE MICROBIOME OF THE PACIFIC WHITELEG SHRIMP (*LITOPENAEUS VANNAMEI*) IN WILD, AQUACULTURED, AND AHPND EMS OUTBREAK CONDITIONS **Cornejo-Granado*, Lopez-Zavala, Gallardo-Becerra, Mendoza-Vargas, Sánchez, Vichido, Brieba, Viana, Sotelo-Mundo, Ochoa-Leyva**	*PLOIOMYSIDIUM* IN MOLLUSCS FROM WESTERN AUSTRALIA **Dang, Jenkins, Miller, Snow, Caraguel, Go, Bogema**
3:45 PM	CONSERVATION PALEOBIOLOGY AS A TOOL TO SUPPORT OLYMPIA OYSTER RESTORATION **Martinelli & Padilla-Gamiño**	TRENDS IN OYSTER-ASSOCIATED MICROBIAL TRANSCRIPTOMES **Stevick*, Post, Gómez-Chiarri**	SUPPORTING MANAGEMENT OF THE EMERGING JONAH CRAB FISHERY AND THE IONIC LOBSTER FISHERY IN THE NORTHEAST USA: A COLLABORATIVE FISHING VESSEL RESEARCH FLEET APPROACH **Ellertson, Mercer, Spencer, Glenn**		UNDER THE RADAR! EMERGING *HAPLOSPORIDIUM* SPP. IN WILD COMMON COCKLE, *CERASTOIDERMA EDULE*, AND MUSSELS, *MYTILUS* SPP., AT PACIFIC OYSTER, *CRASSOSTREA GIGAS*, CULTURE SITES **Lynch, Rivero, Kelly, Quinn, Coughlan, Culloty**
4:00 PM		GENETIC MAPS AND ASSEMBLY OF THE PACIFIC OYSTER GENOME **Hedgecock, Yin, Kitapci, Perez**	MENTAL MODELING AND PARTICIPATORY SCIENCE TO INVESTIGATE PRIBILOF ISLAND BLUE KING CRAB **McDonald, Reum, Holsman, Lang, Armstrong, Armstrong, Scellacek**		REPORT ON THE UNKNOWN HAPLOSPORIDIAN PARASITE FROM THE GRAY MUSSEL, *CHAMAEMELIS GRAPHITUS*, FROM GANGNEUNG ON THE EAST SEA OF KOREA **Cho*, Lee, Choi, Kang, Kim**
4:15 PM		THE EASTERN OYSTER GENOME: A RESOURCE FOR COMPARATIVE GENOMICS IN SHELLFISH AQUACULTURE SPECIES **Gómez-Chiarri, Warren, Miux, Tomlinson, Guo, Proestou**	ENGAGING FISHERMEN TO ADDRESS DATA GAPS AND EVOLVE MANAGEMENT OF THE QUAHOG (*MERCENARIA MERCENARIA*) IN NARRAGANSETT BAY **Mercer, Leavitt, McManus, Heimann**	EVALUATION OF MARINE BACTERIA AND THEIR POTENTIAL USE AS FEED ADDITIVE AS PROBIOTIC AGENT AGAINST PATHOGENIC *VIBRIO PARAHAEMOLYTICUS* (AHPND) IN WHITE SHRIMP, *LITOPENAEUS VANNAMEI* **Sánchez-Díaz*, Ocampo-Ayala, Herrera-Pazüio, Molina-Garza, Cruz-Suárez, Gómez-Gil, Silva, Ibarra-Gámez**	HIGH MORTALITY, RETARDED REPRODUCTION, AND POOR GROWTH OF THE MANILA CLAM, *RUDITAPES PHILIPPINARUM*, CAUSED BY HIGH LEVELS OF THE PARAMYXEAN PARASITE, *MARTEILIA GRANULA*, INFECTION OBSERVED ON THE SOUTH COAST OF KOREA **Lee*, Kang, Cho, Hong, Lee, Choi**
4:30 PM		DEVELOPING AN EFFECTIVE TRANSFECTION PROTOCOL FOR GENE EDITING IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS* **Wang* & Guo**	COLLABORATING FOR OYSTER SUSTAINABILITY: COMMUNICATIONS ASSESSMENT AND NETWORK ANALYSIS OF RESTORATION STAKEHOLDERS ON THE GULF COAST **Brown* & Jacobson**		DO PARASITES OF THE GENUS *MYOXOZOIDES* PRESENT A RISK FOR THE PRODUCTION OF SHELLFISH IN EUROPE? **Arzul, Lupo, Engelsma, Garcia**
4:45 PM		EXPRESSED EQUIMOLECAPTURE SEQUENCING (EECSEQ): A METHOD FOR COST-EFFECTIVE EXOME SEQUENCING NONMODEL ORGANISMS **Puritz & Lotterhos**		DIGITAL PATHOGEN SURVEILLANCE: A ONE HEALTH APPROACH TO PREVENTING INFECTIOUS DISEASES IN HUMANS AND ANIMALS **Gardy**	INSIGHTS INTO MORTALITIES AFFECTING SILVER-LIPPED PEARL OYSTER *PINCTADA MAXIMA* IN THE KIMBERLEY SINCE 2006 **Dang, Snow, Miller, Irving**
5:00 PM	**FOCUS GROUP DISCUSSION: BUILDING A COAST-WIDE OLYMPIA OYSTER NETWORK FROM BAJA CALIFORNIA TO BRITISH COLUMBIA**	DIFFERENCES IN MEIOTIC INSTABILITY BETWEEN CHEMICAL AND MATED TETRAPLOID LINES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Sousa & Allen, Jr.**			PUBLIC HEALTH AND PERSONAL LIVELIHOODS: A CASE STUDY OF OYSTERS AND NORVIRUS IN HAMMERSLEY INLET, PUGET SOUND **Nixon**
5:15 PM					CARDIAC RESPONSES TO BIOGENIC AMINES IN SELECTED MOLLUSCAN SPECIES **Guilbeaux* & Deaton**
5:30 PM			**Discussion**		ISOLATION AND TESTING OF PROBIOTICS AS A POTENTIAL TOOL FOR THE MANAGEMENT OF EPIDOTIC SHELL DISEASE IN THE AMERICAN LOBSTER, *HOMARUS AMERICANUS* **Hoffman*, Castro, Underwood, Ranson, Hatzipetro, Somers, Rowley, Nelson, Gomez-Chiarri**
5:45 PM					SHELLFISH INDUSTRY IN EU: AN EXERCISE OF STAKEHOLDERS MAPPING **Arzul, Prou, Delangle, Venier, Cheslett, Furones, Moreira, Ventura, Figueras, Feist, Lupo**
6:00 PM					

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

TUESDAY March 20, 2018					
8:00-8:50AM	**PLENARY: Peter Beninger – *Centering on functional anatomy unlocks neat stuff from the molecular to the ecological levels*** **Courtyard Ballroom**				
ROOM	**Federal**	**Superior**	**Municipal**	**James**	**North**
SESSION TITLE	**SCIENCE, ART, AND COMMUNICATION** **Sandra Shumway**	***VIBRIO*** **Kristin DeRosia-Banick, John Jacobs & Rohine Paranjpe**	**HARMFUL ALGAL BLOOMS** **Vera Trainer**	**GENOMICS: AN INTRODUCTORY PRIMER WORKSHOP** **Sarah Kingston & Maureen Krause**	**GENERAL CONTRIBUTED II** **Lewis Deaton**
9:00AM	ART, SCIENCE, AND HUMOR: THE IMPORTANCE OF EFFECTIVE COMMUNICATION **McDermott**	**Introduction** MANAGING *VIBRIO PARAHAEMOLYTICUS* RISK IN THE US: INNOVATIVE STRATEGIES FOR RISK REDUCTION **DeRosia-Banick, Jacobs[P], Paranjpe**	FIRST RECORDS OF THE GENUS *AZADINIUM* (DINOPHYCEAE) FROM PUGET SOUND, WASHINGTON STATE **Trainer, Kim, Bill, Adams, Tillmann, Krock, Harrington**	NEW TO THE GENOMICS REVOLUTION, WONDERING WHAT IT IS ALL ABOUT, AND HOW IT CAN BE APPLIED TO SHELLFISH BIOLOGY? THIS INTERACTIVE WORKSHOP WILL INTRODUCE THE NOVICE TO 'OMICS BASICS AND USE A CASE-STUDY APPROACH TO WALK ATTENDEES THROUGH A GENOMICS PROJECT, FROM DATA COLLECTION TO PUBLICATION. PLEASE BRING YOUR LAPTOPS.	USING ARCHAEOLOGICAL OYSTER SHELL TO INFER ANCIENT MARICULTURE **Jenkins***
9:15AM		POPULATION GENETICS, BIOGEOGRAPHY, AND PHYLOGENETICS OF *VIBRIO PARAHAEMOLYTICUS* FROM NORTH AMERICA USING WHOLE GENOME SEQUENCE DATA **Miller, Lüdeke, Weimer, Jones[P]**	*PSEUDO-NITZSCHIA* EARLY WARNING BULLETIN INCREASES CLAMMING OPPORTUNITIES ON PACIFIC NORTHWEST OUTER COAST BEACHES **Trainer, McCabe, Hickey, MacCready, Hunter, Moore, Doucette, Banas, Forster[P]**		FRESHWATER MUSSEL SHELLFISHING AS EVIDENCE OF CULTURE CONTINUITY AND DIVERGENCE DURING THE LATE PREHISTORIC IN WISCONSIN **McTavish***
9:30AM	CONTEMPORARY OBSTACLES TO CREDIBILITY IN SCIENCE **Beninger**	ECOSYSTEM AND GENOMIC RESEARCH IN SUPPORT OF *VIBRIO PARAHAEMOLYTICUS* RISK MANAGEMENT; WHAT ARE THE CRITICAL THEMES? **Jones, Whistler, Hartwick, Taylor, Marcinkiewicz, Foxall, Nash**	IDENTIFYING ENVIRONMENTAL DRIVERS OF *ALEXANDRIUM* HARMFUL ALGAL BLOOMS IN SOUTHEAST ALASKA **Tobin, Crumpton, Wallace, Eckert**		QUANTIFYING OYSTER REEF DEVELOPMENTAL TRAJECTORIES FROM 16 YEARS OF LIVING SHORELINES RESEARCH IN SOUTH CAROLINA, USA **Kingsley-Smith, Hodges, Stone, Sundin, Johnson, Tweel, Sanger**
9:45AM			TRANSFER OF THE HARMFUL ALGAL TOXIN, MICROCYSTIN, FROM FRESHWATER TO MARINE ECOSYSTEMS **Hardy & Preece**		LUNG VOLUME IN THE APPLE SNAIL, *POMACEA MACULATA* **Lee & Deaton**
10:00AM	THE JAPANESE ART OF *GYOTAKU*, THE INTERSECTING OF SCIENCE AND ART **Koike**	ENVIRONMENTAL DETERMINANTS OF *VIBRIO PARAHAEMOLYTICUS* IN THE CHESAPEAKE BAY: CURRENT AND FUTURE WORK **Davis, Jacob, DePaola, Curriero**	USE OF THE ENVIRONMENTAL SAMPLE PROCESSOR FOR NEAR-REAL TIME DETECTION OF HARMFUL ALGAL SPECIES AND DOMOIC ACID IN THE PACIFIC NORTHWEST **Adams, Moore, Mickett, Mikulski, Doucette, Birch**		LACTIC ACID IN THE TISSUES OF THE APPLE SNAIL, *POMACEA MACULATA* **Essajee & Deaton**
10:15AM		NEXT GENERATION *VIBRIO* RISK TOOLS **DePaola, Bowers, Davis, Curriero**	MONITORING HAB TOXINS USING SPATT PROXY FOR SHELLFISH MANAGEMENT **Morton, Haynes, Wang, Hattenrath, Gobler, Leighfield**		QUANTITATIVE METHODS FOR MEASURING MITOTIC, MEIOTIC, AND DIFFERENTIATION ACTIVITY WITHIN GAMETOGENESIS OF TRIPLOID *CRASSOSTREA VIRGINICA* **Matt* & Allen, Jr.**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**SEAGRASS-BIVALVE INTERACTIONS** **Kay McGraw & Brett Dumbauld**	***VIBRIO*** **Kristin DeRosia-Banick, John Jacobs & Rohine Paranjpe**	**HARMFUL ALGAL BLOOMS** **Vera Trainer**	**COMPARATIVE GENOMICS: A HANDS-ON WORKSHOP ON THE EASTERN OYSTER GENOME** **Marta Gomez-Chiarri**	**GENERAL CONTRIBUTED II** **Kristen Linesch & Michael Kendrik**
11:00 AM	BIVALVE – SEAGRASS INTERACTIONS: INTRODUCTION TO THE SESSION **McGraw & Dumbauld**	COLD CHAINS FOR FARMED OYSTERS PRODUCED IN THE CHESAPEAKE BAY AND MODELED *VIBRIO PARAHAEMOLYTICUS* GROWTH **Love, Lane, Claney, Davis, Fry, Harding, Hudson[P]**	SOUNDTOXINS: A PUGET SOUND HAB MONITORING PARTNERSHIP **King, Claassen, Borchert, Trainer, SoundToxins Partnership**	RECENT EFFORTS IN GENOMIC SEQUENCING FOCUSED ON INVERTEBRATE SPECIES PROVIDE AN EXCITING OPPORTUNITY TO ANSWER A MULTITUDE OF BASIC AND APPLIED QUESTIONS RELATED TO SHELLFISH BIOLOGY AND ECOLOGY. IN THIS HANDS-ON WORKSHOP, WE WILL TAKE ADVANTAGE OF THE RELEASE OF THE EASTERN OYSTER GENOME AND DEMONSTRATE HOW TO EXPLOIT THIS AND OTHER GENOMICS RESOURCES TO ANSWER KEY QUESTIONS IN INVERTEBRATE BIOLOGY. PLEASE BRING YOUR LAPTOP.	RADULAR DEVELOPMENT AND LACK OF RADULAR PLASTICITY IN PINTO ABALONE (*HALIOTIS KAMTSCHATKANA*) POSTLARVAE AND YOUNG JUVENILES **Kuehl***
11:15 AM	SHELLFISH AQUACULTURE AND EELGRASS: A GLOBAL META-ANALYSIS **Ferriss, Conway-Cranos, Sanderson, Hoberecht**	FORECASTING *VIBRIO PARAHAEMOLYTICUS* IN LONG ISLAND SOUND OYSTERS AND MANAGEMENT STRATEGIES FOR AQUACULTURE **Whitney, DeRosia-Banick, Deignan-Schmidt**	COMMUNITY-BASED MITIGATION OF HARMFUL ALGAL BLOOMS AND SHELLFISH POISONINGS IN SOUTHEAST ALASKA **Kennedy, Lanphier, Whitehead**		GROWTH OF JUVENILE FRESHWATER MUSSELS (*ANODONTA IMPLICATA*) REARED IN PONDS WITHIN THE DELAWARE ESTUARY **Cheng, Kreeger, Padeletti, Butler, Thomas**
11:30 AM	COASTAL MANAGEMENT USING OYSTER-SEAGRASS INTERACTIONS FOR SUSTAINABLE AQUACULTURE, FISHERIES, AND ENVIRONMENT **Hori, Lagarde, Derolez, Richard, Hamaguchi, Hori, Makino**	EVALUATING LIPOSOMES FOR THE DELIVERY OF OXYTETRACYCLINE TO OYSTER LARVAE (*CRASSOSTREA GIGAS*) AND SUBSEQUENT EFFECTS ON RESISTANCE TO *VIBRIO CORALLILYTICUS* **Blodgett*, Langdon, Hawkyard**	IMPACTS OF TWO HARMFUL ALGAL BLOOM SPECIES ON OYSTERS CULTURED IN LOWER CHESAPEAKE BAY **Robison*, Vogelbein, Reay, Carnegie, Smith, Reece**		ARE OYSTERS IN THE CHESAPEAKE BAY PRIORITIZING THEIR OFFSPRING OVER THEIR HEALTH? **Huey* & Carnegie**
11:45 AM	MANAGING EELGRASS AND SHELLFISH AQUACULTURE IN WASHINGTON: A WORKSHOP TO EXAMINE CHALLENGES AND INCONSISTENCIES **Hoberecht, Sanderson, Ferriss**	BACTERIOPHAGES SIGNIFICANTLY REDUCE LARVAL OYSTER MORTALITY CAUSED BY *VIBRIO CORALLILYTICUS* **Madison*, Langdon, Hase, Richards, Watson, Soffer, Li, Sulakvelidze**	IMPACTS OF TWO HARMFUL ALGAL BLOOM SPECIES ON DIPLOID AND TRIPLOID LARVAL AND JUVENILE OYSTERS **Reece, Hobbs, Jones III, Scott, Harris, Vogelbein**		MOLECULAR CLONING, EXPRESSION PATTERN ANALYSIS, AND IN SITU HYBRIDIZATION OF A DMRT11E GENE IN THE ORIENTAL FRESHWATER PRAWN, *MACROBRACHIUM NIPPONENSE* **Yabing, Hongtuo, Hui, Shengming, Wenyi, Shubo[P], Yongsheng, Sufei, Yiwei, Yan**
12:00 NOON	SOME CONSIDERATIONS FOR EVALUATING OYSTER-SEAGRASS INTERACTIONS AT BROADER SCALES IN US WEST COAST ESTUARIES **Dumbauld**	EFFECT OF ANOXIA ON THE VIRULENCE OF *VIBRIO CORALLILYTICUS* AND ITS IMPACT ON THE MORTALITY AND IMMUNE FUNCTION OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Phippen*, Ivanina, Sokolova, Oliver**	STAGE-SPECIFIC DETRIMENTAL EFFECTS OF THE BIOACTIVE EXTRACELLULAR COMPOUNDS PRODUCED BY *ALEXANDRIUM MINUTUM* ON EARLY DEVELOPMENT OF THE OYSTER *CRASSOSTREA GIGAS* **Castree*, Soudant, Petton, Ratiskol, Le Grand, Le Goïc, Lambert, Boulais, Hégaret, Fabioux**		HORSESHOE CRAB PASSAGE THROUGH RACK-AND-BAG OYSTER FARMS **Munroe, Bushek[P], Woodruff, Calvo**
12:15 PM	COMPARING FISH AND CRAB USE OF THE BOUNDARY BETWEEN TWO TYPES OF PACIFIC OYSTER AQUACULTURE AND EELGRASS IN WILLAPA BAY, WASHINGTON, USA **Muething* & Dumbauld**	THE EFFECTS OF AERIAL EXPOSURE AT LOW TIDE ON *VIBRIO* CONCENTRATIONS IN HARVESTED OYSTERS CULTURED IN THE INTERTIDAL **Ben-Horin, Audemard, Bushek, Calvo, Reece**			PHYSIOLOGICAL IMPACTS OF THE BIOMEDICAL BLEEDING PROCESS ON THE ATLANTIC HORSESHOE CRAB, *LIMULUS POLYPHEMUS*, IN SOUTH CAROLINA, USA **Linesch, Burnett, Burnett, Kalisperis, Fowler**
12:30-1:30 PM	**LUNCH BREAK**				

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

TUESDAY March 20, 2018					
ROOM	**Federal**	**Superior**	**Municipal**	**James**	**North**
SESSION TITLE	**SEAGRASS-BIVALVE INTERACTIONS** **Kay McGraw & Brett Dumbauld**	***VIBRIO*** **Kristin DeRosia-Banick, John Jacobs & Rohine Paranjpe**	**CLAMS** **Matthew Hunter & Daniel Ayres**	**PREPARATION OF SHELLFISH FOR DISEASE DIAGNOSTICS WORKSHOP** **Roxanna Smolowitz & Dale Leavitt**	**NORTHWEST INDIAN TRIBES SHELLFISH MANAGEMENT AND FISHERIES** **Sandy Zeiner**
1:30 PM	QUANTIFYING ECOSYSTEM FUNCTIONS IN MIXED OYSTER CULTURE AND SEAGRASS/MACROALGAL HABITATS **Cheney, Hudson, Dumbauld Cordell, Nash, Kramer**	LEVELS OF *VIBRIO* SPP. AFTER DESICCATION AND RE-SUBMERGENCE OF OYSTERS STORED IN THREE COMMON GEAR TYPES IN ALABAMA **Neil, Pruente, Webb, Walton, Jones**	RAZOR CLAM (*SILIQUA PATULA*) SEASON SETTING IN WASHINGTON STATE **Ayres & Parson**	RISK OF DISEASE IS A CONSTANT THREAT TO SHELLFISH FARMERS ACROSS THE INDUSTRY. THIS WORKSHOP WILL PROVIDE GROWERS WITH INFORMATION TO AID IN THEIR DEFENSE AGAINST LOSING SHELLFISH TO DISEASE. MATERIAL COVERED DURING THE WORKSHOP WILL INCLUDE THE ANATOMY/PHYSIOLOGY OF BIVALVES, SOME OF THE MORE IMPORTANT DISEASES OF OYSTERS AND CLAMS FOUND IN THE U.S., WHAT TO DO IF A DISEASE IS SUSPECTED, AND MEANS OF BIOSECURITY TO REDUCE THE RISK OF DISEASE INITIATING. PARTICIPANTS WILL LEARN BASIC ANATOMY AND PHYSIOLOGY OF BIVALVE THROUGH A HANDS-ON DISSECTION OF CLAMS AND OYSTERS. AFTER DISSECTION, THERE WILL BE AN INTRODUCTION TO IMPORTANT DISEASES OF BIVALVES, INCLUDING DERMO AND ASSOCIATED DISEASES (*PERKINSUS MARINUS* AND *P. OLSENI*), MULTINUCLEATED SPHERE UNKNOWN (MSX – HAPLOSPORIDIUM NELSON), OSTREID HERPES VIRUS 1 (OSHV-1), QUAHOG PARASITE UNKNOWN (QPX) AND TRANSMISSIBLE TUMOR.	TRIBAL CO-MANAGEMENT OF THE SHELLFISH RESOURCES IN WASHINGTON STATE: AN EVOLVING PROCESS **Fyfe**
1:45 PM	COMPARATIVE HABITAT USE OF ESTUARINE HABITATS WITH AND WITHOUT OYSTER AQUACULTURE: CHALLENGES, PARTNERSHIPS, AND INITIAL LESSONS **Meaders, Bloch, Cziesla**	THE EFFECT OF HIGH SALINITY ON THE ABUNDANCE, ANTIBIOTIC RESISTANCE, AND GENETIC DIVERSITY OF *VIBRIO PARAHAEMOLYTICUS* IN AN OYSTER RELAY STUDY **Parveen, Elmahdi, Jahncke, Jacobs, Bowers**	THE OREGON PACIFIC RAZOR CLAM RESOURCE: HISTORIC AND CURRENT MANAGEMENT **Hunter**		TRIBAL SHELLFISH HARVEST MANAGEMENT ON PRIVATELY OWNED TIDELANDS IN WASHINGTON STATE **Moore, Barry, Unsell**
2:00 PM	MONITORING EELGRASS RESPONSES TO AQUACULTURE ACTIVITIES AND DEVELOPMENT OF IMPROVED MONITORING TOOLS **Lummis*, Kroeker, Newkirk, Klausmeyer, Lomonico, Jones, Finger, Sawyer**	EFFECTS OF TUMBLING AND REFRIGERATION ON THE ABUNDANCE OF *VIBRIO VULNIFICUS* AND *VIBRIO PARAHAEMOLYTICUS* IN CULTURED OYSTERS (*CRASSOSTREA VIRGINICA*) **Pruente*, Walton, Jones**	MONITORING THE RECOVERY OF EAST SIDE COOK INLET RAZOR CLAMS **Kerkvliet, Booz, Blackmon, Hansen**		THE SWINOMISH SHELLFISH PROGRAM: MANAGEMENT, RESEARCH, AND RESTORATION EFFORTS **Loomis, Barber[P], Greiner, Grossman**
2:15 PM	OYSTERS SHOW ENHANCED GROWTH IN EELGRASS: DOES pH EXPLAIN THE DIFFERENCE? **Horwith & Lowe**	THE ABUNDANCE AND OCCURRENCE OF *VIBRIO* IN CULTURED OYSTERS GROWN AT VARIOUS DEPTHS WITHIN THE WATER COLUMN **Scro, Agnew, Smolowitz**	RELATIONSHIP BETWEEN THE GROWTH CYCLE OF THE RAZOR CLAM AND THE SEASONALITY OF PHYTOPLANKTON BLOOMS ON THE WASHINGTON COAST **Forster & Berry**		MAINTAINING LIVELIHOODS AND CULTURAL DIVERSITY THROUGH TRIBAL SHELLFISH AQUACULTURE **Riccio, Toy, Parsons, Grinnell**
2:30 PM	OYSTERS SHOW ENHANCED GROWTH IN EELGRASS: DOES DIET EXPLAIN THE DIFFERENCE? **Lowe* & Horwith**	MITIGATION STRATEGIES FOR *VIBRIO PARAHAEMOLYTICUS* IN OYSTER SHELLSTOCK INTENDED FOR RAW CONSUMPTION **Liu & DePaola**	HABITAT EFFECTS OF MACROPHYTES AND SHELL ON THE PERFORMANCE OF JUVENILE CLAMS AND LOCAL pH CONDITIONS **Greiner, Klinger, Ruesink, Horwith**		PACIFIC RAZOR CLAM AND DUNGENESS CRAB FISHERY MANAGEMENT CHALLENGES ON THE WASHINGTON COAST **Schumacker**
2:45 PM	FILTER-FEEDING BIVALVES CAN ENHANCE *ZOSTERA MARINA* REPRODUCTIVE OUTPUT **Peterson, Jackson, Furman**	MANAGING *VIBRIO PARAHAEMOLYTICUS* IN WASHINGTON **Hard**	SPATIAL AND TEMPORAL POPULATION VARIABILITY IN INTERTIDAL CLAMS **Barber, Ruff, McArdle, Hunter, Speck, Rogers, Greiner**		DUNGENESS CRAB TRAP CATCH EFFICIENCY RELATED TO ESCAPE RING LOCATION AND SIZE **Stearns, Conrad, Winfrey, Shippentower-Games, Finley**
3:00 PM	HABITAT COMPLEXITY MEDIATES PREDATOR-BIVALVE INTERACTIONS IN CHESAPEAKE BAY **Seitz & Glaspie**	*VIBRIO PARAHAEMOLYTICUS* MANAGEMENT FOR OYSTERS IN MASSACHUSETTS **Schillaci*, Jones, Whistler, Regan**	THE CASE OF THE "MISSING" ARCTIC BIVALVES AND THE WALRUS, THE BIGGEST [IGNORED] CLAM FISHERY ON THE PLANET **Mann, Powell, Munroe**		IMPLEMENTING A SIZE RESTRICTION TO OFFSET IMPACTS FROM SIZE-SELECTIVE HARVESTING OF GIANT RED SEA CUCUMBERS **Mueller**
SESSION TITLE	**SEAGRASS-BIVALVE INTERACTIONS** **Kay McGraw & Brett Dumbauld**	***VIBRIO*** **Kristin DeRosia-Banick, John Jacobs & Rohine Paranjpe**	**PHYTOPLANKTON CULTURE: A TRIBUTE TO RRL GUILLARD** **Gary Wikfors & Steve Morton**	**PREPARATION OF SHELLFISH FOR DISEASE DIAGNOSTICS WORKSHOP** **Roxanna Smolowitz & Dale Leavitt**	**NORTHWEST INDIAN TRIBES SHELLFISH MANAGEMENT AND FISHERIES** **Sandy Zeiner**
3:15PM	SHELLFISH COMMUNITY PATTERNS IN THE NATIVE AND NON-NATIVE EELGRASS HABITATS OF NETARTS BAY, OREGON, USA **D'Andrea, Perotti, Moffett, Strickland**	**PANEL DISCUSSION: MANAGING *VIBRIO PARAHAEMOLYTICUS* RISK IN THE US: INNOVATIVE STRATEGIES FOR RISK REDUCTION**	THE FUTURE OF THE PROVASOLI-GUILLARD NATIONAL CENTER FOR MARINE ALGAE AND MICROBIOTA **Lomas, Sexton, Preston, Hurd, Blanchette, Reed**	THE WORKSHOP WILL CONCLUDE WITH A DISCUSSION OF HOW TO RESPOND SHOULD ONE SUSPECT A DISEASE IS DEVELOPING ON THEIR FARM; THE TIMING OF MONITORING, SAMPLE COLLECTION AND SHIPPING; TESTING METHODS FOR DISEASE DIAGNOSIS; AND BIOSECURITY PRACTICES FOR THE FARM.	UNUSUAL 2017 MICROALGAL BLOOM HAS RIPPLE EFFECTS ON THE BIVALVES OF HOOD CANAL **Paul & Books**
3:30 PM	EFFECTS OF CONTROLLED, LARGE-SCALE REMOVAL OF *ZOSTERA JAPONICA* ON ESTUARINE FAUNA **Patten & Norelius**		MICROALGAL BIOCHEMICAL COMPOSITION AND BIVALVE NUTRITION: HOW WE KNOW WHAT WE KNOW **Wikfors**		
3:45 PM	ASSESSMENT OF INTERACTIONS BETWEEN SALMON HABITAT RESTORATION ACTIONS AND SHELLFISH RESOURCES **Meaders & Schlenger**		WHAT WE STILL DO NOT KNOW ABOUT FEEDING BIVALVES AND WHAT WE NEED TO DO **Henry & Reed**		
4:00 PM			ESSENTIAL FATTY ACID ASSIMILATION AND SYNTHESIS IN *CRASSOSTREA GIGAS* LARVAE **da Costa, Robert, Quéré, Wikfors, Soudant**		
4:15 PM			ALGAL ECONOMICS FOR SHELLFISH HATCHERIES **Glover & Roulston**		
4:00 – 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Madison Ballroom**				
7:00 PM - ???	**STUDENT ENDOWMENT FUND AUCTION** **Courtyard Ballroom**				

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

WEDNESDAY March 21, 2018					
8:00-8:50AM	**PLENARY: Donal Manahan – *Predicting adaptive responses to ocean change: implications for aquaculture*** **Courtyard Ballroom**				
ROOM	**North**	**West**	**James**	**South**	**East**
SESSION TITLE	**GREEN CRABS** **Sylvia Yamada & Thomas Therriault**	**UNDERGRADUATE RESEARCH COLLOQUIUM** **Edward Catapane**	**CONTAMINANTS OF EMERGING CONCERN** **Aswani Volety & Evan Ward**	**OYSTERS: EAST MEETS SOUTH MEETS WEST** **Chris Davis & Bill Walton**	**GENERAL CONTRIBUTED III** **Vincent Encomio & Michael Doall**
9:00AM	EUROPEAN GREEN CRAB IN BRITISH COLUMBIA: TRACKING THE SPREAD OF A HIGH-RISK INVADER **Therriault, Hodes, Norgard, Curtis, Gillespie**	IMMUNOHISTOFLUORESCENCE STUDY OF THE ACTIONS OF MANGANESE ON THE PHOSPHOLIPASE C AND IP3 RECEPTOR MECHANISMS OF DOPAMINE D2-LIKE POSTSYNAPTIC RECEPTORS IN *CRASSOSTREA VIRGINICA* **Eid*, Amoako, Cummings, Jacobs, Carroll, Catapane**	CAPTURE AND INGESTION OF NANOPARTICLES BY BIVALVES: IMPLICATIONS FOR BIOACCUMULATION AND TOXICITY **Ward, Doyle, Haynes, Holohan**	COMPARTMENTALIZATION OF HEMOCYTE FUNCTIONS IN CONGENERS OF TWO OYSTERS **Little-Jackson, Faltz, Ivanina[P]**	A NOVEL LOW-VOLUME PORTABLE PUMP SYSTEM FOR SAMPLING LARVAL SHELLFISH IN SHALLOW, TURBULENT, "DIRTY" ENVIRONMENTS **Nichols & Hudak**
9:15AM	EUROPEAN GREEN CRAB IN THE WASHINGTON SALISH SEA: SAME STATE, DIFFERENT INVASION **Grason, McDonald, Litle, Adams**	A ROLE FOR PROTEIN KINASE C IN GILL LAMELLA CELL ACTIVITY OF *CRASSOSTREA VIRGINICA* **Johnson*, Ernest, Carroll, Catapane**	A 72-HOUR GRAPHENE OXIDE NANOPARTICLE EXPOSURE STUDY WITH EASTERN OYSTERS **Khan, Adeleye, Russo, Burgess, Ho**	REEXAMINING *BONAMIA OSTREAE* IN MAINE FLAT OYSTERS **Bienfien*, Lane, Carnegie**	COMPARISON OF UNDERWATER PHOTO AND VIDEO SURVEY METHODS WITH DIVER OBSERVATIONS TO ASSESS NEARSHORE ALGAE AND BENTHIC MARINE INVERTEBRATE COMMUNITIES **Bureau & Lessard**
9:30AM	BIOLOGICAL AND PHYSICAL OCEAN INDICATORS PREDICT THE SUCCESS OF THE INVASIVE EUROPEAN GREEN CRAB, *CARCINUS MAENAS* **Yamada, Prickett, Yednock, Geierman, Indivero, Williams, Randall, Peterson, Fisher, Kosro**	THE EFFECTS OF TAURINE ON MANGANESE ACCUMULATIONS IN GILL OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Santos*, Agyei, Griffith, Jr., Carroll, Catapane**	TEMPORAL EFFECTS OF EXPOSURE TO PHARMACEUTICALS AND PERSONAL CARE PRODUCTS AND THEIR MIXTURE ON THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) METABOLOME **Bren* & Black**	A NEW COLLECTION METHOD FOR WILD PACIFIC OYSTER SPAT IN THE INTERTIDAL ZONE FOR COMPLEMENTING SPAT SUPPLY IN JAPAN **Hasegawa, Watanabe, Higano, Tsuchihashi, Kuriyama**	GROWTH AND REPRODUCTIVE CONDITION OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*) RAISED IN AN INTERTIDAL RACK-SUSPENDED CULTURE SYSTEM IN TAEAN OFF THE WEST COAST OF KOREA, THREE YEARS AFTER THE *HEBEI SPIRIT* OIL SPILL **Hong, Lee, Jeong, Park, Choi**
9:45AM	THE MORAN EFFECT AND REGIONAL SYNCHRONY OF EUROPEAN GREEN CRAB POPULATIONS ALONG THE PACIFIC COAST **Grosholz, Chang, Jeppesen, McCann, de Rivera, Ruiz, Therriault, Wasson, Yamada**		LETHAL AND SUB-LETHAL EFFECTS OF THE POLYFLUORINATED COMPOUND, GENX, ON THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* **Volety, Loh, Soudant, Leuentine, Harell, Soudant, Volety**	DENSITY-DEPENDENT CAPTURE EFFICIENCY OF A SURVEY DREDGE AND ITS INFLUENCE ON THE STOCK ASSESSMENT OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) IN DELAWARE BAY **Morson*, Munroe, Ashton-Alcox, Powell, Bushek, Gius**	APPLICATION OF TRIPLOIDY TO AN EMERGENT OYSTER CULTURE INDUSTRY ON THE FLORIDA WEST COAST **Cyr, Markham, Sims, Sturmer**
10:00AM	COMPARING PREDATION IMPACTS OF NATIVE AND INVASIVE CRABS USING A BIOENERGETICS APPROACH **McDonald, Holsman, Armstrong**		INGESTION, BIOACCUMULATION, AND DEPURATION OF MICRO- AND NANO-PLASTIC PARTICLES BY MARINE BIVALVES **Ward, Haynes, Holohan, Mladinich**	THE BILLION OYSTER PROJECT: CHALLENGES, LESSONS, AND OPPORTUNITIES IN RESTORING OYSTERS TO AN URBANIZED ENVIRONMENT **Burmester, McCann, Mosher, Malinowski**	TAURINE REDUCES THE TOXIC EFFECTS OF MANGANESE ON MITOCHONDRIAL MEMBRANE POTENTIAL **Catapane, Carroll, Florestan, Gazca**
10:15AM	EVALUATION OF SHORT-TERM REMOVAL EFFORT TO CONTROL THE EUROPEAN GREEN CRAB, *CARCINUS MAENAS*, POPULATION IN THE BROKEN GROUP ISLANDS, BRITISH COLUMBIA **Yakimishyn & Zharikov**		DETERMINING PRESENCE OF MICROPLASTICS IN SHELLFISH FROM PUGET SOUND, WASHINGTON, USA **Martinelli & Padilla-Gamiño**	SURVEYING BENTHIC INVERTEBRATE COMMUNITIES ASSOCIATED WITH OYSTER AQUACULTURE SITES IN MAINE **Lindsay, Deon, Holmes, Miller, Silverbrand, Rawson[P]**	OYSTER RESTORATION EFFORTS IN THE SOUTHERN INDIAN RIVER LAGOON, FLORIDA – INCORPORATING RESILIENCY TO FRESHWATER DISCHARGES **Encomio**
10:30-11:00AM	**MORNING BREAK**				
SESSION TITLE	**GREEN CRABS** **Sylvia Yamada & Thomas Therriault**	**RIBBED MUSSELS** **Dave Bushek & Danielle Kreeger**	**CONTAMINANTS OF EMERGING CONCERN** **Aswani Volety & Evan Ward**	**OYSTERS: EAST MEETS SOUTH MEETS WEST** **Chris Davis & Bill Walton**	**GENERAL CONTRIBUTED III** **Vincent Encomio & Michael Doall**
11:00 AM	LARGE-SCALE GREEN CRAB REMOVAL AS SITE PREPARATION FOR EELGRASS RESTORATION EFFORTS IN PLACENTIA BAY, NEWFOUNDLAND, CANADA **Best & Le Bris**	SESTON FILTRATION AND RESTORATION POTENTIAL OF RIBBED MUSSELS COMPARED WITH OTHER NATIVE BIVALVES **Kreeger, Moody, Cheng**	EFFECTS OF SURFACE SURFACTANTS ON PARTICLE CAPTURE, CLEARANCE EFFICIENCY, AND CLEARANCE RATES OF THE BLUE MUSSEL (*MYTILUS EDULIS*) **Rosa, Ward, Flores, Sierra, Torres**	FOOD WEB OF THE EASTERN OYSTER AND BLUE CRAB: SCAVENGERS, FACILITATION, COMPETITION, AND KLEPTOPARASITISM **Lipcius & Chei**	IF YOU BUILD IT, WHY DO THEY COME? AN INVESTIGATION INTO THE MOTIVATIONS OF VOLUNTEER OYSTER GARDENERS **Waters, Jr.*, Walton, Petrolia, Swann, Witte**
11:15 AM	ASSESSING SHELLFISH TRANSFERS AS A VECTOR FOR THE EUROPEAN GREEN CRAB (*CARCINUS MAENAS*) AND THE EFFECTIVENESS OF POWER-WASHING TO MITIGATE MOVEMENT **Curtis, Pearce, Hodes, Therriault**	HABITAT CHARACTERIZATION OF THE RIBBED MUSSEL (*GEUKENSIA DEMISSA*) AND ITS RESPONSE TO HARVEST IN SOUTH CAROLINA, USA **Julien*, Tweel, Hadley, McGlinn, Kingsley-Smith**		OYSTER SHELL BUDGETS IN THE CHESAPEAKE BAY: A SUMMARY FROM LONG-TERM SURVEY DATA **Mann, Southworth, Wesson, Tarnowski, Thomas**	OYSTER RESTORATION IN HARRIS CREEK, MARYLAND; A PROGRESS REPORT **Paynter, Needham, McDowell**
SESSION TITLE	**GREEN CRABS** **Sylvia Yamada & Thomas Therriault**	**RIBBED MUSSELS** **Dave Bushek & Danielle Kreeger**	**SHELLS AND MATERIALS** **Karolyn Hansen & Andrew Mount**	**OYSTERS: EAST MEETS SOUTH MEETS WEST** **Chris Davis & Bill Walton**	**GENERAL CONTRIBUTED III** **Vincent Encomio & Michael Doall**
11:30 AM	**Discussion**	EFFECTS OF PREDATION AND SUBSTRATE CHOICE ON RIBBED MUSSEL RECRUITMENT FOR LIVING SHORELINE APPLICATIONS **Moody & Kreeger**	CRACKING THE SHELL: AN INVESTIGATION OF SHELL REPAIR IN THE OYSTER, *CRASSOSTREA VIRGINICA* **Outhwaite*, Hansen, Hansen**	**WORKSHOP: EXPLORING AN INITIATIVE TO TRAIN THE NEXT GENERATION OF SHELLFISH BIOLOGISTS**	ARE SPAWNER SANCTUARIES AN EFFECTIVE RESTORATION STRATEGY FOR THE NORTHERN QUAHOG (= HARD CLAM) *MERCENARIA MERCENARIA*: A COMPARISON OF TWO RESTORATION EFFORTS ON LONG ISLAND, NEW YORK **Doall, Kulp, Peterson, Lobue, Starke, Griffith, Gobler**
11:45 AM		SPATIALLY EXPLICIT ESTIMATES OF THE IMPACTS OF SEA LEVEL RISE AND EROSION ON RIBBED MUSSEL (*GEUKENSIA DEMISSA*) MEDIATED ECOSYSTEM FUNCTIONS **Isdell*, Bilkovic, Hershner**	PHENOTYPIC PLASTICITY IN SHELL CONSTRUCTION AND REMODELING IN THE GASTROPOD, *NUCELLA LAMELLOSA* **Charifson[P] & Bourdeau**		A DYNAMIC MODEL FOR MANAGEMENT OF OYSTER NURSERIES **Soares, Nobre, Hubert**
12:00 NOON		A PILOT STUDY OF NUTRIENT BIOEXTRACTION USING RIBBED MUSSELS AT HUNTS POINT, NEW YORK CITY, FROM CONCEPTION TO CONCLUSION: PATHS, PROCESSES, PARTNERSHIPS, PERCEPTIONS, AND PROJECTIONS **Galimany, Wikfors[P], Dixon, Newell, Meseck, Henning, Li, Tedesco, Dwyer, Rose**	MOLECULAR MODELING AND CHARACTERIZATION OF A MUSSEL ADHESIVE PROTEIN (MEFP-5) **Zimlich*, Hansen, Hansen**		SPAT ON SHELL AS A MEANS FOR STOCK ENHANCEMENT OF PUBLIC REEFS IN ALABAMA, AND THE STANDARDIZATION OF SETTING EFFICIENCY ASSESSMENT **Lappin*, Walton, Rikard, Herrmann**
12:15 PM					BABYSITTING BABY SQUID: *IN SITU* MONITORING OF LONGFIN INSHORE SQUID EGG DEPOSITION AND EMBRYONIC DEVELOPMENT **Nichols, Groglio, Eldredge**
12:30-2:00 PM	**NSA BUSINESS LUNCHEON** **Courtyard Ballroom**				
2:00 - 4:30 PM	**SCALLOP GALLOP** **EXPLORE SEATTLE!!**				
4:30 - 6:00 PM	**POSTER SESSION AND HAPPY HOUR** **Madison Ballroom**				
6:30 PM - ???	**KEN CHEW CHINESE DINNER** **(Tickets must be purchased by 5PM on Monday)**				

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

THURSDAY March 22, 2018					
8:00-8:50AM	**PLENARY: Gary Wikfors – '*The Milford Method*': *Origins, Evolution, and Applications*** **Courtyard Ballroom**				
ROOM	**Federal**	**Superior**	**Municipal**	**North**	**West**
SESSION TITLE	**GEODUCKS** **Joth Davis & Paul Gribben**	**OsHV-1** **Tim Green & Colleen Burge**	**SHELLFISH AND CLIMATE CHANGE** **Hillary Lane Glandon & Sarah Kingston**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT** **Theresa Bert & Harriet Perry**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren**
9:00AM	COMPARISON OF GROWTH CURVES OF THE GEODUCK, *PANOPEA GLOBOSA*, FROM FOUR FISHING ZONES IN NORTHWESTERN MEXICO **Aragón-Noriega, Cruz-Vásquez, Castillo-Vargasmachuca, Rodríguez-Domínguez, Alcántara-Razo, Ponce-Palafox, López-Sánchez**	EXPERIENCES WITH OSTREID HERPESVIRUS 1 (OsHV-1) IN AUSTRALIA – IMPACTS AND POSSIBLE SOLUTIONS **Kirkland, Gestier, Gu**	WINTER IS (NOT) COMING: CHANGES TO OVERWINTER BEHAVIOR OF BLUE CRAB IN RESPONSE TO WARMING TEMPERATURES **Glandon, Kilbourne, Miller**	ENVIRONMENTAL DRIVERS OF THE SPATIAL AND TEMPORAL DISTRIBUTION OF SPAWNING BLUE CRABS, *CALLINECTES SAPIDUS*, IN THE WESTERN GULF OF MEXICO **Anderson, Olsen, Wagner[P], Gelpi, Topping**	ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP **Alcivar-Warren**
9:15AM	THE GEOGRAPHICAL DISTRIBUTION OF THE GEODUCKS, *PANOPEA GENEROSA* AND *P. GLOBOSA* **González-Peláez, Vélez-Arellano, Bautista-Romero, Carvalho-Saucedo, Lluch-Cota**		THE ROLE OF CLIMATE IN DRIVING DISEASE DYNAMICS IN THE COMMERCIALLY IMPORTANT WHITE SHRIMP, *LITOPENAEUS SETIFERUS* **Kendrick, Frischer, Brunson, Gooding, Byers, Geer, Kingsley-Smith**	A REVIEW OF RECENT FISHERY-INDEPENDENT AND FISHERY-DEPENDENT MONITORING DATA FOR BLUE CRABS IN THE GULF OF MEXICO SPECIFIC TO MANAGEMENT OF THE RESOURCE **Wagner, Perry, Collins, Anderson, Burris, Anderson, Olsen, Gelpi, Topping**	PRESENT STATUS OF MANGROVE ECOSYSTEMS IN MEXICO, WITH NOTES ON THEIR KNOWLEDGE AND CONSERVATION CHALLENGES REGARDING NATURAL AND ANTHROPOGENIC IMPACTS **Ruiz-Luna & Berlanga-Robles**
9:30AM	GROWTH MODELING IN TWO POPULATIONS OF *P. GLOBOSA* FROM THE UPPER GULF OF CALIFORNIA: INTEGRATION OF INDIVIDUAL GROWTH PROFILES AND JUVENILE DATA TO TERMINAL SIZE-AT-AGE **Vega-Collazo*, González-Peláez, Hidalgo-de-la-Toba, Bautista-Romero, Lluch-Cota**	GENETIC VARIATION IN PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) FOR RESISTANCE TO OSTREID HERPESVIRUS-1 **Kube, Dove, Cunningham**	ASSESSMENT OF THE DISTRIBUTION SHIFT AND RANGE EXPANSION OF THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA*, USING A SPATIAL DISTRIBUTION FUNCTION MODEL **Timbs*, Mann, Powell**	A REVIEW OF RECENT FISHERY-INDEPENDENT MONITORING DATA FOR BLUE CRABS IN THE GULF OF MEXICO: THE DISCONNECT BETWEEN SETTLEMENT AND SUBSEQUENT JUVENILE ABUNDANCE **Perry, Collins, Anderson, Johnson, Sanchez-Rubio, Burris, Wagner**	
9:45AM	POPULATION GENOMICS OF *PANOPEA GLOBOSA* BASED ON ANALYSIS OF SINGLE NUCLEOTIDE POLYMORPHISM OBTAINED BY DDRAD **López*, Munguía, Cruz**	DOES FIRST BARRIER PASSAGE SHUNT MATTER IN DISEASE REPRODUCTION? UPDATE FROM OSHV-1 – *CRASSOSTREA GIGAS* MODEL **Morga, Picot, Faury, Dégremont, Renault, Lupo, Travers**	THE 'EAST OF NANTUCKET' SURVEY: SURFCLAMS ON THE MARCH OFFSHORE – MUSSELS BEWARE **Kuykendall, Powell, Mann, Long, Timbs**	A HIERARCHICAL BAYESIAN SURPLUS-PRODUCTION MODEL FOR BLUE CRAB (*CALLINECTES SAPIDUS*) IN THE NORTHERN GULF OF MEXICO **Oshima* & Leaf**	
10:00AM	INDIVIDUAL GROWTH PROFILES AS AN ALTERNATIVE TO THE TERMINAL SIZE-AT-AGE METHOD IN *PANOPEA GENEROSA* STUDIES **Hidalgo-de-la-Toba*, González-Peláez, Morales-Bojorquez, Bautista-Romero, Lluch-Cota**	OSTREID HERPES VIRUS IN THE UK: DISEASE CHALLENGES, SNP-ARRAY DEVELOPMENT, AND A GENOME-WIDE ASSOCIATION STUDY FOR HOST RESISTANCE IN PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) **Bean, Gutierrez, Hooper, Stenton, Sanders, Paley, Gharbi, Houston**	THE WARMING OF THE NORTHWEST ATLANTIC AS RECORDED BY THE OCEAN QUAHOG, *ARCTICA ISLANDICA*, WITH A NOTE ON CLIMATE CYCLES **Powell, Pace, Mann, Klinck**	REPRODUCTION IN FEMALE STONE CRABS (GENUS *MENIPPE*) FROM TAMPA BAY, FLORIDA, USA: INTERANNUAL, SEASONAL, AND TEMPERATURE-RELATED VARIATION **Bert, Gerhart, Crawford**	MANGROVEENCODE (2017-2027): DEVELOPING TECHNOLOGIES FOR THE ASSESSMENT OF CO_2, MICROBIOME, ENDOCRINE DISRUPTING CHEMICALS (GLYPHOSATE, METALS) AND MICROBIAL TRANSGENE *BACILLUS THURINGIENSIS* IN MANGROVES SEDIMENT AND AGRICULTURAL SOIL OF SELECTED COUNTRIES **Zuniga*, Espinoza, Ruiz-Luna, Berlanga-Robles, Gómez-Gil, Chouinard, Morell, Ochoa, Alcivar-Arteaga, Asunción, Galindo, Saltos, Zambrano, Alcivar Parrales, Alcivar-Warren, Echevarria, Ikeogu**
10:15-10:45AM	**MORNING BREAK**				
SESSION TITLE	**GEODUCKS** **Joth Davis & Paul Gribben**	**OsHV-1** **Tim Green & Colleen Burge**	**SHELLFISH AND CLIMATE CHANGE** **Hillary Lane Glandon & Sarah Kingston**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT** **Theresa Bert & Harriet Perry**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren**
10:45AM	GEODUCK STOCK ASSESSMENT IN BRITISH COLUMBIA **Bureau**	MAPPING GENES CONFERRING RESISTANCE TO OSHV-1 IN THE PACIFIC OYSTER **Kitapci*, Burge, Closek, Friedman, Hedgecock**	LARGE-SCALE PATTERNS OF TREMATODE PARASITES COMMUNITIES INFECTING *CERASTODERMA EDULE* FROM PORTUGAL TO MOROCCO **Correia*, Magalhães, de Montaudouin, Bazairi, Gam, Freita**	YOUNG-OF-THE-YEAR STONE CRAB (*MENIPPE*) RECRUITMENT IN THE GULF OF MEXICO OFF FLORIDA: KEY SHALLOW-WATER RECRUITMENT HOTSPOTS **Bert, Crawford, Shea**	THE EXCEPTIONALLY HIGH CARBON STOCKS OF MANGROVES AND THEIR POTENTIAL FOR THE GLOBAL MARKET OF CARBON – A REVIEW OF CO_2 LEVELS IN THREE GEOGRAPHIC REGIONS OF ECUADOR **Hernandez, Galindo*, Espinoza**
11:00 AM	EXAMINING WINTERTIME PARALYTIC SHELLFISH TOXICITY IN GEODUCKS IN SOUTHEAST ALASKA **Hart*, Eckert, Tobin, Sullivan, Whitehead, Lanphier, Kennedy, Wallace**	UNSUSPECTED OSHV-1 GENOMIC DIVERSITY AT INTER- AND INTRA-HOST LEVEL **Lamy, Renault, Bietry, Faury, Webb, Pepin, Morga[P]**	VISUAL KEYS SUPPORT OYSTER HEALTH MONITORING AS PART OF OYSTER REEF RESTORATION EFFORTS **Kane, Brooks, Sanchez, Thomas, Havens, Estes, Parker**	TEMPERATURE EFFECTS ON THE BIOENERGETICS OF DUNGENESS AND GRACEFUL CRABS, WITH IMPLICATIONS FOR MANAGEMENT **McDonald, Holsman, Workman, Armstrong**	SHRIMPENCODE (2017-2027): TRANSPOSABLE ELEMENTS OF THE ORIGINAL SPECIFIC PATHOGEN-FREE SHRIMP (SPF), *PENAEUS (LITOPENAEUS) VANNAMEI*, DOMESTICATED IN THE UNITED STATES – REVIEW OF HORIZONTAL TRANSFER OF TRANSPOSONS (HTT) ASSOCIATED WITH SHRIMP DISEASES **Alcivar-Warren, ShrimpENCODE Project Collaborators**
11:15 AM	PROTEOMICS REVEALS GEODUCK PHYSIOLOGICAL RESPONSE TO ENVIRONMENTAL CHANGE **Spencer*, Horwith, Lowe, Timmins-Schiffman, Nunn, Roberts**	AN 'OMICS' APPROACH TO UNDERSTAND OYSTER-OSHV-1 INTERACTIONS **Rosani, Abbadi, Domeneghetti, Venier**	USE OF A QPCR ASSAY TO DETECT THE TREMATODE, *PROCTOCEUS MACULATUS*, IN WATER COLUMN SAMPLES **Agnew, Scro, Smolowitz**	UNDERSTANDING BLUE CRAB, *CALLINECTES SAPIDUS*, PATTERNS OF MOVEMENT ALONG A SALINITY GRADIENT WITHIN THE ASHLEY RIVER, CHARLESTON, SOUTH CAROLINA, USA **Brunson, Kendrick, Czwartacki, Kingsley-Smith**	THE *NONLTR-1_LVA* NON-LTR RETROTRANSPON OF SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *LITOPENAEUS VANNAMEI*, FROM THE UNITED STATES IS HOMOLOGOUS TO THE NLRS NON-LTR RETROTRANSPOSON ASSOCIATED WITH ABDOMINAL SEGMENT DEFORMITY DISEASE (ASDD) OF CULTIVATED SHRIMP FROM THAILAND **Alcivar-Warren, Bao, Espinoza***
11:30 AM	CULTIVATION OF THE NEW ZEALAND GEODUCK, *PANOPEA ZELANDICA* **Le, Alfaro, Young, King, Ragg, Hilton**	MULTI-GENERATIONAL PLASTICITY AND ANTIVIRAL IMMUNITY IN THE OYSTER AGAINST OSHV-1 **Lafont, Goncalves, Guo, Montagnani, Raffos, Green[P]**	LOCATION, LOCATION, LOCATION: POPULATION DIFFERENCES IN RESPONSE TO OCEAN ACIDIFICATION IN BLUE MUSSELS **Padilla, Volkenborn, Gurr, Milke, Meseck, Rugila, Redman, Dixon, Veilleux, Liguori, Rosa**	INTERACTING EFFECTS OF HUMANS AND NATURE: FLOODWATERS, FISHERMEN, AND POPULATION DECLINE OF THE BLUE CRAB **Eggleston**	OLIGOMERIZATION PATTERNS OF PIRA AND PIRB CAUSING ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) AND ITS INTERACTION WITH THE MEMBRANE COMPONENTS OF THE EPITHELIAL CELLS OF THE SHRIMP HEPATOPANCREAS **Victorio-De Los Santos*, Hernández-Santoyo, Soto-Rodriguez**
11:45 AM		THE EFFECTS OF CRUDE AND REFINED ALGAL-DERIVED ANTIVIRAL BIOTHERAPEUTICS ON OSTREID HERPESVIRUS DEVELOPMENT AND PACIFIC OYSTER (*CRASSOSTREA GIGAS*) PERFORMANCE **Bookelaar*, Culloty, Lynch**		REPRODUCTIVE BIOLOGY INFORMS FISHERY MANAGEMENT OF SNOW (*CHIONOECETES OPILIO*) AND TANNER CRABS (*C. BAIRDI*) IN THE EASTERN BERING SEA, ALASKA **Kruse, Rebert, Richar, Slater, Webb**	
12:00-1:00 PM	**LUNCH BREAK**				

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

THURSDAY March 22, 2018					
ROOM	**Federal**	**Superior**	**Municipal**	**James**	**North**
SESSION TITLE	**DOWN ON THE FARM** **LeRoy Creswell & Bobbi Hudson**	**OsHV-1** **Tim Green & Colleen Burge**	**SHELLFISH AND CLIMATE CHANGE** **Hillary Lane Glandon & Sarah Kingston**	**APPLICATIONS OF CRUSTACEAN BIOLOGY TO FISHERIES MANAGEMENT** **Theresa Bert & Harriet Perry**	**ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP** **Acacia Alcivar-Warren**
1:00 PM	A TOOL FOR SEED STOCK MANAGEMENT IN COMMERCIAL OYSTER NURSERIES **Nobre, Soares, Ferreira, Hubert, Valente**	A LIFE IN FLUX: EFFECTS OF FLUCTUATING TEMPERATURES, AIR EXPOSURE, SALINITY, SUSPENDED PARTICULATE MATTER (SPM), AND TURBIDITY ON OSTREID HERPES VIRUS-1 MICROVAR EXPOSED *CRASSOSTREA GIGAS* (VIVALDI PROJECT) **Lynch, Molloy, Mcdonald, Cox, Culloty**	EFFECT OF OCEAN ACIDIFICATION ON PACIFIC OYSTER (*CRASSOSTREA GIGAS*) REPRODUCTION **Venkataraman* & Roberts**	COMPARING INDEPENDENT APPROACHES TO ESTIMATE AGE OF THE JONAH CRAB (*CANCER BOREALIS*): CORROBORATING GASTRIC MILL BAND COUNTS AS A DIRECT AGING METHOD **Huntsberger*, Wahle, Chen, Kilada**	LACCASE-SILICA NANOPARTICLE CONJUGATES CAN EFFICIENTLY REDUCE THE EARLY MATURATION RISK DUE TO BISPHENOL A (BPA) IN FEMALE *ORECHROMIS MOSSAMBICUS* AND ITS TOXIC LOAD FROM THE CONTAMINATED EFFLUENT **Manna* & Amutha**
1:15 PM	COMMERCIAL SCALE COMPARISON OF SELECTED WATER COLUMN OYSTER CULTURE GEAR TYPES AND NATIVE OYSTER STRAINS DEVELOPED FOR THE NORTH CAROLINA INDUSTRY **Weirich, Wilbur, Cerino**	SPATIO-TEMPORAL DYNAMICS OF PACIFIC OYSTERS MORTALITY PATTERNS ALONG THE FRENCH COAST: DISENTANGLING ORIGIN, AGING, AND ENVIRONMENTAL FACTORS **Fleury, Barbier, Normand, Pouvreau, Petton, Daigle, Pernet**	ESTIMATING SEASONAL GROWTH IN SEA SCALLOPS USING ISOTOPIC DATA IN A CHANGING ENVIRONMENT **Stokesbury & Inglis**	FINALLY, A TECHNIQUE TO AGE DECAPODS: PROGRESS WITH THE CARIBBEAN SPINY LOBSTER, *PANULIRUS ARGUS*, AND MANAGEMENT IMPLICATIONS **Gnanalingam, Butler[P], Matthews, Hutchinson, Kilada**	*SHRIMP SCAMPI*: A CITIZEN'S SCIENCE PROJECT TO EXAMINE LEVELS OF GLYPHOSATE AND OTHER ENDOCRINE DISRUPTING CHEMICAL (METALS BISPHENOL A) IN FROZEN SHRIMP SOLD IN SUPERMARKETS IN THE UNITED STATES **Hutchins, Berardi, Tanikella, Reyes, Warren, Yang, Zambrano*[P]**
1:30 PM	DEVELOPING A RESEARCH PROGRAM TO ADDRESS SHELLFISH GROWERS' NEEDS: NINIGRET POND – A CASE STUDY **Leavitt, Rheault, Kinney**	UNDERSTANDING THE PHYSIOLOGICAL MECHANISMS UNDERLYING THE ENHANCED SURVIVAL OF *CRASSOSTREA GIGAS* INFECTED BY THE OSTREID HERPESVIRUS 1 AT HIGH TEMPERATURE **Delisle*, Petton, Burguin, Quéré, Fleury, Pauletto, Morga, Artigaud, Pichereau, Corporeau, Pernet**	WARMING AND fCO_2 EFFECTS ON FLORIDA STONE CRAB LARVAE **Gravinese, Enochs, Manzello, van Woesik**	POPULATION CYCLES IN CRAB FISHERIES **Botsford**	TBA
1:45 PM	AQUACULTURE IN SHARED WATERS – AN AQUACULTURE TRAINING PROGRAM DESIGNED TO EXPLORE THE INTEGRATION OF FISHING AND FARMING IN MAINE **Morse, Bartlett, Battista, Belle, Cleaver, Cowperthwaite, Davis, Johnson, Springuel**	HOPING FOR THE BEST, PREPARING FOR THE WORST: DETERMINING RESISTANCE OF OYSTER SPECIES TO EXPOSURE TO OSHV-1 AND OSHV-1μVARS IN THE UNITED STATES **Burge, Reece, Rivlin, Wippel, Dar, Morga, Dégremont, Faury, Kirkland, Cortez, Sawyer, Moore, Friedman**	AN INTERTIDAL HOST-PARASITE SYSTEM: PREDICTING SOME OF THE EFFECTS OF CLIMATE CHANGE **Magalhães*, de Montaudouin, Figueira, Freitas**	ALIGNING BIOLOGY, ASSESSMENT, AND MANAGEMENT OF BLUE CRAB IN CHESAPEAKE BAY **Miller, Wilberg, Liang, Nesslage**	CHILDRENENCODE (2017-2027): REVIEW OF EPIGENETIC MECHANISMS ASSOCIATED WITH ENDROCRINE DISRUPTING CHEMICALS (GLYPHOSATE, METALS, BISPHENOL A) AND MICROBIAL TRANSGENE *BACILLUS THURINGIENSIS* IN SHELLFISH AND PEOPLE FROM ESTUARIES: A CASE STUDY OF METALS ASSOCIATED WITH MICROCEPHALY AND OTHER CONGENITAL MALFORMATIONS IN CHILDREN FROM SANTA ELENA PENINSULA OF ECUADOR **Alejandro-Tigrero, Alejandro-Rosales, Molina-Vasquez*[P], Espinoza, Matute, Hutchins, Berardi, Tanikella, Reyes, Zambrano, Argandoña, Alcivar-Arteaga, Ikeogu, Asogwa, Obodoefuna, Amutha, Alarcon, Zambrano-Basurto, Alcivar-Warren**
2:00 PM	OBSERVATIONS OF GAMETOGENESIS IN *CRASSOSTREA VIRGINICA* ASSOCIATED WITH TRIPLOID-SPECIFIC SPRING MORTALITIES ON COMMERCIAL FARMS IN THE CHESAPEAKE BAY **Matt*, Guévélou, Allen, Jr.**	HAEMOCYTES FROM *CRASSOSTREA GIGAS* AND OSHV-1: A PROMISING *IN VITRO* SYSTEM TO STUDY HOST/VIRUS INTERACTIONS **Morga, Faury, Guesdon, Chollet, Renault**	THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*, DEMONSTRATES SENSITIVITY TO TEMPERATURE AND RESILIENCE TO PH CHANGE DURING SUMMER GROWTH **Hesketh*, Simpson, Ianson, Kohfeld, Harley**	AN ECOLOGICAL FOUNDATION FOR THE RATIONAL MANAGEMENT OF THE FISHERY FOR CARIBBEAN SPINY LOBSTER (*PANULIRUS ARGUS*) **Butler, Gnanalingam, Kough, Paris**	
2:15 PM	GLYCOGEN CONTENT IN DIPLOID AND TRIPLOID *CRASSOSTREA VIRGINICA* DURING GAMETOGENESIS IN LOWER CHESAPEAKE BAY, USA **Guévélou, Matt, Allen, Jr.**	CHARACTERIZATION OF THE PACIFIC OYSTER MICROBIOME DURING A SUMMER MORTALITY EVENT **King*, Jenkins, Go, Siboni, Seymour, Labbate**	COMPARING NATIVE AND NON-NATIVE ESTUARINE SPECIES: DO MORE TOLERANT SPECIES HARBOR MORE GENES TO COMBAT CLIMATE CHANGE STRESS? **McIntyre*, Der, Zacherl, Walter**	ENCOURAGING DIAMONDBACK TERRAPIN CONSERVATION THROUGH COOPERATION WITH THE MISSISSIPPI BLUE CRAB FISHERY **Burris & Floyd**	BASIC RESEARCH NEEDED TO PRODUCE HEALTHY SHRIMP: A PUBLICLY AVAILABLE, FULLY-ASSEMBLED, REFERENCE GENOME FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) DOMESTICATED STOCKS OF *PENAEUS (LITOPENAEUS) VANNAMEI* IN THE UNITED STATES IS A PRIORITY **Alcivar-Warren, ShrimpENCODE Project Collaborators**
2:30 PM	SUMMER MORTALITY IN FARMED TRIPLOID AND DIPLOID OYSTERS, *CRASSOSTREA VIRGINICA*, IN THE NORTHERN GULF OF MEXICO **Wadsworth* &Walton**	SIMULATED MARINE HEAT WAVE ALTERS ABUNDANCE AND STRUCTURE OF *VIBRIO* POPULATIONS ASSOCIATED WITH THE PACIFIC OYSTER RESULTING IN A MASS MORTALITY EVENT **Green, Siboni, King, Seymour, Raftos**	LINKING GENOTYPE TO PHENOTYPE IN A CHANGING OCEAN: INFERRING THE GENOMIC ARCHITECTURE OF A BLUE MUSSEL STRESS RESPONSE **Kingston, Martino, Melendy, Reed, Carlon**	**Discussion**	**Discussion**
2:45PM	OYSTER INFESTATION: ABUNDANCE OF MUDBLISTER WORMS (*POLYDORA WERSTERI*) IN ALABAMA COASTAL OYSTER FARMS **Cole*, Dorgan, Walton**				
3:00 PM	THE COSTS OF REGULATORY COMPLIANCE ON WEST COAST SHELLFISH FARMS: EFFECTS AND IMPACTS ON PRODUCERS **van Senten & Engle**				
3:15 PM					
3:30 – 6:00 PM	**CLOSING HAPPY HOUR** **Madison Ballroom**				

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

CONTENTS

ORAL PRESENTATIONS

POSTER PRESENTATIONS

RECOGNIZING HOW LNC VARIATIONS EXPOSE OLYMPIA OYSTER POPULATIONS TO THERMAL RISK

John Adams

Sound Fresh Clams and Oysters, SE 222 Sells Dr, Shelton, Washington 98584 USA

johna@skookumpoint.com

The 18.6 year Lunar Nodal Cycle (LNC) shapes ecological conditions and changes risk factors for intertidal organisms. The 2024 LNC maximum presents as many as 40 low tides lower than a -2.5 tide level. This is in contrast to the 2014 LNC minimum which presented 4 low tides lower than the -2.5 level. The ten-fold increase in low tide exposure to summer and winter temperature extremes exploits the thermal vulnerabilities of Olympia oyster populations. Additionally, the LNC creates dramatic differences in current velocities, estuary flushing rates, and air/water temperatures thus impacting estuary ecologies. With these, conditions, one can conclude that multiple thermal events in the years centered upon the 2024 LNC max will result in a 70% mortality of the Olympia oyster populations above the -1.3 tide level.

USE OF THE ENVIRONMENTAL SAMPLE PROCESSOR FOR NEAR-REAL TIME DETECTION OF HARMFUL ALGAL SPECIES AND DOMOIC ACID IN THE PACIFIC NORTHWEST

Nicolaus G. Adams[1*], Stephanie K. Moore[1], John B. Mickett[2], Tina Mikulski[3], Gregory J. Doucette[3], and James M. Birch[4]

[1]NOAA-Fisheries, Northwest Fisheries Science Center, 2725 Montlake Blvd. E., Seattle, Washington, 98112 USA

[2]University of Washington, Applied Physics Laboratory, 1013 NE 40th St., Seattle, Washington, 98105 USA

[3]NOAA-National Ocean Service, National Centers for Coastal Ocean Science, 219 Fort Johnson Rd., Charleston, South Carolina, 29412 USA

[4]Monterey Bay Aquarium Research Institute, 7700 Sandholdt Rd., Moss Landing, California 95039 USA

Nicolaus.Adams@noaa.gov

Closures of shellfish harvesting in the Pacific Northwest (PNW) due to harmful algal bloom (HAB) toxins can occur with little warning and result in significant economic losses to shellfish growers and coastal communities. The Environmental Sample Processor (ESP) is an *in situ*, autonomous robotic platform that can collect water samples and conduct quantitative harmful algal cell and toxin analyses in near real-time. In 2012 and 2013, the ESP was deployed shore side at shellfish beds in Puget Sound and in 2016 and 2017, the ESP was installed on an open-water mooring ~15 miles off the Washington State coast. Harmful algal (e.g., *Alexandrium* spp., *Pseudo-nitzschia* spp.) and bacterial targets (e.g., *Vibrio, Bacteroides*) were detected with DNA- and RNA-based methodologies, while the neurotoxin domoic acid was detected using an antibody-based assay. Low densities/concentrations (e.g., 5 ng/L domoic acid) were detected, demonstrating the ability of the ESP to identify HAB and their toxins before they impact shellfish and threaten public health or economic interests. Near-real time data were distributed to end-users through the PNW regional ocean observing system (NANOOS) of the Integrated Ocean Observing System. In 2017, ESP data were incorporated into the PNW HAB Bulletin, a synthesis of HAB risk to inform management decisions to protect shellfish resources and coastal communities. The ESP platform can be expanded to include new HAB species and toxins in the PNW, such as *Azadinium* spp. or *Dinophysis* spp. and diarrhetic shellfish toxins, making it a powerful tool for detecting HAB of emerging importance in the region.

USE OF A QPCR ASSAY TO DETECT THE TREMATODE, *PROCTOECES MACULATUS,* IN WATER COLUMN SAMPLES

M. Victoria Agnew*, Abigail Scro, and Roxanna Smolowitz

Aquatic Diagnostic Laboratory, Roger Williams University, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

m.victoria.agnew@gmail.com

The digenetic trematode, *Proctoeces maculatus,* is known to infect the blue mussel, *Mytilus edulis.* Recent data collected by this lab demonstrates a strong relationship between severity of infections and mortality events, which may both increase with rising seawater temperatures. *P. maculatus* is known to have a multi-host life cycle. The cercaria produced in an intermediate host leaves the host and enters the water column to infect various fish species, their definitive host. Theoretically, this migration would lead to an increase of trematodes in the water column. Additionally, eggs and the second life stage of the parasite, miracidia, are released into the water column with the fish feces. The ability to detect and quantify the relative abundance of *P. maculatus* in water samples could make it possible to better understand, monitor and manage mass mortality outbreaks in blue mussel culture. Multiple primer pairs were designed to target the 18S ribosomal DNA (rDNA) of *P. maculatus* to be used in a quantitative polymerase chain reaction (qPCR). These primers resulted in false amplification of species other than *P. maculatus*. A published primer pair targeting the 18S rDNA region was also used that was capable of detecting a single cercaria in one liter of water without false amplification. Water samples collected in the summer of 2016 near mussel beds were run in this assay. Although water collection methods require further study, initial results show this is a promising assay to accurately detect *P. maculatus* in water samples.

ONE HEALTH EPIGENOMICS AND MICROBIOMES: FROM SOIL TO PEOPLE WORKSHOP

Acacia Alcivar-Warren

ONE HEALTH Epigenomics – A Global Educational Initiative, Environmental Genomics Inc., P.O. Box 196, Southborough, Massachusetts 01772 USA

environmentalgenomics.warren@gmail.com

The 'ONE HEALTH Epigenomics and Microbiomes: From Soil to People' workshop focus on application of the holistic concept of ONE HEALTH to conserve healthy ecosystems (agricultural soil, sediment of mangroves forests), to maintain healthy animals (shrimp/shellfish, fish), to protect human health long-term (antibiotic resistance, zoonoses, obesity, diabetes, microcephaly and other neural tube defects, among others).

Speakers will address issues related to research projects planned for 2017-2027, discussed at the 'ONE HEALTH Epigenomics and Microbiomes: From Soil to People' Symposium held in Framingham, MA, March 16-18, 2017. Topics include: Present status of mangrove ecosystems in Mexico; MangroveENCODE: developing technologies for assessment of $C0_2$, microbiome, EDCs and microbial transgenes in mangroves sediments and agricultural soil; Transposable elements of specific pathogen-free (SPF) *Litopenaeus vannamei* - review of horizontal transfer of transposons; The *NonLTR-1_LVa* non-LTR retrotranspon of SPF *L. vannamei* is homologous to the NLRS non-LTR retrotransposon associated with abdominal segment deformity disease (ASDD) of cultivated shrimp; Oligomerization patterns of PirA and PirB causing AHPND and its interaction with the membrane components of the epithelial cells of the shrimp hepatopancreas; *Shrimp Scampi*: a Citizen Science project to examine glyphosate and other EDCs in shrimp sold at US supermarkets; Seafood safety and food security – who is in charge?; ChildrenENCODE: epigenetic mechanisms associated with EDCs in shrimp and people from estuaries - a case study of metals associated with congenital malformations of children of the Santa Elena peninsula of Ecuador; and Basic research needed to produce healthy shrimp. A group discussion will follow.

SHRIMP EPIGENOME (SHRIMPENCODE) PROJECT SESSION ACACIA ALCIVAR-WARREN

Environmental Genomics Inc., P.O. Box 196, Southborough, Massachusetts 01772 USA

environmentalgenomics.warren@gmail.com

The 'ShrimpENCODE' session focus on application of the holistic concept of ONE HEALTH to conserve healthy ecosystems (agricultural soil, sediment of mangroves forests and wetlands), to maintain healthy animals (shrimp/shellfish, fish), to protect human health long-term (antibiotic resistance, zoonoses, obesity, diabetes, microcephaly and other neural tube defects, among others).

Speakers will address: efforts towards understanding the epigenetic mechanisms associated with exposure of Pacific white shrimp, *Penaeus* (*Litopenaeus*) *vannamei* to acute hepatopancreatic necrosis disease (AHPND)-causing *Vibrio* spp. and microbial transgenes; epigenetic re-programming upon foreign (viral) DNA invasion into cells; viral diseases of shrimp [white spot syndrome virus (WSSV), infectious hypodermal and hematopoietic necrosis virus (IHHNV)], understanding the molecular basis of susceptibility to WSSV in shrimp, WSSV-like element, *DNAV-1_LVa*, in SPF *L. vannamei* domesticated in the United States; polymorphisms in *RTE-3_LVa* non-LTR retrotransposon of SPF *L. vannamei* from the United States: its association with the *Penaeus monodon* endogenous virus IHHNV from Africa and Australia; the PirAB toxin-producing genes of *Vibrio* spp. have a function similar to the *Bacillus thuringiensis* Cry proteins; Transposase DDE domain and N-6 DNA Methylase family proteins as potential epigenetic marks of pathogenic AHPND-causing *Vibrio* spp. from Asia and Latin America; and a global pathogen surveillance system based on real-time, informed genomic sequencing technologies; the microbiome of the Pacific whiteleg shrimp (*L. vannamei*) in wild, aquacultured and AHPND/EMS outbreak conditions; evaluation of marine bacteria and their potential use as feed additive and probiotic agent against pathogenic *V. parahaemolyticus* (AHPND) in white shrimp *L. vannamei*; and efforts towards a genomics-informed, real-time, global pathogen surveillance system. A group discussion will follow.

BASIC RESEARCH NEEDED TO PRODUCE HEALTHY SHRIMP: A PUBLICLY AVAILABLE, FULLY-ASSEMBLED, REFERENCE GENOME FROM THE FIRST SPECIFIC PATHOGEN-FREE (SPF) DOMESTICATED STOCKS OF *PENAEUS* (*LITOPENAEUS*) *VANNAMEI* IN THE UNITED STATES IS A PRIORITY

Acacia Alcivar-Warren[1,2]* and ShrimpENCODE collaborators

[1]The Shrimp Epigenome (ShrimpENCODE) Project, Environmental Genomics Inc., P.O. Box 196, Southborough, Massachusetts 01772 USA

[2]Fundacion para la Conservacion de la Biodiversidad Acuatica y Terrestre (FUCOBI), Quito, Ecuador

environmentalgenomics.warren@gmail.com

A review of shrimp aquaculture genomics, genetics and breeding will be presented. Evidence of horizontal gene transfer, horizontal transfer of transposons, genome rearrangements, and genome size variation will be discussed, with comments on the current genome assembly of *Litopenaeus vannamei* published by Abdelrahman et al. [BMC Genomics (2017) 18:191], particularly considering the serious Acute Hepatopancreatic Necrosis Disease (AHPND), also known as Early Mortality Syndrome (EMS), caused by *Vibrio* spp.

The presence of a fossilized white spot virus (WSSV)-like element in the genome of the first SPF *L. vannamei* domesticated in

the United States will be used to highlight the need for a publicly available, fully-assembled, new reference genome sequence from the first domesticated stocks of *L. vannamei*. Recommendations for basic research needed to produce healthy shrimp will be made on behalf of shrimp geneticists, breeders, animal welfare and food safety advocates, and experts on genomics and epigenetics.

A group discussion will follow about distribution of tissue or DNA samples from the original SPF broodstock used in the breeding program of the US Marine Shrimp Farming Program funded by the USDA.

SHRIMPENCODE (2017-2027): TOWARDS UNDERSTANDING THE EPIGENETIC MECHANISMS AND TRANSGENERATIONAL INHERITANCE ASSOCIATED WITH EXPOSURE OF SPF SHRIMP, *PENAEUS* (*LITOPENAEUS*) *VANNAMEI*, TO ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND)-CAUSING *VIBRIO* SPP. AND MICROBIAL TRANSGENE INSECTICIDE, *BACILLUS THURINGIENSIS*

Acacia Alcivar-Warren* and ShrimpENCODE collaborators

The Shrimp Epigenome (ShrimpENCODE) Project, Environmental Genomics Inc., P.O. Box 196, Southborough, Massachusetts 01772 USA

environmentalgenomics.warren@gmail.com

Acute hepatopancreatic necrosis disease (AHPND), also known as early mortality syndrome (EMS), causes significant economic losses to the shrimp industry worldwide. AHPND began in China in 2009 and spread quickly to Vietnam (2010), Malaysia (2011), Thailand (2012), Mexico (2013), and Ecuador (2015). The disease affects both *Penaeus monodon* and *Litopenaeus vannamei*, characterized by mass mortalities (up to 100%) during the first 20-30 days of culture (post-stocking in grow-out ponds). Clinical signs include slow growth, corkscrew swimming, loose shells, as well as pale coloration, abnormal hepatopancreas (shrunken, small, swollen or discolored). To date, very limited information is available on the genomic and epigenetic mechanisms associated with *Vibrio* spp. that cause AHPND in the most economically important farmed species, the Pacific white shrimp, *L. vannamei*.

AHPND-causing *Vibrio parahaemolyticus* and *V. campbellii* contain a conjugative plasmid with the transposon Tn6264, also known as PirAB-Tn903, that codes for PirAB toxins that are similar in function to the Cry proteins of *Bacillus thuringiensis* (Bt). A Tn3-like transposon is also present in Vp strains from Latin America.

A review of the scientific literature on health considerations associated with horizontal transfer of microbial transgenes (*Bacillus thuringiensis*, *Agrobacterium tumefaciens*) will be presented. The proposed hypothesis and experimental designs to study the epigenetic mechanisms and transgenerational inheritance of susceptibility to AHPND will be discussed.

SHRIMPENCODE (2017-2027): TRANSPOSABLE ELEMENTS OF THE ORIGINAL SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *PENAEUS* (*LITOPENAEUS*) *VANNAMEI*, DOMESTICATED IN THE UNITED STATES – REVIEW OF HORIZONTAL TRANSFER OF TRANSPOSONS (HTT) ASSOCIATED WITH SHRIMP DISEASES

Acacia Alcivar-Warren* and ShrimpENCODE Project Collaborators

The Shrimp Epigenome (ShrimpENCODE) Project, Environmental Genomics, Inc., Massachusetts, USA

environmentalgenomics.warren@gmail.com

The goal of ShrimpENCODE is to understand the epigenetic mechanisms associated with susceptibility of *L. vannamei* to acute hepatopancreatic necrosis disease (AHPND). It was proposed that transposition of mobile genetic elements [transposable elements (TEs)], among AHPND-causing *Vibrio* spp. occurs via horizontal transfer (HGT) of transposase (Tpase), of transposons (HTT), and transgenerational epigenetic inheritance. To test this hypothesis, a fully-assembled reference genome sequence was needed. HMW DNA from the original SPF stocks of *L. vannamei,* developed by the US Marine Shrimp Farming Program was subject to pilot whole genome sequencing using 20K PacBio SMRTCell libraries and running on Pacific Bioscience RSII platform with P5 chemistry.

Approximately 55% of the assembled 9.6 Mb is repetitive sequences, of which ~50% is simple or satellite sequences, AT-rich (GC%=15.5), other half is interspersed transposons, GC-rich (GC%=45.3). 110 TEs were characterized from 2 LTR retrotransposon clades [Gypsy, BEL], 9 non-LTR retrotransposons [RTE, Penelope, CR1, Jockey, Ingi, Nimb, Proto2, Vingi, SINE, NonLTR], 6 DNA transposons [Harbinger, Mariner, MuDRx, Polinton, Piggyback, Merlin], 2 Satellite sequences, 4 TEs, 11 DNA transposons, and a WSSV-like *DNAV-1_LVa* element. Sequences are deposited in Repbase Reports 2015, Vol 15(4); www.girinst.org.

Two non-LTR retrotransposons are associated with shrimp diseases: *RTE-3_LVa* is associated with the *P. monodon* endogenous virus IHHNV (DQ228358); *NonLTR-1_LVa* with ASDD of cultured *L. vannamei* from Thailand; they are not horizontally transferred. 16 *L. vannamei* TE families are likely to be involved in HTT events; transcripts involved in HTT events may play roles in antiviral immunity. *L. vannamei* transcript FE114166 may originate from Gypsy family (Gypsy-22_GM-I) of soybean, *Glycine max*.

THE *NONLTR-1_LVA* NON-LTR RETROTRANSPON OF SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *LITOPENAEUS VANNAMEI,* FROM THE UNITED STATES IS HOMOLOGOUS TO THE NLRS NON-LTR RETROTRANSPOSON ASSOCIATED WITH ABDOMINAL SEGMENT DEFORMITY DISEASE (ASDD) OF CULTIVATED SHRIMP FROM THAILAND

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

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

[2]UNA SALUD / ONE HEALTH Epigenomics and Microbiomes Program, FUCOBI Foundation, Quito, Ecuador

[3]Genetics Information Research Institute, 465 Fairchild Drive, Suite 201, Mountain View, California 94043 USA

fucobi@gmail.com

Abdominal Segment Deformity Disease (ASDD) of cultivated Pacific white shrimp, *Litopenaeus vannamei,* from Thailand was associated with a partial non-long terminal repeat (non-LTR) element (NLRS) (KC179708, 4161 bp). ASDD was initially associated with the presence of viral-like particles seen by electron microscopy in ventral nerve cords of affected shrimp. Using the NLRS probe, *in situ* hybridization signals were detected in abdominal-ganglion neurons of the distorted abdominal muscles of shrimp with ASDD, but were not detected in normal shrimp. ASDD appears related to inbreeding and long-term use of eyestalk-ablated female broodstock used in commercial hatcheries, and increased prevalence in mysis stage offspring from those broodstock.

Nucleotides 5-4101 of NLRS are 96% identical to nucleotides 1976-6062 of a young non-LTR family, *NonLTR-1_LVa* [6180-bp, Bao 2015, Repbase Reports 15(4), 1579], which is reconstructed from the original SPF *L. vannamei* stocks domesticated by the US Marine Shrimp Farming Program in 1992, and used around the world. *NonLTR-1_LVa* contains 50% CG, two ORF, and three conserved protein domains: RT_nLTR_like, group_II_RT_mat, and RVT_1 [RT, RNA-dependent DNA polymerase].

NonLTR-1_LVa is expressed in *L. vannamei* transcriptomes from ovary of intact and ablated females, testis, hepatopancreas, muscle and other tissues of juveniles and adult shrimp, developmental stages (nauplius, zoea, mysis, poslarvae), and shrimp exposed to environmental stress conditions. Significant identities found in transcriptomes of farmed *L. vannamei* from Thailand, USA and Brazil; wild *L. vannamei* and *Farfanepenaeus aztecus* from Mexico; and wild *P. monodon* and *M. japonicus* from China. Sequence comparisons of NonLTR clade with those of other Penaeid genomes will be presented.

TRANSPOSASE DDE DOMAINS AND N-6 DNA METHYLASE FAMILY PROTEINS AS POTENTIAL EPIGENETIC MARKS OF PATHOGENIC *VIBRIO* SPP. FROM ASIA (CHINA, VIETNAM, THAILAND) AND LATIN AMERICA (MEXICO, ECUADOR) THAT CAUSE ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) IN SHRIMP

Acacia Alcivar-Warren[1,2], Bruno Gomez-Gil[3], Sonia Soto-Rodriguez[3], Zhenkang Xu[1], and Daniela Espinoza[2*]

[1]The Shrimp Epigenome (ShrimpENCODE) Project, Environmental Genomics Inc., P.O. Box 196, Southborough, Massachusetts 01772 USA

[2]Programa 'UNA SALUD / ONE HEALTH Epigenomics and Microbiomes: Somos lo que comemos / We are what we eat', FUCOBI Foundation, Quito, Ecuador

[3]Centro de Investigacion en Alimentacion y Desarrollo (CIAD), AC Mazatlán Unit for Aquaculture AP 711, Mazatlán, Sinaloa, México 82000

fucobi@gmail.com

Transposases (Tpases) cleave the ends of transposons, mediating the spread of virulence and antibiotic resistance genes among bacteria. Horizontal gene transfer (HGT) and DNA methylation contribute significantly to virulence development of *Vibrio parahaemolyticus,* but limited information is available on genomic and epigenetic mechanisms associated with *Vibrio* spp. that cause acute hepatopancreatic necrosis disease (AHPND) in *Penaeus vannamei*. The PirAB toxins in transposon Tn6264 are similar in function to Cry proteins of *Bacillus thuringiensis*. Tn6264 is flanked by ISVal1-like Tpases with domains DDE_Tnp_1 and DDE_Tnp_1_5 (IS5), flanked by N-6 DNA methylases.

A Tn3-like transposon is only in Latin America strains, inserted in an YhgA-like Tpase, contains DDE_Tnp_Tn3 domain and a resolvase. A DNA sequence (Lv1.9b, 739 bp) from ovary of SPF *P. vannamei* is similar to ISEc63 (Tn3) Tpase, and contains DDE_Tnp_Tn3 and LacZ B-galactosidase domains. Lv1.9b is expressed in *P. vannamei* from Brazil (JR494595), contains four GATC motifs. GATC is methylated by DNA adenine methyltransferase (*Dam*), known to silence transposons in some bacterial genomes.

A zinc transporter close to a pathogenic island was HGTed (IS91) to Vp strain from China, providing fitness for Vp. IS91 (Zn-binding domain) transposes when Zn levels in water are very low, interactions with AHPND strains suggest metal complexes are potential virulence mechanism. IS91 locates upstream of N-6 DNA methylase. When the combined IS91, DNA Methylase and Tpase sequences of Tn6264 were blasted against WGS databases, they were only found in pathogenic *Vibrio* spp., suggesting that both DNA transposition and DNA methylation enzymes are potential epigenetic marks for virulence.

CHILDRENENCODE (2017-2027): REVIEW OF EPIGENETIC MECHANISMS ASSOCIATED WITH ENDOCRINE DISRUPTING CHEMICALS (GLYPHOSATE, METALS, BISPHENOL A) AND MICROBIAL TRANSGENE *BACILLUS THURINGIENSIS* IN SHELLFISH AND PEOPLE FROM ESTUARIES: A CASE STUDY OF METALS ASSOCIATED WITH MICROCEPHALY AND OTHER CONGENITAL MALFORMATIONS IN CHILDREN FROM THE SANTA ELENA PENINSULA OF ECUADOR

Diego Alejandro-Tigrero[1], Karina Alejandro-Rosales[1], Kelvin Molina-Vasquez[1]*, Daniela Espinoza[1], Ana Lucia Matute[1], Ryan Hutchins[2], Allison Berardi[2], Sruthi Tanikella[2], Martha Reyes[2], Ayron Zambrano[1], Cristhian Argandoña[1], Miriam Alcivar-Arteaga[1], Chika Ikeogu[3], E.T. Asogwa[3], S.M. Obodoefuna[3], Chinnaiah Amutha[4], Karol Alarcon[1], Sara Zambrano-Basurto[2], Acacia Alcivar-Warren[1,2]

[1]The Coastal People Epigenome (ChildrenENCODE) Project, UNA SALUD / ONE HEALTH Epigenomics: Somos lo que comemos / We are what we eat' Program, FUCOBI Foundation, Quito, Ecuador

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

[3] Nnamdi Azikiwe University, Department of Fisheries and Aquaculture, Awka. Nigeria

[4]School of Biological Sciences, Madurai Kamaraj University, Madurai-625 021, Tamilnadu, India

fucobi@gmail.com

The goal of ChildrenENCODE is to understand epigenetic mechanisms underlying exposure effects to endocrine disrupting chemicals (EDC). About 800 coastal people participated in a pilot project to assess consumption habits and health status, including people from Santa Elena where ~270 cases of neural tube defects (NTD) in children were documented. Most (~100) NTD were anencephaly, also microcephaly, cyclopia, others. NTD causation involves interplay of fetal genes, environmental factors, epigenetics determining susceptibility. Eight of 30 metals in hair of 14 mothers of NTD children had levels above maximum allowed.

Glyphosate (G) causes microcephaly in chicken embryos, is also antimicrobial, biocide. As, Co, Cr, Ni, Pb levels are high in G-based pesticide formulations. Roundup (G) has a direct effect on gut microbiota, changed susceptibility of *E. coli* and *S. enterica* to multiple antibiotics. PirAB toxins in *Vibrio* spp. that cause AHPND in shrimp are similar in function to Cry proteins of *Bacillus thuringiensis* (Bt), also used to control mosquitos (microcephaly-associated Zika). G and Bt are used in shrimp farms near estuaries.

Epigenetic mechanisms associated with G, metals, Bisphenol A (BPA), Bt: G induces DNA methylation in human cells. Cd: global DNA hypermethylation in gastropods, gene-specific hypomethylation cancer, kidney disease. As: hypomethylation, cancer diabetes. Cd and other metals are found in shellfish (oysters, mussels, clams, scallops), concentrations from the Pacific Northwest are greater than values reported for shellfish from other regions of the world. BPA: alters DNA methylation, cancer, heart conditions. Bt resistance influences histone acetylation, DNA methylation, miRNAs in resistant and susceptible larvae, repress genes that confer Bt susceptibility.

FAMILY-BASED GENETIC PARAMETERS FOR TETRAPLOID *CRASSOSTREA VIRGINICA* AND BREEDING IMPLICATIONS

Standish K. Allen, Jr.[1]*, J.M. Small[1], and Peter D. Kube[2]

[1]Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center, Gloucester Point, Virginia 23062 USA

[2]CSIRO Agriculture Flagship, Hobart, 7000, Australia

ska@vims.edu

Aquaculture of triploids *Crassostrea virginica* is popular in the mid-Atlantic and increasingly along the East and Gulf coast of the USA. Production of triploids is driven by the availability of tetraploid brood stock to commercial hatcheries. The Aquaculture Genetics and Breeding Technology Center (ABC) has been trying to determine the important traits to emphasize for tetraploids in our breeding program. Past research has focused on aspects of chromosome instability (CIN) and its contribution to either triploid production or tetraploid propagation.

Recently, ABC has begun a family based breeding program with tetraploids in order to partition the genetic components of traits, not only the "usual suspects," such as growth and survival, but also traits concerning CIN. For example, from within and among 4n families we obtain information on relative DNA content (the amount of DNA in a tetraploid compared to a diploid standard as measured by flow cytometry), extent of mosaicism, and sex ratio. These data are treated as traits in standard ASREML analysis.

From the first set of data from the field from tetraploid families, heritabilities for length, total weight, meat weight and survival are relatively high, ranging from 0.52-0.73. Heritabilities for CIN traits were variable. For example, h^2 for relative DNA content was high, 0.68. Heritability for the degree to which a family becomes a heteroploid mosaic was low, 0.16. There was a strong negative genetic correlation between reversion intensity and morphometric traits (length, total weight, and meat weight) demonstrating the detrimental effects of CIN. The appropriateness of using diploid ASERML models for tetraploids will be discussed.

VARIABLE SPATIAL AND TEMPORAL OCEAN CONDITIONS IMPACT PHYSIOLOGICAL PERFORMANCE OF BIVALVES IN PUGET SOUND, WASHINGTON, USA

Lindsay Alma*[1], Courtney Fiamengo[1], Simone Alin[2], Molly Jackson[1,3], and Jacqueline Padilla-Gamino[1]

[1]University of Washington, School of Aquatic and Fishery Sciences, 1122 NE Boat St., Seattle, Washington 98195 USA

[2]National Oceanic and Atmospheric Administration/Pacific Marine Environmental Laboratory (NOAA/PMEL), 7600 Sand Point Way NE, Seattle, Washington 98115 USA

[3]Taylor Shellfish Hatchery, 701 Broadspit Rd., Quilcene, Washington 98376 USA

lalma@uw.edu

Global change stressors such as hypoxia, ocean acidification, salinity, and thermal stress can heavily affect marine invertebrate physiological performance, survival, metabolism, and shell integrity. The Pacific Coast of North America has already experienced changes in ocean patterns and these conditions are expected to worsen in the near-future as more carbon dioxide is added to the atmosphere at an exponential rate. The results of this project explore how key bivalve physiological performance metrics are impacted by variations in depth and season, specifically in two economically and ecologically important species, the Mediterranean mussel (*Mytilus galloprovincialis*), and the purple-hinge rock scallop (*Crassodoma gigantea*). Organisms were held at two depths (5 m and 30 m) for six months within the Puget Sound, Washington and allowed to acclimate to different environmental regimes. Results of this study reveal that both species had significantly greater growth rates at the 5 m depth in warmer summer months. Shell integrity of mussels was significantly impacted by both depth and season of collection, while scallop shells were only affected by season and not depth of acclimation. Finally, the standard metabolic rate of both species was heavily impacted by laboratory thermal stress treatments, namely those acclimated to 30 m; however, there were no significant differences between groups with varying pH laboratory treatments. These results have contributed to our understanding of seasonal variation on oceanographic conditions and their effects on bivalve performance at multiple levels.

ENVIRONMENTAL DRIVERS OF THE SPATIAL AND TEMPORAL DISTRIBUTION OF SPAWNING BLUE CRABS, *CALLINECTES SAPIDUS,* IN THE WESTERN GULF OF MEXICO

Joel Anderson[1], Zachary Olsen[2], Tom Wagner[3]*, Carey Gelpi[4], and Darin Topping[3]

[1]Texas Parks & Wildlife Department, Perry R Bass Marine Fisheries Research Station, 3864 FM 3280, Palacios, Texas 77465 USA

[2]Texas Parks & Wildlife Department, 6300 Ocean Drive, Unit 5845, Corpus Christi, Texas 78412 USA

[3]Texas Parks & Wildlife Department, 702 Navigation Circle, Rockport, Texas 78382 USA

[4]Texas Parks & Wildlife Department, 601 Channelview, Port Arthur, Texas 77640 USA

Tom.Wagner@tpwd.texas.gov

Recent declines in abundance of blue crabs, *Callinectes sapidus,* throughout the species range have driven progressive management, including protection of spawning females by establishing "no-take" zones on the Atlantic coast. To date, no-take zones have not been established in the western Gulf of Mexico, although annual closures associated with mitigation of derelict traps exist in both Texas and Louisiana. Long-term fishery-independent data collected by the Texas Parks and Wildlife Department were used to assess spatial and seasonal distribution of spawning females in order to inform future evaluations of no-take areas in Texas. The presence of spawning females was modeled statistically by using water quality and spatial variables as predictors. Distance to the nearest Gulf pass was the most reliable predictor of presence, accounting for over 43% of the deviance observed in models from two independent sampling eras. Salinity and temperature were also reliable predictors, and the values of salinity and temperature that were associated with peak presence remained consistent over an approximately 30-year span despite increasing mean annual values of both variables through time. Peak presence in spawning grounds now occurs in early spring (March–April), contrasting with historical peak presence in the summer (June–July). These data imply seasonal shifts in spawning behavior despite relative spatial consistency through time, suggesting that Gulf pass areas would be ideal for protection of spawning blue crabs via no-take zones if such a measure is deemed necessary.

SHELLFISH LEASING AND PERMITTING: CASE STUDIES FOR OVERCOMING COMMON LEGAL BARRIERS

Elizabeth Andrews

Virginia Coastal Policy Center, William & Mary Law School, PO Box 8795, Williamsburg, Virginia 23187 USA

eaandrews@wm.edu

Aquaculturists today face challenges such as a state permitting landscape that can be confusing and complicated, and waterfront use conflicts that can arise due to the growth of the shellfish industry in highly populated coastal areas. This presentation will feature two case studies highlighting these issues and potential solutions that can be used to advance aquaculture.

The first case study concerns the development of a quick-use guide for novice aquaculturists in Virginia. The guide will discuss issues such as operation startup costs, the process for determining available locations for aquaculture, fulfillment of bonding requirements, filling out state and federal forms, and responsibilities associated with aquaculture farming.

The second case study focuses on the relationship between aquaculturists, homeowners, the state regulatory agency, and legislators in Virginia, focusing on the events surrounding the resurgence of aquaculture in the Lynnhaven River as water quality has improved. The case study will feature successful communication between groups, problems still unresolved, changes in statutory requirements in response to the situation, and future steps to improve communication and cooperation between the varying groups.

COMPARISON OF GROWTH CURVES OF THE GEODUCK, *PANOPEA GLOBOSA,* FROM FOUR FISHING ZONES IN NORTHWESTERN MEXICO

E. Alberto Aragón-Noriega[1*], Rolando Cruz-Vásquez[2], Sergio G. Castillo-Vargasmachuca[2], Guillermo Rodríguez-Domínguez[3], Edgar Alcántara-Razo[1], Jesús T. Ponce-Palafox[2], and J. Armando López-Sánchez[2]

[1]Centro de Investigaciones Biológicas del Noroeste, Unidad Sonora. Km 2.35 Camino al Tular, Estero Bacochibampo, Guaymas, Sonora 85454, Mexico

[2]Posgrado en Ciencias Biológico Agropecuarias, Universidad Autónoma de Nayarit, Carretera Tepic-Compostela Km 9 Xalisco, Nayarit 63780, Mexico

[3]Universidad Autónoma de Sinaloa, Facultad de Ciencias del Mar, Paseo Claussen S/N, Col. Los Pinitos, Mazatlán, Sinaloa 82000, Mexico

aaragon04@cibnor.mx

The Kimura's likelihood ratio test was used to compare growth curves of *Panopea globosa* from four fishing zones in Northwestern Mexico, three inside the Gulf of California (Guaymas, Puerto Peñasco, and San Felipe), and one in the Pacific coast of southern Baja California Peninsula (Bahía Magdalena). The curves were generated using the von Bertalanffy growth model. The lengths-at-age data for each location were obtained from fishery-independent data each location. The average asymptotic lengths were 114.4 mm, 156.6 mm, 161.5 mm, and 168.4 mm, respectively, for each location in the order listed above. These findings provided good evidence that the largest individuals are present in the northern fishing zones and the Pacific coast there were no significant differences in length between them. The location from the central Gulf of California was the shortest with a significant difference in length at the others three sites. Because the fishing management strategy for this species uses the minimum legal size (MLS), the conclusion is that MLS should be regionally different to achieve a sustainable exploitation.

DO PARASITES OF THE GENUS *MIKROCYTOS* PRESENT A RISK FOR THE PRODUCTION OF SHELLFISH IN EUROPE?

Isabelle Arzul*[1], Coralie Lupo[1], Marc Engelsma[2], and Céline Garcia[1]

[1]Ifremer, SG2M-LGPMM, av de Mus de Loup, 17390 La Tremblade, France

[2]Wageningen Bioveterinary Research, P.O. Box 65, 8200 AB Lelystad, The Netherlands

Isabelle.Arzul@ifremer.fr

For many years, *Mikrocytos mackini* had been the only representative of the genus *Mikrocytos*. Its geographic range appears restricted to the west coast North America. It has never been reported in Europe. Parasites similar to *M. mackini* have recently been observed in bivalve species in different parts of the world. Such parasites have notably been detected during mortality events in oysters and clams in Europe. A new species, *M. mimicus*, has been described in cupped oysters, *Crassostrea gigas,* in the United Kingdom and The Netherlands. Two additional species, *M. donaxi* and *M. veneroïdes* have also been characterized from clams, *Donax trunculus,* in France.

The presence of the genus *Mikrocytos* in Europe questions its potential risks for the local shellfish production. An exercise has been undertaken in order to identify zones suitable for *M. mackini* introduction and spread in Charente Maritime, the main oyster producing area in France. Geographical data were obtained for risk factors identified from the literature and prioritized based on experts' opinion. This study has estimated that the risk of introduction of *M. mackini* is low whereas there is a high risk of establishment of the infection in February to March in few areas.

The detection of several *Mikrocytos* species in Europe in the context of bivalve mortality and the identification of suitable sites for the establishment of infection of *M. mackini* suggest that these parasites present a risk for the shellfish production and highlight the need for an active surveillance regarding this parasite genus at the European level.

SHELLFISH INDUSTRY IN EU: AN EXERCISE OF STAKEHOLDERS MAPPING

Isabelle Arzul[1], Jean Prou[1], Estelle Delangle[1], Paola Venier[2], Deborah Cheslett[3], Dolors Furones[4], Rebeca Moreira[5], Romina Ventura[4], Antonio Figueras[5], Steve Feist[6], and Coralie Lupo[1]

[1] IFREMER-SG2M-LGPMM-av de Mus de Loup, 17390 La Tremblade-France

[2]Universita Degli Studi Di Padova, Dipartimento di Biologia, Viale Giuseppe Colombo,3 - Via Ugo Bassi,58/B – Padova, Italy

[3]Marine Institute, Rinville, Galway, Ireland

[4]Investigacion y Technologia Agroalimentarias (IRTA), Crta. Poble Nou, km. 5'5 43540 Sant Carles de la Ràpita, Spain

[5]Consejo Superior de Investigaciones Científicas (CSIC) Instituto de Investigaciones Marinas, Rúa de Eduardo Cabello, 6, 36208 Vigo, Pontevedra, Spain

[6]Cefas, Weymouth Laboratory, Barrack Road, The Nothe, Weymouth, Dorset. DT4 8UB, United Kingdom

Isabelle.Arzul@ifremer.fr

The European project VIVALDI (PreVenting and mItigating farmed bivalve DIseases) aims at increasing the sustainability and competitiveness of the shellfish industry in Europe, developing tools and approaches with a view to better preventing and controlling marine bivalve diseases. In order to improve the dialogue among the parties affected by shellfish diseases and to disseminate results of the project, a mapping of stakeholders has been undertaken. Two distinct online cross-sectional surveys were conducted. The first survey was aimed at identifying all potential stakeholders and their perceptions regarding shellfish diseases and disease management measures. The second survey evaluated the nature and intensity of the relationships between stakeholders. The surveys were edited in five languages: English, French, Spanish, Catalan and Italian. Seven categories of stakeholders were identified: politicians; public institutions; education/training organisations; research organisations; knowledge transfer and technological development organisations or individual experts; shellfish industry and related sectors; and, finally, society including NGO and media.

Shellfish diseases appear as a major issue and have an important impact, generally negative, on stakeholders' activities. Preventing and mitigating bivalve diseases seem possible for most of the respondents which take part in different actions related to the control of diseases: definition, implementation, application and transfer. Producers are important interlocutors for most of stakeholders. Moreover producers, research and health-related Institutions are the most connected stakeholders. Results from this analysis can inform an improved risk communication process and the development of a better targeted communication approach about shellfish disease management either at the EU and national levels.

RAZOR CLAM (*SILIQUA PATULA*) SEASON SETTING IN WASHINGTON STATE

Dan L. Ayres* and Clayton E. Parson

Washington State Department of Fish and Wildlife, 48 Devonshire Road, Montesano, Washington 98563 USA

daniel.ayres@dfw.wa.gov

Significant intertidal populations of the Pacific razor clam (*Siliqua patula*) are found along the Washington Pacific Ocean coast. Fisheries managers annually take specific steps to insure the sustainability of the large and economically important recreational and commercial fisheries that are dependent on these populations. During the summer fishery closure, assessments using the Pumped Area Method are conducted by both state and tribal fisheries managers. This method requires water to be pumped from the surf or a nearby lagoon, directed through a handheld PVC wand, and then used to liquefy the sand within an aluminum ring (½ square meter in area). Razor clams in the area of the ring float to the surface and are removed, measured and returned. This process is repeated along randomly selected transects with one transect per mile of suitable razor clam habitat. The Pumped Area Method provides data used to calculate the total number (abundance) and size frequency of razor clam populations and divide those into pre-recruit and recruit portions of the total population. The individual total allowable catch (TAC) for each of five fishery management areas are set with a goal to maximize harvest opportunities while maintaining stable populations. This is accomplished using a harvest rate dependent on the ratio of the current recruit portion of the populations to the Biological Maximum Sustained Yield (BMSY.) In this presentation we will also review Washington razor clam population and harvest trends.

WHITE SPOT SYNDROME VIRUS-LIKE ELEMENT, *DNAV-1_LVA*, IN ORIGINAL SPECIFIC PATHOGEN-FREE (SPF) SHRIMP, *LITOPENAEUS VANNAMEI*, DOMESTICATED IN THE UNITED STATES

Weidong Bao[1], Acacia Alcivar-Warren[2,3*], Robert Bogden[4], Quanzhou Tao[4], Suresh Iyer[4], Galina Mikhaylenko[4], Jon Wittendorp[4], Amy Mraz[4], Evan Hart[4], Emily Hatas[5], Steven Kujawa[5], Joan Wilson[5], and Karl Voss[5]

[1]Genetics Information Research Institute (GIRI), 465 Fairchild Drive, Suite 201, Mountain View, California 94043 USA

[2]UNA SALUD / ONE HEALTH Epigenomics and Microbiomes Program, Fundacion para la Conservacion de la Biodiversidad Acuatica y Terrestre (FUCOBI), Quito, Ecuador

[3]Environmental Genomics, Inc. (EGI), P.O. Box 196, Southborough, Massachusetts 01772 USA

[4]Amplicon Express, Pullman, Washington 99163 USA

[5]Pacific Biosciences, Menlo Park, California, USA

environmentalgenomics.warren@gmail.com

To understand the mechanisms associated with susceptibility of *Litopenaeus vannamei* to bacterial and viral diseases, a broodstock of the first specific pathogen-free (SPF) *L. vannamei*, developed by the U.S. Marine Shrimp Farming Program, was subject to a pilot whole genome sequencing using PacBio SMRT method.

453,089 subreads were generated from 89,716 genome loci, totaling 1.2 Gb sequences. ~424 Mb (~1/7 of the genome) is reclaimed as non-redundant genomic sequence. More than 330 diverse repetitive families, including 113 DNA tansposons, 94 LTR retrotransposons, 75 Non-LTR retrotransposons, 17 satellite sequences, and some 27 unclassified repeats were found. Remarkably, a family of white spot syndrome virus (WSSV)-like sequences is identified,

named as *DNAV-1_LVa*. The genome of *DNAV-1_LVa* is ~279-kb, supported by 3-6 copies throughout the whole length, all flanked by the putative telomeric (GGTTA)n. Consequently, ~0.39% of the whole shrimp genome consists of *DNAV-1_LVa*. Due to the low accuracy of the sequence, 66 hypothetic ORFs are recognized. 15 are significantly homologous to WSSV of shrimp (NC_003225.3), and 6 other ORFs show marginal similarity.

The shrimp genome exhibits high abundance of repetitive sequences: at least 55% of the genome is estimated transposons and other repetitive sequences. Identification of a large fossil WSSV-like DNA virus in large quantity in shrimp genome not only reveals one unidentified lineage of WSSV, consistent with previous reports of fossilized relatives of WSSV in decapod crustacean genomes, it also provides a model for studying the mutual relationship between host and pathogen.

QUANTIFYING PARAMETERS OF ECOLOGICAL CHANGE BEFORE AND AFTER OLYMPIA OYSTER RESTORATION

Julie S. Barber[1*], Sarah K. Grossman[1], Jeffery R. Cordell[2], James T. McArdle[1], Lindy L. Hunter[1], and Courtney M. Greiner[1]

[1]Swinomish Indian Tribal Community, Fisheries Department, 11426 Moorage Way, La Conner, Washington 98257 USA

[2]University of Washington, School of Aquatic and Fishery Sciences, Seattle, Washington 98195 USA

jbarber@swinomish.nsn.us

Restoration of oyster beds is important for both rebuilding populations of native species and for the reestablishment of biological communities that co-evolved with these ecosystem engineers. Research investigating the biology and ecology of Olympia oysters, *Ostrea lurida*, has increased over the last decade, but little information exists on how the reintroduction of this species affects local biological communities. To address this gap, the Swinomish Indian Tribal Community developed a long-term monitoring program to quantify ecological change before and after Olympia oyster restoration efforts in northern Puget Sound. It was hypothesized that the restoration effort would change habitat complexity, resulting in changes in species abundance and diversity within tidal lagoons. Epifaunal, sessile, and mobile invertebrate surveys were conducted in the spring for two years prior to the reintroduction of Olympia oysters and for one year following oyster reintroduction; post-oyster restoration data collection is planned for the next decade. Sites were located within tidal lagoons in Skagit and Similk Bays such that two lagoons served as the treatment sites (oysters reintroduced) and one served as the control site (no oyster reintroduction). Prior to oyster restoration, epibenthic results show that all three lagoons have distinct biological communities despite relative proximity. These results highlight the importance of collecting ecological data before beginning restoration efforts and will serve as a baseline for post-restoration data comparisons.

SPATIAL AND TEMPORAL POPULATION VARIABILITY IN INTERTIDAL CLAMS

Julie S. Barber[1*], Casey P. Ruff[2], James T. McArdle[1], Lindy L. Hunter[1], Camille Speck[3], Douglas Rogers[3], and Courtney M. Greiner[1]

[1]Swinomish Indian Tribal Community, Fisheries Department, 11426 Moorage Way, La Conner, Washington 98257 USA

[2]Skagit River System Cooperative, 11426 Moorage Way, La Conner, Washington 98257 USA

[3]Washington Department of Fish and Wildlife, 375 Hudson Street, Port Townsend, Washington 98368 USA

jbarber@swinomish.nsn.us

Although long-term datasets can be particularly useful for parsing out factors influencing populations, few studies have utilized continuous datasets to quantify population synchrony in bivalve mollusks. Dynamic factor analysis was used on a clam biomass dataset spanning 28 years and four distinct regions in the southern Salish Sea to determine (1) if native intertidal clam populations exhibit spatial or temporal coherence and (2) what environmental covariates influence population trends. The model with the most data support included three predominant trends to describe decadal change in mean clam biomass. Results demonstrate that intertidal clam population coherence can vary spatially and temporally by species. Intraspecific coherence was the highest in *Leukoma staminea*, followed by *Saxidomus gigantea*, with lowest synchrony in *Clinocardium nuttallii*. Population dynamics on three beaches (two in Hood Canal and one in Admiralty Inlet) showed similar temporal trends regardless of species. No other beaches showed synchrony in temporal trends across species indicating that species-specific trends (regardless of location) were more common than beach-specific trends (regardless of species). Eight covariates were evaluated in their ability to explain variability in annual mean biomass not captured in the latent trends. Of these, the North Pacific Gyre Oscillation lagged four years prior to the observation year received the strongest data support. While this large-scale oceanographic factor may play a valuable and previously undescribed role in population variation of venerid clams, local factors are also likely to account for variance not explained by our model.

OSTREID HERPES VIRUS IN THE UK: DISEASE CHALLENGES, SNP-ARRAY DEVELOPMENT, AND A GENOME-WIDE ASSOCIATION STUDY FOR HOST RESISTANCE IN PACIFIC OYSTERS (*CRASSOSTREA GIGAS*)

Tim P. Bean*[1], Alejandro Gutierrez[2], Chantelle Hooper[1], Craig A. Stenton[1], Matthew B. Sanders[1], Richard K. Paley[1], Karim Gharbi[3], and Ross D. Houston[2]

[1]Cefas Weymouth Laboratory, Barrack Road, Weymouth, UK DT4 8UB

[2]University of Edinburgh, The Roslin Institute and Royal (Dick) School of Veterinary Studies, Midlothian EH25 9RG, United Kingdom

[3]University of Edinburgh, Edinburgh Genomics, Ashworth Laboratories, EH9 3FL, United Kingdom

tim.bean@cefas.co.uk

Ostreid Herpesvirus (OsHV-1) has recently been associated with sporadic mass mortality events in UK Pacific oysters (*Crassostrea gigas*). Sites along the South coast have suffered varying levels of infection with OsHV-1 µVar and, except for the practice of rigorous biosecurity, there are limited methods through which shellfish farmers can control the disease; however, shifts in susceptibility of breeding populations have demonstrated that some oysters carry an inherent level of survivability when challenged by the pathogen, and that this "resistance" is heritable. This study was designed to characterise the genetics of resistance and enhance efforts to breed resilient animals. To this end a large-scale controlled disease challenge of roughly 1000 oysters was performed, and samples taken from mortalities and survivors for genotyping and for qPCR measurement of viral loading. Genotypes were analysed by high density single nucleotide polymorphism array (SNP-chip), which had been developed via whole genome sequencing of *C. gigas* oysters and sampled from hatcheries and farm locations in the UK and France. Genetic parameters of OsHV-1 resistance were estimated and indicate significant, but low heritability for both survival and for viral loading. In addition, genome-wide association studies highlight significant QTLs which affect host resistance. Efforts will now be made to design and utilise assays to identify these QTLs in breeding populations and provide a basis for producing animals with reduced susceptibility to OsHV-1.

THE EFFECTS OF AERIAL EXPOSURE AT LOW TIDE ON *VIBRIO* CONCENTRATIONS IN HARVESTED OYSTERS CULTURED IN THE INTERTIDAL

Tal Ben-Horin[1*], Corinne Audemard[2], Dave Bushek[3], Lisa Calvo[3], and Kimberly S. Reece[2]

[1]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, College of the Environment and Life Sciences, Kingston, Rhode Island 02881, USA

[2]Virginia Institute of Marine Sciences, College of William and Mary, Gloucester Point, Virginia 23062, USA

[3]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Ave, Port Norris, New Jersey 08349 USA

tbenhorin@uri.edu

Understanding how aquaculture practices influence levels of harmful *Vibrios* in harvested oysters is of paramount importance to the oyster aquaculture industry. Results from a regional field study examining variation in concentrations of total *Vibrio parahaemolyticus* (*Vp*), pathogenic *V. parahaemolyticus* (*trh+ Vp* and *tdh+ Vp*), and total *Vibrio vulnificus* (*Vv*) in oysters grown under intertidal or subtidal conditions at low (12-15), moderate (18-25), and high (27-35) salinity sites in Delaware and Chesapeake Bays will be reported. For oysters grown under intertidal conditions, it was found that *Vibrio* concentrations increase with aerial exposure at low tide, but the magnitude of this increase depends on the *Vibrio* species and duration of aerial exposure. Concentrations of pathogenic *Vp* increased with as little as two hours of exposure to aerial conditions, but only weak evidence for increases in total *Vp* and *Vv* over this time frame was found. The maximum duration of aerial exposure for intertidal-cultured oysters at the sampling sites ranged from three and a half to four hours, and over this period of exposure, levels of total *Vp* were found to be approximately two to thirty times that of oysters in the subtidal. Levels of *trh+ Vp* and *tdh+ Vp* in intertidal oysters sampled at maximum emergence were found to be two to fifteen and one to ten times that of oysters in the subtidal. Weaker evidence indicates that emergence at low tide increases concentrations of total *Vv* in oysters. *Vibrio* concentrations in intertidal oysters returned to levels found in subtidal oysters by the following tide series, if not sooner. Hence, intertidal farms themselves do not present an increased risk with respect to *Vibrio* concentrations. Many aquaculture harvest regulations presently consider the time of initial aerial exposure as the harvest starting time for oysters grown under intertidal conditions, which is supported by these data, and growers should be cautious when harvesting intertidal oysters as close to initial aerial exposure as possible.

CENTERING ON FUNCTIONAL ANATOMY UNLOCKS NEAT STUFF FROM THE MOLECULAR TO THE ECOLOGICAL LEVELS

Peter G. Beninger

Laboratoire de Biologie Marine, Faculté des Sciences, Université de Nantes, 2 rue de la Houssinière, Nantes, Cedex France

Peter.Beninger@univ-nantes.fr

The organism is the mid-point on the scale of organization of life. Centering on this level allows one to extend in both directions – toward both the molecular and the ecosystem levels, concomitantly extending the reach of one's research. Over several decades

of organism-centered research, largely involving functional anatomy, I have been able to discover/elucidate some important biological phenomena, as well as opening several very active and current fields of research. What more could a scientist want (besides money…)? Research case histories from the following fields will be presented:

- Bivalve feeding
- Bivalve reproduction
- Gastropod reproduction
- Crab reproduction
- Shorebird feeding

CONTEMPORARY OBSTACLES TO CREDIBILITY IN SCIENCE

Peter G. Beninger

Laboratoire de Biologie Marine, Faculté des Sciences, Université de Nantes, 2 rue de la Houssinière, Nantes, Cedex France

Peter.Beninger@univ-nantes.fr

Science is a unique approach to understanding the physical universe. It comprises two complementary types of reasoning: inductive and deductive, and three types of methodology: direct observation, empirical, and experimental. Appropriately combining these components is not a natural human enterprise; and the central place of science in modern civilization is largely due to its success in medicine and technology, rather than to its ease of practice. The Achilles heel of science is the rest of human cognition, characterized by thought processes and behaviours antithecal to science. These elements have hindered and discredited science from its outset. In the contemporary world, the credibility of science is plagued most acutely by its instrumentalisation for the advancement of power agendas, by faulty reasoning (especially statistical), and by dilution/inactivation due to the massive input of 'research' which has little or no quality control. These themes will be presented, with a view to providing what can only be a difficult 'solution'.

YOUNG-OF-THE-YEAR STONE CRAB (*MENIPPE*) RECRUITMENT IN THE GULF OF MEXICO OFF FLORIDA: KEY SHALLOW-WATER RECRUITMENT HOTSPOTS

Theresa M. Bert*, Charles Crawford, and Colin Shea

Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, 100 Eighth Avenue SE, St. Petersburg, Florida 33701 USA

theresa.bert@myfwc.com

Knowledge of juvenile recruitment is instrumental for conserving heavily harvested species and their critical habitats. At multiple hierarchical spatial scales and for multiple stone crab generations, geographical, seasonal, and interannual variation in the distribution and relative abundance of megalopal and post-settlement juvenile stone crabs inhabiting the Gulf of Mexico off peninsular Florida and north of the Florida Keys are defined. Then the influences of the relative abundance of spawning females, temperature, salinity, depth, distance from shore, habitat, red tide blooms, tropical cyclones, and ENSO events on the patterns of variation are described. Two principal and two secondary recruitment grounds, stable through decades, account for approximately 75% of the YOY stone crabs recruited in the Florida Gulf. Approximately 65% - 75% of the recruits were collected August – October; but with movement southward, the timing of the recruitment season shifts to later in the year and the season's duration increases. Monthly patterns of relative abundance can differ among locations within a year and among years within locations. Water temperature, salinity, depth, and habitat are important factors in structuring recruitment. Highest relative abundances of recruits were collected from sites off large, pristine estuaries in murky water less than 5 m deep, with salinities ranging 24 – 36 and temperatures near and at summer high values. Annual variation in relative abundance was influenced significantly only by the occurrence of tropical cyclones in the vicinity. Because stone crabs support an intense fishery throughout the Florida Gulf, recruitment grounds and associated estuaries should be protected.

REPRODUCTION IN FEMALE STONE CRABS (GENUS *MENIPPE*) FROM TAMPA BAY, FLORIDA, USA: INTER-ANNUAL, SEASONAL, AND TEMPERATURE-RELATED VARIATION

Theresa M. Bert[1]*, Susan D. Gerhart[2], and Charles Crawford[1]

[1]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, 100 Eighth Avenue SE, St. Petersburg, Florida 33701 USA

[2]National Marine Fisheries Service, Southeast Regional Office, 263 13th Avenue South, St. Petersburg, Florida 33701 USA

theresa.bert@myfwc.com

Knowledge of short- and long-term reproductive patterns is basic for fisheries management. Using data from over 22 years of sampling commercially-valuable female stone crabs (genus *Menippe*) in Tampa Bay, Florida, size-specific inter-annual and intra-annual patterns in ovarian development and spawning were defined; relationships between the molting cycle and the intra-annual patterns were explored; and the influence of water temperature on those interrelationships was identified. Frequency of gravid females (frequency-gravid) shifted in multiyear cycles, but frequency of ovigerous females (frequency-ovigerous) did not. Frequency-gravid and frequency-ovigerous increased with size class except in the largest females. Inter-annual variation in frequency-ovigerous was the product of multiple patterns differing principally between size-class-70 and -80 (mm CW) females and size-class-90 and -100+ females. Ovarian development, spawning, and molting in females of size classes 20-50

occurred principally during peak temperatures (August-September). In females of size classes 70-100+, ovarian development--tightly and inversely linked to molting--occurred principally February-August; and spawning--influenced by both water temperature and molting--occurred principally April-September. Size-class-60 females exhibited a mosaic of those patterns. Ovarian development and spawning ceased in all size classes when temperature decreased to 25°C during October. Other temperatures were associated with additional shifts in reproduction and molting. Decreases through years in frequency-ovigerous of females in size classes 70-110, concomitant with increases in frequency-ovigerous of females in size classes 50-60, and coupled with possible decreases in size-at-maturity and minimum spawning size, suggest fisheries selection. Shortening harvesting season by six weeks during the spring would protect females during the first spawning pulse in the spring.

LARGE-SCALE GREEN CRAB REMOVAL AS SITE PREPARATION FOR EELGRASS RESTORATION EFFORTS IN PLACENTIA BAY, NEWFOUNDLAND, CANADA

Kiley Best* and Arnault Le Bris

Marine Institute of Memorial University,Centre for Fisheries Ecosystems Research, 155 Ridge Road, St. John's, Newfoundland, Canada, A1C 5R3

Kiley.best@mi.mun.ca

The invasive green crabs were discovered in Placentia Bay, Newfoundland in 2007 and have established a significant population. Eelgrass habitat coverage has decreased 50-100% in areas of Placentia Bay that are within this invasion range. It has been surmised that green crab invasion is one of the major contributors to the decrease of this ecologically significant species. Eelgrass habitat provides nursery habitat for many ecologically and commercially important species like Atlantic cod, scallop and American lobster. In response to this issue efforts are underway to restore eelgrass beds to historical coverage in areas of Placentia Bay. In preparation for eelgrass restoration and to increase likelihood of success green crab must be reduced in the areas of interest. Using removal methods established by the Department of Fisheries and Oceans Canada, green crab removal started in the fall of 2017 with an intensive eight week fishery. Ten fisherman with a fleet of 70 Fukui pots each fished nine areas, using 12 hours soaks. Over 30 metric tons of crabs were removed from the system. Catch per unit of effort did not decrease over the eight weeks but number of crab per kilo increased. Many lessons learned in the first season of fishing will be assessed and taken into account for planning future efforts in 2018. As this site maintenance continues for five years, data collected will provide information on population abundance, help define threshold levels for control of target population's levels and contribute to recommendations for future control of green crab.

REEXAMINING *BONAMIA OSTREAE* IN MAINE FLAT OYSTERS

Lydia M. Bienlien[1]*, Henry S. Lane[2], and Ryan B. Carnegie[1]

[1]Virginia Institute of Marine Science, College of William & Mary, P.O. Box 1346, Gloucester Point, Virginia 23062, USA

[2]Department of Zoology, University of Otago, PO Box 56, Dunedin 9054, New Zealand

lmbienlien@vims.edu

The oyster parasite genus, *Bonamia,* infects numerous hosts worldwide. These "microcell" protozoans, characteristically infecting oyster hemocytes, are directly transmissible among hosts and can cause substantial mortality in oyster fisheries and aquaculture, as exemplified by damage caused to European *Ostrea edulis* populations following invasion of *Bonamia ostreae* in the 1970s. Major pathogens, *B. ostreae* and *Bonamia exitiosa,* are notifiable to the World Organisation for Animal Health (OIE) and have received significant research attention. Yet questions remain about *Bonamia* biology and ecology, including the evolution of interactions with hosts long exposed to the pathogens. In Maine, USA, *O. edulis* is locally abundant and *B. ostreae* has been present since at least 1991, at prevalences up to 45% and with up to 75% of infections reaching advanced moderate to heavy intensities. Oysters from Casco Bay, Maine infected with *B. ostreae* were reanalyzed to determine infection status 17 years after its last assessment. In May 2017 adult and juvenile *O. edulis* were collected and evaluated using PCR diagnostics and histology. Adult oysters had a 15% detection prevalence and juveniles a 55% prevalence by PCR. Histologically confirmed prevalence was 10% (67% of these advanced) in adult oysters and 25% (18% advanced) in juveniles. It is clear that *B. ostreae* persists in Casco Bay, albeit with no indication of significant host mortality. Results suggest that a modest infection prevalence, though with a number of these infections developing to high intensities, may represent a stable state ensuring reasonable fitness of both host and pathogen populations.

AN UPDATE ON THE STATUS OF OYSTER AQUACULTURE (*CRASSOSTREA VIRGINICA*) IN GEORGIA

Thomas Bliss[1*], Dominic Guadagnoli[2], Jill Andrews[2], and Mark Risse[3]

[1]University of Georgia, Marine Extension and Georgia Sea Grant, 20 Ocean Science Circle, Savannah, Georgia 31411 USA

[2]Georgia Department of Natural Resources, Coastal Resources Division, One Conservation Way, Brunswick, Georgia 31520 USA

[3]Univeristy of Georgia, Marine Extension and Georgia Sea Grant, Chicopee Building No. 1, 1180 East Broad St., Athens, Georgia 30602 USA

tbliss@uga.edu

The University of Georgia, Georgia Department of Natural Resources, and Georgia Department of Agriculture are partners to

working to expand shellfish aquaculture industry in Georgia. Aquaculture in Georgia is dominated by the northern quahog (=hard clam) (*Mercenaria mercenaria*) and the development of sustainable single oyster (*Crassostrea virginica*) is of highest importance to the Georgia Shellfish Growers Association diversify the shellfish industry. In 2016, a Blueprint for Georgia Oyster Aquaculture was developed to start to process and lay the groundwork for development of oyster aquaculture. An update on the status of the Georgia aquaculture industry and changes to the Blueprint for Georgia Oyster Aquaculture will be provided as Georgia works to transition from an oyster industry based on wild harvest to an aquaculture based industry.

EVALUATING LIPOSOMES FOR THE DELIVERY OF OXYTETRACYCLINE TO OYSTER LARVAE (*CRASSOSTREA GIGAS*) AND SUBSEQUENT EFFECTS ON RESISTANCE TO *VIBRIO CORALLIILYTICUS*

Lianne Blodgett[1*], Chris Langdon[2], and Matt Hawkyard[2]

[1]University of Chicago, Chicago, Illinois 60637, USA

[2]Oregon State University, Coastal Oregon Marine Experiment Station and Department of Fisheries and Wildlife, Corvallis, Oregon 97331, USA

lblodgett@uchicago.edu

A leading cause of disease-associated mortality in oyster larviculture is the outbreak of *Vibrio* spp. Improved methods for preventing and treating bacterial infections are needed to ensure reliable larval culture. Current treatments used in research often require dissolving large quantities of antibiotics in culture water, a method that wastes antibiotics and may promote the development of antibiotic-resistant bacteria. In this study, microparticles (liposomes) were investigated for the delivery of antibiotics to Pacific oysters (*Crassostrea gigas*), and the effects of additions of antibiotic-liposomes on larval resistance to *Vibrio coralliilyticus* were determined. To measure uptake of liposomes by larval oysters, larvae were fed fluorescently-labeled liposomes and then examined using an epifluorescent microscope. The fluorescent images revealed that two-day and nine-day old oyster larvae readily ingested and partially digested liposomes, liberating water-soluble fluorescein from liposomes into their guts. In addition, oxytetracycline (OTC), a water-soluble antibiotic known to be highly effective against *V. coralliilyticus*, was successfully encapsulated within liposomes. However, oyster larvae treated with OTC-liposomes and exposed to *V. coralliilyticus* for 48 hours did not show increased survival. Similarly, while larvae were shown to take up dissolved OTC from culture water, pre-treatment with dissolved OTC before exposure to *V. coralliilyticus* did not increase larval survival. Taken together, these results indicate that more research is needed to evaluate the use of liposomes for treatment of oyster larvae against bacterial infections. Utilization of liposomes by oyster larvae suggests that they may be useful in the delivery of other water-soluble compounds, such as dietary supplements, to oyster larvae.

THE EFFECTS OF CRUDE AND REFINED ALGAL-DERIVED ANTIVIRAL BIOTHERAPEUTICS ON OSTREID HERPESVIRUS DEVELOPMENT AND PACIFIC OYSTER (*CRASSOSTREA GIGAS*) PERFORMANCE

B.E. Bookelaar*, S.C. Culloty, and S.A. Lynch

Aquaculture and Fisheries Development Centre, School of Biological, Earth and Environmental Sciences & Environmental Research Institute, University College Cork, Cork, Ireland

b.bookelaar@umail.ucc.ie

Aquaculture species are exposed to artificial and stressful conditions resulting in disease development and even mortalities. Sulphated polysaccharides (SP) are compounds found in seaweed species and have been showing positive effects on immune systems in marine vertebrate and invertebrate species. Pacific oysters *Crassostrea gigas* are important commercial aquaculture species worldwide; however, over the past few decades *C. gigas* have been suffering summer mortalities related to a complex aetiology including pathogens like ostreid herpes virus variants (OsHV-1) and *Vibrio* spp. The future sustainability of the Irish Pacific oyster industry is dependent on new modified measures and husbandry techniques. In this study, the impact of seaweed and derivatives on innate immunity and ability to understand OsHV-1 infection was assessed through lab based trials. Naïve and naturally pathogen exposed oysters were exposed to two different seaweed species in the lab for 26 days under elevate temperature regime. Results indicated that, seaweed species had a positive effect on disease development of naturally pathogen exposed oysters. Those oysters showed significant lower prevalence of ostreid herpes virus when exposed to seaweed species compared to control oysters; however, over the limited study period no significant differences in oyster performance, like mortality and lysozyme activity were observed between the treatments. It would be of high interest to carry out further studies to test new seaweed species, shorter/longer exposure times, different seaweed concentrations, and endorse this approach as a new tool for disease control in Pacific oysters.

POPULATION CYCLES IN CRAB FISHERIES

Louis W. Botsford

University of California, Davis, Department of Wildlife, Fish, and Conservation Biology, One Shields Ave., Davis, California 95616 USA

lwbotsford@ucdavis.edu

Dungeness crab populations along the US west coast experience cyclic variability period near 10 years, and cyclic variability with various periods also appears in snow crab populations in the Bering Sea and eastern Canada. These cycles could be caused by two different population dynamic mechanisms. Cycles of the type seen in Dungeness crab are of period 2T (T=generation time), require

over-compensatory density-dependent recruitment, and are mathematically a deterministic local instability. The cycles in the Bering Sea snow crab appear to be of period 1T, and they may be due to a recently discovered phenomenon termed cohort resonance. Such cycles of period 1T occur with compensatory density-dependent recruitment, and they arise in a locally stable population driven by a random environment. The consequences of these differences for the detection of mechanisms and the management of fisheries are described.

TEMPORAL EFFECTS OF EXPOSURE TO PHARMACEUTICALS AND PERSONAL CARE PRODUCTS AND THEIR MIXTURE ON THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) METABOLOME

David W. Brew* and Marsha C. Black

University of Georgia, Department of Environmental Health Science, Athens, Georgia, USA

dbrew@uga.edu

Oysters are keystone species in estuaries, and are routinely exposed to complex mixtures of contaminants, which can frequently include pharmaceuticals and personal care products; however, the biological effects of these exposures are poorly characterized. Untargeted GC-MS metabolomics were utilized to quantify the responses of oysters exposed to fluoxetine, N,N-diethyl-meta-toluamide (DEET), 17α-ethinylestradiol (EE2), diphenhydramine and their mixture. Contaminant exposure lasted for ten days, followed by an eight-day depuration period, and adductor muscle tissue was sampled at days 0, 1, 5, 10 and 18. Changes in the relative abundance of individual metabolites in each treatment were used to identify potential biomarkers of exposure. Detected metabolites were associated with the Krebs cycle, cellular signaling, fatty acid, carbohydrate, and amino acid metabolism, and the urea cycle. Over the first 10 days, the observed metabolite changes in the individual treatments were related to their respective mechanism-of-action (MOA). The mixture treatment response shared certain characteristics with the EE2, diphenhydramine and fluoxetine treatments; however, most metabolite changes were unique to the mixture. Several generalized stress responses (anaerobic metabolism, osmotic stress, and oxidative stress) were also detected at least once during the course of each exposure. After depuration, both partial least-squares discriminant analysis and changes in metabolite expression showed that minimal biochemical recovery occurred, as most of the detected metabolites were still statistically different from the controls. This research highlights the utility of untargeted metabolomics in developing exposure biomarkers for compounds with differing MOA, while also highlighting challenges in interpreting single chemical versus mixture responses in bivalves.

COLLABORATING FOR OYSTER SUSTAINABILITY: COMMUNICATIONS ASSESSMENT AND NETWORK ANALYSIS OF RESTORATION STAKEHOLDERS ON THE GULF COAST

Hannah O. Brown[1]* and Susan Jacobson[2]

[1]University of Florida, School of Natural Resources and Environment, 103 Black Hall, 1128 Center Drive, Gainesville, Florida 32611-6455 USA

[2]University of Florida, Department of Wildlife Ecology and Conservation, 110 Newins-Ziegler Hall, Gainesville, Florida 32611-0430 USA

hannahobrown@ufl.edu

Oyster restoration projects on the Gulf Coast present a possible solution to mitigating decreasing oyster populations. To ensure the success of restoration projects, it is essential to understand the communication strategies used by stakeholder groups involved in restoration projects. This research will analyze how mass media represent stakeholder perspectives, assess the factors that influence network structure among stakeholder groups, map the flow of information between stakeholders, and create an expert-driven set of communication recommendations for future restoration projects. A mixed-methods approach will be used to investigate the sociological dynamics of communication between and preferences of stakeholder groups, including content analyses, a multi-state survey, semi-structured interviews, a social network analysis, and a Delphi panel.

UNDERSTANDING BLUE CRAB, *CALLINECTES SAPIDUS*, PATTERNS OF MOVEMENT ALONG A SALINITY GRADIENT WITHIN THE ASHLEY RIVER, CHARLESTON, SOUTH CAROLINA, USA

Jeff Brunson*, Michael Kendrick, Stephen Czwartacki, and Peter Kingsley-Smith

South Carolina Department of Natural Resources (SCDNR), 217 Fort Johnson Road, Charleston, South Carolina 29422, USA

brunsonj@dnr.sc.gov

Across its life stages, the Atlantic blue crab (*Callinectes sapidus*) occupies a diversity of habitats with different environmental characteristics, particularly in regards to salinity. Within this broader distribution, temporal and spatial segregation by size, sex, and reproductive status have been observed and are reflected in a dynamic commercial blue crab fishery in South Carolina. Monitoring of blue crab populations by the SCDNR has historically focused on year-round trawl and fall commercial-style crab pot sampling. Crab pot sampling is effective at capturing larger subadult and adult crabs and allows for sampling of habitats that are not amenable to trawl-based techniques, such that this sampling approach constitutes an informative tool for characterizing habitat use by blue crab. Monitoring of blue crab populations by the SCDNR was recently expanded to include year-round sampling at a range of habitat conditions in the main-stem of the Ashley

River. The primary goal of the study presented here was to better characterize the distribution of blue crab across a salinity gradient. Monthly sampling was conducted for two years using triplicate crab pots deployed at six stations along a salinity gradient (0.1 – 26.5 psu). High numbers of mature males were captured at all stations, females and immature males were generally captured in lower numbers, and mature females were more commonly captured at the higher salinity stations. Temporal and spatial variability in blue crab distribution suggest that modifications to current sampling regimes may improve indices of abundance, particularly if management actions are recommended that target specific blue crab demographics.

HOPING FOR THE BEST, PREPARING FOR THE WORST: DETERMINING RESISTANCE OF OYSTER SPECIES TO EXPOSURE TO OSHV-1 AND OSHV-1 MVARS IN THE UNITED STATES

Colleen A. Burge[1*], Kimberly S. Reece[2], Natalie D. Rivlin[1], Bryanda T. Wippel[3], Arun K. Dar[4], Benjamin Morga[5], Lionel Dégremont[5], Nicole Faury[5], Peter D. Kirkland[6], Daniel Mancilla Cortez[7], D. Terry Sawyer[7], James D. Moore[8], and Carolyn S. Friedman[3]

[1]University of Maryland Baltimore County, Institute of Marine and Environmental Technology, 701 East Pratt Street, Baltimore, Maryland 21202 USA

[2]Virginia Institute of Marine Sciences, College of William and Mary, 1375 Greate Rd, Gloucester Point, Virginia 23062 USA

[3]University of Washington, School of Aquatic and Fishery Sciences, Box 355020, Seattle, Washington 98195 USA

[4]University of Arizona, Animal and Comparative Biomedical Sciences, 1117 E Lowell Road, Tucson, Arizona 85721 USA

[5]Ifremer, SG2M-LGPMM, Station La Tremblade, 17390 La Tremblade, France

[6]Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, NSW 2568, Australia

[7]Hog Island Oyster Company, PO Box 829, Marshall, California 94940 USA

[8]California Department of Fish and Wildlife and UC Davis-Bodega Marine Laboratory, PO Box 247, Bodega Bay, California 94923 USA

colleenb@umbc.edu

The Ostreid herpesvirus 1 (OsHV-1) and its variants, particularly the OsHV-1 µvars are virulent and emerging pathogens known to infect and kill *Crassostrea gigas*, globally. Since 2008, an increase in *C. gigas* mortality in France has been associated with a new genetic variant, OsHV-1 µvar. OsHV-1 µvars are continuing to spread in Europe and similar variants cause severe losses in Australia, New Zealand, and Asia. In the US, OsHV-1 has been detected only in California, mostly notably in Tomales Bay where since 1993 an OsHV-1 variant (not considered a µvar) has caused losses of juvenile oysters each summer. Given the emergence and rapid spread of OsHV-1 µvars, it may be only a matter of time before oyster culture in the US is threatened by OsHV-1 µvars. The goal of the present work is to demonstrate differential survival of US oyster species and genetic stocks in the face of OsHV-1 and OsHV-1 µvars. In 2017, three species of oysters grown on the US West Coast (*C. gigas, C. sikamea*, and *Ostrea lurida*) were planted in Tomales Bay and monitored for survival and OsHV-1 quantification. Results suggest that *C. sikamea* and *O. lurida* are more resistant to OsHV-1 than *C. gigas*. Susceptibility to OsHV-1 varied among *C. gigas* stocks planted in Tomales Bay. We are investigating whether resistance to OsHV-1 confers resistance to OsHV-1 µvar exposure using laboratory challenge experiments exposing stocks of *C. gigas*, *C. virginica*, *C. sikamea*, and *O. lurida* to OsHV-1 µvars from France and Australia.

GEODUCK STOCK ASSESSMENT IN BRITISH COLUMBIA

Dominique Bureau

Inshore Assessment Section, Pacific Biological Station, Fisheries and Oceans Canada, 3190 Hammond Bay Road, Nanaimo, British Columbia, Canada, V9T 6N7

Dominique.Bureau@dfo-mpo.gc.ca

An overview of the stock assessment framework for the British Columbia (BC) Geoduck fishery will be provided. Geoducks are found in discrete beds of soft substrates throughout the coast of BC. The stock is spatially structured with over five thousand Geoduck beds identified in BC. The framework in place for assessment of the BC Geoduck fishery consists of estimating biomass for each bed.

Geoduck biomass on a bed is estimated from bed area, mean weight and density data. Bed area is estimated in a Geographic Information System (GIS) from fishing event positions, dive survey and substrate mapping data. Mean weight is estimated from data provided on commercial fishery logbooks. Density is estimated through fishery-independent dive surveys. There is a strong collaboration between Fisheries and Oceans Canada and the Geoduck fishing industry (Underwater Harvesters Association). The industry has been involved in stock assessment and survey activities for the last 25 years and provides significant funding towards Geoduck stock assessment.

Regional annual harvest rates between 1.2% and 1.8% are applied to estimates of current biomass to provide harvest options to fishery managers. A Limit Reference Point (LRP) was defined for the BC Geoduck fishery as current biomass being equal to 40% of estimated unfished exploitable biomass and is applied on a bed-by-bed basis.

COMPARISON OF UNDERWATER PHOTO AND VIDEO SURVEY METHODS WITH DIVER OBSERVATIONS TO ASSESS NEARSHORE ALGAE AND BENTHIC MARINE INVERTEBRATE COMMUNITIES

Dominique Bureau* and Joanne Lessard

Marine Spatial Ecology and Analysis Section, Pacific Biological Station, Fisheries and Oceans Canada, 3190 Hammond Bay Road, Nanaimo, British Columbia, Canada, V9T 6N7

Dominique.Bureau@dfo-mpo.gc.ca

Data collection for benthic marine invertebrates and algae in the shallow subtidal zone is challenging and often done through SCUBA diving surveys. Other survey methods (e.g. underwater photo and/or video) are sometimes proposed as alternatives to direct data collection underwater by divers. A study was conducted to compare underwater photo and video data collection methods with direct data collection underwater by SCUBA divers.

The survey was conducted in the Central Coast of British Columbia and consisted of collecting presence/absence data of algae and benthic marine invertebrate species along transects placed perpendicular to shore. Each transect was swum twice, first to record video and still images, and a second time for divers to directly record algae and benthic marine invertebrate species presence/absence. Photos and videos were later reviewed to estimate presence/absence of algae and benthic marine invertebrate species. For diver and video surveys, data were recorded in 1m x 5m quadrats along each transect while, for photo surveys, one photo of a 0.5m x 0.5m quadrat was taken every 5 m along each transect.

The number of species encountered was greatest when using direct observation by divers, followed by video and photo methods. Field time required to survey transects with video and photo methods were similar to direct underwater data recording by divers; however, photo and video methods require more post-processing after the survey to extract data. Direct data collection underwater by divers is therefore more efficient in terms of both detection ability and time requirements.

THE BILLION OYSTER PROJECT: CHALLENGES, LESSONS, AND OPPORTUNITIES IN RESTORING OYSTERS TO AN URBANIZED ENVIRONMENT

Elizabeth M. Burmester*[1], Michael J. McCann[2], Katie Mosher[1], and Peter Malinowski[1]

[1]Billion Oyster Project, Governor's Island, 10 South St. Slip 7, New York, New York 10004 USA

[2]The Nature Conservancy, 322 8th Ave, New York, New York 10001 USA

lburmester@nyharbor.org

The New York Harbor (NYH) represents a complex marine ecosystem impacted by dynamic and dramatic human use. Specifically, this ecosystem once supported the largest known population of the eastern oyster (*Crassostrea virginica*), creating a reef system that is estimated to have covered 220,000 acres. Today, NYH supports a diverse population of over 8.5 million people and a functionally extinct population of oysters. The Billion Oyster Project (BOP) is a non-profit organization dedicated to the improvement of NYH and the restoration of its once native oyster population through education and community engagement. Challenges to the restoration and conservation of NYH are socially and physically complex and include raw sewage discharge, heavy use by marine and shipping vessels, a lack of natural shoreline, and urban pollution. Toward that end, BOP engages students and community members across four community reef projects, two community nurseries, two oyster hatchery nurseries, two restoration pilot projects, and three planned oyster restoration projects as well as through 105 partnering schools, 84 oyster research stations, and six career and technical education programs in association with the New York Harbor School. This presentation will explore the challenges, lessons, and opportunities associated with marine restoration in an urbanized environment, specifically in relation to BOP's (1) ecological and restoration, (2) community engagement, and (3) educational goals and efforts.

ENCOURAGING DIAMONDBACK TERRAPIN CONSERVATION THROUGH COOPERATION WITH THE MISSISSIPPI BLUE CRAB FISHERY

Rick Burris* and Traci Floyd

Mississippi Department of Marine Resources, 1141 Bayview Avenue, Biloxi, Mississippi 39530 USA

rick.burris@dmr.ms.gov

In the Gulf of Mexico, Diamondback terrapin (Malaclemys terrapin) mortality rates have been linked to nest predation, habitat loss through increased coastal development, and bycatch within the blue crab (Callinectes sapidus) fishery. Derelict crab traps lost by fishermen also pose a threat to terrapins through ghost fishing. The Mississippi Department of Marine Resources (MDMR), Office of Marine Fisheries has been actively promoting terrapin conservation through a variety of cooperative approaches such as increasing public awareness about the potential threats to the Mississippi terrapin population, encouraging the use of Terrapin Excluder Devices (TEDs) in the blue crab fishery, utilizing commercial crab fishermen to provide useful geospatially referenced data on localized populations of terrapins, and through the removal of derelict crab traps in Mississippi marine waters.

The Mississippi Derelict Crab Trap Removal Program, the most successful terrapin conservation initiative, largely through the help of Mississippi commercial crab fishermen, has removed and recycled over 21,600 derelict traps from Mississippi waters since its inception of the program in 1999. The MDMR is also exploring and

applying innovative technology to locate and remove submerged derelict traps that may otherwise go unnoticed. The Mississippi Crab Trap Bycatch Reduction Device (BRD) /TED Program has also been highly effective in distributing over 19,500 TEDs (4,800 traps equipped) and over 54,500 BRDs (27,250 traps equipped) to both commercial and recreational blue crab fishermen.

IMPACTS OF OCEAN ACIDIFICATION ON THE SETTLEMENT OF *CRASSOSTREA GIGAS*

Andrea Burton[1*], Eli Meyer[1], Evan Durland[2], and Chris Langond[2]

[1]Oregon State University, 3029 Cordley Hall, 2701 SW Campus Way, Corvallis, Oregon 97331 USA

[2]Hatfield Marine Science Center, 2030 SE Marine Science Dr, Newport, Oregon 97365 USA

Burtoand@oregonstate.edu

Ocean acidification (OA) resulting from increasing atmospheric P_{CO2} impairs the growth of calcifying organisms, especially in early developmental stages. Little is known about how this impacts the process of metamorphosis in organisms such as marine bivalves that require rapid rates of calcification during metamorphosis. To investigate functional consequences of OA for settlement and metamorphosis, larvae of the Pacific oyster (*Crassostrea gigas*) were grown and induced to settle in acidified and control conditions, using selected families from the Molluscan Broodstock Program. To study the mechanisms underlying effects of OA on settlement success, gene expression was profiled using RNASeq in larvae and settled spat from each condition. Differences in gene expression were evaluated, which were compared using a negative binomial model including the factors of age, settlement treatment (epinephrine), and OA condition. The OA treatments used in this study reduced the settlement rate of spat by 73%. At the same time, the treatments produced significant changes in gene expression with 50 upregulated and 51 downregulated genes in the OA treatment. Together, these findings identify genes and biological processes associated with effects of ocean acidification on settlement and metamorphosis of marine bivalves and other calcifying invertebrates.

INTERACTIVE TALK: BUILDING A SHELLFISH HEALTH DATABASE TO FACILITATE SHELLFISH TRANSFERS

David Bushek[1]*, Lisa Calvo[1], Lucas Marxen[2], Ryan Carnegie[3], Robert Rheault[4], and Lori Gustafson[5]

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

[2]Rutgers University, NJAES Office of Research Analytics, 88 Lipman Drive, New Brunswick, New Jersey 08901-8525 USA

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

[3]East Coast Shellfish Growers Association, 1623 Whitesville Rd., Toms River, New Jersey 08755 USA

[4]Centers for Epidemiology and Animal Health, USDA APHIS Veterinary Services, 2150 Centre Ave, Building B, Mail Stop 2E6, Fort Collins, Colorado 80526 USA

bushek@hsrl.rutgers.edu

Aquaculture is the fastest growing segment of food production with molluscan shellfish aquaculture leading the way. Oyster aquaculture alone has doubled production in just the past five years leading to seed shortages in many states and subsequent increases in requests for seed importation across state lines. The East Coast Shellfish Growers Association estimates there are around 50 shellfish hatcheries along the East Coast of the United States producing a dozen or more different species that support more than 1,400 shellfish farms with production growing at 8-10% annually. Several species are impacted by pathogens that decrease survival and production while also threatening native stocks. Knowing which pathogens pose risks and which do not in any particular situation is key to protecting cultured stocks and wild populations. Without access to such information, regulators are pushed toward more precautionary measures, up to and including bans on transfers.

With support from the NOAA Saltonstall-Kennedy Program, this interactive session will present progress toward developing a shellfish health management database for the East Coast of the US. Attendees will critique the proposed database structure to identify weaknesses and oversights, and provide feedback on features that would encourage and facilitate its use by industry, managers and academics.

IMPLEMENTING PHASE II OF THE WASHINGTON SHELLFISH INITIATIVE

Laura Butler[1*] and Laura Hoberecht[2]

[1]Washington Department of Agriculture, 1111 Washington St. SE Natural Resources Building, Washington 98504 USA

[2]National Marine Fisheries Service (NMFS) West Coast Region (WCR), 7600 Sand Point Way NE, Seattle, Washington 98115 USA

LButler@agr.wa.gov

The Washington State Shellfish Initiative (WSI) is an innovative partnership among state government, federal government, tribes, the shellfish industry and nonprofit organizations to promote clean water commerce, create family-wage jobs and elevate the role that shellfish play in keeping our marine waters healthy. The WSI was originally introduced in 2011 by Governor Gregoire in conjunction with the NOAA National Shellfish Initiative. After the completion of over 30 action items, a new work plan was developed and Phase II of the WSI was launched in 2016 by Governor Inslee. Phase II includes a new suite of action items to advance the goals of healthy, abundant shellfish resources for the Washington residents and Native American tribes, as well as a thriving shellfish aquaculture industry. Highlights from the Phase II workplan and progress to date will be presented.

AN ECOLOGICAL FOUNDATION FOR THE RATIONAL MANAGEMENT OF THE FISHERY FOR CARIBBEAN SPINY LOBSTER (*PANULIRUS ARGUS*)

Mark Butler[1*], Gayathiri Gnanalingam[1], Andrew Kough[2], and Claire Paris[3]

[1]Old Dominion University, Department of Biological Sciences, Norfolk, Virginia 23529 USA

[2]John G. Shedd Aquarium, Daniel P. Haerther Center for Conservation and Research, Chicago, Illinois 60605 USA

[3]University of Miami, Rosenstiel School of Marine and Atmospheric Science, Miami, Florida 33149 USA

mbutler@odu.edu

The Caribbean spiny lobster, *Panulirus argus* is an iconic species in the Caribbean where it supports one of the largest and most economically valuable fisheries in the region whose estimated worth approaches $1B US. Over the past few decades, landings in the Caribbean have declined by ~30% and the average size of adult *P. argus* in most areas has decreased, patterns that are indicative of a dramatic loss of spawning stock biomass due to over-fishing. Yet, the more than 35 nations that share the Caribbean Sea struggle for a sensible basis upon which to manage and restore the lobster fishery, see-sawing between parochial management of each nation's lobster resources and the implementation of uniform, Caribbean-wide regulations. In recent years, scientific information has emerged that provides an ecological foundation for the rational management of the *P. argus* fishery in the Caribbean - one based on an understanding of larval connectivity and size-specific reproductive dynamics. Laboratory studies of larval life history and size-dependent male and female reproductive success, when integrated into biophysical models of larval dispersal and spatially-explicit stage-based models that explore the interplay of an MPA and harvest slot-limits, provide insight into new avenues for the cooperative international management of *P. argus* in the Caribbean. This novel schema that merges traditional and ecosystem-based management approaches appears promising as a means to rebuild and sustain stocks of a widespread decapod crustacean, although its implementation may perhaps be politically unpalatable.

STAGE-SPECIFIC DETRIMENTAL EFFECTS OF THE BIOACTIVE EXTRACELLULAR COMPOUNDS PRODUCED BY *ALEXANDRIUM MINUTUM* ON EARLY DEVELOPMENT OF THE OYSTER *CRASSOSTREA GIGAS*

Justine Castrec[1*], Philippe Soudant[1], Bruno Petton[2], Dominique Ratiskol[2], Jacqueline Le Grand[2], Nelly Le Goïc[1], Christophe Lambert[1], Myrina Boulais[1], Hélène Hégaret[1], and Caroline Fabioux[1]

[1]LEMAR UMR 6539, Technopole Brest Iroise, 29280 Plouzané, France

[2]Ifremer/ LEMAR UMR 6539, Presqu'île du vivier, 29840 Argenton, France

justine.castrec@gmail.com

Harmful algal blooms have increasingly disrupted coastal ecosystems for the last few decades with dinoflagellates of the genus *Alexandrium* being of global importance due to its widespread distribution. In France, blooms of toxic *Alexandrium minutum*, known to produce Paralytic Shellfish Toxins (PST) and uncharacterized Bioactive Extracellular Compounds (BEC), appear generally during the season of the reproduction of most bivalves. These blooms could impact larval development or recruitment of juveniles, therefore causing real issues for economically important species, such as the oyster *Crassostrea gigas*.

To test the sensitivity of early life stages of *C. gigas* to *A. minutum* blooms, whether fertilized eggs, veliger larvae (too small to feed on *A. minutum*) or eyed larvae were experimentally exposed for one or two days to *A. minutum*, at environmentally realistic concentration. To discriminate the respective effects of PST and BEC produced by *A. minutum*, the effects of two strains of *A. minutum* known to produce either only BEC, or both PST and BEC, on larval growth, mortality, and settlement were analyzed.

The most deleterious effects have been observed with exposure to the BEC-producing *A. minutum* strain. This treatment i) totally inhibited embryo development by inducing lysis of fertilized eggs, ii) delayed competence for metamorphosis of veliger larvae, partly because of a reduction in larval growth, and iii) reduced larval settlement rate after exposure at veliger or eyed stages. This study provides evidence that BEC produced by *A. minutum* have stage-specific deleterious effects on early development of *C. gigas*.

TAURINE REDUCES THE TOXIC EFFECTS OF MANGANESE ON MITOCHONDRIAL MEMBRANE POTENTIAL

Edward J. Catapane*[1], Margaret A. Carroll[1], Christina Florestan[1], and Kelly Gazca[2]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

[2]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New York 11235 USA

catapane@mec.cuny.edu

Manganese causes Manganism, which is similar to Parkinson's disease. The neurotoxic mechanism is not understood. Some propose manganese causes oxidative stress damaging dopaminergic systems. Results showed manganese reduced oxygen consumption and depolarized mitochondrial membrane potential in *Crassostrea virginica* gill mitochondria. These effects were reduced by EDTA and p-aminosalicylic acid, and taurine reduced deleterious effects of manganese on cilio-inhibitory actions of dopamine on gill lateral cell cilia (GLC). Since taurine alleviate symptoms in other neurodegenerative diseases, we hypothesize taurine will prevent manganese neurotoxicity on GLC mitochondrial membrane potential. TMRM, a mitochondrial probe, was used to study taurine in

manganese treated GLC. The gills of *C. virginica* were exposed to manganese, taurine, or manganese and taurine (125 µM each) and compared to controls. Sections were viewed on a Leica microscope with DFC400 camera, 50 watt HBO mercury lamp and Texas Red filters. Photomicrographs were taken at 0, 10 and 20 min, all with the same camera settings. Mitochondria fluorescence was measured using ImageJ from NIH. Control and taurine treated cells were brightly fluorescing indicating strong mitochondrial membrane potentials. Manganese treatment reduced fluorescence by 40%. Co-treatments with manganese and taurine reduced fluorescence by only 20%. This study showed taurine protects against manganese on mitochondrial membrane potential, supporting our physiology studies demonstrating taurine's neuro-protective ability against manganese on dopaminergic, cilio-inhibitory innervation of GLC. These finding should be of interest to those exploring therapeutic treatments for Manganism.

PHENOTYPIC PLASTICITY IN SHELL CONSTRUCTION AND REMODELING IN THE GASTROPOD, *NUCELLA LAMELLOSA*

David M. Charifson[1]* and Paul E. Bourdeau[2]

[1]Stony Brook University, Department of Ecology and Evolution, 650 Life Sciences Building, Stony Brook, New York 11794-5245 USA

[2]Humboldt State University, Department of Biological Sciences, 1 Harpst St., Arcata, California, 95521 USA

david.charifson@stonybrook.edu

Many marine gastropods exhibit inducible defenses, or phenotypic plasticity in response to increased predation risk. Often, inducible responses result in a thicker shell that is more difficult for predators to break; however, little is known about the fine scale construction of the shell under inducible shell thickening. Studies of inducible shell thickening tend to only examine recent shell growth or do not make a distinction between recent growth and modifications to parts of the shell present before exposure to predators (shell remodeling). Snails may remodel older regions of their shell in response to increased predation risk. The intertidal gastropod, *Nucella lamellosa*, exhibits inducible shell thickening in response to the predatory crab, *Cancer productus*. The role of shell construction and remodeling in inducible shell thickening was examined using hard tissue histology. The thickness of microstructural shell layers was examined at various parts of the shell, from newly produced shell material at the aperture to older parts of the shell at the apex. *N. lamellosa* exposed to chemical cues from *C. productus* had thicker shells compared to the controls, not only near the aperture, but near the apex as well. All *N. lamellosa* exposed to crabs had an inner crossed lamellar layer at the aperture, while most control snails had no detectable crossed lamellar layer at the aperture. These results demonstrate that increased predation risk effects how snails construct their shells and that such alterations are not limited to shell growth that occurs after exposure to the predator.

QUANTIFYING ECOSYSTEM FUNCTIONS IN MIXED OYSTER CULTURE AND SEAGRASS/MACROALGAL HABITATS

Daniel Cheney[1*], Bobbi Hudson[1], Brett Dumbauld[2], Jeff Cordell[3], Fiona Nash[4], and Sharon Kramer[5]

[1]Pacific Shellfish Institute, 120 State Ave NE #1056, Olympia, Washington 98502 USA

[2]USDA-Agricultural Research Service, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport Oregon 97365-5296 USA

[3]University of Washington, School of Aquatic and Fishery Sciences, P.O. Box 355020, Seattle Washington 98195-5020 USA

[4]Oregon State University, Dept. of Fisheries and Wildlife, Corvallis, Oregon 97331 USA

[5]HT Harvey and Associates Ecological Consultants, 1125 16th Street, Suite 209 Arcata, California 95521 USA

cheney@pacshell.org

Considerable effort is directed at studies of ecosystem functions in shellfish culture and associated aquatic vegetation. The application of the Habitat Suitability Index (HSI) as a simplified tool to quantify and map aspects of ecosystem functions in mixed oyster culture and seagrass habitats will be described. Epibenthic taxa were examined in areas used for oyster long-line and flip-bag culture, and adjacent eelgrass and edge habitats at multiple locations in Humboldt, Tillamook, Willapa, and Samish Bays, four major U.S. west coast shellfish producing regions. The epibenthic data were assigned numerical ratings based on the total number of taxa, total taxa abundance, and mean abundance of selected prey taxa. Oyster culture ratings were then calibrated using data from available assessments of epibenthic taxa on long-line clusters and ground cultured oysters, and eelgrass and macroalgae densities.

Based on project field data, seagrass/macroalgae habitat had the highest overall average ratings. Ratings were lower and similar for oyster culture and bare or mixed sediment habitat types. Calibrating oyster culture ratings with epibenthic densities from long-line clusters resulted in ratings which were nearly equivalent to the eelgrass ratings. Limited sampling from flip-bags elsewhere in the region also indicates epibenthic production on these structures was also similar to the long-line clusters. Finally, this work applies the HSI ratings in a preliminary examination of the areal extent of predator prey functions across a range of mapped shellfish culture methods and habitat types.

GROWTH OF JUVENILE FRESHWATER MUSSELS (*ANODONTA IMPLICATA*) REARED IN PONDS WITHIN THE DELAWARE ESTUARY

Kurt Cheng*[1], Danielle Kreeger[1,3], Angela Padeletti[1], Lance Butler[2], and Roger Thomas[3]

[1]Partnership for the Delaware Estuary, 110 South Poplar St. Suite 202, Wilmington Delware, 19801 USA

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

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

kcheng@delawareestuary.org

North America is home to nearly 300 of 840 identified species of freshwater mussels (Bivalvia: Unionoida). These filter-feeding bivalves have gained recent attention due in part to their conservation status, with over 70% of North American species at risk of extinction. In the Delaware River Basin, freshwater mussels have been declining in range, abundance, and species richness. A Freshwater Mussel Recovery Program (FMRP) was formulated in 2008 in attempt to reverse these declines, pairing traditional conservation measures with new restoration tactics aimed at promoting bivalve-delivered ecosystem services. One facet of the FMRP is propagation of freshwater mussel seed for restoration projects. With hatchery support from the Harrison Lake National Fish Hatchery, over 80,000 juvenile alewife floaters (*Anodonta implicata*) were produced in spring 2017 using Delaware River brood stock. Several thousand juveniles were deployed into floating baskets in rearing ponds at six different locations throughout Pennsylvania and Delaware. Initial stocked mussel size varied between 0.3 to 0.5 mm in shell length. Within seven months, juveniles reared in some ponds demonstrated high survival with growth to 60 mm shell length. Juveniles reared in other ponds initially experienced 100% mortality but mussels did survive and grow when stocked at 10 mm or greater shell length. Size at deployment may therefore influence site-specific survival, possibly due to variability in biofouling or food conditions. Future studies include comparing juvenile mussel condition and seston composition among ponds. Optimization of juvenile rearing protocols will strengthen restoration outcomes as the FMRP expands its hatchery propagation program.

REPORT ON THE UNKOWN HAPLOSPORIDIAN PARASITE FROM THE GRAY MUSSEL, *CRENOMYTILUS GRAYANUS,* FROM GANGNEUNG ON THE EAST SEA OF KOREA

Young-Ghan Cho[1*], Hye-Mi Lee[1], Kwang-Sik Choi[1], Hyun-Sil Kang[2], and Chul-Won Kim[3]

[1]Jeju National University, School of Marine Biomedical Science (BK21 PLUS), 102 Jejudaehakno, Jeju 690-756, Republic of Korea

[2]Tidal Flat Research Institute, National Institute of Fisheries Science (NIFS), Kunsan 54014, Republic of Korea

[3]Korea National College of Agriculture and Fisheries, Department of Aquaculture, Kongjwipatjwi-ro, Wansan-gu, Jeonju-si, Jeollabuk-do, 54874, South Korea

youngghan@jejunu.ac.kr

The phylum Haplosporidia contains 52 described species and several unidentified species. In this study, unidentified Haplosporidian member was found from the gray mussel, *Crenomytilus grayanus* (Dunker, 1853) on the East Sea of Korea. From September 2012 to August 2013, 30 mussels were collected monthly and prepared for histology. For the assay, a longitudinal section was cut in the middle of the body, fixed in the Davison's fixative, dehydrated and embedded in paraffin. The histo-blocks were sectioned to 6 µm, stained with hematoxylin and counter-stained with eosin Y. In September 2012, Haplosporidian-like organisms exhibiting spherical multinucleate plasmodia could be seen in the digestive tubules of the mussel. These plasmodia developed into sporocysts called sporonts forming walls around each nucleus. Immature sporonts and group of spores were also observed in the epithelium of the digestive tubules. Heavy infection with the Haplosporidian-like organisms was associated with hemocytic infiltration around the infected digestive gland. The small subunit ribosomal DNA (SSU rDNA, 1784bps) and DNA sequence similarity analysis revealed that the Haplosporidian-like organisms discovered from the mussel was closely related to the genus Minchinia and Bonamia with the highest sequence similarity of 87.1% with *Minchinia tapetis.* Twelve mussels out of 300 examined exhibited the unidentified Haplosporidian parasite. Currently ultrastructure of the unknown Haplosporidian parasite from the gray mussel is analyzed using the transmitted electron microscope.

FACILITATING BETTER DECISION-MAKING: IS SHELLFISHING RIGHT FOR YOU?

Antoinette Clemetson[1*], Michael Ciaramella[1], and Gregg Rivara[2]

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

[2]Cornell Cooperative Extension of Suffolk County, 423 N Griffing Avenue, Suite 100, Riverhead, New York 11901-3071 USA

aoc5@cornell.edu

There is substantial interest in shellfish cultivation throughout the northeast. In New York, hard clams and oysters represent the most commonly cultivated species. Access to submerged (or underwater) lands is a major constraint to the expansion of the shellfish cultivation industry, and the Suffolk County Aquaculture Lease Program (SCALP) was enacted in 2014 to address this need. With the designation of a 30,000 acre Shellfish Cultivation Zone, SCALP presents a relatively inexpensive option for private parties to establish a marine business. While the first two cycles of SCALP focused on converting shellfish leases carried over from earlier access programs, SCALP began accepting applications for new shellfish leases in 2010.

Many of the new applicants for SCALP were novice farmers who lacked prior knowledge or experience with shellfish cultivation. As a result, there was a significant failure rate of startup shellfish businesses on account of their unfamiliarity with the industry and good aquaculture practices. In 2016, New York Sea Grant partnered with Cornell Cooperative Extension and other local agencies to develop an online course for new aquaculturists with interest in shellfish cultivation. This course includes an overview of the shellfish regulatory requirements, common pre-to-post harvest requirements, BMPs, capital requirements and investment insights etc. This serves as an educational tool to help entrepreneurs make informed decisions before starting a shellfish farm. This session will be used to describe: 1) steps involved in building the course platform, 2) topics and issues summarized; and 3) major challenges and constraints experienced to develop this online course.

OYSTER INFESTATION: ABUNDANCE OF MUDBLISTER WORMS (*POLYDORA WEBSTERI*) IN ALABAMA COASTAL OYSTER FARMS

Sarah M. Cole[1,2*], Kelly M. Dorgan[2,1], and William Walton[3,2]

[1]University of South Alabama, Department of Marine Sciences, Mobile, Alabama 36688 USA

[2]Dauphin Island Sea Lab, 101 Bienville Blvd, Dauphin Island, Alabama 36528 USA

[3]Auburn University, AUSL, 150 Agassiz Street, Dauphin Island, Alabama, 36528 USA

scole@disl.org

Mudblister worms (*Polydora websteri*) infest oyster shells in off-bottom oyster farms across the northern Gulf of Mexico. Worms bore into oysters, which cover mud-filled boreholes with layers of shell, creating the mudblister. When shucked, infested oyster shells break easily and mudblisters can burst, releasing anoxic mud. The half shell market is growing and mudblister worms potentially decrease oyster marketability. This study quantified settlement of worms over a full season of oyster growth in coastal Alabama, with the aim of identifying preventative methods for oyster farmers. Diploid and triploid oysters at three different densities were deployed at four Alabama oyster farms, and collected at different seasons. Worms were extracted from oysters and condition index was quantified. Ploidy and stocking density showed minimal effects on infestation, although abundances varied among seasons and sites. More frequent sampling was conducted in the summer, during the peak of infestation, in combination with monitoring of environmental data to determine if salinity, temperature, oxygen, or turbidity are correlated with *P. websteri* infestation. Re-infestation of previously heavily infested and lightly infested shell was compared during peak infestation to determine if *P. websteri* are re-infesting oysters that have previously been treated for heavy infestation over uninfested oysters. Ongoing experiments are characterizing larval growth rates, planktonic durations, and larval dispersal. Knowing when higher abundances of *P. websteri* occur and under what conditions will help inform oyster farmers in making decisions about when and how frequently to perform treatments to prevent high infestation and reduce mud blisters in oyster shells.

DEFINING THE MICROBIOME OF THE PACIFIC WHITELEG SHRIMP (*LITOPENAEUS VANNAMEI*) IN WILD, AQUACULTURED, AND AHPND/EMS OUTBREAK CONDITIONS

Fernanda Cornejo-Granados[1]*, Alonso A. Lopez-Zavala[2], Luigui Gallardo-Becerra[1], Alfredo Mendoza-Vargas[3], Filiberto Sánchez[1], Rodrigo Vichido[4], Luis G. Brieba[5], Maria Teresa Viana[6], Rogerio R. Sotelo-Mundo[7], and Adrián Ochoa-Leyva[1]

[1]Departamento de Microbiología Molecular, Instituto de Biotecnología (IBT), Universidad Nacional Autónoma de México (UNAM), Cuernavaca, México

[2]Departamento de Ciencias Químico Biológicas, Universidad de Sonora (UNISON), Sonora, México

[3]Instituto Nacional de Medicina Genómica, Secretaría de Salud (INMEGEN), Ciudad de México, México

[4]Centro Nacional de Servicios de Constatación en Salud Animal (CENAPA), Morelos, México

[5]Laboratorio Nacional de Genómica para la Biodiversidad (LANGEBIO), Centro de Investigación y Estudios Avanzados (CINVESTAV Unidad Irapuato) Guanajuato, México

[6]Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California (UABC), Baja California, México

[7]Laboratorio de Estructura Biomolecular, Centro de Investigación en Alimentación y Desarrollo, A.C. (CIAD), Sonora, Mexico

mafercg@ibt.unam.mx

Crustaceans form the second largest subphylum on Earth, which includes the Pacific whiteleg shrimp, *Litopeneaus vannamei*, one of the most cultured shrimp worldwide. Despite efforts to study the shrimp microbiota, little is known about it from shrimp obtained from the open sea and the role that aquaculture plays in microbiota remodeling.

The microbiota from the hepatopancreas and intestine of wild type (wt) and aquacultured *L. vannamei* and pond sediment from hatcheries were characterized using sequencing of seven hypervariable regions of the 16S rRNA gene. Additionally, cultured shrimp with AHPND/EMS disease symptoms were included.

The analysis showed that (i) the microbiota and its predicted metagenomic functions were different between wt and cultured shrimp; (ii) independent of the shrimp source, the microbiota of the hepatopancreas and intestine was different; (iii) the microbial diversity between the sediment and intestines of cultured shrimp was similar; and (iv) associated to an early development of AHPND/EMS disease. Changes in the microbiota structure and the predicted functions as well as the appearance of disease-specific bacteria were observed. Notably, the analysis of cultured conditions showed bacterial taxa enriched only in healthy shrimp, such as *Faecalibac-*

terium prausnitzii and *Pantoea agglomerans,* and communities enriched in diseased shrimp, such as *Aeromonas taiwanensis*, *Simiduia agarivorans* and *Photobacterium angustum* suggesting their use as probiotics for *L. vannamei*. These findings strongly suggest that the microbiota manipulation could be utilized as a new approach against shrimp diseases.

LARGE-SCALE PATTERNS OF TREMATODE PARASITE COMMUNITIES INFECTING *CERASTODERMA EDULE* FROM PORTUGAL TO MOROCCO

Simão Correia[1*], Luísa Magalhães[1,2], Xavier de Montaudouin[2], Hocein Bazairi[3], Mériame Gam[3], and Rosa Freitas[1]

[1]Departamento de Biologia & CESAM, Universidade de Aveiro, 3810-193 Aveiro, Portugal

[2]Université de Bordeaux, EPOC, UMR 5805 CNRS, 2, rue du Pr Jolyet, F-33120 Arcachon, France

[3]University Mohammed V in Rabat, Faculty of Sciences, 4 Av. Ibn Battota, Rabat, Morocco

simaocorreia@ua.pt

Trematodes are common coastal macroparasites with complex life cycle using generally three hosts. The exploited cockle, *Cerastoderma edule*, is a dominant bivalve distributed along northeastern Atlantic coasts hosts several trematode species. Extensive spatial sampling of cockles from Portugal to South Morocco (2500 km) was performed in order to 1) analyze cockle parasites south of 31°N. and 2) identify drivers of parasite community structure.

Most of the 12 trematode species were observed along the whole latitudinal gradient, demonstrating the high dispersal ability of these parasites; however, one species was absent in the southern stations, in relation with host distribution area. Multivariate analysis related to trematode communities in cockles clustered: 1) a series of poorly connected sites with low infection, corresponding to northern Portuguese stations under the influence of cold water (upwelling proximity) and coarse sediments; 2) sites characterized by the dominance of the trematode *Parvatrema minutum* in habitat suitable for intermediate host, *Scrobicularia plana*; 3) lagoons (or bays) with high oceanic influence and characterized by high trematode diversity.

This study highlighted that the most important limiting factor was the presence of the other hosts. The results also suggest that temperature is an important trigger to predict parasite infection, with coastal upwelling system operating for Portugal as a shield against trematode infection. These vertical currents provide cool surface temperature and mask latitudinal gradients of temperature (and trematode infection). This study figures out what could be the consequence of thermal modification mediated by oceanographic global circulation changes on cockle populations.

ESSENTIAL FATTY ACID ASSIMILATION AND SYNTHESIS IN *CRASSOSTREA GIGAS* LARVAE

Fiz da Costa[1,2]*, René Robert[1,3], Claudie Quéré[1], Gary H. Wikfors[4], and Philippe Soudant[5]

[1]Ifremer/Laboratoire des sciences de l'Environnement Marin (UMR 6539, LEMAR), 29280 Plouzané, France

[2]Present Address: Oceano Fresco Lda., Edifício Mira Center, Rua do Matadouro, piso 2, Lab. B2, Valeirinha, 3070-436 Mira, Portugal

[3]Ifremer, Unité Littoral, Centre Bretagne, ZI de la Pointe du Diable-CS 10070, 29280 Plouzané, France

[4]Northeast Fisheries Science Center, NMFS, NOAA, 212 Rogers Avenue, Milford, Connecticut 06460, USA

[5]Laboratoire des Sciences de l'Environnement Marin (UMR 6539, LEMAR), IUEM/UBO, Technopole Brest Iroise, Plouzané, France

fiz.dacosta@oceano-fresco.pt

Essential fatty acids (EFA) are of utmost importance for bivalve larval survival and growth. The objective of this study was to calculate accurately using a mass-balance approach dietary EFA incorporation and synthesis by *Crassostrea gigas* larvae. A first experiment was performed using two single diets (*Tisochrysis lutea* (T) and *Chaetoceros neogracile* (Cg)) and a bi-specific diet (TCg). A second experiment using a similar design was carried out to confirm and validate the results observed in the first experiment. Use of a flow-through larval rearing has allowed to control accurately food supply and measurement of ingestion. Fatty acid desaturase Δ5 was actively involved in non-methylene-interrupted fatty acids synthesis from precursors supplied in the diet (16:1n-7 and 18:1n-9). This Δ5 desaturase presumably participated in the conversion of 20:3n-6 and 20:4n-3 to 20:4n-6 and 20:5n-3 in oyster larvae, respectively, when diets were deficient in these EFA, as when larvae were fed T exclusively. Under the experimental conditions, 22:6n-3 was not synthetized, *de novo* or from precursors; however, 22:6n-3 incorporation into larval tissues occurred selectively under non-limiting dietary supply to maintain optimal levels in the larvae. This approach, which combines flow-through larval rearing and fatty acid quantification, could be useful to precisely define optimal levels of EFA supply in bivalve larval diets.

ASSESSING SHELLFISH TRANSFERS AS A VECTOR FOR THE EUROPEAN GREEN CRAB (*CARCINUS MAENAS*) AND THE EFFECTIVENESS OF POWER-WASHING TO MITIGATE MOVEMENT

Lyanne J.F. Curtis*, Christopher M. Pearce, Vanessa R. Hodes, and Thomas W. Therriault

Department of Fisheries and Oceans Canada, Pacific Biological Station, 3190 Hammond Bay Rd. Nanaimo, British Columbia, V9T 6N7 Canada

lyanne.curtis@dfo-mpo.gc.ca

The European green crab (*Carcinus maenas*) is a high-risk global invader that has been redistributed via many anthropogenic vectors, including the movement of live seafood and aquaculture products. In 2012, shellfish movements were confirmed as a vector for green crabs in British Columbia (BC, Canada), transferring this species from the west coast of Vancouver Island to Sooke Basin (Salish Sea). A conceptual framework was developed that identified potential control points that could be used to reduce the risk of inadvertently spreading green crabs. The first control point occurs at the culture/collection site and involves an effort to prevent entrainment with the vector. Present conditions of license in British Columbia require the "rinsing" of shellfish product prior to movement, however, the efficacy and potential utility of this mitigation measure have not been evaluated and no specific guidance (*i.e.*, duration, intensity, *etc.*) has been provided. Results of a project evaluating the efficacy of power-washing (at different intensities and durations), relative to taking no action (*i.e.*, control) and present industry practice (*i.e.*, dipping), in removing green crabs from Pacific oysters (*Crassostrea gigas*) will be presented. The potential utility of these results for management will be discussed.

APPLICATION OF TRIPLOIDY TO AN EMERGENT OYSTER CULTURE INDUSTRY ON THE FLORIDA WEST COAST

Carter Cyr[1]*, Reggie Markham[1], Charles A. Sims[2], and Leslie N. Sturmer[1]

[1]University of Florida/IFAS, Shellfish Aquaculture Extension Program, Senator Kirkpatrick Marine Lab, 11350 SW 153rd Court, Cedar Key, Florida 32625 USA

[2]University of Florida/IFAS, Food Science and Human Nutrition Department, 530 Newell Drive, Gainesville, Florida 32611 USA

ccyr399@ufl.edu

To address increased interest in oyster culture on the Florida west coast, replicated field trials were conducted to document the production performance of diploid and triploid oysters *Crassostrea virginica* and quantify the effects of stocking densities, gear modifications, and seasonal harvests. Single-set oysters (shell height [SH] average: 25 mm) were cultured in 9 and 12 mm mesh floating bags from August (2016) through April (2017) at final densities of 125, 150, and 175/bag (n=6). Triploid oysters (averages: 84.2 mm SH, 140.0 g total weight [TW], 12.8 g meat weight [MW], 3.1 g dry MW, 12.8 condition index [CI]) were significantly ($P<0.05$) larger than diploids (averages: 75.8 mm SH, 109.4 g TW, 9.2 g MW, 1.7 g dry MW, 9.8 CI); in contrast, survival of diploid oysters (97.7 %) was higher ($P<0.0001$) than triploid oysters (90.4%). Stocking densities had little effect on production. Although biofouling control methods consisted of weekly aerial drying of bags, natural overset was problematic; over 70 % of the oysters harvested were fouled with wild spat. Another set of trials conducted from April through November (2017) compared float type (square versus bullet), float placement (side versus top), and anti-fouling coatings on bags stocked with oysters at 150/bag (n=4). Production results will be presented. The sensory attributes of cultured oysters harvested seasonally were also evaluated. In the spring (May), triploid oysters rated higher ($P<0.10$) in appearance and acceptability than diploids. Results may improve awareness of the benefits of triploidy and accelerate adoption of a new bivalve species for culture.

SHELLFISH COMMUNITY PATTERNS IN THE NATIVE AND NON-NATIVE EELGRASS HABITATS OF NETARTS BAY, OREGON, USA

Anthony F. D'Andrea*, Elizabeth A. Perotti, Cinamon Moffett, and Stacy Strickland

Oregon Department of Fish and Wildlife, Marine Resources Program, 2040 SE Marine Science Drive, Newport, Oregon 97365 USA

tony.f.dandrea@state.or.us

The non-native eelgrass *Zostera japonica* was introduced in the 1930s to the Pacific Northwest (PNW) and has since become well-established in many Oregon estuaries. Several of these estuaries have expansive native *Zostera marina* beds and support communities of ecologically, recreationally, and commercially important shellfish; however, there is limited information about the effects of *Z. japonica* expansion on these communities. In 2013-2014, the Oregon Department of Fish and Wildlife conducted a comprehensive shellfish community and estuarine habitat survey of Netarts Bay. The survey used a whole estuary randomized approach stratified by region of the estuary and tide level on the intertidal. There were four major bed types identified in the bay: unvegetated (UV), *Z. marina* only (ZM), *Z. japonica* only (ZJ), and mixed eelgrass beds (MX). Multivariate analyses showed evidence for differences in community structure between sites with eelgrass relative to UV sites. Among the eelgrass bed types, there was a transition in community composition from ZM to MX to ZJ bed types. A canonical analysis of principle coordinates (CAP) was used to test for distinct communities between the bed types. The CAP model explained more than 75% of the variability in community structure. This variability was due to species compositional changes and characteristic species found within the different bed types. The results of this study support the assertion that the expansion of *Z. japonica* in Netarts Bay has led to shifts in shellfish communities and improve our understanding of the ecological effects of this non-native eelgrass in PNW estuaries.

INSIGHTS INTO MORTALITIES AFFECTING SILVER-LIPPED PEARL OYSTER *PINCTADA MAXIMA* IN THE KIMBERLEY SINCE 2006

Cecile Dang*[1], Mike Snow[1], Terry Miller[1], and Aaron Irving[2]

[1]Fish Health Laboratory, Department of Primary Industry and Regional Development Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia

[2]Pearl Producers Association, PO Box 1605, Fremantle, WA 6959, Australia

cecile.dang@dpird.wa.gov.au

The pearl oyster industry is one of the most valuable and iconic fisheries in Australia, creating significant economic and employment opportunities across Northern Australia; however, health issues have been persistent obstacles affecting productivity of the Australian pearling Industry. One of the largest mass mortality events of farmed silver-lipped pearl oysters (*Pinctada maxima*) occurred in the Exmouth Gulf of Western Australia (WA) in 2006, where an estimated 2.8 million individual oysters died. Oysters involved in this event displayed a marked oedema, a retraction of the mantle and a lack of inflammation in tissues, which led to the Oyster Oedema Disease case definition to describe affected animals. An infectious agent was suspected following some initial epidemiological investigations. Since 2006, *P. maxima* pearl culture productivity has been limited by morbidity and mortality of spat and adults, as well as by a decrease in the quality of the pearl across all regions of northern Australia. A common sign across all affected oysters is a retraction of the mantle. Several research projects tasked with identifying and characterising an infectious agent over the last 10 years have failed to identify a pathogen as the cause. More work is required to investigate and better understand the cause of recent mortalities in the Kimberley. This presentation will provide some insights into mortality events since 2006, into the research projects undertaken over the past 10 years, as well as into recent new leads and planned future research to better understand and address this loss of productivity for industry.

PERKINSUS OLSENI IN MOLLUSCS FROM WESTERN AUSTRALIA

Cecile Dang*[1], Cheryl Jenkins[2], Terry Miller[1], Mike Snow[1], Charles Caraguel[3], Jeffrey Go[2], and Daniel Bogema[2]

[1]Fish Health Laboratory, Department of Primary Industry and Regional Development Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia

[2]Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, NSW 2568, Australia

[3]University of Adelaide, School of Animal and Veterinary Science, Roseworthy, SA 5371, Australia

cecile.dang@dpird.wa.gov.au

Abalone are an economically important species, which contributes approximately AU$190 million annually to the Australian economy. First described in South Australia in 1981 as a parasite of the abalone, *Haliotis rubra, Perkinsus olseni*, is responsible for large-scale mollusc mortalities worldwide, and is notifiable to the Word Organisation in Animal Health (OIE). This parasite has been reported from other mollusc hosts in most Australian states. Recent surveys in Western Australia using Ray's Fluid Thioglycollate medium method (RFTM) have revealed that this parasite infects several farmed and wild mollusc species such as greenlip abalone, *H. laevigata*, Roe's abalone, *H. roei*, scallops, *Amusium balloti*, pearl oysters, *Pinctada margaritifera, P. maxima* and *P. fucata*, and cockles, *Circe plicatina* and *Costacallista impar*. These recent investigations have revealed limitations in the analytical and diagnostic sensitivity and specificity of current OIE recommended testing protocols. The industry has highlighted the need for a reliable, rapid and specific method to detect this parasite. The ability to detect *P. olseni* in abalone tissues as well as in haemolymph and water samples will provide critical tools for surveillance and on-farm management of *Perkinsus* infections of commercial stocks. A current research project, funded by the Fisheries Research and Development Corporation (FRDC), aims to optimise diagnostic capabilities for *Perkinsus* spp. isolates, including developing a rapid and specific method to detect the parasite using an antibody-based approach. An overview of the *P. olseni* infection status in WA molluscs as well as the objectives and progress of the FRDC project will be presented.

ENVIRONMENTAL DETERMINANTS OF *VIBRIO PARAHAEMOLYTICUS* IN THE CHESAPEAKE BAY: CURRENT AND FUTURE WORK

Benjamin J.K. Davis[1]*, John M. Jacobs[2], Angelo DePaola[3], and Frank C. Curriero[1]

[1]Johns Hopkins School of Public Health, Department of Epidemiology, 615 N. Wolfe Street, Baltimore, Maryland 21205 USA

[2]National Oceanic and Atmospheric Administration, National Ocean Service, National Centers for Coastal Ocean Science, Cooperative Oxford Lab, 904 S. Morris Street, Oxford, Maryland 21654 USA

[3]Angelo DePaola Consulting, 12719 Dauphin Island Parkway, Coden, Alabama 36523 USA

bdavis64@jhmi.edu

One of the leading causes of seafood-borne illness in the United States is *Vibrio parahaemolyticus* and it occurs naturally in brackish waters. Given the natural presence of the bacterium, an improved understanding of its environmental determinants is necessary for future preventative measures. This work attempts to elucidate the environmental determinants of this bacterium in the tidal waters of the Chesapeake Bay using a uniquely large data set (n = 1,385) collected from 148 monitoring stations between 2007-2010. Interval-censored regression models with splines were developed using water samples analyzed by qPCR for *V. parahaemolyticus* abundance along with spatially- and temporally-indexed water quality data. Previously identified relationships with water

temperature and turbidity were confirmed, while more complex and non-linear relationships were identified for many forms of nitrogen and phosphorus. Non-linear associations with salinity were determined to be a function of both low temperature and turbidity. Associations with dissolved oxygen and phosphate also appeared stronger when samples were taken near human developments.

This analysis of environmental *Vibrio parahaemolyticus* is one of only a few analyses that utilize a large data set measured over a wide geographic and temporal range. This work contributes to a larger NIH-funded research project with the overall goal of developing *V. parahaemolyticus* predictions and forecasts to be used by shellfish harvesters and regulators. Details of this project, including the regionalization of existing quantitative microbial risk assessments for *V. parahaemolyticus* in shellfish for the Chesapeake Bay and Washington State harvesting waters, will also be discussed.

EXPLORING AN INITIATIVE TO TRAIN THE NEXT GENERATION OF SHELLFISH BIOLOGISTS

Chris Davis*[1], Joth Davis[2], and Bill Walton[3]

[1]Pemaquid Oyster Company, PO Box 302, Waldoboro, Maine 04572 USA

[2]Baywater, Inc., 10610 Manitou Park Blvd, Bainbridge Island, Washington 98110 USA

[3]Mississippi-Alabama Sea Grant, Auburn University Shellfish Lab, 150 Agassiz St., Dauphin Island, Alabama 36528 USA

cdavis@midcoast.com

In an effort to produce well-rounded shellfish biologists, the moderators will lead a discussion to explore the feasibility of forming intensive graduate-level summer workshops focusing on a broad range of bivalve research methods. These Bivalve Boot Camps would rotate annually around the three coastlines of the US and be taught by leading researchers within the NSA community. The overall goal is to train NSA recruits in a broad suite of shellfish research methods so that they become more well-rounded shellfish biologists. This workshop seeks to develop interest and input among NSA meeting attendees regarding this concept.

DEVELOPMENT OF AQUACULTURE PRODUCTION TECHNIQUES FOR PURPLE-HINGE ROCK SCALLOPS

Joth Davis

Baywater, Inc., 10610 NE Manitou Park Blvd., Bainbridge, Washington 98110 USA

jothpdavis@gmail.com

There is growing interest in aquaculture development of the purple-hinge rock scallop (*Crassadoma gigantea*), a species with high market potential in the Pacific coastal states. Information on grow out technologies, rate of growth, survivorship and methods to reduce the behavioral tendency for scallops to cement to hard substrates is necessary prior to widespread aquaculture development. A field study describing size at age, survivorship, and cementation behavior at seven Puget Sound sites indicates that scallops grow rapidly to a market size of 100mm in under three years. Survivorship was observed to be generally high and in excess of 80% from seed to harvestable size at most sites. Importantly, once scallops reach 50-60mm, the tendency to cement onto hard substrates is significantly reduced. Obstacles remain to full commercialization in Washington State due mainly to regulatory concerns associated with wild cultured interactions. This may necessitate the development of triploid seed stocks prior to widespread efforts at commercial cultivation of this species. Recent efforts at producing triploid scallops will be discussed with a discussion of opportunities and obstacles in the development of aquaculture methods for this scallop.

ALASKAN MARICULTURE INTIATIVE – TANGIBLE INDICATIONS OF PROGRESS AS A RESULT OF A THREE-YEAR COMPREHENSIVE PLANNING PROCESS

Julie Decker*[1] and Paula Cullenberg[2]

[1]Alaska Fisheries Development Foundation, P.O. Box 2223, Wrangell, Alaska 99929 USA

[2]Alaska Sea Grant Marine Advisory Program, 1007 W. 3rd Avenue, Suite 100, Anchorage, Alaska 99501 USA

jdecker@afdf.org

Alaska produces over 50% of the seafood in the United States; its coastline is over 33,000 miles long; and Alaska has a reputation for responsible resource management. The potential for mariculture in Alaska represents a tremendous opportunity for renewable, supplemental, and diversified economic development; however, industry growth is stagnant at around $1 million in annual production.

In 2014, the Alaska Fisheries Development Foundation (AFDF) was funded through a NOAA Saltonstall-Kennedy grant to spearhead the Alaska Mariculture Initiative (AMI) in order to expedite development of the mariculture industry in Alaska. As a result of the initiative, Governor Walker established the Alaska Mariculture Task Force by Administration Order #280 in 2016 with the directive to deliver a comprehensive plan by March 1, 2018. This presentation will cover the highlights of this comprehensive plan, the unique components of the planning process (including the three-phase iterative economic analysis), and the tangible indications of progress to date.

UNDERSTANDING THE PHYSIOLOGICAL MECHANISMS UNDERLYING THE ENHANCED SURVIVAL OF *CRASSOSTREA GIGAS* INFECTED BY THE OSTREID HERPESVIRUS 1 AT HIGH TEMPERATURE

Lizenn Delisle[1*], Bruno Petton[2], Jean-François Burguin[1], Claudie Quéré[1], Elodie Fleury[1], Marianna Pauletto[3], Benjamin Morga[4], Sébastien Artigaud[5], Vianney Pichereau[5], Charlotte Corporeau[1], and Fabrice Pernet[1]

[1]Ifremer/LEMAR UMR 6539, Technopole de Brest-Iroise, 29280 Plouzané, France

[2]Ifremer/LEMAR UMR 6539, Presqu'île du vivier, 29840 Argenton, France

[3]Dipartimento di Biomedicina Comparata e Alimentazione (BCA), Università di Padova, Italy

[4]Ifremer/Laboratoire de génétique et Pathologie, avenue de Mus de Loup, 17390 La Tremblade, France

[5]LEMAR UMR 6539 CNRS/UBO/IRD/Ifremer, Université de Bretagne Occidentale, Institut Universitaire Européen de la Mer, 29280 Plouzané, France

lizenn.delisle@ifremer.fr

Among all the environmental factors, seawater temperature plays a decisive role in triggering marine diseases. Like fever in vertebrates, high seawater temperature could modulate the aptitude of the parasite to colonize a host and the ability of the host to defend itself in ectothermic animals. In France, massive mortality of Pacific oysters (*Crassostrea gigas*) caused by the Ostreid herpes virus 1 (OsHV-1) occurs when seawater temperature ranges between 16°C and 24°C.Results show that oysters exposed to OsHV-1 at 29°C exhibited 86% survival compared to only 52% at 21°C and 44% at 26°C. These differences in survival likely reflect a protective metabolism of the host at high temperature because there was no evidence of change in OsHV-1 virulence.

The objective of this session is to investigate the physiological mechanisms underlying the enhanced survival of oysters infected by OsHV-1 at high temperature by means of RNA sequencing analysis, 2-DE proteomics, and specific biochemical analyses (energetic reserves, enzyme activities and fatty acids). First results indicate that antioxidant metabolism and level of heat shock proteins were strongly modulated at 29°C and may reflect a protective metabolism of the host.

NEXT GENERATION *VIBRIO* RISK TOOLS

Angelo DePaola[1]*, John C. Bowers[2], Ben Davis[3], and Frank Curriero[3]

[1]Angelo DePaola Consulting, 12719 Dauphin Island Pkwy, Coden, Alabama 36523 USA

[2]FDA, Division of Public Health and Biostatistics, 5001 Campus Dr., College Park, Maryland 20740 USA

[3]Johns Hopkins Bloomberg School of Public Health, Department of Epidemiology, 615 North Wolfe Street, Baltimore, Maryland 21205 USA

andydepaola@gmail.com

The risk of illness caused by *Vibrio parahaemolyticus* and *V. vulnificus* after consuming raw oysters and clams is managed in the US by the National Shellfish Sanitation Program (NSSP) using risk prediction tools (calculators) derived from risk assessments developed by the Food and Drug Administration and the United Nations. Predicted exposure at harvest is determined by water temperature and at consumption by additional post-harvest growth based on time and ambient temperatures. These risk calculations are currently provided using Excel spreadsheets with fixed relationships for different regions and production practices and allow control authorities to conduct scenario analyses for proposed post-harvest controls. Since the risk assessments were released in 2005 higher resolution temporal and spatial data that better address the relationship between environmental conditions and risk have become available and could be used to improve the accuracy and reliability of predictions. R-shiny is a flexible and free menu driven analytic and visualization program that is based on the powerful R Statistical Software and has been used in the US/Canada Norovirus Risk Assessment for raw shellfish. It is well-suited for updating and regionalizing *Vibrio* risk prediction tools. Architectural options for scenario analysis and visualization including expansion of shellfish species, pre-harvest controls and input variables that contribute to risk will be presented. Examples of incorporating new data will use ongoing research at Johns Hopkins University and other sources. Additionally, other emerging tools based on risk models including ecological forecasting and verification of cold chain by time/temperature indicators will round out next generation *Vibrio* risk management.

ARE SPAWNER SANCTUARIES AN EFFECTIVE RESTORATION STRATEGY FOR THE NORTHERN QUAHOG (= HARD CLAM) *MERCENARIA MERCENARIA*: A COMPARISON OF TWO RESTORATION EFFORTS ON LONG ISLAND, NEW YORK

Michael H. Doall[1*], Rebecca E. Kulp[1], Bradley J. Peterson[1], Carl Lobue[2], Adam Starke[2], Andrew W. Griffith[1], and Christopher J. Gobler[1]

[1]Stony Brook University, School of Marine and Atmospheric Sciences, 239 Montauk Highway, Southampton, New York 11968 USA

[2]The Nature Conservancy, 250 Lawrence Hill Rd., Cold Spring Harbor, New York 11724 USA

michael.doall@stonybrook.edu

The creation of "spawner sanctuaries", harvest-free areas where adult shellfish are planted at high densities, has been employed as a restoration strategy for the northern quahog (= hard clam), *Mercenaria mercenaria,* in several U.S. east coast estuaries. Recently, New York State has announced a $10.4 million initiative to establish hard clam spawner sanctuaries in five Long Island es-

tuaries; however, the efficacy of this restoration strategy has not been demonstrated in Long Island bays. This study investigates the effectiveness of hard clam spawner sanctuaries through comparison of two ongoing restoration efforts in separate Long Island bays: 1) the Nature Conservancy Great South Bay (GSB) program, which began establishing spawner sanctuaries in 2004, and 2) the Stony Brook University Shinnecock Bay (SB) Restoration Program started in 2012. Intensive monitoring has revealed significant differences in the performance of spawner transplants between and within bays, with condition index, gonad ripeness, and post-stocking survivorship higher in SB across years. In GSB, interannual variability in recruitment has been observed, with greater recruitment occurring in years of higher clam condition, but there has been little overall improvement in hard clam populations due to high juvenile mortality. Recent data from SB, on the other hand, has indicated improvements in bay-wide recruitment and harvest levels since restoration activities began in 2012. Overall, results indicate: 1) proper siting of spawner sanctuaries is essential to maximize survivorship and reproductive output of spawner transplants, 2) high juvenile mortality can limit population recovery despite increases in recruitment, and 3) monitoring is essential to adaptively manage restoration.

EPIGENETIC RE-PROGRAMMING UPON FOREIGN (VIRAL) DNA INVASION INTO CELLS

Walter Doerfler

University of Cologne, Institute for Virology, Erlangen University Medical School, D-91054 Erlangen, Institute of Genetics, D-50674 Cologne, Germany

walter.doerfler@t-online.de

Sequence-specific CpG methylation of promoters is an important epigenetic signal for long-term eukaryotic gene silencing. To elucidate the epigenetic consequences of the intrusion of viruses or of foreign DNA into mammalian cells, we have studied human adenoviruses 2 and 12 (Ad2, 12), frog virus 3 (FV3), bacteriophage lambda (λ), human immunodeficiency virus 1 (HIV1), and African swine fever virus (ASFV). The investigated viral genomes often escape the cellular defense of *de novo* methylation and remain unmethylated when they elicit productive infection cycles. In contrast, upon viral (foreign) DNA integration into the host genome, the integrated viral genomes become extensively *de novo* methylated. Ad12, bacteriophage λ or bacterial plasmid DNA as foreign DNA integrates lead to changes in cellular methylation and transcription patterns with far-reaching consequences for the functional stability of the recipient cell genomes. In Ad12-infected human cells in culture, cellular DNA methylation profiles undergo distinct changes. HIV1 proviral genomes become hyper-methylated in cell culture systems; however, HIV proviral genomes in peripheral mononuclear blood cells isolated from HIV-infected humans with a wide spectrum of reactions to infection remain unmethylated, except in rare cases. The FV3 genome, the odd ball in viral DNA methylation, is hypermethylated in the virion, and the hypermethylated FV3 genomes are actively transcribed both in mammalian and fish cells. The fate of food-ingested bacterial plasmid DNA in the gastrointestinal tract of mice was followed as well as the small amount of persisting food-derived DNA in the mouse organism.

SOME CONSIDERATIONS FOR EVALUATING OYSTER-SEAGRASS INTERACTIONS AT BROADER SCALES IN US WEST COAST ESTUARIES

Brett R. Dumbauld

USDA-ARS, Hatfield Marine Science Center, Newport, Oregon 97365, USA

brett.dumbauld@ars.usda.gov

Oysters have contributed to the local economy of several communities along the US West Coast for over 100 years and in most of the estuaries where Pacific oyster (*Crassostrea gigas*) culture occurs, it has coexisted with the native seagrass (eelgrass, *Zostera marina*). Eelgrass is protected by no net loss provisions and other laws, in part because it provides numerous ecosystem services including nursery habitat for juvenile fish and invertebrates. Most US west coast estuaries are small relative to the nearby coast, experience less riverine influence than estuaries where oysters are cultured on eastern edges of continents, and the majority of oyster culture takes place in intertidal areas. The ecology of eelgrass and cultured oysters as well as their role as habitat is thus directly influenced by bathymetry and proximity to the coastal ocean. Recent initiatives to expand shellfish aquaculture have received increased regulatory scrutiny because eelgrass is declining in many locations worldwide and concern over documented negative effects of culture on eelgrass at local scales. An examination of effects over the larger estuarine seascape scale in Willapa Bay suggests, however, that these may not be negative for eelgrass or for Dungeness crab that use this estuary as a nursery. Instead of using a permit process that simply attempts to preclude negative effects of oyster culture on eelgrass at small spatial and immediate temporal scales, managers should consider a more adaptive approach that considers bathymetric and along estuary gradients that affect both eelgrass and oysters and therefore the services they provide.

STAGE-SPECIFIC EFFECTS OF ELEVATED SEAWATER *P*CO_2 ON THE GENETIC COMPOSITION OF LARVAL PACIFIC OYSTERS (*CRASSOSTREA GIGAS*)

Evan Durland*, Eli Meyer, Pierre De Wit, and Chris Langdon

Oregon State University, Coastal Oregon Marine Experiment Station, Department of Fisheries and Wildlife, Newport, Oregon, 97365 USA

evan.durland@oregonstate.edu

Negative impacts of acidified seawater on oyster larvae have been well documented and several recent studies have shown that physiological responses of these larvae to elevated pCO_2 conditions are dependent on genotype. In 2015 and 2016 trials were conducted in static-culture laboratory and commercial hatchery settings to compare phenotypic and genetic changes in populations of Pacific oysters (*Crassostrea gigas*) reared under both ambient and elevated pCO_2 conditions. It was found that the impacts of elevated seawater pCO_2 upon larval *C. gigas* are stage-specific and distinctly different among veliger developmental periods.

In order to investigate the coincident genetic changes in these larval groups under ambient and elevated pCO_2 conditions, 2bRAD libraries were created from genomic DNA of larval samples collected during the 2015 trial and sequenced on an Illumina HiSeq 2500. More than 15,000 single nucleotide polymorphisms (SNPs) were identified and used to compare changes in the genetic composition of larval pools in both ambient and high pCO_2 cultures.

Initial results indicate that changes in the genetic composition of larval Pacific oyster populations from fertilization to settlement are temporally dynamic. The stage-specific physiological sensitivity of larval oysters to elevated seawater pCO_2 is mirrored by concurrent changes in the genetic composition of these larval pools. Furthermore, among the SNPs which were significantly affected by seawater pCO_2 treatment, ~28% of them displayed directional selection which differed among development periods. The overall nature of genetic changes in larval pools across veliger life stages in response elevated pCO_2 suggests that genetic components of larval fitness are highly epistatic and pleiotropic across developmental periods.

IDENTIFYING REGULATORY BARRIERS TO NATIVE OYSTER RESTORATION IN WASHINGTON, USA

Danielle Edelman

University of Washington, School of Marine and Environmental Affairs, 3707 Brooklyn Ave NE, Seattle, Washington 98105 USA

dedelman@uw.edu

The Olympia oyster (*Ostrea lurida*) suffered a population crash in the early 1900s, and it has yet to recover to historical estimates. Though there are many biological and ecological reasons why the Olympia oyster struggles to return to its former population size, regulatory barriers exist which make it difficult to launch and sustain restoration projects. The author determined that there is a need to define the current permitting pathways for Olympia oyster restoration projects, as well as the points along those pathways which may delay or prevent permit approval. This research explored the permitting framework for oyster restoration projects in Washington State, with a focus on the following aspects: 1) Determining the common pathways for restoration projects based on the paths of least resistance which have been utilized by various restoration groups; 2) Using Multi-Criteria Decision Analysis to identify ideal permitting pathways based on the priorities for restoration projects. Identifying current strategies for navigating the permitting process, as well as those permitting pathways which best align with project priorities, may help to streamline the permitting process and increase the number of successful and ambitious projects.

INTERACTING EFFECTS OF HUMANS AND NATURE: FLOODWATERS, FISHERMEN, AND POPULATION DECLINE OF THE BLUE CRAB

David B. Eggleston

North Carolina State University, Department of Marine, Earth & Atmospheric Sciences, Raleigh, North Carolina 27695 USA

Center for Marine Sciences & Technology, Morehead City, North Carolina 28557 USA

eggleston@ncsu.edu

Ecosystems or populations exposed to multiple perturbations, either simultaneously or at a rate faster than the rate of recovery, can suffer striking changes or "ecological surprises" that are stable over time. This study documents a precipitous and concurrent decline and lack of recovery in different life stages of the commercially important blue crab (*Callinectes sapidus*) population in Pamlico Sound, North Carolina, the second largest estuary in the U.S., following three sequential hurricanes in 1999. Spawning stock declined by 72%, young-of-the-year (YOY) by 63%, and postlarvae by 84%. Fisheries-dependent and -independent data suggest that the decline was due to intense, localized fishing pressure as crabs migrated en masse with hurricane floodwaters down rivers to eastern portions of Pamlico Sound, and once crabs were resident in Pamlico Sound, where catch rates increased state-wide by 369% compared to average catch. Despite a decrease in fishing effort of over 50% since 1999, spawning stock as not recovered to pre-1999 levels. The present study is one of few documented cases of human influence (fishing pressure) and environmental catastrophe (multiple hurricanes) interacting synergistically to cause the rapid and precipitous decline of a fishery stock. The critical lesson is that we must anticipate how mobile animals will respond to large, infrequent disturbances and implement adaptive management strategies that can reduce excessive human extraction at times and places where animals form hyper-aggregations. This lesson is especially important to the southeastern coast of the U.S. where the frequency of hurricanes is expected to increase.

IMMUNOHISTOFLUORESCENCE STUDY OF THE ACTIONS OF MANGANESE ON THE PHOSPHOLIPASE C AND IP3 RECEPTOR MECHANISMS OF DOPAMINE D2-LIKE POST-SYNAPTIC RECEPTORS IN *CRASSOSTREA VIRGINICA*

Mohamed Eid[1]*, Peter Amoako[1], Delilah Cummings[1], Maxine Jacobs[2], Margaret A. Carroll[1], and Edward J. Catapane[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

[2]Kingsborough Community College, 2001 Oriental Ave, Brooklyn, New York 11235 USA

meedeid@gmail.com

Manganese causes Manganism a Parkinson's-like disease. Reports postulate the neurotoxic mechanism is related to dopamine neuron dysfunction, not degeneration. Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine is cilio-inhibitory. Previous work showed the dopamine receptors are D2 type (D2DR) and manganese disrupts the cilio-inhibition of GLC cilia, suggesting D2DR is a site of action in manganese neurotoxicity. The D2DR pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC synthesizes inositol trisphosphate (IP3), which activates IP3 receptors (IP3R) increasing intracellular Ca^{2+}. PLC has not been well studied in bivalves, nor have effects of manganese on PLC or IP3R. It is hypothesized that PLC and IP3R are present in GLC, and if so, any effects of manganese will be determined. Gill sections were prepared with PLC and IP3R antibodies and viewed on a Leica microscope. All sections were photographed with the same camera setting. It was found that GLC displayed green fluorescence in cytoplasm and along cell membranes indicating the presence of PLC and IP3R. Gills threated with manganese had reduced PLC and reduced IP3R fluorescence compared to untreated cells. Zinc treated gills showed no differences. The study shows PLC and IP3R presence in GLC and that manganese did cause a small, significant reduction in PLC and IP3R fluorescence. This study provides new knowledge of manganese actions on D2DR pathway in bivalve gill. Future experiments will test if manganese negatively effects physiological actions of PLC and IP3R on GLC cilia activity.

UNIQUE AND COMMON PATTERNS IN THE STRESS RESPONSE OF THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*

Jose M. Eirin-Lopez[1]* and Victoria Suarez-Ulloa[2]

[1]Florida International University, Department of Biological Sciences, 3000 NE 151st St., North Miami Beach, Florida 33181, USA

[2]University of Namur, Department of Biology, Rue de Bruxelles 61, 5000 Namur, Belgium

jeirinlo@fiu.edu

The application of transcriptomic data series provides a better understanding of the dynamics in the responses of organisms to environmental stress. Accordingly, co-expression networks, classification methods and discriminant analyses represent valuable approaches for this purpose, given their ability to synthesize large amounts of information and to unravel hidden patterns. The present work builds on this knowledge to provide a better understanding of the molecular strategies used by the oyster *Crassotrea gigas* during responses to changing environments and stress. Such information is critical to distinguish expression changes and altered biological processes specifically linked to particular environmental conditions from a core response to stress in general. With this in mind, transcriptomic data series corresponding to different environmental variables were analyzed (temperature, salinity, exposure to the heavy metal Zinc and exposure to *Vibrio* pathogens). The observed general similarities in functional profiles support the notion of a core response to stress. Co-expression network analysis of time-series further revealed a dynamic response to stress allowing the chronological organization of responsive transcript modules. Lastly, the most informative genes in each dataset were identified using sPLS-DA, constituting candidate biomarkers with predictive power for specific stressors. These findings support the value of transcriptomic data series and data mining techniques to promote new hypotheses and convey relevant insights for the development of stress biomarkers in the oyster *C. gigas* useful in oceans biomonitoring.

SUPPORTING MANAGEMENT OF THE EMERGING JONAH CRAB FISHERY AND THE ICONIC LOBSTER FISHERY IN THE NORTHEAST USA: A COLLABORATIVE FISHING VESSEL RESEARCH FLEET APPROACH

Aubrey A. Ellertson[1*], Anna Malek Mercer[1], David Spencer[1,2], and Robert Glenn[3]

[1]Commercial Fisheries Research Foundation, P.O. Box 278, Saunderstown, Rhode Island 02874 USA

[2]F/V Nathaniel Lee, Newport, Rhode Island, USA

[3]Massachusetts Division of Marine Fisheries, 1213 Purchase Street, New Bedford, Massachusetts 02740 USA

aellertson@cfrfoundation.org

Despite the economic and cultural importance of the lobster (*Homarus americanus*) and Jonah crab (*Cancer borealis*) fisheries, research scientists, managers, and industry members agree that the data being used to assess these stocks lack sufficient spatial and temporal coverage, particularly in Southern New England. Specifically, there is a mismatch between the location of primary lobster fishing grounds in this region (10-200 miles offshore) and the location where data are being collected (0-3 miles from shore). Similarly, Jonah crab fishery management efforts are hindered by major gaps in the understanding of the catch compostion and operational characteristics of the fishery.

The Commercial Fisheries Research Foundation developed the Lobster and Jonah Crab Research Fleet in 2013 to begin addressing these data needs and inform the assessment and management of

these valuable fisheries resources. Research Fleet participants use a specialized tablet app, digital calipers, and wireless temperature sensors to record information about their lobster and Jonah crab catch and the environment during routine fishing practices. Since 2013, the 18 fishermen participating in the Research Fleet have collected biological data from over 105,000 lobsters and 44,000 Jonah crab as well as coupled bottom water temperatures from the Gulf of Maine to the Mid-Atlantic. The data collected by the Research Fleet are integrated into federal biosamples databases and used extensively in the lobster stock assessment and Jonah crab management plan. Ultimately, the project's approach increases the transparency of the assessment process and promotes the fishing industry's trust in the data sources being used for management.

OYSTER RESTORATION EFFORTS IN THE SOUTHERN INDIAN RIVER LAGOON, FLORIDA - INCORPORATING RESILIENCY TO FRESHWATER DISCHARGES

Vincent Encomio

Florida Oceanographic Society, Stuart, FL. 890 NE Ocean Blvd. Stuart, Florida 34996 USA

vencomio@floridaocean.org

The St. Lucie River Estuary in southeast Florida is periodically beset by freshwater releases from Lake Okeechobee and other drainage canals that have significantly expanded the St. Lucie's watershed since the 1930s. Extended freshwater conditions, as a result of these releases, can devastate oyster resources in this estuary. In 2013, severe wet season rainfall and resulting freshwater discharges resulted in near to complete extirpation of oysters from the St. Lucie. Recovery of lost oyster resources was initiated in 2014-2015. An important facet of this effort was to build resiliency to future discharge events. To achieve this, oyster reef habitat was constructed in seven locations in the southern Indian River Lagoon, downstream from the St. Lucie River. These oyster reefs were incorporated as a component of living shoreline restoration, along with seagrass and shoreline plantings. In 2016, high dry season rainfall due to El Niño conditions, led to freshwater discharges (primarily from Lake Okeechobee) persisting for nine months. Throughout this period, losses of oysters at these downstream sites were minimal, reflective of higher salinities found at these sites. Timing of oyster reef construction at four sites coincided with high spatfall in May and remained consistent for five months following construction. Live oyster densities were extremely high (2000-10,000+ oysters m^{-2}). Although other factors (predation, sea level rise, storms) may influence these sites' long-term persistence as oyster habitat, oysters at these sites were unaffected by the discharges. Future efforts will expand reef creation and continue monitoring of their long-term success.

POLYMORPHISMS IN *RTE-3_LVA* NON-LTR RETROTRANSPOSON OF SPF *PENAEUS VANNAMEI* FROM THE UNITED STATES: ITS ASSOCIATION WITH THE *PENAEUS MONODON* ENDOGENOUS VIRUS IHHNV (INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS) FROM AFRICA AND AUSTRALIA

Daniela Espinoza[1]*, Acacia Alcivar-Warren[1,2], Jurgenne Primavera[3], Leobert De la Pena[3], Kathy Tang, Gladys Zuniga[1,3], and Zhenkang Xu[1]

[1]Fundación para la Conservación de la Biodiversidad Acuática y Terrestre (FUCOBI), Quito, Ecuador

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

[3]SEAFDEC Aquaculture Department, Tigbauan 5021, Iloilo, Philippines

fucobi@gmail.com

The *RTE-3_LVa* non-LTR retrotransposon (3,654 bp) is among the most abundant (3.5%) transposable elements characterized in SPF *P. vannamei* genome (Bao. 2015. Repbase Reports 15(4), 1592; http://www.girinst.org/censor/index.php). *RTE-3_LVa* is 82% identical to the reverse transcriptase (RT, nucleotides 3511-4655) of unnamed retrotransposon in *P. monodon* endogenous virus IHHNV from Africa and Australia (DQ228358, 4,655 bp), a non-infectious strain. IHHNV is prevalent in penaeid shrimp and associated with runt deformity syndrome (slow growth).

RTE-3_LVa contains four conserved domains: L1-EN [endonuclease domain of non-LTR retrotransposon LINE-1], RT_nLTR_like [non-LTR retrotransposon, non-LTR retrovirus reverse transcriptase (RT)], group_II_RT_mat [group II intron RT/maturase]; and RVT-1 [RT: RNA-dependent DNA polymerase]; and is identical to microsatellites and ESTs from SPF *P. vannamei*, wild and farmed *P. monodon*, and cultured *P. stylirostris*. Microsatellites were tested for polymorphisms, some located on to the sex linkage group LG4 of *P. vannamei* (*ShrimpMap*2). Penaeid microsatellites may be generated from the RTE non-LTR retrotransposon clade.

Both infectious and non-infectious IHNNV were amplified by PCR in wild shrimp of Thailand, Ecuador and Gulf of Mexico USA; in frozen shrimp sold in US supermarkets, and SPF *P. vannamei* lines from Hawaii USA (Kona, High Growth, Mexican WSSV-resistant). Infectious IHHNV fragments were identified in *P. monodon* genome, and in isolates from imported SPF *P. vannamei,* wild *P. monodon* (Palawan, Negros Occidental), and cultured *P. monodon* (SEAFDEC) of the Philippines. It is possible that IHHNV is inserted into *RTE-3_LVa* of *P. vannamei,* but a mechanism remains to be determined until a fully-assembled reference genome of SPF *P. vannamei* is available.

LACTIC ACID IN THE TISSUES OF THE APPLE SNAIL, *POMACEA MACULATA*

Sal Essajee and Lewis E. Deaton*

Biology Department, University of Louisiana at Lafayette, Lafayette, Louisiana 70504 USA

led9784@louisiana.edu

The apple snail, *Pomacea maculate,* belongs to the Family Ampullariidae. Species in this group are generally characterized by tolerance of long term exposure to air. For example, *Pila virens* and *P. urceus* can survive six months or more of aerial exposure in aestivation. During aerial exposure, *P. virens* accumulates lactic acid but *P. urceus* does not. *P. maculata* is capable of surviving many months of aerial exposure. When exposed to air, the animals enter a state of aestivation characterized by inactivity; both oxygen uptake and heart rate decrease markedly. To assess the metabolic biochemistry of active snails and snails in aestivation, test strips were used to determine the presence of D- and L-lactate in the tissues of the animals. In active animals the foot and gill contained about higher levels of L-lactate than other tissues. D-lactate levels were higher in the gill than in other tissues. The tissues of snails in aestivation for several months will be assayed for comparison and these results presented.

SHELLFISH AQUACULTURE IN THE COASTAL (INLAND) BAYS OF DELAWARE 2018: STATUS AND OUTLOOK

John W. Ewart

Delaware Sea Grant Marine Advisory Service, College of Earth, Ocean, and Environment, University of Delaware, 700 Pilottown Road, Lewes, Delaware 19958 USA

ewart@udel.edu

After more than a decade of field demonstration research to evaluate shellfish aquaculture technologies for oyster restoration and seafood production in the coastal bays of Delaware, and subsequent public discussion to identify policy and legal constraints, Delaware Governor Jack Markell signed legislation authorizing reinstatement of commercial shellfish aquaculture bottom leases in August 2013.

The Delaware Department of Natural Resources and Environmental Control (DNREC) Division of Fish and Wildlife, charged with developing a bottom leasing program and regulatory framework, completed the drafting and public education/hearing stages with release of final regulations in August 2014. Strong public opposition involving 2 proposed bottom lease tracts adjacent to waterfront residential communities stalled implementation of the leasing program and its review and approval by the US Army Corps of Engineers (ACOE). The issue was resolved in December 2016 through the reduction or elimination of available bottom acreage in the contested locations. The DNREC resumed the shellfish aquaculture leasing program in May 2017 by holding a public lottery as an impartial site selection process for 343 acres of ACOE permitted coastal bay bottom.

Of the 58 individuals participating in the lottery, 34 continued to participate by selecting a total of 206 acres now identified as pending and subject to a formal lease application process. The present status and outlook for the Delaware leasing program and coastal (inland) bays commercial shellfish aquaculture development for 2018 and beyond is reviewed. Additional regulatory and background information is available at the Delaware Inland Bays Shellfish Aquaculture website <darc.cms.udel.edu/ibsa>.

SHELLFISH AQUACULTURE AND EELGRASS: A GLOBAL META-ANALYSIS

Bridget E. Ferriss[1*], Tish Conway-Cranos[2], Beth L. Sanderson[1], and Laura Hoberecht[3]

[1]Northwest Fisheries Science Center, National Oceanic and Atmospheric Administration, 2725 Montlake Blvd. East, Seattle, Washington 98112, USA

[2]Washington Department of Fish and Wildlife, 1111 Washington St. SE Olympia, Washington 98501, USA

[3]NOAA West Coast Region, Sand Point Way Northeast, Seattle, Washington 98115, USA

bridget.ferriss@noaa.gov

The inter-tidal zone is optimal habitat for bivalve aquaculture and eelgrass (*Zostera* spp.), a valuable and protected nearshore habitat. It is important to understand how bivalve aquaculture interacts with eelgrass in order to sustainable develop this globally expanding, industry. This study provides a comprehensive understanding of the positive and negative effects of bivalve aquaculture on eelgrass by conducting the first, quantitative, global meta-analysis of aquaculture-eelgrass studies. The meta-analysis focused on: (1) how eelgrass responds to on-bottom and off-bottom shellfish aquaculture; and (2) the resilience of eelgrass after harvesting disturbances. On-bottom culture (e.g., laying directly on the sediment) corresponded to significant increases in eelgrass biomass, growth, and reproduction. Off-bottom culture (e.g., longline and suspended bag) resulted in significant decreases in biomass, density, percent cover, and reproduction. A US West coast case study (relative to the remaining global average) revealed more negative impacts on biomass, density, and percent cover from off-bottom culture and more positive impacts on biomass from on-bottom culture. Eelgrass densities recovered after all shellfish harvest methods, however mechanical harvesting created greater initial impact and longer recovery times than manual harvest methods. The time-period over which observations were reported was an important variable that was not included in the analysis but could influence results. These analyses suggest the response of eelgrass to shellfish aquaculture varies depending on eelgrass characteristic, grow-out approaches, and harvesting methods, with potential regionally specific relationships. Questions remain, regarding how these cycles of eelgrass and aquaculture habitat relate to ecological functions and services in the nearshore environment.

SPATIO-TEMPORAL DYNAMICS OF PACIFC OYSTERS MORTALITY PATTERNS ALONG THE FRENCH COAST: DISENTANGLING ORIGIN, AGING, AND ENVIRONMENTAL FACTORS

Elodie Fleury[1*], Pierrick Barbier[1], Julien Normand[2], Stéphane Pouvreau[1], Bruno Petton[1], Gatean Daigle[3], and Fabrice Pernet[1]

[1]Ifremer, UMR LEMAR 3539 (UBO/CNRS/IRD/Ifremer), Technopôle Brest Iroise, BP70, 29280 Plouzané France

[2]Laboratoire Environnement Ressources Normandie, Avenue Général de Gaulle

BP 32, 14520 Port-en-Bessin France

[3]Département de Mathématiques et de Statistiques, Faculté des sciences et de génie, Pavillon Alexandre Vachon, Université Laval, Québec, QC G1V 0A6 Canada

elodie.fleury@ifremer.fr

Since 2009, the RESCO monitoring network has been surveying sentinel batches of the cupped oyster, *Crassostrea gigas,* in several study sites over the entire French coast. This network was designed to collect a nationally-spread dataset on diseased induced mortality, to contribute to the understanding of the spatio-temporal dynamics of mortality of this species. Sentinel batches of oysters corresponding to different origins and to two rearing age classes are deployed simultaneously in 13 sites covering the main shellfish growing regions of the French coastline. Mortality and growth are monitored every fifteen days along with environmental parameters and data associated with the presence of infectious agents in sentinel oysters (DNA detection of OsHV-1 and *Vibrio aestuarianus*). The RESCO network actions thus contribute to disentangle the biotic and abiotic parameters involved in mortality phenomena, by implementing a proactive and integrative approach, accounting for the different compartments (environment / host / infectious agents) likely to interact with the evolution of the mortality. Logistic regression model was used to investigate the effect of sites and batches on the oyster final survival and the survival time curves were compared using a Cox regression model with sites and batches as fixed effects, and environmental factors as covariates. A second Cox regression model was performed with level of OsHV-1 and *V. aestuarianus* DNA copy as time-dependant covariates. The results highlight spatial patterns of disease-induced mortalities and the contributions of the main environmental factors adversely affecting oysters' survival.

RELATIONSHIP BETWEEN THE GROWTH CYCLE OF THE RAZOR CLAM AND THE SEASONALITY OF PHYTOPLANKTON BLOOMS ON THE WASHINGTON COAST

Zach Forster* and Charlotte Berry

Washington State Department of Fish and Wildlife, 26700 Sandridge Road, Ocean Park, Washington 98640 USA

zachary.forster@dfw.wa.gov

The ecology of Washington coastal sandy beaches is endemic to only a few places in the world. The exposed, wide and gently sloping beaches have persistent dense accumulations of the surf diatom *Attheya armatus.* The sandy habitat and highly concentrated food source sustain large populations of the Pacific razor clam (*Siliqua patula*), an important resource to the coastal economies of Washington. Razor clam body condition has been routinely monitored by the Washington Department of Fish and Wildlife since 2013. Comparing annual growth cycles using the body condition index (BCI) calculation ((meat dry weight) *100)/ (dry shell weight) peak condition of clams typically occurs in early spring prior to spawning with a subsequent recover of body mass late in the fall. Cell concentrations of *Attheya armatus* increase with intensified wave action in the fall and winter providing high amounts of nutrients during a time of otherwise low productivity. Chlorophyll measurements of surf zone waters are highest in the fall to spring when overall phytoplankton species diversity remains low. While this relationship undoubtedly effects the recruitment of clams on Washington beaches, recent population trends can also be correlated with larger climate indices such as the Pacific Decadal Oscillation (PDO).

TRIBAL CO-MANAGEMENT OF THE SHELLFISH RESOURCES IN WASHINGTON STATE: AN EVOLVING PROCESS

David Alan Fyfe

Northwest Indian Fisheries Commission, 19472 Power Hill Place NE, Suite 210, Poulsbo, Washington 98370 USA

dfyfe@nwifc.org

Treaty tribes of the Pacific Northwest have lived in harmony with the land and seas from time immemorial. As seasons changed, summer camps would be left behind, in favor more suitable locations to survive the winter. Each tribe had Usual and Accustomed fishing areas, sometimes overlapping with neighboring tribes, and sometimes being exclusive to a particular tribe. As European settlers moved westward, interaction and confrontation grew, with two very different ways of life often conflicting. By the mid-1800s, there was a desire to resolve differences peacefully and the U.S. Government signed treaties with these tribes. A few years later, Washington State was carved out of the Oregon Territory. As the population grew, so did the number of regulations necessary to protect the natural resources. Increasingly, the state and tribes clashed over harvest limits, times and areas. The tribes, having reserved their rights to the natural resources in their treaties with the federal government, did not feel bound by regulations developed by the state. After a series of 'Fish Wars' between the state and tribes, the tribes filed within the federal court system to specifically determine what their reserved rights meant. The federal government aligned with the tribes and sat opposite the state in a court hearing and decision that was ultimately referred to the U.S. Supreme Court. This presentation will review events leading up to that decision 40 years ago, known as *U.S. v. Washington*, and how the state and tribes have since implemented the Court's findings.

A PILOT STUDY OF NUTRIENT BIOEXTRACTION USING RIBBED MUSSELS AT HUNTS POINT, NEW YORK CITY, FROM CONCEPTION TO CONCLUSION: PATHS, PROCESSES, PARTNERSHIPS, PERCEPTIONS, AND PROJECTIONS

Eve Galimany[1], Gary H. Wikfors[1*], Mark S. Dixon[1], Carter R. Newell[2], Shannon L. Meseck[1], Dawn Henning[3], Yaqin Li[1], Mark Tedesco[4], Lynn Dwyer[5], and Julie M. Rose[1]

[1]NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford, Connecticut 06460 USA

[2]Maine Shellfish R&D, 7 Creek Lane, Damariscotta, Maine 04543 USA

[3]Rocking the Boat, 812 Edgewater Road, Bronx, New York 10474 USA

[4]EPA Long Island Sound Study, Stamford Government Center, 888 Washington Blvd., Stamford, Connecticut 06904 USA

[5]National Fish & Wildlife Foundation, 1133 15th Street, Washington, DC 20005 USA

Gary.Wikfors@noaa.gov

The term "Nutrient Bioextraction" was coined by three of us in 2009 while planning a workshop held at UCONN Stamford, CT, later that year. The EPA Long Island Sound Study and Milford Laboratory were prompted to explore alternate nutrient management tools by models indicating that water-quality goals could not be met in LIS with conventional technologies. We were inspired by the pioneering work of Odd Lindahl, who employed farmed blue mussels in Lysekil, Sweden, to assimilate and remove nitrogen that evaded the local wastewater treatment plant. The workshop concluded with an agreement to pursue a pilot study. Hunts Point, Bronx, NYC, was chosen because funding from a local environmental damages settlement was available. A coalition of NOAA, EPA, NY State, National Fish & Wildlife Foundation, Maine Shellfish R&D, and local youth development organization Rocking The Boat planned and executed a 2-year study evaluating the use of commercial blue mussel cultivation practices to grow and harvest ribbed mussels in Hunts Point for the purpose of removing nitrogen from the ecosystem. The ribbed mussel, Geukensia demissa, was chosen because it is an environmentally-resilient native species, and there is no commercial market for the species and, therefore, reduced risk of human illness from theft and consumption of the mussels. During this study, much was learned about the ribbed mussel, about the local environment and its suitability for nutrient bioextraction, and about the social context of innovative methods to improve the quality of heavily-degraded environments. Major findings and lessons learned will be highlighted.

DIGITAL PATHOGEN SURVEILLANCE: A ONE HEALTH APPROACH TO PREVENTING INFECTIOUS DISEASES IN HUMANS AND ANIMALS

Jennifer Gardy

Canada Research Chair in Public Health Genomics, School of Population and Public Health, University of British Columbia, Vancouver, Canada, British Columbia Centre for Disease Control, 655 West 12th Ave, Vancouver, BC V5Z 4R4

jennifer.gardy@bccdc.ca

In the human health domain, outbreaks and epidemics of infectious diseases are typically studied through a combination of molecular epidemiology and traditional field epidemiology - we can ask questions of the pathogen itself and ask questions of the individuals who are ill in an attempt to understand how the outbreak started and how it's spreading. Recently, technological advances in multiple areas, from genome sequencing to detecting signals of infectious disease using data from the internet, are changing the way we investigate outbreaks like Ebola and Zika virus – a new paradigm, known as Digital Pathogen Surveillance, is emerging.

This talk will introduce some of the technologies underlying this new approach, discuss some of the successes of the approach in the human health domain, and show how, by adopting a One Health ethos, the approach can be extended to improve disease surveillance in other ecosystems, including the marine world.

RECREATIONAL HARVEST OF BAY SCALLOPS IN FLORIDA

Stephen P. Geiger[1]*, Jennifer Granneman[1], and Brittany J. Scharf[2]

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

[2]Florida Sea Grant, University of Florida, 16110 Aviation Loop Drive, Brooksville, Florida 34604 USA

steve.geiger@MyFWC.com

Commercial fisheries landings in the United States have been reported since the 1800s sporadically and with increasing consistency since the 1950s, but commercial harvest of bay scallops, *Argopecten irradians*, in Florida was prohibited in 1995. Recreational fishing effort is currently estimated through a federally funded statistically model, but bay scallops are not included in those recreational surveys, so neither common method is available to manage the Florida stock based on harvest. Fishing mortality caused by the recreational fishery in Florida in 2002 was estimated to be small, relative to natural mortality, but the fishery appears to have expanded since then.

Pre-season and post-season abundance surveys were conducted in 2011 – 2014 to update estimates of natural and fishing mortality. Direct estimates of effort were conducted in 2016 and 2017 using aerial surveys. Indirect estimates were also collected by monitoring boating activity from launch points known to be frequented by scal-

lop harvesters. Finally, harvest rates were estimated using self-reported post cards and on-line surveys. An estimate of mortality due to harvest was then created based on extrapolating from direct and indirect measures of harvest combined with catch data.

Both methods indicate scallop harvest and total mortality in the open-harvest regions have increased, though fishing mortality remains smaller than natural mortality. Improved estimates could be achieved with more frequent aerial surveys using refined spatial resolution, improved responses from harvesters (including angler-intercept style interviews), and an improved understanding of what proportion of the total population range is being exploited.

LISTENING, LEARNING, AND LEADING TO SUPPORT RESPONSIBLE AQUACULTURE DEVELOPMENT IN CONNECTICUT

Tessa Getchis*, Sylvain De Guise, Nancy Balcom, and Anoushka Concepcion

Connecticut Sea Grant, 1080 Shennecossett Road, Groton, Connecticut 06340 USA

tessa.getchis@uconn.edu

The Connecticut Shellfish Initiative is an effort to grow commercial, recreational, and natural shellfish sectors, and increase public awareness about their importance for maintaining a healthy Long Island Sound and providing maritime jobs.

Shellfish are an important part of the environment, economy, and culture. Shellfish depend upon, and also contribute to, clean water. There are forty-six companies with over 300 people employed in shellfishing-related jobs. Commercial shellfish harvest contributes greater than $30 million dollars annually, while sales of recreational harvest permits generate $110,000 annually in revenue to local communities. Citizens, shellfishermen, regulators, scientists, and other interested parties collaborated to develop and publish the *Connecticut Shellfish Vision Plan* (http://shellfish.uconn.edu). Announced in October 2016, the plan contains specific recommendations.

1. Key successes include:
2. Eight new/expanded commercial shellfish operations
3. Approval of hiring plan for three new staff at public health offices
4. An alternative route for access to shellfish grounds
5. Expanded public outreach
6. Bioextraction coordinator position announced

7. The next phase will include a focus on:
8. Staff and infrastructure for public health offices
9. Streamlining laws, regulations, and policies
10. Strategies to address water quality impairments in shellfish harvest areas
11. Establishing restoration priorities
12. Expanding outreach on the regulatory process for aquaculture
13. Setting research goals for priority issues

These efforts may result in improved recreation, economic development, and a healthier ecosystem; however, to support the responsible growth, outreach is focused on facilitating discussions about how aquaculture can fit into the culture, economy and ecology of local communities.

WINTER IS (NOT) COMING: CHANGES TO OVERWINTER BEHAVIOR OF BLUE CRAB IN RESPONSE TO WARMING TEMPERATURES

Hillary Lane Glandon*[1,2], K. Halimeda Kilbourne[1], and Thomas J. Miller[1]

[1]Chesapeake Biological Laboratory, University of Maryland Center for Environmental Science

P.O. Box 38, Solomons, Maryland 20688 USA

[2]University of North Carolina Wilmington, Biology and Marine Biology, 601 S. College Road,

Wilmington, North Carolina 28403 USA

hillaryannelane@gmail.com

Understanding how increases in water temperature may affect the duration of the winter dormancy period and the overwinter survival are important for the effective conservation and management of estuarine species in the face of a warming climate. In this study, the length of the overwintering period and the probability of overwinter survival of blue crab (*Callinectes sapidus*), an ecologically and economically important estuarine crustacean, was determined. Overwintering period length and probability of overwinter survival were determined using water temperature predictions up to the year 2100 which were derived from a harmonic model that utilized air temperatures predicted in multiple regional-scale climate projections. Estimates of warming water temperatures by 2100 in Chesapeake Bay indicate that the overwintering period in this species will be up to 50% shorter and overwinter survival will increase by at least 20% compared to current conditions. The warmer conditions will lead to faster and prolonged seasonal growth, which, when combined with lower winter mortality, will lead to increased population productivity. The level of expression of this increased productivity will depend on the response of other elements of the Chesapeake Bay food web, and on the response of fishery management policies.

FROM PILOT EFFORT TO A REGIONAL MONITORING PROGRAM: THE COAST-WIDE VENTLESS LOBSTER TRAP SURVEY

Robert P. Glenn[1] and Tracy L. Pugh[2]

Massachusetts Division of Marine Fisheries, 1213 Purchase St, New Bedford, Massachusetts 02740 USA

Massachusetts Division of Marine Fisheries, 30 Emerson Ave., Gloucester, Massachusetts 01930 USA

robert.glenn@state.ma.us

American lobster (*Homarus americanus*) support the most valuable fishery in the northeastern United States with commercial landings exceeding 140 million pounds and ex-vessel value exceeding $500,000,000 since 2014. Historically, stock assessments for American lobster have relied on indices of relative abundance generated from state and federal trawl surveys. This reliance on trawl survey data for assessing American lobster has been a major concern for the fishing industry who astutely point out that trawl surveys cannot tow on rocky hard bottom that is preferred by lobsters. In 2004, a random stratified ventless lobster trap survey was initiated in Massachusetts Bay as a pilot effort in collaboration with Massachusetts commercial fishers. The goal of this survey was to develop an additional fishery independent survey to monitor lobster abundance. Survey methodology was developed with industry input, and the initial success and strong industry support lead to a survey expansion. In 2006, the pilot effort was expanded regionally to a "Coast-wide" monitoring program covering coastal waters from Rhode Island to Maine. In 2015, the ventless lobster trap survey indices were incorporated into population models in the Atlantic States Marine Fisheries Commission American lobster benchmark stock assessment. This marks the first time that an industry-collaborative survey was formally used to assess American lobsters. Industry collaboration has been key to establishing long term funding for the survey and to promoting "buy-in" to survey results.

ALGAL ECONOMICS FOR SHELLFISH HATCHERIES

Shawn D. Glover* and Robert S. Roulston

Industrial Plantkon Inc., 3378 Burns Avenue, Victoria British Columbia, Canada V8Z 3P2

shawn@industrialplankton.com

Algae are undoubtedly one of the biggest bottlenecks in bivalve hatcheries. Whether feed limitation is stifling larval production currently or limiting the potential for expansion, economical solutions for reliable and clean algae production hold the key to making hatcheries more efficient, and ultimately more profitable. Most traditional systems for algal production (i.e. batch or continuous bag systems) have relatively low capital costs; however, they are labour intensive and their output is operator dependant, making the production cost of hatchery-grade algae challenging to accurately quantify. Coutteau and Sorgeoloos (1992) had six of nine hatcheries estimate that 1 kg of algal dry weight (DW) cost them between $300-$400 to produce. Assuming efficiency increases and inflation balance each other to keep this estimate in the same range 25 years later, this can be used as one data point for comparing CAPEX and OPEX with modern production methods. Another metric of comparison, though not comparing like items, has much easier math: concentrated or spun down algae paste. Concentrated algae costs roughly $450-$650/kg DW depending on the species. Including amortized capital costs, Industrial Plankton's PBR 1250 L converges on the value of ~250$/kg DW, making it a cost effective solution to the algal feed bottleneck in hatcheries.

FINALLY, A TECHNIQUE TO AGE DECAPODS: PROGRESS WITH THE CARIBBEAN SPINY LOBSTER, *PANULIRUS ARGUS*, AND MANAGEMENT IMPLICATIONS

Gaya Gnanalingam[1], Mark J. Butler IV[1*], Thomas R. Matthews[2], Emily Hutchinson[2], and Raouf Kilada[3]

[1]Old Dominion University, Department of Biological Sciences, Norfolk, Virginia, USA

[2]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, Marathon, Florida, USA

[3]University of New Brunswick, Biology Department, Saint John, New Brunswick, Canada

butler@odu.edu

Conventional ageing methods used for a variety of marine taxa have proven inapplicable for decapods because of the loss and replacement of calcified structures during ecdysis. However, in 2012 Kilada and colleagues demonstrated that age could be estimated by counting bands deposited in the eyestalk and ossicles of the gastric mill in four temperate decapod species. The technique has since been applied to a few other crustaceans with promising results. Whether tropical species would exhibit the same biannual banding was questionable, but the same banding pattern has been confirmed in the tropical Caribbean spiny lobster (*Panulirus argus*), which supports the most valuable fishery in the Caribbean. Clearly distinguishable bands have been discovered in the mesocardiac and zygotic ossicles of the gastric mill (but not eyestalks) that differ logically between animals of different sizes and those of known age. Experiments have demonstrated that the deposition of bands is indicative of chronological age, but not influenced by the frequency of ecdysis. Lobsters tagged with calcein also retained the tag through several molts and now calcein and heavy metal marked bands are being used in experiments to validate band counts and to estimate time of postlarval settlement. Robust fisheries management of crustaceans has long been hampered by an inability to disentangle patterns of size and age, but this technique stands to rectify that shortcoming.

THE EASTERN OYSTER GENOME: A RESOURCE FOR COMPARATIVE GENOMICS IN SHELLFISH AQUACULTURE SPECIES

Marta Gomez-Chiarri[1*], Wesley C. Warren[2], Patrick Minx[2], Chad Tomlinson[2], Ximing Guo[3], and Dina A. Proestou[4]

[1]University of Rhode Island, Kingston, Rhode Island 02881 USA

[2]Washington University School of Medicine, McDonnell Genome Institute, St Louis, Missouri 63108 USA

[2]Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, New Jersey 08349 USA

[3]USDA ARS National Cold Water Marine Aquaculture Center, Kingston, Rhode Island 02881 USA

gomezchi@uri.edu

Oyster aquaculture is an important sector of world food production. As such, it is imperative to develop a high quality reference genome for the eastern oyster, *Crassostrea virginica,* to assist in the elucidation of the genomic basis of commercially and ecologically important traits. It is predicted that the use of all types of sequence variants (e.g. genetic, gene expression, methylation) will expand the association of allelic states with trait variance. Genetic, gene expression, and methylation studies depend on the use of accurate assembled consensus base sequences. Major challenges to the assembly of molluscan genomes are the high rate of polymorphism and the unique repeat architecture present in these species. To partially address these challenges, DNA from an eastern oyster produced by gynogenesis within an inbred line was used for single molecule real time sequencing of the genome (~87x coverage). All reads were assembled using FALCON to a total size of 684Mb with an N50 contig length of 1.9Mb. The predicted genome size is reported to be 578-675Mb. Total repetitive elements were estimated to be ~36% using WindowMasker. A majority of sequences (>99%) were scaffolded into the known number of 10 chromosomes using a HiC proximity map then aligned to an eastern oyster genetic linkage map to confirm correct association. Gene annotation using the automated NCBI pipeline predicts the presence of 34,596 protein coding genes and 4,230 non-coding. This reference resource should facilitate discovery of a wealth of information about traits important to oyster health and development.

THE PIRAB TOXIN-PRODUCING GENES OF *VIBRIO* SPP. HAVE A FUNCTION SIMILAR TO THE *BACILLUS THURINGIENSIS* CRY PROTEINS

Bruno Gómez-Gil* and Sonia Soto-Rodríguez

CIAD, AC Mazatlan Unit for Aquaculture. AP 711, Mazatlán, Sinaloa México 82000

bruno@ciad.mx

Recently, cultured shrimps have been affected by the Acute Hepatopancreatic Necrosis Disease (AHPND), previously known as Early Mortality Syndrome (EMS). Affected shrimps show signs of a severe necrosis of the hepatopancreatic cells within hours of the disease onset. This effect has been associated to the presence of two genes in a conjugative plasmid (pVp-AP) found in several strains of related species of *Vibrio*.

The pVp-AP plasmid has one or two transposons inserted, depending on the origin of the strain. The large 5.5 Kbp transposon in pVp-AP is composed of two inverted repeats of 55 bp at the extremes followed by the transposases of 921 bp; six CDS are found within, three hypothetical proteins, one putative cell surface anchor family protein (CSAP), and two potential delta endotoxins similar to the PirAB toxins of *Photorhabdus luminescens*. The Pir toxins are encoded in two genes within a 1,776 bp operon (including the 50 bp promoter, and the -10 and -35 signals). The *pirA* gene encodes for a 111 amino acid 12.7 kDa protein and the *pirB* for a 438 amino acid 50.1 kDa protein. The probable quaternary structure of these proteins resembles the tertiary structure of the Cry3A toxin of *Bacillus thuringiensis*.

All these proteins (PirAB and Cry) have a similar function in the digestive tract of invertebrates. They are pore-forming toxins that induce cell death by forming ionic pores into the membrane of the midgut epithelial cells in their target host, either in insect (for Cry and PirAB) or shrimp (for PirAB).

THE GEOGRAPHICAL DISTRIBUTION OF THE GEODUCKS, *PANOPEA GENEROSA* AND *P. GLOBOSA*

Sergio Scarry González-Peláez*, Mónica Nurenskaya Vélez-Arellano, J. Jesús Bautista-Romero, Liliana Carvalho-Saucedo, and Daniel B. Lluch-Cota

Centro de Investigaciones Biológicas del Noroeste. Av. Instituto Politécnico Nacional 195.

Col. Playa Palo de Santa Rita Sur, La Paz, B.C.S., México 23096

scarry04@cibnor.mx

The development of the geoduck fishery in northwest of Mexico have resulted in the identification of new populations of this resource in recently years; however, the similar shape of *Panopea generosa* and *P. globosa* makes their identification misleading. As a consequence, it is also hard to define correct management policies for each species. A sample of 480 geoduck shells from Punta Eugenia (27°51'12.15"N, 115° 5'26.92"W), in the Pacific coast of Baja California, was analyzed using a Discriminant Function to identify the species. The shell length, distance from the umbo to the ventral margin along the shell surface, and the weight from a single shell, were used as morphological variables. The results indicated that 247 individuals belonged to *P. generosa* and 233 to *P. globosa*. This demonstrates that both geoduck species cohabit at Punta Eugenia, being the first confirmation of different geoduck living species coexisting in the North Pacific of America. This report also extends the equatorward distribution of *Panopea generosa* ~170 km, and *P. globosa* distribution increases poleward ~470 km.

EUROPEAN GREEN CRAB IN THE WASHINGTON SALISH SEA: SAME STATE, DIFFERENT INVASION

Emily W. Grason*[1], P. Sean McDonald[2], Kate Litle[1], and Jeff Adams[1]

[1]Washington Sea Grant, University of Washington, 3716 Brooklyn Ave NE, Seattle, Washington 98105-6716 USA

[2]University of Washington, Program on the Environment, School of Aquatic and Fisheries Science, 3737 Brooklyn Ave NE, Seattle, Washington 98105 USA

egrason@uw.edu

Though the European green crab, *Carcinus maenas*, has been periodically abundant in coastal embayments of Washington State since the late 1990s, the recent range expansion into the Washington Salish Sea has the potential for more destructive impacts and dynamics. Green crab spread is currently being tracked by a citizen science network of early detection sites along Washington inland shorelines: Washington Sea Grant (WSG) Crab Team. The network of volunteer, tribal, and agency partners of the Crab Team monitors 52 sites across Puget Sound, the San Juan Islands and the Strait of Juan de Fuca, with the goals of assessing the status and impacts of the nascent invasion.

In 2016, volunteers captured the first confirmed green crab from Washington inland shorelines, and, to date, 108 European green crabs have been captured across six locations in the Washington Salish Sea. Green crab populations are currently extremely small, but without swift intervention, have the potential to grow rapidly. Based on the size of crabs captured, all individuals are recent arrivals, likely recruiting in as larvae dispersed from nearby populations in 2015 and/or 2016. These arrival dates coincide with two years of particularly strong El Nino – Southern Oscillation indices, which have been observed to correlate with successful larval dispersal events. The present rarity of the crab, infrequent dispersal, and apparent relative isolation of Salish Sea populations, sets up a promising scenario for effective intervention. A collaborative, coordinated, and rapid response is required to offer the greatest changes for successful protection of natural, economic, and cultural resources.

WARMING AND *P*CO_2 EFFECTS ON FLORIDA STONE CRAB LARVAE

Philip M. Gravinese*[1,2], Ian C. Enochs[3,4], Derek P. Manzello[4], and Robert van Woesik[1]

[1]Florida Institute of Technology, Department of Biological Sciences, 150 W. Univ. Blvd. Melbourne, Florida 32901, USA

[2]Mote Marine Laboratory, Fisheries Ecology and Enhancement, 1600 Ken Thompson Way, Sarasota, Florida 34236, USA

[3]University of Miami, Cooperative Institute for Marine and Atmospheric Studies, Rosenstiel School of Marine and Atmospheric Science, Miami, Florida, 4600 Rickenbacker Causeway, Key Biscayne, Florida 33149, USA

[4]Atlantic Oceanographic and Meteorological Laboratories, National Oceanic and Atmospheric Administration, 4301 Rickenbacker Causeway, Miami, Florida, 33149, USA

pgravinese@mote.org

Anthropogenic activities are deteriorating coastal habitats by increasing nutrients, changing coastal carbonate chemistry, and reducing seawater pH. The emission of greenhouse gases is also increasing oceanic temperatures. Although the adult stages of many marine organisms are capable of tolerating fluctuations in environmental conditions, marine larvae that hatch in coastal habitats may not have the ability to detect, respond to and/or tolerate such perturbations. This study examined the response of the commercially important Florida stone crab, *Menippe mercenaria,* to determine the impacts of simultaneous exposure to both elevated temperature and ocean acidification (OA) on larval survival, growth, and geotactic swimming behavior. Larvae were raised in a fully crossed experiment with ambient and elevated treatments for temperature (30°C and 32°C) and pCO_2 (~450 ppm and ~1100 ppm). Exposure to elevated pCO_2 and ambient temperatures increased larval mortality, an effect which was further exacerbated by elevated temperature. The larval molt-stage duration was shorter when individuals were exposed to elevated temperature, however late stage larvae exhibited a significantly longer molt-stage duration under OA conditions than the in controls. Geotactic responses changed throughout ontogeny and directional movement was reversed under OA conditions. The decrease in survival at elevated temperatures and the change in swimming orientation may have a negative effect on larval supply, and limit the potential for larval dispersal. These results suggest that the future of the fishery may be threatened in the absence of the stone crabs ability to acclimatize or adapt to future changes in seawater conditions.

SPATIALLY EXPLICIT ESTIMATES OF OLYMPIA OYSTER (*OSTREA LURIDA*) FILTRATION SERVICES: A MODEL-BASED APPROACH FOR AUGMENTING ECOSYSTEM SERVICES AND REDUCING RESOURCE USE DURING RESTORATION

Matthew Gray*[1], Philine zu Ermgassen[2], Jonathan Gair[3,4], Chris Langdon[5], Emily Lemagie[6], and Jim Lerczak[6]

[1]University of Maryland Center of Environmental Science, Horn Point Laboratory, Cambridge, Maryland, USA

[2]University of Edinburgh, School of Geosciences, Edinburgh, U.K.

[3]Biomathematics and Statistics Scotland, Edinburgh, U.K.

[4]School of Mathematics, The University of Edinburgh, U.K.

[5]Oregon State University, Coastal Oregon Marine Experimental Station, Hatfield Marine Science Center, Newport, Oregon, USA

[6]Oregon State University, College of Earth, Ocean, and Atmospheric Sciences, Corvallis, Oregon, USA

mgray@umces.edu

Recovery of oyster ecosystem services, such as water filtration, that is derived from their suspension feeding activities (termed fil-

tration services; FS), often serves as the primary incentive for restoration of *O. lurida* along the US west coast. To better understand the ecological outcome of *O. lurida* restoration in Yaquina Bay, Oregon, an improved FS model that accounts for *in situ* feeding behavior of this species and the complex hydrodynamics of the estuary is provided. As the Pacific oyster (*Crassostrea gigas*) currently dominates most of the habitat historically occupied by *O. lurida*, an FS model was also developed of this non-native species in Yaquina Bay. The total area and the order of locations chosen for oyster restoration in Yaquina Bay was examined to determine how oyster FS could be maximized with limited resources. Model outcomes indicate hydrodynamics play the dominant role in the ability of oysters to improve water quality. In contrast to previous modeling attempts, *O. lurida*, and equivalent populations of *C. gigas*, were estimated to clear substantial portions of the Bay's volume (e.g. 28% and 33%, respectively). Populations of *C. gigas* consistently contributed greater FS than equivalent populations of *O. lurida* across all model scenarios. Importantly, model results point to a novel restoration strategy for augmenting ecosystem services and more efficient use of resources; prioritizing areas with the longer residence times used 25% (dry season) and 40% (wet season) of the area required when restored oysters were planted haphazardly in historic habitats in order to achieve the same FS outcomes.

SIMULATED MARINE HEAT WAVE ALTERS ABUNDANCE AND STRUCTURE OF *VIBRIO* POPULATIONS ASSOCIATED WITH THE PACIFIC OYSTER RESULTING IN A MASS MORTALITY EVENT

Timothy Green*[1], Nachshon Siboni[2], William King[2], Justin Seymour[2], and David Raftos[1]

[1]Macquarie University, Department of Biological Sciences, Sydney Australia

[2]University of Technology Sydney, Climate Change Cluster (C3) Ocean Microbes and Healthy Oceans, Australia

tim.green@mq.edu.au

Marine heat waves are predicted to become more frequent and intense due to anthropogenic climate change, which will impact global production of seafood from aquaculture. Links between rising seawater temperature and disease have been documented convincingly for the Pacific oyster, *Crassostrea gigas*. The oyster harbors a diverse microbial community, which may act as a source of opportunistic pathogens during temperature stress. Whether the oyster's microbial community can cause disease during a simulated marine heat wave was assessed. Mortality occurred in *C. gigas* when the seawater temperature was rapidly raised from 20°C to 25°C, however, mortality did not occur at 25°C when *C. gigas* was treated with antibiotics. 16S rRNA amplicon sequencing revealed a large change in the oyster's bacterial community at 25°C, with a notable increase in the proportion of *Vibrio*. TaqMan® Real-Time PCR revealed *Vibrio harveyi* and *Vibrio fortis* increased in abundance by 300-fold and 10-fold at 25°C, respectively. Findings provide evidence that bacteria associated with the oyster can cause disease during elevated seawater temperatures and highlight the potential negative consequences of marine heat waves on food production by aquaculture.

HABITAT EFFECTS OF MACROPHYTES AND SHELL ON THE PERFORMANCE OF JUVENILE CLAMS AND LOCAL PH CONDITIONS

Courtney M. Greiner[1]*, Terrie Klinger[2], Jennifer L. Ruesink[3], and Micah Horwith[4]

[1]Swinomish Indian Tribal Community, Fisheries Department, 11426 Moorage Way, La Conner, Washington 98225 USA

[2]University of Washington, School of Marine and Environmental Affairs, 3707 Brooklyn Ave NE, Seattle, Washington 98105 USA

[3]University of Washington, Department of Biology, Box 351800, Seattle, Washington 98195 USA

[4]Washington Department of Natural Resources, Aquatic Resources Division, PO Box 47027, Olympia, Washington 98504-47026 USA

cgreiner@swinomish.nsn.us

Dissolution of shell and photosynthesis by macrophytes have potential to raise local pH and therefore improve conditions for shell-forming organisms, but habitat-specific performance could also derive from altered water flow or food web dynamics. This study involved a split plot design to examine two habitat treatments (macrophytes, shell) on (1) juvenile *Venerupis philippinarum* settlement, survival, and growth and (2) local water chemistry at Fidalgo Bay and Skokomish Delta, Washington. Results show no macrophyte or shell hash treatment effect on *V. philippinarum* settlement or survival. A significant macrophyte treatment effect was detected on clam growth, with mean length higher when macrophytes were absent regardless of the presence or absence of shell hash. Additionally, there was no significant difference in porewater pH between the habitat treatments; however, the macrophyte treatment had an unexpected correlation with pH in the overlaying water, where pH was higher outside of macrophyte beds than inside. Although these results do not support the use of either treatment as an ocean acidification adaptation strategy, the mixed results reported in the literature for both treatments highlight the nascent nature of this research and the need to continue studying the effectiveness of potential strategies in the field. Such research could help guide local adaptation actions, especially among resource-dependent communities that rely on sustainable fisheries for their health and well-being.

UNDERSTANDING TOP-DOWN, BOTTOM-UP, AND SUPPLY SIDE INFLUENCES ON OLYMPIA OYSTER POPULATIONS FOR MORE SUCCESSFUL RESTORATION

Edwin Grosholz*[1], David Kimbro[2], and Will White[3,4]

[1]University of California Davis, Department of Environmental Science and Policy, Davis, California 95616 USA

[2]Northeastern University, Department of Marine and Environmental Science, Nahant, Massachusetts 01908 USA

[3]University of North Carolina Wilmington, Department of Biology and Marine Biology, Wilmington, North Carolina 28403 USA

[4]Oregon State University, Coastal Oregon Marine Experiment Station, Department of Fisheries and Wildlife, Newport, Oregon 97365 USA

tedgrosholz@ucdavis.edu

Many populations are by a combination of top-down, bottom-up, and supply-side (i.e., juvenile recruitment) factors. Establishing how these processes interact remains a fundamental challenge, particularly for populations with open recruitment. It is known that recruitment, growth, and mortality of Olympia oysters (*Ostrea lurida*) can vary along multiple environmental and biological gradients within the estuary in Tomales Bay, CA, but the relative importance of those differences is unknown despite the importance of these factors for oyster restoration. A state-space model was fitted to oyster size and abundance data over a ten year period. Using model selection criteria, the results showed that spatio-temporal variation in juvenile oyster mortality spatial, but not temporal variation in oyster growth, and temporal, but not spatial variation in larval recruitment best explained oyster population dynamics over the past decade. Targeted field experiments also demonstrated that predation (top-down control) accounted for 50% of natural mortality, therefore, rapid growth of mid-bay oysters at the phytoplankton maxima (bottom-up control) can create a size refuge from predation. These results demonstrate how these key processes affecting Olympia oyster populations in Tomales Bay and provide a guide for understanding how restoration could be more effectively achieved throughout the Bay.

THE MORAN EFFECT AND REGIONAL SYNCHRONY OF EUROPEAN GREEN CRAB POPULATIONS ALONG THE PACIFIC COAST

Edwin Grosholz*[1], Andrew Chang[2], Rikke Jeppesen[3], Linda McCann[2], Catherine de Rivera[4], Gregory Ruiz[2], Thomas Therriault[5], Kerstin Wasson[3], and Sylvia Yamada[6]

[1]University of California, Department of Environmental Science and Policy, 1 Shields Ave., Davis, California 95616 USA

[2]Smithsonian Environmental Research Center, 3152 Paradise Drive, Tiburon, California 94920 USA

[3]Elkhorn Slough National Estuarine Research Reserve, 1700 Elkhorn Rd, Royal Oaks, California 95064 USA

[4]Portland State University, Department of Environmental Science, 1825 SW Broadway, Portland, Oregon 97201 USA

[5]Fisheries and Oceans Canada, 3190 Hammond Bay Rd., Pacific Biological Station, Nanaimo, BC V9T 6N7 Canada

[6]Oregon State University, Department of Integrative Biology, 1500 SW Jefferson St., Corvallis, Oregon 97331 USA

tedgrosholz@ucdavis.edu

Populations of marine and estuarine species can be influenced climatic and oceanographic process that influence broad geographic areas. Synchrony at scales larger than the scale of dispersal would likely represent a Moran effect at large-scales possibly due to oceanographic drivers. These effects have been observed for outer coast and subtidal species, but have only recently been examined for estuarine species that are also subject to similar regional forcing. Data were analyzed for European green crabs collected over twenty years from up to a dozen sites along the west coast of North America. Unlike outer coast species, there was no evidence of spatial synchrony among estuaries as a function of distance between them; however, there were patterns of synchrony among estuaries that differed strongly between regions. Similar to earlier studies, there was strong synchrony among estuaries in Washington and Oregon. In contrast, there was no synchrony among California estuaries over the same period. Tests of the effects of oceanographic processes on the degree of synchrony showed highly significant effects of El Niño-Southern Oscillation on synchrony that varied strongly with latitude. There was also a moderate effect of the Pacific Decadal Oscillation, but no significant effect of local upwelling strength on the degree of synchrony among estuaries. These results are compared with recent findings for synchrony of Olympia oysters in the same region. Lastly, the consequences of these results are discussed in the context of future management of the European green crabs on the west coast.

GLYCOGEN CONTENT IN DIPLOID AND TRIPLOID *CRASSOSTREA VIRGINICA* DURING GAMETOGENESIS IN LOWER CHESAPEAKE BAY, USA

Eric Guévélou*, Joseph L. Matt, and Standish K. Allen, Jr.

Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center (ABC), Gloucester Point, Virginia 23062, USA

Gueveloueric@yahoo.fr

Since, at least 2012, shellfish aquaculturists in the Virginia portion of the Chesapeake Bay have observed annual mortality events that have typically peaked between May and June and resulted in the reported loss of about 30% of *Crassostrea virginica* oysters approaching market size. These events have been unusual in that they have not been associated with pathogens. In oyster species, glycogen is a major storage material with marked seasonal variation being linked to survival and success of reproduction. Glycogen content is known to be influenced by internal factors, such as growth and sexual maturation, but also external factors, such as food avail-

ability and other environmental factors. Because glycogen content varies depending on the physiological state of the organism, it can be used to evaluate physiological condition and therefore serves as an indicator for physiological distress in these sessile organisms. Aquaculture Genetics and Breeding Technology Center (ABC) has been developing Near-infrared spectroscopy (NIRS) technology for use in its breeding program and has developed several models suited for compositional analysis in *C. virginica*. NIRS technology provides a fast, safe, and eco-friendly alternative to traditional analytical methods which may need the use of chemicals that are toxic to humans and the environment. The glycogen model was optimized and used to quantify glycogen content in diploid and triploid oysters in order to determine whether a variation in this major storage material can be correlated with the mortalities observed during spring and summer in the lower part of the Chesapeake Bay.

CARDIAC RESPONSES TO BIOGENIC AMINES IN SELECTED MOLLUSCAN SPECIES

Trey Guilbeaux* and Lewis Deaton

University of Louisiana at Lafayette, Department of Biology, 104 East University Avenue, Lafayette, Louisiana 70504 USA

txg6456@louisiana.edu

Biogenic amines have been documented as cardioregulatory in a few species of molluscs, but little work has been done to continue their documentation. Octopamine, apomorphine, and histamine were tested in a few bivalve gastropod species alongside the classic cardioregulatory chemicals serotonin, acetylcholine, epinephrine, and FMRFamide in varying concentrations to determine the basic pharmacology of each. Animals were collected among wild populations of available species which included members of *Thais*, *Pomacea*, *Mytilus*, *Mercenaria*, *Melongena*, and *Geukensia*. The hearts were isolated from the animals to remove neural influences and stabilized either in an organ bath for bivalves or internally perfused for gastropods. The test chemicals were administered through the bathing solutions and effects measured via changes in contractile force. Shifts in beat frequency, tone, amplitude, and duration were observed to discern the effects of the drugs. Serotonin, while being classically defined as cardioexcitatory, was observed to have varying effects even among different populations of the same species in addition to having mixed effects in other cases. Epinephrine often only showed effects in high concentrations possibly indicating receptor cross talk. Octopamine and apomorphine often acted consistently, but weakly cardioregulatory with one or two exceptions. Histamine seldom had noticeable effects. It appears that the number and variety of receptors and their expression may be quite high as well as utilizing several different signaling pathways in order to increase the variety of responses available to the organisms.

MOLECULAR ADAPTATIONS OF BIVALVE MOLLUSCS REVEALED BY GENOMIC ANALYSES

Ximing Guo

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

xguo@hsrl.rutgers.edu

Bivalve molluscs are superbly adapted to benthic life. They are remarkable calcifiers that produce strong shells for support and protection, key to their evolutionary success. As successful colonizers of intertidal zones and estuaries, bivalves have developed remarkable resilience against wide fluctuations in temperature, salinity and air exposure. Bivalves are powerful filter-feeders that thrive in microbe-rich environments without adaptive immunity. Recently, whole genomes of several bivalves such as *Crassostrea gigas, Pinctada fucata martensii, Patinopecten yessoensis, Chlayms farreri, Bathymodiolus platifrons, Modiolus philippinarum,* and *Crassostrea virginica,* have been sequenced, and genomic analyses have provided insights into molecular bases of bivalve adaptation. All bivalve genomes are highly polymorphic and show lineage-specific expansion of certain gene families. The *C. gigas* genome is rich in genes related to stress and immune responses. The expansion of heat shock proteins, inhibitors of apoptosis and immune receptors is common to bivalves. Key genes related to shell formation are expanded in both *C. gigas* and *P. f. martensii*. In *C. farreri*, advanced eyes are supported by expanded opsins, and neurotoxin tolerance is enabled by mutations in sodium channel proteins. The *P. yessoensis* genome shows unprecedented conservation of ancestral bilaterian chromosomes, suggesting the bivalve karyotype is slow-evolving. Overall, genomic analyses indicate that gene expansion and diversification provide an important mechanism for the adaptation of bivalve molluscs.

OBSERVATIONS ON TETRAPLOID EASTERN OYSTERS, *CRASSOSTREA VIRGINICA,* AND IMPLICATIONS IN GENETIC IMPROVEMENT OF TRIPLOIDS

Ximing Guo

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

xguo@hsrl.rutgers.edu

Triploid oysters are valuable for aquaculture because of their sterility, superior growth and improved summer meat quality. Triploid oysters are produced by mating diploids with tetraploids. Tetraploid eastern oysters have been produced and bred for over 10 generations. Breeding over the years has produced observations on the biology and reproduction of tetraploid oysters. The production of tetraploids from triploid females is difficult and highly variable. Tetraploid oysters are fertile and can be reproduced by tetraploid x

tetraploid mating, although the survival of the mated tetraploids is significantly lower than that of diploids. The first-generation tetraploids are smaller than diploids and triploids. Later generations of tetraploids can be significantly larger than diploids and triploids during the first year. Tetraploid oysters take longer time to condition. Tetraploid females produce fewer eggs than diploids, averaging about 1 million per female at one year of age. Eggs from tetraploids show multivalent pairing during meiosis and produce more aneuploids than eggs from diploids. Sperm from tetraploids have large heads and move slowly compared with normal sperm. Tetraploid genome is unstable, and tetraploid oysters may lose chromosomes in some cells and revert to triploid/tetraploid mosaics. The germline cells of tetraploids are more stable than somatic cells. Tetraploids show improved growth and survival after several generations of selective breeding. Tetraploid parents have a larger effect on the performance of triploid offspring than diploid parents, probably due to their contribution of two-sets of chromosomes. Genetic improvements of tetraploids are important for the production and improvement of triploid oysters.

MANAGING *VIBRIO PARAHAEMOLYTICUS* IN WASHINGTON

Clara H. Hard

Washington State Department of Health, 243 Israel Road SE, Tumwater, Washington, 98501 USA

clara.hard@doh.wa.gov

The Washington State Department of Health (DOH) manages for *Vibrio parahaemolyticus* (Vp) using several strategies: regular environmental sampling during summer months, implementation of a Vp Control Plan for the commercial shellfish industry, and a health advisory for recreational harvesters. For over two years, DOH worked with an advisory group comprised of industry representatives, regulators and researchers, with an objective to revise the Vp Control Plan to make it more preventative of illness, rather than reactionary. As part of this revision, each growing area in the state was assigned a risk category based how many illnesses are attributed to that area in the previous five years. Each risk category outlines how much time companies have to cool oysters to less than 50 degrees after harvest using the air, water, and internal tissue temperatures taken at the time of harvest. Harvest is prohibited on the highest risk days when temperature thresholds are exceeded. This revised rule was adopted by the Washington State Board of Health in March 2015, and implemented in May 2015. This presentation will discuss Washington's experience with this process and the first three years of the rule implementation.

TRANSFER OF THE HARMFUL ALGAL TOXIN, MICROCYSTIN, FROM FRESHWATER TO MARINE ECOSYSTEMS

F. Joan Hardy[1*] and Ellen Preece[2]

[1]Washington State Department of Health, 111 Israel Road SE, Tumwater, Washington 98501 USA

[2]Robertson-Bryan, Inc., 9888 Kent Street, Elk Grove, California 95624 USA

nwaquaticecology@gmail.com

Harmful algal blooms (HAB) are a persistent, worldwide environmental problem in marine, estuarine and fresh waters. Climate change and expanding human populations are expected to exacerbate the frequency, intensity and distribution of HAB. In freshwater environments, cyanobacteria, especially microcystins (MC), are the most prolific toxin producers. Acute and chronic MC exposures can cause death or permanent liver damage and have been implicated in carcinogenesis. Until recently, MC in marine environments have been largely ignored; however, it is suspected that MC-contaminated fresh water is polluting the land-sea interface in many areas throughout the world. Recent investigations documented the transport and accumulation of MC from freshwater lakes to Puget Sound shellfish. A handful of other studies have also found freshwater-derived MC in nearshore marine environments. The freshwater origin of MC contamination reinforces the importance of freshwater nutrient reduction and management efforts. It also highlights the connectivity of terrestrial, freshwater and marine ecosystems. This review highlights new research findings and discusses how a changing climate is expected to intensify this ecological and human health threat.

A GENOMIC TEST FOR HYBRIDIZATION BETWEEN SELECTIVELY BRED EASTERN OYSTER AQUACULTURE STRAINS AND WILD NEW YORK POPULATIONS

Matthew P. Hare* and Yuka Kutsumi

Cornell University, Department of Natural Resources, Ithaca, New York 14853 USA

mph75@cornell.edu

When agricultural crops have been shown to hybridize with wild relatives, more often than not the introgression of alleles from domesticated strains to the wild relative lowers fitness-related performance in at least some natural environments. In aquaculture the most thoroughly studied case involves domesticated Atlantic salmon. Several studies have shown widespread hybridization of domesticated escapees with wild stocks, inferring reduced wild population fitness based on changes in life history and demography. Wild regional eastern oyster stocks represent a priceless source of germplasm for future selective breeding, and in some cases provide direct annual benefits to the aquaculture industry in the form of seed. Where the eastern oyster aquaculture industry is growing, such as northeastern U.S., it is providing jobs, producing local protein-rich food and improving the local coastal environmental;

however, a growing industry also increases the risk of hybridization with wild stocks. Tests of this hybridization hypothesis will be presented based on genomic analyses of Hudson and East River oyster samples (New York, USA). Using double-digest RADseq polymorphisms assayed in both spat and adult samples from 2012 and 2013, indications of sweepstakes reproduction are weak and the average population differentiation is extremely low, as expected for this typically high gene flow species. Most of the observed allele frequency differentiation was between the Hudson and East River sample sets, and when analyzed with a reference aquaculture strain, the East River (but not Hudson) showed levels of introgression consistent with hybridization followed by two generations of backcrossing to wild oysters.

EXAMINING WINTERTIME PARALYTIC SHELLFISH TOXICITY IN GEODUCKS IN SOUTHEAST ALASKA

Courtney E. Hart[1]*, Ginny L. Eckert[1], Elizabeth D. Tobin[1,4], Kate Sullivan[2], Christopher D. Whitehead[3], Kari Lanphier[3], Esther Kennedy[3], and Chelsea Wallace[1]

[1]University of Alaska, Fairbanks, College of Fisheries and Ocean Science, 17101 Point Lena Loop Road, Juneau, Alaska 99801 USA

[2]Southeast Alaska Regional Dive Fishery Association, 1225 Tongass Avenue, Ketchikan, Alaska 99901 USA

[3]Sitka Tribe of Alaska Environmental Research Lab, 456 Katlian Street, Sitka, Alaska, 99835 USA

[4]Jamestown S'Klallam Tribe, Natural Resources, 1033 Old Blyn Hwy, Sequim, Washington, 98382 USA

chart16@alaska.edu

The commercial fishery for geoduck clams (*Panopea generosa*) in Southeast Alaska is a small but lucrative fishery, with annual ex-vessel value averaging $4.9 million (2010-2015). Harvest in recent year has declined as a result of lack of fishery openings because of failed tests for paralytic shellfish toxins (PST). Seventy-six percent of management areas failed weekly PST testing over four harvest seasons. High PST levels cause substantial economic loss to the fishery through increased sampling costs for repeated tests (paid for by the fishery) and by delaying or closing harvest. Paralytic shellfish toxins bioaccumulate in filter feeders when springtime blooms of the toxin producer, *Alexandrium* sp., occur. Clam toxicity within a harvest area varies substantially from week-to-week, fluctuating well above (e.g., 600µg saxitoxins/100g shellfish tissue) and below (e.g., 40µg/100g) the regulatory limit of 80µg/100g. Such week-to-week variation in toxicity is occurring throughout winter months, long after the toxic blooms are gone. It is hypothesized that ingestion of overwintering *Alexandrium* cysts is a mechanism for toxicity during winter months, however there is a paucity of information regarding the relationship between cysts and geoduck clam toxicity. This project will: 1) determine if *Alexandrium* cysts are ingested by geoduck clams and if cyst ingestion is linked to toxicity; 2) map *Alexandrium* benthic cyst distributions and identify locations of high density cyst near clam harvest areas; and 3) determine if *Alexandrium* cysts are re-suspended during geoduck harvest. This research will improve understanding of temporal and spatial variability in toxicity, with a goal to better inform the fishery.

A NEW COLLECTION METHOD FOR WILD PACIFIC OYSTER SPAT IN THE INTERTIDAL ZONE FOR COMPLEMENTING SPAT SUPPLY IN JAPAN

Natsuki Hasegawa[1*], Satoshi Watanabe[1], Junya Higano[2], Yasushi Tsuchihashi[3], and Isami Kuriyama[3]

[1]National Research Institute of Aquaculture, Japan Fisheries Research and Education Agency, Nakatsuhamaura 422-1, Minami-ise, Mie 516-0193, Japan

[2]National Research Institute of Fisheries and Environment of Inland Sea, Japan Fisheries Research and Education Agency, Maruishi 2-17-5, Hatsukaichi, Hiroshima 739-0452, Japan

[3]Mie Prefecture Fisheries Research Institute, Hamajima 3564-3, Shima, Mie 517-0404, Japan

hasena@fra.affrc.go.jp

Pacific oyster *Crassostrea gigas* aquaculture in Japan widely uses wild spat collected and transplanted from Miyagi and Hiroshima Prefectures; however, the wild spat supply from these prefectures has been insufficient, and its price increasing in recent years. For complementing the shortage in the spat supply, a simple and inexpensive method was developed to collect the wild spat in intertidal zones by using mesh cage collectors containing pelletized oyster shell powder (commercial product called careshell). This method is advantageous in that it does not require monitoring of the planktonic larvae for optimal collection. Careshell functions as a settlement substrate for oyster larvae for several months in the intertidal zone because its surface is not fouled with other sessile organisms. Single-seed careshell (i.e. only one spat on each pellet) can also be obtained by this method and used for single-seed oyster culture. The proportion of single-seed careshell decreased with the increased spat collection rate, and the spat collection rate and proportion of single-seed varied depending on the location, tide level and mesh size of the collectors, suggesting site-specific adjustments are required for optimal collection.

GENETIC MAPS AND ASSEMBLY OF THE PACIFIC OYSTER GENOME

Dennis Hedgecock[1]*, Xiaoshen Yin[1], Tevfik Hamdi Kitapci[1], and Alberto Arias Perez[1,2]

[1]University of Southern California, Department of Biological Sciences, 3616 Trousdale Pkwy, Los Angeles, California 90089-0371 USA

[2]University of Cádiz, Área de Genética, Facultad de Ciencias del Mar y Ambientales, 11510 Cádiz, Spain

dhedge@usc.edu

Linkage maps can help verify the assembly of genome sequences and permit mapping of quantitative trait loci (QTL) that influence production traits (e.g. survival, growth, sex-determination, and reproductive maturation). Co-linearity of genetic and physical maps facilitates identification of candidate genes underlying QTL. This study compiles linkage-map data for 10,583 single-nucleotide polymorphisms (SNPs) across 13 full-sib families of the Pacific oyster. These include five previously published maps (Hedgecock et al. 2015 *G3*), which were based on Illumina Golden Gate SNP assays along with previously mapped microsatellite DNA markers, and eight maps constructed using genotyping-by-sequencing (GBS) of reduced-representational genomic libraries. Altogether, these efforts yield high-density genetic maps of 10 linkage groups (the haploid chromosome number), with total lengths of ~600 cM and average marker spacing, in the GBS maps, of ~0.7 cM. Locating these mapped markers on the published genome (Zhang et al. 2012 *Nature*), we assign the mapped SNPs to 1,628 (of 7,659) genome scaffolds and 96 independent genome contigs. Of 1,212 genome scaffolds containing two or more mapped markers, 572 (47.2%) have SNPs that map to two or more linkage groups. This observation suggests that the current genome assembly comprises a large number of miss-assembled, chimeric scaffolds, which will hinder progress in identifying candidate genes underlying QTL. A new genome assembly, based on linkage mapping, comprises those genome contigs and scaffolds that map consistently to one linkage group, as well as unambiguously mapped contigs and sub-scaffolds extracted from chimeric scaffolds.

WHAT WE STILL DO NOT KNOW ABOUT FEEDING BIVALVES AND WHAT WE NEED TO DO

Eric Henry*and Tim Reed

Reed Mariculture, 900 E. Hamilton Ave., Suite 100, Campbell, California 95008 USA

eric@reedmariculture.com

Although much hard work during recent decades has generated a sizeable literature on bivalve feeding, much remains to be learned. Significant gaps in our knowledge persist due to the differences in the biology among the diversity of bivalves, variability in culture management among hatcheries, and often poorly understood effects of diseases and variable water quality. Such confounding factors will always be with us, but improvements in the design of feeding studies could accelerate progress: 1) The particular strain of any alga used as feed must be clearly identified, and if it is "new" its nutritional content should be analyzed. 2) Algae well-known to have limited nutritional value (e.g. *Chlorella*, *Dunaliella*) are unlikely to be useful components of diets. 3) Studies should seek to identify optimal algae combinations, not to discover a single panacea feed species. 4) The choice of algal species should take into account sterol profile, which can vary considerably among similar strains. 5) Algal cell size, palatability and digestibility should be considered. 6) Feeding should be quantified in the most biologically meaningful ways, such as biomass, carbon content, or energy content. rather than simple cell counts. This is especially important when algae with great differences in cell size or constituents are compared. 7) Feeding efficiency should be measured. 8) In larviculture studies, the condition of broodstock and quality of gametes (especially egg lipid stores) should be assessed. 9) The microbial community (microbiome) existing in bivalve culture systems should be optimized to suppress pathogens and enhance gut functions.

THE EXCEPTIONALLY HIGH CARBON STOCKS OF MANGROVES AND THEIR POTENTIAL FOR THE GLOBAL MARKET OF CARBON – A REVIEW OF CO_2 LEVELS IN THREE GEOGRAPHIC REGIONS OF ECUADOR

Iris J.C. Hernandez, Mayra Galindo*, Daniela Espinoza

Fundación para la Conservación de la Biodiversidad Acuática y Terrestre de Ecuador (FUCOBI), Quito, Ecuador

fucobi@gmail.com

The role of land forests as a source and sink of greenhouse gases (GHG) is well known. A major source of GHG release is through the conversion of land use, from carbon (C) stored in coastal and marine ecosystems such as mangroves, tidal marshes and seagrasses. They sequester and store large C quantities in plants and sediment. Mangroves are highly productive and biologically diverse wetlands, serve as nurseries and habitats to many juvenile fishes, molluscs, and crustaceans. They support microorganisms such as fungi and bacteria associated with biogeochemical transformations of nutrients via extensive root systems. Marine ecosystems are disappearing due to ozone depletion, freshwater diversion, ocean acidification, atmospheric pollution, natural disasters, introduction of exotic chemicals and modified organisms in shrimp farms nearby mangrove habitats. In some countries, large tracts of mangroves are cut down for coastal development, agricultural/aquaculture purposes, other uses. Mangroves trap sediments and assimilate nutrients, along with associated contaminants (to be reviewed).

Carbon stocks in mangroves of Asia Pacific is 500-1200 megagram (Mg) of C/ha, which is equivalent to 1603-8023 Mg/ha of CO_2. Deforestation cause C sediment destabilize, increase microbial activity, GHG release, impacting rising sea level and frequency of extreme weather events. High emissions from degradation is an untapped opportunity of C mitigation through U.N. 'Reduction

of C Emissions caused by Deforestation and Forest Degradation (REDD)' program -economic incentives are considered to maintain C forests. The biomass C map of Ecuador will be used to discuss CO_2 emissions, biodiversity and ecosystems services in three provinces where mangroves were converted to shrimp farms.

THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*, DEMONSTRATES SENSITIVITY TO TEMPERATURE AND RESILIENCE TO PH CHANGE DURING SUMMER GROWTH

Amelia V. Hesketh[1*], Eleanor Simpson[2], Debby Ianson[3], Karen Kohfeld[2], and Christopher D.G. Harley[1]

[1]University of British Columbia, Department of Zoology, 6270 University Blvd., Vancouver, BC, Canada V6T 1Z4

[2]Simon Fraser University, School of Resources and Environmental Management, 8888 University Drive, Burnaby, BC, Canada V5A 1S6

[3]Fisheries and Oceans Canada, Institute of Ocean Sciences, 9860 West Saanich Road, Sidney, BC, Canada V8L 4B2

hesketh@zoology.ubc.ca

Understanding how ecologically and economically important marine organisms will respond to climate change is critical to predicting community structure and the future of aquaculture. Field studies, which capture the inherent complexity of conditions *in situ*, are needed to accurately predict how organisms will fare under climate change. Farmed populations of the Pacific oyster, *Crassostrea gigas*, are being monitored in an ongoing field study to determine their response to different growing conditions in a oceanographically heterogeneous estuarine sea, the Strait of Georgia (British Columbia, Canada) when grown on rafts (fully submerged) and beaches (periodically emersed). Results to date indicate that *C. gigas* grow faster and are healthier (better condition) when grown on rafts compared to beaches. Throughout the summer, *C. gigas* growth and condition correlated with mean temperature and showed some dependence on maximum temperature, though the effect of increasing temperature varied depending on growing environment (raft vs. beach). Salinity and pH had limited and no effect, respectively, on growth, condition, and mortality of *C. gigas*. Field observations indicate that local predator abundance or disease may exert a greater effect on mortality than environmental conditions, and these indirect effects will be examined in future studies. This study demonstrates that temperature changes expected in the Strait of Georgia this century may affect *C. gigas* more than acidification and changing salinity, though an assessment of oyster responses to corrosive winter-time conditions is needed to holistically predict how the British Columbian aquaculture industry will fare as climate change progresses.

INDIVIDUAL GROWTH PROFILES AS AN ALTERNATIVE TO THE TERMINAL SIZE-AT-AGE METHOD IN *PANOPEA GENEROSA* STUDIES

José Angel Hidalgo-de-la-Toba[*], Sergio Scarry González-Peláez, Enrique Morales-Bojorquez, J. Jesús Bautista-Romero, and Daniel Bernardo Lluch-Cota

Centro de Investigaciones Biológicas del Noroeste, SC, Instituto Politécnico Nacional 195, Col. Playa Palo de Santa Rita. CP. 23096, La Paz, B. C. S., México

jahidalgo@pg.cibnor.mx

The description of the individual growth is closely related to the quality and quantity of the data. When working with a species with infrequent recruitment events and prone to sampling bias, it is common to gather incomplete length to age data where some age classes are missed, predominantly the first ones. This has been a recurrent concern in long-lived species as the geoduck, *P. generosa*, therefore, it was proposed that the individual growth profile (IGP) as an alternative method to improve the modeling of their individual growth. This method consist in relating the inner annual growth marks from transversal cross sections with their respective external growth mark in the whole shell to determinate the shell length attained at each age. The IGP of 32 geoducks from the locality of Punta Canoas, in the west coast of the Baja California Peninsula was determined and consisted of 260 age-to-length data, increasing to 292 by including size data at terminal ages. The individual growth was analyzed following a multimodel inference approach contrasting five growth models. According to Akaike information and Schwartz-Bayesian criteria, Schnute growth model is the best candidate model; which describes a growth that reaches its asymptotic stage at ages over 15 years (L_∞=126.53 mm). Comparatively with a previous work based on terminal length-to-age data, the IGP modelling allowed an agreement between both selection criteria and estimated a different growth curve with a lower L_∞. The advantage granted by this proposal is to include information about sizes in the first years of life, thus providing less uncertainty in the growth prediction by avoiding an overestimation of the older ages as consequence of missing age classes.

TRACE ELEMENTAL FINGERPRINTS: AN ECOLOGICAL DETECTIVE'S TOOL TO TRACK OLYMPIA OYSTERS (*OSTREA LURIDA*)

Megan Hintz[1]*, Bonnie Becker[2], Henry Carson[3], Brian Rusk[4], Marco Hatch[4], Brian Allen[5], Brent Vadopalas[1], and Steven Roberts[1]

[1]University of Washington School of Aquatic and Fishery Sciences, Seattle, Washington 98105 USA

[2]University of Washington Tacoma School of Math and Sciences, Tacoma, Washington 98402 USA

[3]Washington Department of Fish and Wildlife, Olympia, Washington 98501 USA

[4]Western Washington University, Bellingham, Washington 98225 USA

[5]Puget Sound Restoration Fund, Bainbridge Island, Washington 98110 USA

hintzm@uw.edu

Olympia oysters (*Ostrea lurida*), a species of concern in Washington State, have failed to fully recover after both over-exploitation and environmental degradation. Although state agencies, tribal nations, and environmental groups in Washington have made it a priority to restore *O. lurida* because they are the only native oyster on the west coast of North America and provide key habitat and ecosystem services to the Puget Sound, our understanding of *O. lurida* larval dispersal patterns remains limited. The early stages of the Olympia oyster play a key role in their restoration because it is the only stage where they can disperse to other populations. Brooded Olympia oyster larvae incorporate trace elements present in estuarine waters into their shell, creating a chemical "signature" of their natal site before release and dispersal. With the use of laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS), the provenance signatures of larvae and recruits can be compared, and potentially matched, to signatures of source populations. Unique elemental fingerprints of *O. lurida* larval shells were found to three regions in Puget Sound. This provides an approach to quantifying larvae dispersal that can be used to determine the extent to which these *O. lurida* populations self-seed, seed other sites, and exchange larvae with other populations.

MANAGING EELGRASS AND SHELLFISH AQUACULTURE IN WASHINGTON: A WORKSHOP TO EXAMINE CHALLENGES AND INCONSISTENCIES

Laura Hoberecht[1*], Beth L. Sanderson[2], and Bridget E. Ferriss[2]

[1]National Marine Fisheries Service (NMFS) West Coast Region (WCR), 7600 Sand Point Way NE, Seattle, Washington 98115 USA

[2]NMFS Northwest Fisheries Science Center, 2725 Montlake Blvd. East, Seattle, Washington 98112 USA

laura.hoberecht@noaa.gov

Native eelgrass (*Zostera marina*) occurs in bays, estuaries, and nearshore areas across Washington and is currently managed in different ways by different agencies. In an effort to move toward a common understanding of how eelgrass is managed in and around shellfish farms, NMFS WCR hosted an all-day workshop on April 11, 2017. Over 70 scientists and agency, tribal, and shellfish industry representatives convened to discuss challenges related to the management of eelgrass and shellfish aquaculture in Washington. Specifically, the workshop sought to: increase understanding about eelgrass and shellfish aquaculture interactions; determine where and why inconsistencies in eelgrass management related to shellfish aquaculture exist; and develop a path forward for addressing inconsistencies. Five scientific experts gave presentations on the state of the science and addressed questions posed by participants in a pre-workshop survey. The scientific presentations were followed by a discussion about ecosystem functions and services of eelgrass and shellfish aquaculture. Presentations were then made on eelgrass management related to shellfish aquaculture from both the regulatory and industry perspectives. The management presentations were followed by discussions about management challenges, and recommendations for future actions. As a general outcome of the workshop, participants agreed that industry and the regulatory community should embrace a management approach that supports the protection of eelgrass functions and services as well as sustainable aquaculture, and that scientists should be involved in development of this approach. To achieve this goal, a more open dialogue between shellfish growers, scientists, and regulators, as provided through this workshop, should be continued.

ISOLATION AND TESTING OF PROBIOTICS AS A POTENTIAL TOOL FOR THE MANAGEMENT OF EPIZOOTIC SHELL DISEASE IN THE AMERICAN LOBSTER, *HOMARUS AMERICANUS*

Melissa Hoffman[1]*, Kathy Castro[1], Grace Underwood[2], Hilary Ranson[3], Mitch Hatzipetro[1], Barbara Somers[1], David Rowley[3], David R. Nelson[2], and Marta Gomez-Chiarri[1]

[1]University of Rhode Island, Department of Fisheries, Animal, and Veterinary Sciences, Kingston, Rhode Island, USA

[2]University of Rhode Island, Department of Cell and Molecular Biology, Kingston, Rhode Island, USA

[3]University of Rhode Island, Department of Biomedical and Pharmaceutical Sciences, Kingston, Rhode Island, USA

melissahoffman@uri.edu

Epizootic shell disease (ESD) in the American lobster, *Homarus americanus*, has a major impact on the southern New England lobster industry, yet there are no practical tools for managing the disease. The goal of this study was to identify bacterial probiotics that could be used to decrease the intensity of ESD in wild lobster populations. Candidate bacterial isolates (n = 24) have been identified from lobsters in Narragansett Bay as having probiotic characteristics against ESD-associated bacteria *Thalassobius* sp. and *Aquimarina 'homaria',* or the fish pathogen *Vibrio anguillarum*. Healthy lobster post-larvae were exposed to 5 of the candidate strains isolated from lobsters and a probiotic isolated from the eastern oyster, *Crassostrea virginica* (*Phaeobacter inhibens* S4). After several weeks of treatment, there were no significant differences in molting, mortality, or growth of treated lobsters when compared with the control, indicating the candidate probiotics do not exhibit toxicity to the lobster post-larvae. The effect of selected candidate probiotics (n = 3) on progression of ESD in adult lobsters was tested for three months. Frequent molting due to strong disease severity confounded long-term effects of the treatments, and no signifi-

cant differences were seen in mortality, molting, growth, or disease progression. These results highlight the challenges involved in the development of tools for the management of a chronic disease with poorly understood etiology. Future research should focus on a better understanding of microbial-microbial-host interactions in ESD, and the effect of environmental conditions on these interactions.

GROWTH AND REPRODUCTIVE CONDITION OF PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) RAISED IN AN INTERTIDAL RACK-SUSPENDED CULTURE SYSTEM IN TAEAN OFF THE WEST COAST OF KOREA, THREE YEARS AFTER THE *HEBEI SPIRIT* OIL SPILL

Hyun-Ki Hong[1]*, Hee-Jung Lee[2], Hee-Do Jeung[2], Heung-Sik Park[3], and Kwang-Sik Choi[1]

[1]Jeju National University, School of Marine Biomedical Science (BK21 PLUS), Jeju 63243, Republic of Korea

[2]Tidal Flat Research Institute, National Institute of Fisheries Science (NIFS), Kunsan 54014, Republic of Korea

[3]Marine Ecosystem and Biological Research Center, Korea Institute of Ocean Science and Technology (KIOST), Busan 49111, Republic of Korea

hyunki0203@gmail.com

In December 2007, Hebei Spirit oil tanker released 10,800 tons of crude oil by accident, and the oil covered oyster farms in Taean coast on the west coast Korea. In 2010, the residual oil in the water, sediment, and oyster tissue in the spilled area returned to the level previous level. Growth and reproduction of the Pacific oyster three years after the oil spill was monitored at one of the most heavily damaged oyster farming area. Annual gametogenesis and reproductive effort of oysters were assessed using histology and ELISA using the oyster egg protein-specific polyclonal antibody. In September 2013, two-year-old oysters reached to 6.5 cm in shell length and 5.8 in somatic tissue wet weight. Histology indicated that the two-year-old oysters spawned during July and September. An indirect-ELISA indicated that the fully ripe oysters produced 20-23 % of their body weight as egg prior to spawn. Reproductive effort and the annual gametogenic pattern of the rack suspended cultured oysters in the oil spilled area measured in this study was similar to the pattern of oysters in oil-spill free areas. Consequently, it was believed that oyster aquaculture in Taean coast could be resumed, although monitoring on the environmental quality and the oyster physiology in this area should be continued.

COASTAL MANAGEMENT USING OYSTER-SEAGRASS INTERACTIONS FOR SUSTAINABLE AQUACULTURE, FISHERIES AND ENVIRONMENT

Masakazu Hori[1*], Franck Lagarde[2], Valérie Derolez[2], Marion Richard[2], Masami Hamaguchi[1], Juri Hori[3], and Mitsutaku Makino[3]

[1]National Research Institute of Fisheries and Environment of Inland Sea, 2-17-5 Maruishi, Hatsukaichi, Hiroshima 739-0452, Japan

[2]Ifremer/UMR MARBEC, 34200, Sete, France

[3]National Research Institute of Fisheries Science, Yokohama, Kanagawa 236-8648, Japan

mhori@affrc.go.jp

Recently the quality of coastal waters has been gradually improved from eutrophication for past several decades in some regions; however, oligotrophication by this improvement has caused another issue which reduces pelagic productivity and therefore fisheries products in the coastal ecosystems. Therefore, harmonizing coastal fisheries with water-quality improvement is now essential for the sustainable use of coastal ecosystem services. Here, the interaction between oyster aquaculture and eelgrass vegetation was chosen as a key factor for the harmonization using an interdisciplinary approach including ecological actions, socio-economical actions and psychological actions. Coastal organisms have adapted their traits to the environment over a long period of time, so that restoration of natural mixed habitats represents reconstruction of the original process of coastal production. Subtidal seagrass vegetation with intertidal oyster reefs is the original mixed habitats in Japan, which would be expected to enhance coastal production by improving the production efficiency without adding nutrients. A simple field experiment with carbon and nitrogen contents and the stable isotope analyses revealed that oyster spats cultivated on a tidal flat adjacent to seagrass beds had higher nitrogen contents and higher δ13C ratios than spats cultivated in an offshore area using only pelagic production. This result suggests that utilization of the traditional mixed habitats, which enables oysters to use both pelagic and various benthic production, has potential to sustain food provisioning service for humans even in oligotrophic environment.

MONITORING THE GENETIC DIVERSITY OF HATCHERY-PRODUCED COHORTS AND SUPPLEMENTED REEFS OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Katherine M. Hornick* and Louis V. Plough

University of Maryland Center for Environmental Sciences, Horn Point Laboratory, 2020 Horns Point Road, Cambridge, Maryland 21613 USA

khornick@umces.edu

Hatchery-based enhancement of marine fisheries is being undertaken on a large worldwide scale, but the genetic impacts of these practices, specifically their effects on genetic diversity and long-term population resilience, are often not fully understood. Intensive hatchery-based restoration is underway in the Chesapeake Bay for depleted eastern oyster, *Crassostrea virginica,* populations, but the potential genetic impacts remain poorly understood. To evaluate the effect of hatchery propagation on genetic diversity, microsatellite-based parentage analysis were conducted on nine hatchery cohorts to evaluate how genetic diversity changes across generations, calculating variance in parental contribution and the effective number of breeders (N_b) represented in offspring at

the spat stage. Diversity of hatchery planted (restored) reefs and 'wild' source populations were also examined. Examination of hatchery-produced cohorts revealed high variance in parental contribution and significant reproductive skew, particularly in males, which lead to a reduction in N_b from the total number that spawned. Offspring also showed decreased allelic richness and observed heterozygosity relative to their parents. The relative reduction in N_b decreased as the sex ratio of parents approached one, in line with theory. Attempts to reduce variance in contribution among males via separate fertilizations had mixed success, and might not be practical in a large-scale hatchery restoration program. Genomic SNP data is currently being used to quantify effective size (N_e) and genetic diversity in a number of 'wild' oyster populations and in restored reefs with variable planting efforts to further characterize how diversity is maintained in the field over time.

OYSTERS SHOW ENHANCED GROWTH IN EELGRASS: DOES PH EXPLAIN THE DIFFERENCE?

Micah Horwith[1]* and Alex Lowe[2]

[1]Washington State Department of Natural Resources, 1111 Washington St SE, Olympia, Washington 98504 USA

[2]University of Washington, Department of Biology, 24 Kincaid Hall, Seattle, Washington 98105 USA

micah.horwith@dnr.wa.gov

Many bivalve species are likely to suffer negative consequences from progressing ocean acidification. Natural resource managers are at pains to mitigate these consequences and to adapt to anthropogenic change. In the face of acidification, seagrasses and kelp have received attention for their phytoremediation potential: through photosynthesis, these primary producers may remove enough carbon dioxide from the water to increase local pH and aragonite saturation state. In 2016 and 2017, this potential was tested by transplanting juvenile Pacific oysters, Olympia oysters, and geoducks from a hatchery setting into field settings in- and outside of eelgrass. At five intertidal sites in Washington State, the transplanted juveniles were co-located with autonomous sensors measuring pH, dissolved oxygen, salinity, and temperature. Following exposure periods ranging from 40 to 80 days, Pacific and Olympia oysters in eelgrass showed enhanced growth, while geoducks showed no such response. Bivalve performance will be compared to sensor measurements to evaluate whether local differences in carbon chemistry can explain biological outcomes.

ARE OYSTERS IN THE CHESAPEAKE BAY PRIORITIZING THEIR OFFSPRING OVER THEIR HEALTH?

Lauren I. Huey* and Ryan B. Carnegie

Virginia Institute of Marine Science, College of William and Mary, P.O. Box 1346, Gloucester Point, Virginia 23062, USA

lhuey@vims.edu

The Chesapeake Bay region is steeped in appreciation for the eastern oyster. This stems from the ecosystem services, lucrative fishery, and historical significance that the species embodies; however, over the last half century, intense parasitism paired with anthropogenic impacts has reduced oyster abundances to historical lows. Today, the population is recovering, evidenced by increasing catches and spatial expansion of the oysters. Based on anecdotal observations, a contributor to the recovery seemed to be an increase in reproductive investment. To validate this, three measurements were made on slides of oysters from a histological archive collected during the summer at Wreck Shoal in the James River from 1988–present: oocyte diameter, oocyte density, and gonad area fraction. While oocyte diameter has remained fairly constant, oocyte density and gonad area fraction increased sharply around 2003. Mean oocyte densities increased by a factor of 1.691 (n=722) and gonad area fraction by a factor of 2.245 (n=411). Wild oysters have maintained this heightened reproductive investment to the present. What is responsible for such a sudden shift? The hypothesis presented here is that the increase is indicative of a tolerance response to the native parasite *Perkinsus marinus*; the oysters have adjusted their energy budgets to invest more in reproduction, increasing their fitness, in response to high disease pressure. An intense outbreak of *P. marinus* in the early 2000s seems the likely trigger for the response, though trends in environmental conditions are being investigated and insights into long-term temporal patterns in reproduction are included.

THE OREGON PACIFIC RAZOR CLAM RESOURCE: HISTORIC AND CURRENT MANAGEMENT

Matthew Hunter

Oregon Department of Fish and Wildlife, 2001 Marine Drive, Astoria, Oregon 97103 USA

Matthew.v.hunter@state.or.us

The Oregon Department of Fish and Wildlife (ODFW) has been monitoring the Pacific razor clam (*Siliqua patula*) resource and its fisheries in some capacity since 1935. The region of coast on the most northern 18 mile stretch of beach, known as Clatsop Beach, supports the largest recreational and commercial razor clam fisheries in Oregon. An estimated 90% of the overall harvest and effort occurs in this region as does the research and management of the resource.

Following improved transportation that subsequently led to easier access to beach harvest areas and a shift to more leisure activities in the American culture in the late 1940s, a dramatic shift in user profiles took place. Prior to this improvement, commercial harvest accounted for 75% of the use. By the middle 1950s this ratio had completely reversed and the recreational component accounted for nearly 80% of the total use. Historical monitoring focused heavily on the commercial fishery but with the user profile change, monitoring efforts and regulation changes began to focus

primarily on the recreational fishery. These monitoring data sets included; 1) effort indices during harvest time periods, 2) harvest rates and estimates, and 3) annual age and length composition.

As these fisheries continue to evolve and the resource adapts to changing environmental conditions, adaptive monitoring to account for and anticipate future issues is becoming more necessary. This presentation will illustrate management strategies to mitigate current and future issues as well as projects and policies that are currently being conducted to facilitate a sustainable natural resource.

COMPARING INDEPENDENT APPROACHES TO ESTIMATE AGE OF THE JONAH CRAB (*CANCER BOREALIS*): CORROBORATING GASTRIC MILL BAND COUNTS AS A DIRECT AGING METHOD

Carl Huntsberger[1*], Richard Wahle[1], Yong Chen[2], and Raouf Kilada[3]

[1]University of Maine, School of Marine Sciences, Darling Marine Center, 193 Clarks Cove Road, Walpole, Maine 04573 USA

[2]University of Maine, School of Maine Sciences, 225 Libby Hall, Orono, Maine 04469 USA

[3]OceAge, 41 Stratford Way, B3S Halifax, Nova Scotia, Canada

carlton.huntsberger@maine.edu

Age determination is essential to understanding key life history parameters for fisheries management. Direct aging methods for fishes and mollusks typically rely on counting annual growth bands preserved in calcified structures. Crustaceans pose a unique challenge in this respect because all calcified structures are lost with each molt. Recent evidence from several taxa of decapod crustaceans suggests that the bands present in histological sections of the gastric mill, a gizzard like structure of the foregut, may accumulate with age. The current project describes the application of this method to the Jonah crab (*Cancer borealis*), an ecologically important species and a newly managed fishery in New England, for which no direct aging method has been established.

Gastric mill band counts have been collected from Jonah crabs from two contrasting temperature regimes along the Maine coast. To date the gastric mill band counts correlate with size, suggesting they may be a promising indicator of age. Existing growth data are sparse and only available for larger, older crabs. To improve estimates of absolute age at size, and to corroborate the band count method, a laboratory growth study and a length frequency analysis of benthic survey data, including crabs collected in the earliest juvenile stages is underway. The three independent aging methods will be compared to determine if the use of gastric mill band counts can be corroborated by the indirect methods possibly providing the first direct method for aging Jonah crabs.

***SHRIMP SCAMPI*: A CITIZEN'S SCIENCE PROJECT TO EXAMINE THE LEVELS OF GLYPHOSATE AND OTHER ENDOCRINE DISRUPTING CHEMICALS (METALS, BISPHENOL A) IN FROZEN SHRIMP SOLD AT SUPERMARKETS IN THE UNITED STATES**

Ryan Hutchins[1], Sruthi Tanikella[1], Allison Berardi[1], Martha Reyes[1], Caroline Warren[1], Jennifer Warren[1], Mulan Yang[1], Ayrton Zambrano[1]*, Sara Zambrano-Basurto[1], Acacia Alcivar-Warren[1,2]

[1]ONE HEALTH Epigenomics – A Global Educational Initative; *Shrimp Scampi*: A Citizens Science Project, P.O. Box 196, Southborough, Massachusetts 01772 USA

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

environmentalgenomics.warren@gmail.com

The ONE HEALTH Epigenomics Educational Initative (OHEEI) was initiated by students to assess the adverse health effects to the environment, wildlife, pets, seafood, and people, caused by the antimicrobial and herbicide Glyphosate (RoundUp) and other endocrine disrupting chemicals (EDC), such as metals and Bisphenol A (BPA).

Shrimp is the favorite seafood of Americans, most of the shrimp we eat is imported, causing a yearly US$4.5 billion trade deficit. Although shrimp viruses (WSSV, IHHNV) and metals have been detected in frozen shrimp sold at Massachusetts (MA) supermarkets, no official compulsory testing of imported seafood is performed. The goals of '*Shrimp Scampi'* are to (a) review the scientific literature about epigenetic mechanisms associated with EDC [Glyphosate (G), metals, BPA] associated with antibiotic resistance, obesity, diabetes and neural tube defects (NTD), and (b) detect the levels of these EDC in frozen shrimp sold at US supermarkets.

The effects of Glyphosate (G) alone and 14 of its formulations in plant and human cells will be reviewed. Petroleum-based compounds in herbicides were highly more toxic than G. Arsenic, chromium, cobalt, lead, and nickel were found in the pesticide formulations.

Epigenetic mechanisms (DNA methylation, histone modifications, non-coding RNAs) associated with 15 metals tested before 2017 in shrimp sold at MA supermarkets will be summarized. All three epigenetic mechanisms are associated with exposure to G and BPA, linked to antibiotic resistance (G), obesity, diabetes, cancer (BPA, G) and NTD (G). Preliminary results on levels of metals and G in shrimp sold at MA and New Jersey supermarkets will be presented.

THE MISSING LINK: TRANSMISSION OF APICOMPLEXAN INFECTION IN GRAY MEAT ATLANTIC SEA SCALLOPS

Susan Inglis*[1], Jennifer Koop[2], Árni Kristmundsson[3], Mark A. Freeman[4], and Daniel Georgianna[1]

[1]University of Massachusetts Dartmouth, School for Marine Science and Technology, 706 South Rodney French Boulevard, New Bedford, Massachusetts USA

[2]University of Massachusetts Dartmouth, Department of Biology, Dartmouth, Massaschusetts USA

[3]University of Iceland, Institute for Experimental Pathology at Keldur, Reykjavik, Iceland

[4]Ross University School of Veterinary Medicine, Basseterre, St. Kitts, West Indies

singlis@umassd.edu

Scallops with small, darkened and stringy adductor muscle (gray meat) occur episodically along the eastern Atlantic seaboard. This condition is linked to a highly pathogenic apicomplexan parasite that targets muscle tissue and is lethal to scallop hosts with severe infections. A series of laboratory infection trials were conducted to test whether live gray meat scallops or freshly shucked gray meat tissue were vectors for infection to naïve scallops. Experimental and control groups were monitored for number of mortalities, clinical symptoms (meat color and weight/gonad condition) and the presence and intensity of apicomplexan infection through molecular and histological analysis. Results from these experiments confirmed the parasite could be directly transmitted to scallops from freshly dead gray meat scallop tissue; however, infection trials conducted with live gray meat scallops as a vector did not transmit the infection.

Apicomplexan parasites have complex life histories that often include both asexual and sexual reproduction. Histological analysis identified all asexual reproductive forms, but no sexual gametes in scallop tissue. These findings are explained by the recent identification of the definitive host for this parasite in Iceland waters; the common whelk (*Buccinum undatum*). Molecular analysis confirmed that the apicomplexan infecting sea scallops is *Merocystis kathae* in common whelks.

Sea scallops are thus the intermediate host for this parasite and transmission can be direct from highly infected scallops when they die, or from infected whelks in scallop populations. Current studies focus on identifying the presence and range of the infection in whelks associated with Atlantic sea scallops.

SPATIALLY EXPLICIT ESTIMATES OF THE IMPACTS OF SEA LEVEL RISE AND EROSION ON RIBBED MUSSEL (*GEUKENSIA DEMISSA*) MEDIATED ECOSYSTEM FUNCTIONS

Robert E. Isdell*, Donna M. Bilkovic, and Carlton Hershner

Virginia Institute of Marine Science, College of William and Mary, Center for Coastal Resources Management, 1375 Greate Rd., Gloucester Point, Virginia 23062 USA

risdell@vims.edu

Ribbed mussels are a highly abundant yet undervalued resource throughout the marshes of the US Atlantic coast. In the Chesapeake Bay, ribbed mussels are most abundant along the edges of marshes in more exposed creeks and rivers, and are least abundant in very narrow, fringing marshes near the heads of tidal creeks. With an estimated population in excess of 1.3 billion, ribbed mussels in the Chesapeake Bay also have an enormous potential to facilitate nitrogen removal; however, as sea level rises and marshes recede, both the mussels and their capacity to improve water quality are at risk. To address this, we used spatially explicit estimates of ribbed mussel abundance and condition, paired with nitrogen removal and transformation rates to project current and future ecosystem service provision of ribbed mussels throughout Virginia given an expected 0.6 m sea level rise. The results were placed within surrounding land use context to identify where services were most likely to be lost.

USING NOAA OBSERVATIONAL AND MODELING TOOLS TO ADDRESS *VIBRIO* RISK

John Jacobs[1], Rohinee Paranjpye[2], Clara Hard[3], and Bob Daniels[4]

[1]NOAA/National Ocean Service, National Centers for Coastal Ocean Science, Cooperative Oxford Lab, Oxford, Maryland 21654 USA

[2]NOAA/National Marine Fisheries Service, Northwest Fisheries Science Center, Seattle, Washington 98112 USA

[3]Washington Department of Health, Seattle, Washington 98501 USA

[4]NOAA/National Weather Service/National Center for Environmental Prediction/Ocean Prediction Center, College Park, Maryland 20740 USA

John.Jacobs@noaa.gov

The presence of *Vibrio parahaemolyticus* in oysters has been a persistent issue for producers and consumers of raw oysters in the United States, and necessarily, much effort has been directed towards strategies for risk reduction. To date, most states use time and temperature controls to minimize post - harvest growth, and seasonal temperature averages to initiate and end control strategies. In recent years, NOAA has embarked on an effort to work with the States, FDA, and industry to apply NOAA forecast modeling and observational assets to better inform harvest and control strategies. In this presentation, we will demonstrate: 1) how hydrodynamic models are being used to provide spatially explicit predictions of *Vp* concentration in oysters, 2) the use of weather models to pro-

vide scaled projections of *Vp* growth under different control strategies, and 3) efforts underway in the Pacific Northwest to predict *Vp* levels in intertidal oysters based on substrate type and modeled atmospheric data. These products are developed from stakeholder workshops and requests, and are distributed via the web https://products.coastalscience.noaa.gov/vibrioforecast/.

USING ARCHAEOLOGICAL OYSTER SHELL TO INFER ANCIENT MARICULTURE

Jessica A. Jenkins

University of Florida, Department of Anthropology, Turlington Hall, PO Box 117305, Gainesville, Florida 32611 USA

jajenkins@ufl.edu

Shell is one of the most ubiquitous and enduring materials recovered from archaeological sites, demonstrating the importance of shellfish in many aspects of ancient lifeways. Shellfish were not only a source of food for coastal dwellers, but the shells were also used as tools, jewelry, and building material. The challenge of sustaining and intensifying marine resource production today was shared by coastal dwellers of the ancient past. In order to explore how large-scale oyster exploitation was sustained by indigenous communities thousands of years ago, methods for inferring oyster mariculture using proxies on archaeological shell will be presented. These methods are then applied to oyster shells recovered from a large feasting and ceremonial site, Shell Mound (8LV42), on the Florida Gulf Coast, where approximately 1.2 billion oysters were harvested from local reefs in less than two centuries. Results indicate that maricultural practices were likely used by ancient coastal inhabitants when the scale and intensity of oyster procurement increased during a time of ritualized feasting and mound-building during the fifth and sixth centuries A.D.

A ROLE FOR PROTEIN KINASE C IN GILL LATERAL CELL ACTIVITY OF *CRASSOSTREA VIRGINICA*

Alexcia Johnson[1]*, Krystle Ernest[2], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New York 11235 USA

[2]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

alexciajohnson1997@gmail.com

Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine causes cilio-inhibition, serotonin cilio-excitation. GLC dopamine postsynaptic receptors are D2-like (D2DR). The D2DR signaling pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC generates second messengers diacylglycerol (DAG) and inositol trisphosphate (IP3). IP3 binds to IP3 receptors causing release of intracellular calcium. DAG with calcium activates protein kinase C (PKC). While high cytoplasmic calcium slows GLC cilia beating, the role of PKC on GLC cilia has not been studied. It is hypothesized that PKC activation is involved in the cilio-inhibitory response caused by dopamine in *C. virginica*. The PKC activator SC9 [N-(6-Phenylhexyl)-5-chloro-1-naphthalenesulfonamide] and PKC inhibitor rottlerin were tested. Neither SC9 (10^{-6}–10^{-3}M) nor rottlerin (10^{-6}–10^{-4}M) applications to gill altered GLC cilia beating, nor did they alter cilio-excitatory actions of serotonin; however, rottlerin treated gills did not respond to dopamine, an SC9 did not alter the cilio-inhibitory effects of dopamine. These finding indicate PKC is involved in dopamine induced slowing of GLC cilia in *C. virginica.* Inhibiting PKC prevents actions of dopamine, while activating PKC by itself did not significantly alter cilia beating rates. The study suggests PKC plays a role in cilio-inhibition caused by dopamine, but alone PKC activation is insufficient to generate the cilio-inhibitory response and other aspects of the D2DR signaling pathway also must be involved. These findings are helpful in furthering the understanding of the D2DR mechanism of GLC and provides a foundation for further research.

ECOSYSTEM AND GENOMIC RESEARCH IN SUPPORT OF *VIBRIO PARAHAEMOLYTICUS* RISK MANAGEMENT: WHAT ARE THE CRITICAL THEMES?

Stephen H. Jones[1]*, Cheryl A. Whistler[2], Meghan Hartwick[2], Michael Taylor[2], Ashley L. Marcinkiewicz[2], Randi Foxall[2], and W. Christopher Nash[3]

[1]University of New Hampshire, Department of Natural Resources and the Environment, 85 Adams Point Rd., Durham, New Hampshire 03824 USA

[2]University of New Hamphire, Department of Molecular, Cellular and Biomedical Sciences, 46 College Rd., Durham, New Hampshire 03824 USA

[3]University of New Hampshire, Department of Environmental Services, Shellfish Program, 222 International Drive, Suite 175, Portsmouth, New Hampshire 03801 USA

Stephen.jones@unh.edu

The shellfish industry of the Northeast US has recently faced the challenge of significant increases in shellfish-borne *Vibrio parahaemolyticus* (Vp) illnesses. Several different factors have contributed to this problem, and industry and regulators have responded with an array of management strategies to reduce the risks of illness. Application of risk management strategies from other regions have had mixed results, suggesting conditions are uniquely different here. Introduced pathogenic strains and the warming of regional coastal waters have required development and application of new and modified existing management strategies, all of which benefit from research support to gain accuracy and optimization that reduce unnecessary costs while minimalizing risks.

Ecosystem and genomic research related to managing Vp risks at UNH has focused on detection methods for pathogenic strains,

oyster relay, depuration and re-submergence, ecosystem modeling of Vp populations, and the estuarine microbiome. Integration of these topics is needed to provide the scientific foundation and understanding for developing more accurate and effective management strategies. Recent progress will be discussed along with future research directions.

HABITAT CHARACERIZATION OF THE RIBBED MUSSEL (*GEUKENSIA DEMISSA*) AND ITS RESPONSE TO HARVEST IN SOUTH CAROLINA, USA

Asa Julien[1], Andrew Tweel[2], Nancy Hadley[2], Dan McGlinn[3], and Peter Kingsley-Smith[2]

[1]Graduate School at the University of Charleston South Carolina, Grice Program in Marine Biology, 205 Fort Johnson Road, Charleston, South Carolina, 29412 USA

[2]South Carolina Department of Natural Resources, Marine Resources Research Institute, 217 Fort Johnson Road, Charleston, South Carolina, 29412 USA

[3]College of Charleston, Department of Biology, 66 George Street, Charleston, South Carolina 29424 USA

julienar@g.cofc.edu

The ribbed mussel, *Geukensia demissa*, is an ecosystem engineer that promotes salt marsh functioning throughout its range along the eastern coast of North America. Over the past five years, commercial landings of *G. demissa* in South Carolina have increased considerably, yet the fishery lacks species-specific regulations. While habitat characterization is commonly used as a management tool for other commercially important bivalves (e.g., the eastern oyster, *Crassostrea virginica*), such information for *G. demissa* in South Carolina is currently lacking. As part of a broader study to improve understanding of the ecological role of *G. demissa* in the salt marsh community, its elevational range and inundation period were characterized along a salinity gradient in Charleston, S.C. In spring 2017, transects were established at eight sites along the Ashley River (8 – 24 ppt). Elevation was determined using survey-grade GNSS equipment, and inundation period was determined by placing temperature sensors at several sites for a month. A logistic regression model was developed to determine the probability of *G. demissa* occurrence, which was greatest at elevations slightly below mean high water and at intermediate salinities (18 ppt). The model is relevant to managing the emerging fishery, as it can be applied to improve mapping of *G. demissa* habitat, although the model has yet to be tested in systems outside of the Ashley River. In addition to the characterization of *G. demissa* habitat, results from a manipulative experiment looking at the effects of harvesting practices on salt marsh health and *G. demissa* recovery will be presented.

VISUAL KEYS SUPPORT OYSTER HEALTH MONITORING AS PART OF OYSTER REEF RESTORATION EFFORTS

Andy Kane[1*], Ross Brooks[1], Felipe Sanchez[1], Shelby Thomas[1], Karl Havens[2], Jim Estes[3], and Melanie Parker[3]

[1]University of Florida, Department of Environmental and Global Health, Aquatic Pathobiology Laboratory, PO Box 110885, Gainesville, Florida 32611 USA

[2]Florida Sea Grant Program, Building 803 McCarty Drive, PO Box 110400, Gainesville, Florida 32611 USA

[3]Florida Fish and Wildlife Conservation Commission, Division of Marine Fisheries Management, Fish and Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, Florida 33701 USA

kane@ufl.edu

Health observations are an integral component of monitoring oyster reef restoration projects. This project developed and applied visual keys to facilitate consistency in ranking severity scores for stained *Perkinsus marinu*s hypospores, empirical meat ranks (volume within the left shell, plumpness, translucency), and severity of boring shell parasites affecting eastern oyster, *Crassostrea virginica*. Measurement of shell parasite prevalence and severity for *Polydora websteri* (polychaete), *Diplothyra smithii* (clam) and *Cliona celata* (sponge) is important since these organisms excavate shell matrix throughout the life of the oyster (and in the case of *Cliona*, throughout the life of the shell). Further, these parasites reduce shell density and dramatically increase surface area of the shell exposed to the environment. Higher salinity conditions foster the severity of these shell parasites, and shells with extensive excavation and high surface area may dissolve more rapidly in saltwater, break down into shell fragments, and destabilize reef structure in the long term. Visual keys that support these metrics will be demonstrated and their utility for training students and providing quality control for diagnostic health assessments will be discussed. Consistency in reporting health metrics as part of oyster resource monitoring will become increasingly important as restoration efforts with limited resources focus more on sustainable, measureable outcomes. This project was supported in part through the National Fish and Wildlife Foundation Gulf Environmental Benefit Fund, Florida Fish and Wildlife Conservation Commission, and Florida Sea Grant.

ISOLATION AND CHARACTERIZATION OF *FRANCISELLA HALIOTICIDA* FROM ABSCESS LESIONS IN THE ADDUCTOR MUSCLE OF THE YESSO SCALLOP, *PATINOPECTEN YESSOENSIS*

Miku Kawahara[1]*, Makoto Kanamori[2], Tomoyoshi Yoshinaga[1], and Naoki Itoh[1]

[1]The University of Tokyo, Laboratory of Fish Diseases, Graduate School of Agricultural and Life Sciences, Tokyo 113-8657, Japan

[2]Hakodate Fisheries Research Institute, Fisheries Research Department, Hokkaido Research Organization, Hakodate 040-0051, Japan

39mirai-2869mk@g.ecc.u-tokyo.ac.jp

Presence of abscess lesions in the adductor muscle of Yesso scallops, *Patinopecten yessoensis,* has been reported in northern Japan. In addition to loss of marketability in the diseased scallops, it is considered that this disease is associated with mortality and poor growth of scallops. Analyses of bacterial 16S rRNA in the lesions revealed that *Francisella halioticida* was the most dominant bacteria species in the abscess lesions. Moreover, *F. halioticida* was detected from most of the abscess lesions by PCR, whereas very rarely in healthy scallops. Based on these results, *F. halioticida* is considered as the causative agent of this disease. Later, isolation of this bacterium was conducted using modified Eugon agar plates supplemented with antibiotics, and 3 isolates were successfully established from the adductor muscle lesions. 16S rRNA sequence of these scallop isolates were identical to the type strain of *F. halioticida* isolated from the giant abalone *Haliotis gigantea*, however, there were slight differences in *tpiA*, *rpoA* and *pgm* genes between these scallop isolates and the abalone strain. Commercial biochemical test kits showed that all of these scallop isolates lack proline arylamidase activity, and also growth rate of scallop isolates in modified Eugon broth was apparently slower than that of the abalone strain. These results clearly indicate that *F. halioticida* causing the adductor muscle lesions of Yesso scallops is genetically and phenotypically different from the type strain from the giant abalone.

THE ROLE OF CLIMATE IN DRIVING DISEASE DYNAMICS IN THE COMMERCIALLY IMPORTANT WHITE SHRIMP, *LITOPENAEUS SETIFERUS*

Michael R. Kendrick*[1], Marc E. Frischer[2], Jeff Brunson[1], Elizabeth Gooding[1], James E. Byers[3], Pat Geer[4], and Peter R. Kingsley-Smith[1]

[1]South Carolina Department of Natural Resources, Marine Resources Research Institute, 217 Fort Johnson Road Charleston, South Carolina 29422 USA

[2]University of Georgia, Skidaway Institute of Oceanography, 325 Sanford Drive Athens, Georgia 30602-3636 USA

[3]University of Georgia, Odum School of Ecology, 140 E. Green St., Athens, Georgia 30602 USA

[4]Georgia Department of Natural Resources, Coastal Resources Division, 1 Conservation Way, Brunswick, Georgia 31520 USA

kendrickm@dnr.sc.gov

Climate-driven shifts in environmental conditions are anticipated to increase the intensity of host-pathogen interactions, posing substantial potential impacts to host population dynamics. For commercially important species, natural resource managers will require a more comprehensive and predictive understanding of how changing climate conditions relate to pathogen prevalence in order to better manage these species. In the southeastern USA, recent increases in the occurrence of shrimp black gill have coincided with declines in commercial white shrimp (*Litopenaeus setiferus*) landings in the region, suggesting that black gill may be contributing to population declines in white shrimp. While black gill has been associated with a number of different causative agents, recent outbreaks in the southeast have been attributed to infection by an apostome ciliate. The objective of this study was to assess the role of climate conditions in determining the prevalence of black gill in white shrimp in South Carolina and Georgia estuaries. Data were compiled for monthly black gill prevalence and white shrimp abundance data collected over the past 12-15 years from seven estuaries along the South Carolina and Georgia coasts. Phenology of black gill was variable among years, but mean fall black gill prevalence was significantly correlated with climate indices including the El-Niño Southern Oscillation index (ENSO) and the Pacific Decadal Oscillation (PDO). These data suggest an important role of climate in determining black gill prevalence and provide an important baseline for understanding how future climate change might relate to the temporal and spatial dynamics of this condition in white shrimp.

COMMUNITY-BASED MITIGATION OF HARMFUL ALGAL BLOOMS AND SHELLFISH POISONINGS IN SOUTHEAST ALASKA

Esther Kennedy*, Kari Lanphier, and Christopher Whitehead

Sitka Tribe of Alaska Resource Protection Department, 429 Katlian Street, Sitka, Alaska 99835 USA

esther.kennedy@sitkatribe-nsn.gov

Paralytic shellfish toxins have been known in Alaskan shellfish for thousands of years and remain a present threat to all recreational and subsistence shellfish harvesters in the state. Limited State resources, dispersed and remote populations, and long coastlines have precluded the development of a statewide monitoring program or testing facilities for wild shellfish. As climate change has extended the HAB season in Alaska, traditional risk mitigation strategies such as harvesting only during winter months have become increasingly unreliable, causing many would-be harvesters to forgo shellfish entirely. To reduce the threats of PSP and harmful algal blooms in Southeast Alaska, the Sitka Tribe of Alaska has taken the lead in developing a community-based harmful algal

bloom monitoring and biotoxin testing program. The Sitka Tribe's partners, fourteen tribal governments that comprise the Southeast Alaska Tribal Ocean Research (SEATOR) group, each monitor one or more local shellfish sites. Samplers collect and analyze weekly phytoplankton samples at each site and ship bi-weekly shellfish samples to the Sitka Tribe Environmental Lab for analysis using the Receptor Binding Assay. Results are available within one to two business days and are immediately communicated to each local community. The Sitka Tribe and SEATOR group are building a regional database of shellfish toxins and phytoplankton abundances to make shellfish available as a safe, reliable wild food source. The SEATOR group success has implications for all monitoring programs that rely heavily on community participation as well as programs that struggle to effectively serve remote sites.

MONITORING THE RECOVERY OF EAST SIDE COOK INLET RAZOR CLAMS

Carol M. Kerkvliet[1]*, Michael D. Booz[1], Timothy J. Blackmon[1], and Patricia A. Hansen[2]

[1]Alaska Department of Fish and Game, Division of Sport Fish, 3298 Douglas Place, Homer, Alaska 99603 USA

[2]Alaska Department of Fish and Game, Division of Sport Fish, 333 Raspberry Road, Anchorage, Alaska 99518 USA

carol.kerkvliet@alaska.gov

The Alaska Department of Fish and Game, Division of Sport Fish has assessed razor clam populations (*Siliqua patula*) along the east side of Cook Inlet since 1964. This 81 km stretch of beach has supported the largest razor clam sport fishery in Alaska. Historically the population and fishery have been monitored using 4 data sets: 1) periodic estimates of abundance of juvenile and mature size razor clams since 1989; 2) annual estimates of age and length composition since 1985; 3) annual estimates of harvest and effort since 1970; and 4) periodic estimates of harvest success since 1969.

In the early 2000s, a downward trend in harvest combined with shift towards younger razor clams with fewer age classes, suggested decreased productivity. In 2011 even though, abundance of mature razor clams at Ninilchik reached a record high and exploitation was low (~6%), concerns ensued because most of the abundance was composed of one age class. The fishery was progressively restricted, then closed in 2015 because of poor recruitment and high natural mortality of mature size razor clams. The causes for poor recruitment are unknown but thought to be related to poor spawning and/or settling success. The causes for the high rate of natural mortality may include winter storms, predation and other unknown factors.

Monitoring efforts have been refined to better assess recruitment and natural mortality at Ninilchik and Clam Gulch. This presentation will focus on recent razor clam studies and recent increases of juvenile size razor clams detected.

A 72-HOUR GRAPHENE OXIDE NANOPARTICLE EXPOSURE STUDY WITH EASTERN OYSTERS

Bushra Khan[1*], Adeyemi Adeleye[1], Stephen Russo[2], Robert M. Burgess[3], and Kay T. Ho[3]

[1]National Research Council Postdoctoral Research Associate, 27 Tarzwell Drive, Narragansett, Rhode Island 02882 USA

[2]Oak Ridge Associated Universities Student Services Contractor, 27 Tarzwell Drive, Narragansett, Rhode Island 02882 USA

[3]US Environmental Protection Agency, ORD-NHEERL, Atlantic Ecology Division, 27 Tarzwell Drive, Narragansett, Rhode Island 02882 USA

khan.bushra@epa.gov

Graphene family nanomaterials (GFN) are widely used in the field of electronics and biomedicine. Gaps in our knowledge about fate and toxicity of GFN, such as graphene oxide (GO), raise concerns regarding their environmental impacts. Filter feeding bivalves, such as *Crassostrea virginica* (eastern oysters), are good models to study the effects of GO exposures. The goal of this pilot study is to evaluate effects of *in vivo* GO exposures on oysters using a static renewal design. Oysters were exposed to 1 and 10 mg/L GO and fed a mixed algal diet. Each oyster was placed in a beaker with 1 liter of 0.22 µm filtered natural seawater and three renewals were performed daily. For every renewal, a GO suspension was prepared and sonicated before addition to beakers. Water samples were analyzed for GO concentration and effective diameter. At the end of 72 hours, oysters were placed in clean seawater for three hours and gill and digestive gland tissues were harvested. Tissues were analyzed for lipid peroxidation, a marker of oxidative damage, and for activity of glutathione-s-transferase (GST), a detoxification enzyme. Elevated lipid peroxidation in GO exposed oysters was found. No significant changes in GST activity were observed, but reduced total protein levels were noted in exposed oysters. Results indicate that short-term GO exposures can induce oxidative stress and adversely affect overall health in oysters. Evaluation of sublethal effects of exposures to an emerging contaminant, such as GO, is critical to understanding the risks associated with increasing commercial usage of nanoparticles.

SOUNDTOXINS: A PUGET SOUND HAB MONITORING PARTNERSHIP

Teri King[1]*, Lyndsey Claassen[1], Jerry Borchert[2], Vera Trainer[3], and SoundToxins Partnership[1]

[1]Washington Sea Grant, P.O. Box 2347, Shelton, Washington 98584 USA

[2]Washington Department of Health, 101 Israel Road SE, Tumwater, Washington 98501 USA

[3]NOAA Northwest Fisheries Science Center, 2725 Montlake Blvd E, Seattle, Washington 98112 USA

guatemal@uw.edu

SoundToxins is a diverse partnership of aquaculture businesses, federal, tribal, state, and local governments, education institu-

tions, and Puget Sound residents that monitor for harmful algae in Puget Sound, managed by the NOAA Northwest Fisheries Science Center and Washington Sea Grant. The intensively trained partners provide early warning of harmful algal bloom (HAB) events by evaluating water samples gathered weekly from 35 stations throughout Puget Sound looking specifically for *Dinophysis, Alexandrium, Pseudo-nitschia* and *Azadinium* species, and alerting health and natural resource agencies of their presence. The online database and mapping allows for near-real time viewing of data entered by SoundToxins partners and is reviewed daily by Sea Grant staff for quality and accuracy. Participants have partnered on several research projects providing samples, data and endorsement of scientist and their projects. The SoundToxins program has helped to minimize the risks to human health and reducing the economic losses to Puget Sound fisheries since its formation in 2006.

CHARACTERISATION OF THE PACIFIC OYSTER MICROBIOME DURING A SUMMER MORTALITY EVENT

William L. King[1,2*], Cheryl Jenkins[3], Jeffrey Go[3], Nachshon Siboni[2], Justin R. Seymour[2], and Maurizio Labbate[1]

[1]University of Technology Sydney, The School of Life Sciences, Sydney, NSW, Australia

[2]University of Technology Sydney, Climate Change Cluster, Sydney, NSW, Australia

[3]NSW Department of Primary Industries, Elizabeth Macarthur Agricultural Institute, Menangle, NSW, Australia

William.King@student.uts.edu.au

The Pacific oyster, *Crassostrea gigas*, is a key commercial species that is cultivated globally. In recent years, disease outbreaks have heavily impacted *C. gigas* stocks worldwide, with many losses incurred during summer. A number of infectious agents have been associated with these summer mortality events, including viruses (particularly Ostreid herpesvirus 1, OsHV-1) and bacteria, however, cases where no known aetiological agent can be identified are common. In this study, the microbiome of *C. gigas* was examined during a 2013-2014 summer mortality event in Port Stephens (Australia) where OsHV-1 was not detected. The adductor muscle microbiomes of 70 *C. gigas* samples across 12 study sites in the Port Stephens estuary were characterised using 16S rDNA (V1-V3 region) amplicon sequencing. The oyster microbiome composition from disease-affected sites was significantly determined by location. Furthermore, a comparison of oyster microbiomes from stocks affected or unaffected by the mortality event within the same site identified rare OTUs belonging to *Vibrio harveyi* and an unidentified member of the *Vibrionaceae*, as significantly more abundant in the microbiomes from the disease-affected stock indicating a potential role in disease and supporting a previously conducted culture-based study.

QUANTIFYING OYSTER REEF DEVELOPMENTAL TRAJECTORIES FROM 16 YEARS OF LIVING SHORELINES RESEARCH IN SOUTH CAROLINA, USA

Peter Kingsley-Smith*, Michael Hodges, Benjamin Stone, Gary Sundin, Sharleen Johnson, Andrew Tweel, and Denise Sanger

South Carolina Department of Natural Resources (SCDNR), 217 Fort Johnson Road, Charleston, South Carolina, 29412 USA

kingsleysmithp@dnr.sc.gov

High rates of recruitment in South Carolina, USA lead to the rapid development of intertidal oyster (*Crassostrea virginica*) reef habitat when suitable settlement substrate is provided. Utilizing this "substrate limitation" phenomenon, the SCDNR has a long (>16 years) and productive history of oyster restoration. Recent focus for these restoration efforts has centered on the ability of living shorelines to counteract saltmarsh (*Spartina alterniflora*) habitat loss, and to function as a viable or even preferred erosion control alternative to bulkheads and seawalls.

Through funding from the NOAA NERRS Science Collaborative, SCDNR researchers are leading an effort to better understand the performance of living shoreline approaches across a range of estuarine environmental conditions. This project involves four complementary components: 1) monitoring previously created living shorelines; 2) analyzing historical living shorelines data; 3) creating new living shorelines; and 4) gathering information on homeowner perspectives regarding adopting living shoreline approaches.

This presentation will focus on the first of these components. Through re-visiting reefs dating back to 2001, the project team is determining the temporal trajectories of living shorelines at timepoints beyond those typically captured within individual project timelines. Data will be presented on temporal changes in surface elevation and marsh edge location as key determinants of the saltmarsh protection services offered by living shorelines. Ultimately the data gathered through this project will be incorporated into a guidance document provided to the state regulatory agency as part of the generation of state-level regulations for the permitting of living shorelines in South Carolina.

LINKING GENOTYPE TO PHENOTYPE IN A CHANGING OCEAN: INFERRING THE GENOMIC ARCHITECTURE OF A BLUE MUSSEL STRESS RESPONSE

Sarah E. Kingston*[1,2], Pieter Martino[1,2], Marko Melendy[2], Floyd A. Reed[3], and David B. Carlon[1,2]

[1]Bowdoin College, Schiller Coastal Studies Center, 240 Bayview Rd, Orrs Island, Maine 04066 USA

[2]Bowdoin College, Department of Biology, 6500 College Station, Brunswick, Maine 04011 USA

[3]University of Hawai'i at Mānoa, Biology Department, 2538 McCarthy Mall, Edmondson Hall 216, Honolulu, Hawai'i 96822 USA

skingsto@bowdoin.edu

A key component to understanding the evolutionary response to a changing climate is linking underlying genetic variation to phe-

notypic variation in stress response. A genome-wide association approach (GWAS) and differential expression analysis were used to understand the genetic architecture of calcification rates under simulated climate stress. The genomic gradient across the blue mussel hybrid zone (*Mytilus edulis* and *Mytilus trossulus*) in the Gulf of Maine was leveraged to link genomic and RNA expression variation with variance in calcification rates in response to simulated climate change. Wild mussels were sampled and net calcification phenotype quantified after mussels were exposed to a "climate change" common garden (+3°C, -0.2 pH units, and limited food supply compared to ambient GOM conditions in the summer). This climate change exposure greatly increased phenotypic variation in net calcification rates compared to ambient conditions. Regression models were used to link the phenotypic variation with over 170,000 single nucleotide polymorphism loci (SNPs) generated by genotype by sequencing to identify genomic locations associated with calcification phenotype, and estimate heritability and architecture of the trait. Differential gene expression analysis on mRNA sequences revealed transcripts exhibiting perturbed expression, a dynamic response to the simulated multivariate stressors of climate change. At least one of potentially 2-10 genomic regions responsible for 30% of the phenotypic variation in calcification rates that are potential targets of natural selection by climate change was identified. Hundreds of potential expression quantitative trail loci, those significantly differentially expressed under climate stress, were elucidated.

EXPERIENCES WITH OSTREID HERPESVIRUS 1 (OSHV-1) IN AUSTRALIA—IMPACTS AND POSSIBLE SOLUTIONS

Peter D. Kirkland*, S. Gestier, and X. Gu

Virology Laboratory, Elizabeth Macarthur Agriculture Institute. Woodbridge Rd, Menangle NSW, Australia

peter.kirkland@dpi.nsw.gov.au

The variant strain of OsHV-1 (µvar) emerged in Pacific oysters in Australia in November 2010 at Sydney, NSW in the Georges River estuary and has subsequently been detected at two other locations in Australia, most recently in Tasmania in December 2015. When initially detected in a susceptible population, there has been extensive and rapid spread with extremely high mortality rates in Pacific oysters of most ages. Since the first detection through to the current time, oyster producers have experienced devastating impacts – whether through direct losses from mortalities, movement restrictions between affected and unaffected growing areas or from a shortage of seedstock for production in both affected and unaffected regions. Extensive research has been undertaken to identify management strategies that may reduce losses and to commence breeding of stock with resistance to OsHV-1 infection. This presentation will compare the geographical spread of the outbreak in Australia with the distribution of Pacific oyster production in the USA. Studies to develop an experimental virus transmission model and its application to assessment of the susceptibility of other species of oysters and for the selection of genetically resistant Pacific oyster lines will be reviewed.

MAPPING GENES CONFERRING RESISTANCE TO OSHV-1 IN THE PACIFIC OYSTER

Tevfik Hamdi Kitapci[1*], Colleen Burge[2], Collin Closek[3], Carolyn Friedman[4], and Dennis Hedgecock[5]

[1,5]University of Southern California, Department of Biological Sciences, Los Angeles, California 90089, USA

[2]University of Maryland, Institute of Marine and Environmental Technology, 701 East Pratt St. Baltimore, Maryland 21202, USA

[3]Stanford University, Center for Ocean Solutions, Stanford, California, USA

[4]School of Aquatic and Fishery Sciences, University of Washington, Box 355020, Seattle, Washington 98195, USA

tkitapci@usc.edu

Understanding the genetic basis of resistance to ostreid herpes virus 1 (OsHV-1) by the Pacific oyster is important for the global oyster industry. The virulent µVar forms of OsHV-1 have caused devastating losses of farmed Pacific oysters in Western Europe, Australia, New Zealand, and Asia, and it is expected eventually to arrive on the U.S. West Coast. Since 1993, OsHV-1 has caused mass mortalities of seed and juvenile Pacific oysters in Tomales Bay, CA, with losses ranging from 50% to 100% during the warmest summer months. This project, therefore, was designed to generate high-density linkage maps to detect QTL (quantitative trait loci) for resistance to OsHV-1 infection or mortality. Two full-sib families (1252 and 5819) from four unrelated parents were produced and planted in Tomales Bay before OsHV-1-caused mass mortalities in late September 2015. Over a two-week period, family 1252 experienced 55%, and family 5819, 16% mortality. Reduced representational genomic libraries were constructed for pre- and post-exposure samples (268 individuals from 1252 and 290 individuals from 5819) as well as the parents of the two families. Individual libraries were bar-coded and sequenced in pools, using genotyping-by-synthesis methods. Changes in genotypic frequencies particular to the exposure period suggest that, 10 and 7 viability QTLs in families 5819 and 1252 respectively, are associated with resistance to OsHV-1 and survival. Although the current state of the assembly of the Pacific oyster genome impedes identification of candidate genes, these findings strongly suggest that marker-assisted selection could be used to select oyster family resistant to OsHV-1 infection or mortality.

THE JAPANESE ART OF *GYOTAKU*, THE INTERSECTING OF SCIENCE AND ART

Bruce Koike

Little Pond Nature Prints, 322 SE Harney St, Newport, Oregon 97365 USA

koike.bruce@gmail.com

Though definitive knowledge of how and when *Gyotaku* (pronounced Ghio-tah-ku) started is unknown, it is recognized that in the 1800's Lord Sakai was the driving patron of *Gyotaku* as art. This technique of nature printing requires the use of the actual specimen in making the "impression". *Gyotaku* was initially used by fishermen to communicate to commoners the types of fish that were caught and available for purchase. Upon his death the popularity of *Gyotaku* waned, but re-emerged decades later as a bona fide art form.

Today fish printing has the potential to engage students, fulfill Next Generation Science Standards, and promote science literacy. This presentation, accompanied by a short video, will detail the methodology and possibilities of using fish printing as an outreach element for your research and institution.

EXPERIMENTAL INFECTION TO ASSESS PATHOGENICITY OF *PERKINSUS BEIHAIENSIS* AGAINST DOMESTIC BIVALVE SPECIES IN JAPAN

Yoshiki Komatsu, Tomoyoshi Yoshinaga, and Naoki Itoh*

The University of Tokyo, Laboratory of Fish Diseases, Department of Agricultural and Life Sciences, 1-1-1 Yayoi, Bunkyo, 113-8657 Tokyo, Japan

aitoh-nk@mail.ecc.u-tokyo.ac.jp

In 2016, the presence of *Perkinsus beihaiensis* from the Mediterranean mussel *Mytilus galloprovincialis* was found in Japan by histological, RFTM, and PCR assays. Field surveys in 2016 – 2017 revealed that most of mussels in Tokyo Bay were infected with this parasite, while mussels in the other examined areas were free from infection. This geographically limited distribution suggested a possibility that *P. beihaiensis* invaded into Tokyo Bay recently and has not spread throughout the country, therefore, assessment of its pathogenicity to domestic bivalve species in Japan is required. In this study, a primary isolate of *P. beihaiensis* was established from infected gill tissues of mussels using an *in-vitro* proliferation medium JL-ODRP2-A and another cholesterol enriched medium, and then the proliferated cells (1.0 x 10^3 cells/individual) were injected into the adductor muscles of the Manila clam, *Ruditapes philippinarum*, the Pacific oyster, *Crassostrea gigas,* the Pearl oyster, *Pinctada fucata martensii,* and the Mediterranean mussel. Two weeks after the injection, *P. beihaiensis* was detected in Manila clam, Pearl oyster and Mediterranean mussel, but not in Pacific oyster. During the experimental infection, there was no significant mortality in any challenged bivalves, suggesting that *P. beihaiensis* is able to infect the Manila clam, the Pearl oyster and the Mediterranean mussel, but may not cause lethal damage to these species. Additionally, it is likely that the Pacific oyster is highly resistant to *P. beihaensis* infection.

SESTON FILTRATION AND RESTORATION POTENTIAL OF RIBBED MUSSELS COMPARED WITH OTHER NATIVE BIVALVES

Danielle Kreeger*, Josh Moody, and Kurt Cheng

Partnership for the Delaware Estuary, 110 S. Poplar Street, Suite 202, Wilmington, Delaware 19801 USA

DKreeger@DelawareEstuary.org

Of the dozens of bivalve species native to the Delaware River Basin, ribbed mussels (*Geukensia demissa*) are believed to filter the most particles from natural seston (>1,000 metric tons per hour). Although their clearance rates are on par with other species, typical filtration rates are higher because they inhabit shoreline areas having high seston concentrations. Ribbed mussel populations are also still relatively abundant in the marsh-rich Delaware Estuary, whereas populations of many other native bivalves are far below historic levels. Unfortunately, high rates of salt marsh loss are undermining ecosystem services provided by ribbed mussels. To guide strategic investments aimed at promoting water quality, seston filtration outcomes were predicted and compared among tactics to enhance ribbed mussels, oysters (*Crassostrea virginica*), and alewife floaters (*Anodonta implicata*). Species-specific physiological and abundance data were integrated with seston data for sites where projects are being implemented to enhance ribbed mussels (living shorelines), oysters (shellplanting), or alewife floaters (reseeding). All shellfish-based strategies were estimated to yield a high return on investment (e.g., for particulate nitrogen filtration) compared with established nature-based investments. Since bivalves inhabit diverse niches along the river-to-sea salinity gradient, there are many opportunities to address water quality targets. These include projects to restore oyster and freshwater mussel beds as well as living shoreline tactics to stem the decline of ribbed mussels. Greatest improvements in water quality will result from tactics tailored to the unique life history needs of the target species and situated in areas with high particulate pollutant concentrations.

REPRODUCTIVE BIOLOGY INFORMS FISHERY MANAGEMENT OF SNOW (*CHIONOECETES OPILIO*) AND TANNER CRABS (*C. BAIRDI*) IN THE EASTERN BERING SEA, ALASKA

Gordon H. Kruse[1*], April Rebert[1,2], Jonathan I. Richar[1,3], Laura M. Slater[1,4], and Joel B. Webb[1,5]

[1]University of Alaska Fairbanks, College of Fisheries and Ocean Sciences, Juneau, Alaska USA

[2]Alaska Department of Fish and Game, Mark, Tag, and Age Laboratory, Juneau, Alaska USA

[3]National Marine Fisheries Service, Kodiak Fisheries Research Center, Kodiak, Alaska USA

[4]Alaska Department of Fish and Game, Division of Commercial Fisheries, Kodiak, Alaska USA

[5]Alaska Department of Fish and Game, Division of Commercial Fisheries, Juneau, Alaska USA

ghkruse@alaska.edu

Snow (*Chionoecetes opilio*) and Tanner crab (*C. bairdi*) stocks support boom-and-bust fisheries in the eastern Bering Sea. Management of these male-only crab fisheries may be enhanced by improved understanding of functional relationships between male harvest and female reproductive potential. In the genus *Chionoecetes*, females possess paired spermathecae, an organ for sperm storage from previous matings. For Tanner crab in Southeast Alaska, mean sperm cell counts of primiparous females by location were negatively correlated with an exploitation rate index, suggesting that male-only harvest decrease levels of stored sperm available for fertilization of a subsequent clutch. For Tanner crab in the eastern Bering Sea, a 13-14 year cycle in recruitment and total population size may indicate that long-term environmental variability mediates recruitment strength; however, this cycle is also approximately double the estimated mean age of maturity, suggesting the possibility of an endogenous rhythm associated with a stock-recruit relationship. For snow crab, fecundity increases with increasing female size and decreases for older multipara (age) likely due to senescence. Attempts to improve upon estimates of reproductive potential, which are affected by relationships with life history, female size, shell condition, temperature during embryogenesis, and other factors, will be presented. Additionally, research is ongoing to determine whether structures in *Chionoecetes* are retained through molting and whether band counts in these structures correspond to age. If so, results would provide a boon to estimates of age at maturity and rates of natural mortality and growth, which are critical for sustainable fishery management of these stocks.

GENETIC VARIATION IN PACIFIC OYSTERS (*CRASSOSTREA GIGAS*) FOR RESISTANCE TO *OSTREID HERPESVIRUS*-1

Peter D. Kube[1*], Michael C. Dove[2], and Matthew Cunningham[3]

[1]CSIRO Agriculture and Food, Castray Esplanade, Hobart, TAS, 7000, Australia

[2]New South Wales Department of Primary Industries, Taylors Beach, NSW, 2316, Australia

[3]Australian Seafood Industries, Hobart, TAS, 7010, Australia

peter.kube@csiro.au

The *Ostreid herpesvirus*-1 (OsHV-1) is a causative agent of mass mortalities of cultured Pacific oysters (*Crassostrea gigas*) in different regions worldwide and has devastated farmed stocks in France, New Zealand, and Australia. Genetic selection for disease resistance is one potential management tool and research on the Australian Pacific oyster population has provided knowledge of the genetic architecture of disease resistance. This knowledge has been the basis for a resistance breeding strategy which has been implemented via the existing Australian Pacific oyster selective breeding program.

Data were collected from a series of field trials in two regions (New South Wales and Tasmania) where animals were exposed to natural disease challenges. Trials tested both spat (6 months old) and adults (12 months old) over six genetically linked year classes using approximately 125,000 animals from 395 families. Genetic variation has been present in all trials and resistance is a trait under strong genetic control. In a combined analysis, the heritabilities of spat and adult survival were 0.49 and 0.39, respectively.

Operational breeding has progressed in parallel to the research program to address the immediacy of the disease threat. Genetic gains have accumulated in each annual cycle of breeding, increasing the survival of one year old oysters by at least 10% per year, and the economic benefits of resistance breeding are clearly evident. Whilst ongoing breeding is still required to address the challenges faced by industry, resistant oysters are now commercially available and resistance breeding has emerged as the central element of disease management.

RADULAR DEVELOPMENT AND LACK OF RADULAR PLASTICITY IN PINTO ABALONE (*HALIOTIS KAMTSCHATKANA*) POSTLARVAE AND YOUNG JUVENILES

Lillian Kuehl

Western Washington University, Department of Biology, 516 High Street, Bellingham, Washington 98225 USA

kuehll@wwu.edu

Young abalone (family Haliotidae) feed by using their radula to rasp microalgae from the substratum. Radular development has been characterized in several species of abalone, but never in pinto abalone (*Haliotis kamtschatkana*), the only abalone native to northwest North America. Other workers have shown that environment and food type induce a plastic morphological response in radulae of Littorinidae and other gastropod taxa, but such plasticity has not been studied in Haliotidae.

In this study, radulae of pinto abalone postlarvae and young juveniles, aged 12 days to 6 months, were examined using scanning electron microscopy. Postlarvae were raised on one of six different diatom species until day 61 post-settlement. Juveniles were fed a mixed diet of naturally occurring biofilm and macroalgae. Correlation was examined between age, shell length, and radular characteristics including radula length, radula width, row spacing, teeth per row, rachidian tooth shape and dimensions, and lateral tooth cusp shape. Traditional (linear) morphometrics, landmark analysis, and principal component analysis were used to assess changes over time and between diets, using the R software packages “lme4”, “Momocs” and “geomorph”.

As abalone grow, radula teeth become larger and more numerous, and change shape. At 61 days post-settlement, there was no sign that the diatom species postlarvae were fed induced morphological plasticity in the radula. Changes in radular morphology as pinto abalone develop will be presented in detail and compared with reported development in other abalone species.

THE 'EAST OF NANTUCKET' SURVEY: SURFCLAMS ON THE MARCH OFFSHORE – MUSSELS BEWARE

Kelsey M. Kuykendall[1]*, Eric N. Powell[1], Roger Mann[2], M. Chase Long[2], and Jeremy Timbs[1]

[1]Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, Mississippi 39564 USA

[2]Virginia Institute of Marine Science, Rt. 1208 Greate Road, Gloucester Point, Virginia 23062-1346 USA

Kelsey.kuykendall@usm.edu

Despite supporting an important part of the Atlantic surfclam commercial fishery, the region between Nantucket and the Great South Channel has never been comprehensively surveyed. The formation of a working group to redesign the federal surfclam survey provided impetus to survey this region. Large surfclams (>150 mm) were distributed inshore of smaller surfclams with very limited overlap. Recent recruitment is concentrated offshore. The pattern is consistent with the observed movement of surfclams into deeper water throughout the Delmarva to Georges Bank range. Large surfclams (>150 mm) and surfclam shell overlap relatively consistently. Surfclam shell is taphonomically robust – thus presence of shell is indicative of long-term habitation. Smaller surfclams and shell overlap relatively poorly; this absence of shell is indicative of recent habitation. The abundance of surfclams >170 mm transcends values in any other portion of the species' range. Hydroids were very common at many sites; they attached to any hard substrate including cobbles, rocks, boulders, and surfclam shell. Hydroids are the only common epibiont in areas inhabited by large surfclams and were found preferentially attached to surfclam shell suggesting that the fishery may be important in maintaining this epibiont in the community. Mussels (*Mytilus* sp. and *Modiolus* sp.) were very common at a number of sites. These sites generally supported significant numbers of crabs; sea urchins were frequently encountered. The surveyed region has two primary community types: surfclams and associated sandy biota; mussels and associated mobile epifauna. Both are likely in transition as surfclams invade deeper water, potentially displacing mussels.

MULTI-GENERATIONAL PLASTICITY AND ANTIVIRAL IMMUNITY IN THE OYSTER AGAINST OSHV-1

Maxime Lafont[1,2], Priscila Goncalves[1,3], Ximing Guo[4], Caroline Montagnani[2], David Raftos[1,3], and Timothy Green[1,3*]

[1]Sydney Institute of Marine Science, Chowder Bay, Sydney, Australia

[2]Ifremer, IHPE, UMR 5244, University of Montpellier, F-34095, Montpellier, France

[3]Macquarie University, Department of Biological Sciences, Sydney, Australia

[4]Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, New Jersey, USA

tim.green@mq.edu.au

The oyster immune system is capable of adapting upon primary exposure to a pathogen or an antigen to have an enhanced secondary response to the same type of pathogen. This has been demonstrated using a viral mimic (polyI:C) to elicit an antiviral response in the Pacific oyster, *Crassostrea gigas* against Ostreid herpesvirus. Improved survival following exposure to polyI:C was found later in life (within generational immune priming) and in the next generation (multi-generational immune priming). The mechanism that the oyster uses to transfer immunity to the next generation is not known. Understanding this aspect of immunology in the oyster is of great importance to the aquaculture industry. Global oyster production from aquaculture has declined due to the worldwide emergence of Ostreid herpesvirus. These data show that *C. gigas* larvae have higher survival to Ostreid herpesvirus when their mothers received an intramuscular injection of polyI:C prior to spawning, with a notable increase in the expression of antiviral effector genes in the unfertilised eggs; however, survival of larvae was not significantly improved when fathers were injected with polyI:C prior to spawning. RNAseq did not identify any differentially expressed mRNA transcripts between larvae produced from parents treated with polyI:C or seawater. These observations are consistent with the hypothesis that the improved survival of larvae occurs from maternal provisioning of antiviral compounds in the eggs.

UNSUSPECTED OSHV-1 GENOMIC DIVERSITY AT INTER- AND INTRA-HOST LEVEL

Jean-Baptiste Lamy[1], Tristan Renault[2], Antoine Bietry[1], Nicole Faury[1], Steve Webb[3], Jean-François Pepin[4], and Benjamin Morga[1]*

[1]Ifremer, SG2M-LGPMM, Laboratoire de Génétique et Pathologie des Mollusques Marins, Avenue de Mus de Loup, 17390 La Tremblade, France

[2]Ifremer, Département Ressources Biologiques et Environnement, Nantes, France

[3]Cawthon institute, 98 Halifax Street East, Nelson 7010, New Zealand

[4]Ifremer, Laboratoire Environnement Ressources des Pertuis Charentais (LER PC), La Tremblade, France

benjamin.morga@ifremer.fr

Ostreid herpesvirus 1 (OsHV-1) is a major pathogen affecting *Crassostrea gigas* production, as well as some other edible mollusc species in France and in the world (Australia, New Zealand, Sweden, etc.).

The aim of this study is to characterize the simple and complex nucleotide polymorphisms of various OsHV-1 viral population on infected individuals collected worldwide, in order to determine the existing phylogeny (using genome-wide dataset) between OsHV-1 specimens and to determine the inter and intra-host diversity to get better insights how disease is built during infection.

First results show that OsHV-1 samples from France and New Zealand infecting *C. gigas* did not cluster together, meaning that

New-Zealand OsHV1 viral population is another structural variant compare to OsHV-1 µVar. In addition, results confirmed the proximity of AVNV to OsHV-1 µVar-like cluster that suggest a recent host shift from *C. gigas to C. farreri.* The genome-wide study of simple and complex polymorphism suggests that some genomic regions are deleted in several specimens or accumulate a high level of substitution. This nonrandom pattern of polymorphism suggests that some genomic regions are under selective process. Contrary to a common belief, variants within all infected individuals were found. The biological interpretation of these observations is discussed in detail.

SPAT ON SHELL AS A MEANS FOR STOCK ENHANCEMENT OF PUBLIC REEFS IN ALABAMA, AND THE STANDARDIZATION OF SETTING EFFICIENCY ASSESSMENT

David Lappin*[1], William Walton[1], Scott Rikard[1], and Jason Herrmann[2]

[1]Auburn University Shellfish Laboratory, Auburn University School of Fisheries, Aquaculture and Aquatic Sciences, 150 Agassiz Street, Dauphin Island, Alabama, 36528 USA

[2]Alabama Department of Conservation and Natural Resources, Marine Resource Division, 2 Iberville Drive, Dauphin Island, Alabama 36528 USA

dlappin93@gmail.com

Oysters in the Gulf of Mexico region have significant environmental and socioeconomic impacts. Variability in natural population reproductive success over time has stressed the need to investigate methods for stabilization and enhancement of existing stocks. Here, remote set of hatchery reared oyster larvae on shell cultch was assessed as a potential method for the augmentation of existing oyster populations in Alabama. Small-scale experimental trials were conducted to assess site location, density of spat, and size of spat at the time of the plantings. Quantification of both survival and growth for experimental sites, in comparison to large scale planting sites, provides insight into the effectiveness of remote set planting for this region.

In addition to the field based experimental trials, tank experiments were conducted in an attempt to establish a standard method of assessment for oysters set on shell. Given the high degree of variability in size, and in shape, between oyster shells, a standardized assessment for setting efficiency across tanks is a valuable metric. The use of standard setting sticks provides insight into the efficiency of the setting process as well as the spatial distribution of spat across the tank.

CULTIVATION OF THE NEW ZEALAND GEODUCK, *PANOPEA ZELANDICA*

Dung Viet Le[12*], Andrea C. Alfaro[2], Tim Young[2], Nick King[3], Norman L.C. Ragg[3], and Zoë Hilton[3]

[1]Vietnam National University of Agriculture, College of Fisheries, Trau Quy, Gia Lam, Ha Noi, Vietnam

[2]Auckland University of Technology, Institute for Applied Ecology New Zealand, Private Bag 92006, Auckland 1142, New Zealand

[3]Cawthron Institute, 98 Halifax Street East, Private Bag 2, Nelson 7042, New Zealand

levietdung@vnua.edu.vn

The geoduck, *Panopea zelandica,* has been signaled as a new emerging species for aquaculture in New Zealand. To pave the way for the establishment of a geoduck aquaculture industry, information on how to grow this species over its life cycle needs to be determined. The aim of this project was to identify conditions that optimize *P. zelandica* broodstock conditioning, fertilization, larval growth and metamorphosis, and juvenile and young adult growth. Hence, the reproductive development and biochemical composition of broodstock conditioned within different water temperature and algal feeding rations were investigated. The embryogenesis and functional morphology of larvae were described. The practical fertilization and larval rearing methods under hatchery conditions were then developed. This project also determined the thermal window for aerobic scope and clearance rates of juvenile and young adults. In addition, the physiological responses of both two size classes to hypoxia were examined. The achievements of this project not only provided some fundamental information for the industry application but also gained better understanding of the ontogeny and physiology of *P. zelandica*.

DEVELOPING A RESEARCH PROGRAM TO ADDRESS SHELLFISH GROWERS' NEEDS: NINIGRET POND - A CASE STUDY

Dale Leavitt[1]*, Robert Rheault[2], and Heather Kinney[1]

[1]Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

[2]East Coast Shellfish Growers Association, 1121 Mooresfield Rd., Wakefield, Rhode Island 02879 USA

dleavitt@rwu.edu

Recently, there has been a rapid and substantial increase in oyster plantings on farms in a concentrated portion of Ninigret Pond (Charleston, RI). Since the initial development of Ninigret oyster farms, farmers have noted decreasing growth rates and increasing mortality leading to speculation that the carrying capacity of the coastal pond had been exceeded. A coalition of Ninigret farmers worked with local scientists to develop a study of the dynamics of the pond to explain why their oyster production seemed to be decreasing. The objectives were: 1) Monitor seasonal variation in food levels along a transect through the existing farms in Ninigret Pond; 2) Measure oyster survival and growth at various stocking densities within the six participating farms; and 3) Evaluate the condition of oysters growing at the various stocking densities.

The growers evaluated the effect of varying bag stocking densities on oyster growth and mortality while the research team monitored flow patterns and food supply in the vicinity of the farms on three separate occasions, representing three seasonal conditions.

The results suggested that while food resources in the pond were consistently adequate, a localized effect of growth depression was noted in bags as the stocking density increased. Growth depression with increasing stocking density was likely the result of a low rate of food flux through the bags, due to a low flow of water moving through the farms. Farmers must adjust their stocking density or modify their growing methods to allow increased flow and food flux through the culture system.

LUNG VOLUME IN THE APPLE SNAIL, *POMACEA MACULATA*

Andrea Lee and Lewis E. Deaton*

University of Louisiana at Lafayette, Biology Department, Lafayette, Louisiana 70504 USA

led9784@louisiana.edu

The invasive apple snail, *P. maculata*, is a freshwater gastropod that possesses both a functional gill and an air sac formed from mantle tissue that is used to breathe air. Rates of oxygen uptake in this species in air are higher than they are in water. The air sac can be inflated when the snails are in water and used as a flotation device. Floating snails of various sizes were weighed immersed in water and then induced to empty the air sac and re-weighed. The difference in the two measures provides an estimate of the volume of the air sac. The lung volume is about 0.2 mL/g live weight (including the shell).

HIGH MORTALITY, RETARDED REPRODUCTION, AND POOR GROWTH OF THE MANILA CLAM, *RUDITAPES PHILIPPINARUM*, CAUSED BY HIGH LEVELS OF THE PARAMYXEAN PARASITE, *MARTEILIA GRANULA,* INFECTION OBSERVED ON THE SOUTH COAST OF KOREA

Hye-Mi Lee[1*], Hyun-Sil Kang[2], Young-Ghan Cho[1], Hyun-Ki Hong[1], Hee-Jung Lee[2], and Kwang-Sik Choi[1]

[1]Jeju National University, School of Marine Biomedical Science (BK21 PLUS), 102 Jejudaehakno, Jeju 690-756, Republic of Korea

[2]Tidal Flat Research Institute, National Institute of Fisheries Science (NIFS), Kunsan 54014, Republic of Korea

hmlee@jejunu.ac.kr

Manila clam landings in Korea have been declined for the past decades, while increase in parasitic diseases may responsible for the decline. In this study, Manila clams were transplanted to an intertidal beach and subtidal cage to enhance the growth. Shell and tissue growth, reproduction and types of parasite were monitored monthly from October 2015 to May 2016. The SL of clams in the intertidal and subtidal cage increased from 23.1 mm to 25.9 mm and 26.6 mm over 8 months, respectively. From October to February, clam tissue weight increased markedly from 0.46 g to 1.51 g in the suspended cage, while the tissue weight increase was substantially lower (0.46 to 0.90 g) in the intertidal. *Marteilia*-like organisms were first observed in January from clams in the suspended cage (62.1 %) and the intertidal (16.7 %). PCR assay using *Marteilia* species-specific markers confirmed that the pathogen was *M. granula*. In histology, *M. granula* was focalized in the digestive gland causing digestive tubule tissue necrosis. Prevalence of *M. granula* in clams in the suspended cage increased dramatically from January to February (100 %) and remained 100 % until May. Mortality of clams in the suspended cage increased dramatically from March (3.3 %) to April (39.1 %) and May (67.4 %), which was coincided with the rapid increase of *M. granula* infection. Histology also indicated that the gonad development of clams in the suspended cage as well as in intertidal was retarded, possibly due to the heavy infection with *M. granula*.

SURVEYING BENTHIC INVERTEBRATE COMMUNITIES ASSOCIATED WITH OYSTER AQUACULTURE SITES IN MAINE

Sara M. Lindsay, Hanna Deon, Samantha Holmes, Emily Miller, Samantha Silverbrand, and Paul D. Rawson*

University of Maine, School of Marine Sciences, Orono, Maine 04469 USA

prawson@maine.edu

Compared to finfish aquaculture, shellfish aquaculture is predicted to have less impact on benthic communities because organic enrichment and biodeposition rates are typically lower, but impacts are likely to vary with species cultured, site characteristics, and farming methods. Oyster aquaculture is a growing industry in Maine and little is known about its impacts on the benthos. Benthic biodiversity was surveyed under and adjacent to suspended oyster cages at three farms on different rivers in Maine during 2015 and 2016. Sediment samples were collected using ponar grabs, sieved (0.5 mm mesh) and all retained material preserved for later identification. Approximately 6000 individual invertebrates were sorted and identified to the lowest taxonomic level possible (i.e., species, genus or family). Annelids and molluscs were the most abundant fauna at all three farms. Taxonomic similarity (percentage similarity) of fauna collected under and adjacent to oyster cages differed by farm, ranging from ~43% to 79%. At two farms, Capitellid polychaetes and Oligochaetes were most abundant under cages (dominance index=0.3-0.4), while Veneriid bivalves, Nereidid and Spionid polychaetes were most abundant in samples taken adjacent to cages at the same farms (dominance index=0.2-0.4). The spionid *Streblospio benedicti* was the most abundant taxon at the third farm, regardless of sample location in the farm (dominance index ~0.8). Sediment organic content was slightly enriched under cages at only one site (12% vs. 10% organic carbon). The results of this study suggest that the oyster farms are having relatively minor impacts on the benthic community at these sites.

PHYSIOLOGICAL IMPACTS OF THE BIOMEDICAL BLEEDING PROCESS ON THE ATLANTIC HORSESHOE CRAB, *LIMULUS POLYPHEMUS*, IN SOUTH CAROLINA, USA

Kristin Linesch[1]*, Louis Burnett[2,3], Karen Burnett[2,3], Rachel Kalisperis[4], and Amy Fowler[5]

[1]South Carolina Department of Natural Resources, Marine Resources Research Institute, 217 Fort Johnson Road, Charleston, South Carolina 29412 USA

[2]College of Charleston, Grice Marine Laboratory, 205 Fort Johnson Road, Charleston, South Carolina 29412 USA

[3]Hollings Marine Laboratory, 331 Fort Johnson Road, Charleston, South Carolina 29412 USA

[4]South Carolina Aquarium, 100 Aquarium Wharf, Charleston, South Carolina 29401 USA

[5]George Mason University, Potomac Environmental Research and Education Center, 650 Mason Ferry Ave., Woodbridge, Virginia 22191 USA

lineschk@dnr.sc.gov

Over 550,000 horseshoe crabs (HSC) are harvested annually by the biomedical industry in the United States to produce Limulus Amebocyte Lysate, a medical product used to detect endotoxins. The biomedical harvest is unique in South Carolina (SC) in that HSC can be kept in holding ponds for the duration of the spawning season (spanning 1 day to 8 weeks) before bleeding. In this study, current SC biomedical bleeding practices were simulated by holding female HSC in experimental ponds for up to eight weeks before bleeding. A subset of individuals (n=24) was removed from ponds biweekly, of which half were bled immediately and half remained unbled. Hemocyanin concentration ([Hc]) and total hemocyte counts (THC) were monitored 0, 2, 6, and 12 days after bleeding as indicators of physiological health during recovery. The amount of hemolymph biomedically extracted ranged from 3% to 51% (average 33%) of the total hemolymph volume of individual HSC. HSC held in ponds for more than four weeks had lower THC and [Hc] prior to treatment, and those that were bled were not able to return to baseline values as quickly as controls. Total mortality in the ponds was 5% prior to bleeding, but after removal from ponds overall mortality was 11% for bled and control HSC up to 12 days after being removed from the ponds and subjected to bleeding. Results from this study provide important information on harvest impacts in SC and could contribute to best management practices along the east coast of the United States.

FOOD WEB OF THE EASTERN OYSTER AND BLUE CRAB: SCAVENGERS, FACILITATION, COMPETITION, AND KLEPTOPARASITISM

Romuald N. Lipcius[1]* and Emily Chei[1,2]

[1]Virginia Institute of Marine Science, College of William and Mary, PO Box 1346, Gloucester Point, Virginia 23062 USA

[2]Present address: Cornell University, Ithaca, New York, USA

rom@vims.edu

Eastern oyster predation is well understood, but little is known about oyster scavenging. It is assumed that oyster carrion is decomposed or consumed by smaller organisms. Pathways of carrion were examined by attaching dead oysters to an artificial oyster reef on the York River, Chesapeake Bay. The effect of treatment (gaping and crushed oysters) and shell height (25 mm to 100 mm shell height) on scavenger behavior was tested. Underwater video was used to identify species and record exact times to encounter, feeding, and total trial duration. The most common scavengers were mud crabs, the striped blenny (*Hypsoblennius hentz*), the naked goby (*Gobiosoma bosc*), and mature blue crabs (*Callinectes sapidus*). On average, gaping oysters took three times longer to be consumed than crushed oysters, but all trials were fully scavenged within a few hours. Blue crabs acted as a facilitator by prying open gaping oysters and allowing smaller scavengers to enter and feed, but they acted as competitors to smaller scavengers for crushed oysters. Gobies opportunistically kleptoparasitized oysters that were opened by blue crabs. Short scavenging times suggests that most oyster carrion moves to higher trophic levels rather than being decomposed, and food web pathways are influenced by the blue crab.

COMPARTMENTALIZATION OF HEMOCYTE FUNCTIONS IN CONGENERS OF TWO OYSTERS

Naoko Little-Jackson[1], Dametria Faltz[1], and Anna V. Ivanina[2]*

[1]Johnson C. Smith University, 100 Beatties Ford Rd, Charlotte, North Carolina 28216 USA

[2]University of North Carolina at Charlotte, 9201 University City Blvd, Charlotte, North Carolina 28223 USA

aivanina@uncc.edu

Oyster hemocytes (HC) play an important role in immune homeostasis while representing a diverse set of cell types that are morphologically and functionally heterogeneous. Two congeners of oysters, *Crassostrea gigas* and *Crassostrea virginica,* differ in their disease resistance. Although closely related, *C. gigas* can withstand a wide variety of diseases compared with the more disease-susceptible *C. virginica*, however, the physiological basis of this disparity to biotic stressors remains unknown. Four different fractions of HC were isolated on a density gradient and mRNA transcripts of pattern recognition molecules and stress response elements were compared between HC fractions of both species. In *C. virginica* pattern recognition genes (TLR3, TLR4 and Mannose Rec2) were expressed in all HC subpopulations. In *C. gigas* expression of TLR3 was similar in all HC fractions, whereas TLR4 and Mannose Rec2 were overexpressed in the H1 fraction. Among all HC, only the H2 and H1 fractions in *C. virginica* and *C. gigas,* respectively, played role in recognizing tissue damage (based on expression of scavenger receptor cysteine rich). Expression of humoral and inflammatory genes were higher in the H1 fraction of *C. gigas*, and had similar expression patterns in all HC fractions of *C. virginica*. These results indicate considerable functional specialization (revealed by the gene expression patterns) between different subpopulations of HC in both species, which may contribute to differences in biotic stress resistance.

MITIGATION STRATEGIES FOR *VIBRIO PARAHAEMOLYTICUS* IN OYSTER SHELLSTOCK INTENDED FOR RAW CONSUMPTION

Chengchu Liu[1]* and Angela DePaola[2]

[1]University of Maryland Extension, 11868 College Backbone Rd, Princess Anne, Maryland 21853 USA

[2]Angelo DePaola Consulting, 12719 Dauphin Island Parkway, Coden, Alabama 36523 USA

cathyliu@umd.edu

Bivalve molluscan shellfish such as oysters, mussels, and clams, are filter-feeders and can concentrate microbial contaminants from growing waters through filtering large volumes of seawater. The marine bacteria, *Vibrio parahaemolyticus,* naturally inhabit coastal waters and shellfish and are most abundant during summer. It has been a leading cause of human acute gastroenteritis associated with consumption of raw oysters in the United States and throughout the world. The Centers for Disease Control and Prevention (CDC) estimates that 45,000 cases of *V. parahaemolyticus* infection occur each year in the U.S. Several post-harvest processes, such as low-temperature pasteurization, flash-freezing followed by frozen storage, and high pressure processing, have been developed for inactivating *V. parahaemolyticus* in raw oysters; however, these treatments require either significant amounts of initial investment or operation costs and oysters are generally killed during processing. This presentation will provide an overview and discuss potential application of controlled wet-storage and other post-harvest practices for purging *V. parahaemolyticus* from oysters.

THE FUTURE OF THE PROVASOLI-GUILLARD NATIONAL CENTER FOR MARINE ALGAE AND MICROBIOTA

Michael W. Lomas*, Julie Sexton, Mike Preston, Mark Hurd, Joan Blanchette, and Rimar Reed

Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, Maine 04544 USA

mlomas@bigelow.org

The global economy is actively undergoing a green revolution, not just one based on biofuels and bioenergy, but one also based on bioproducts and sustainable food chains. Algae are at the heart of this multi-billion dollar industry sector that provides secure food resources as well as a broad source of nutritional and pharmaceutical supplements. The National Center for Marine Algae and Microbiota (NCMA), originally founded as the Culture Collection of Marine Phytoplankton by Bob Guillard and Luigi Provasoli, has been and continues to be a living library supporting this dizzying array of applied and basic research. For example, in the past six months we have distributed nearly 1000 strains of algae to researchers and companies in 26 countries around the world.

This talk will present a new initiative spearheaded by the NCMA called the Maine Algal Research and Innovation Accelerator (MARIA). The MARIA mission is to connect researchers and entrepreneurs, accelerate innovation and the translation of knowledge, and foster growth of a sustainable, ecologically sound and profitable algal value pyramid in Maine, the U.S. and internationally. This initiative leverages the NCMA collection and extensive algal growth expertise, the range of algae cultivation services offered by the NCMA, and a state-of-the-art research greenhouse designed to support pilot-scale (versus bench scale) research and development activities for both micro- and macroalgae. The overarching goal of MARIA is to help provide a stabilization mechanism for the future success and growth of NCMA in the face of a rapidly changing and uncertain financial climate.

GROWTH RATE MEASUREMENTS IN SCALLOPS: REVISITING MERRILL AFTER 50 YEARS ON THE LIBRARY SHELF

Matthew C. Long[1*], Roger Mann[1], David Rudders[1], Sally Roman[1], Toni Chute[2], Kelly Cronin[3], and Sally Walker[3]

[1]Virginia Institute of Marine Sciences, The College of William and Mary, Rt. 1208 Greate Road, Gloucester Point, Virginia 23062 USA

[2]Northeast Fisheries Science Center, Woods Hole, Massachusetts, 02453 USA

[3]Department of Geology, University of Georgia, Athens, Georgia, 30602 USA

mclong@vims.edu

Scallops are of both economic and ecological interest. In an effort to develop methods describing scallop growth as accurately and efficiently as possible from shell samples, a comparison was made between growth rate estimators (von Bertalanffy k and L_{inf} values) generated using two different methods of measuring annual growth. The first method, which did not require ageing, used the distances between annual signatures on the external surface of the shell (a Ford-Walford approach). The second method relied on age estimates from hinge resilia to produce length-at-age points to which a curve was fit. The latter approach was described over 50 years ago by Merrill (Merrill et al. 1966. Fish Bull. 65:299–311), but has enjoyed little use since that time. Estimates based on external shell signatures are limited to larger shells with multiple annual signatures, potentially compromised where erosion or infestation of the shell surface is significant. While a more comprehensive comparison between the two methods is recommended, results to date suggest a general utility for the resilium approach. Examples are provided for both *P. magellanicus* from the mid-Atlantic and the Antarctic scallop *Adamussium colbecki*, a species living in the coldest waters on Earth.

THE SWINOMISH SHELLFISH PROGRAM: MANAGEMENT, RESEARCH, AND RESTORATION EFFORTS

Lorraine Loomis, Julie S. Barber*, Courtney M. Greiner, and Sarah K. Grossman

Swinomish Indian Tribal Community, Fisheries Department, 11426 Moorage Way, La Conner, Washington 98257 USA

jbarber@swinomish.nsn.us

The Swinomish Indian Tribal Community (SITC) Fisheries Department focuses much of its work on finfish and shellfish resources. The Shellfish Program provides the Tribe with research, restoration, and technical assistance to achieve optimal benefits for its member fishers. Currently, the program supports numerous projects including: shellfisheries management, bait clam fishery administration, subtidal and intertidal shellfish surveys, native clam population variability research, intertidal ecological research, clam garden development, Olympia oyster restoration and research, aquaculture ventures, and dive safety. Within the Shellfish Program, SITC also supports the Swinomish Fisheries Climate Change Program (SFCCP), which works to (1) assess climate change risks and vulnerabilities for shellfisheries and (2) execute research efforts to fill knowledge gaps. The SFCCP is also in the process of developing an adaptation strategy for the Tribe and will work with tribal members to promote dynamic adaptive management practices. This talk will include examples of ongoing and upcoming research projects including the development of a clam garden site selection model, evaluating juvenile Dungeness habitat limitations, and decadal change in intertidal ecology.

POPULATION GENOMICS OF *PANOPEA GLOBOSA* BASED ON ANALYSIS OF SINGLE NUCLEOTIDE POLYMORPHISM OBTAINED BY DDRAD

Víctor López[1]*, Adrian Munguía[2], and Pedro Cruz[1]

[1]Centro de Investigaciones Biologicas del Noroeste, S.C., Av. Instituto Politécnico Nacional 195, La Paz, B.C.S., México, 23096

[2]University of Arizona, Conservation Genetics Laboratory, School of Natural Resources and the Environment, Tucson, Arizona 85721 USA

jvlopez@pg.cibnor.mx

The geoduck, *Panopea globosa*, is one of the most important fishing resources in Northwestern Mexico, generating over 74M dollars annually. This species shows a wide distribution and remote fishing sites complicate its management. As such, identifying alternatives for the proper management is of great importance. Currently, single nucleotide polymorphisms (SNPs or 'snips') are the molecular markers with the greatest potential for genomic population analyzes. A total of 139,214 SNPs and 84,314 loci were obtained from a pilot library of 33 geoduck clams from 3 locations (Upper Gulf of California: San Felipe and Puerto Peñasco; Pacific Ocean: Bahia Magdalena) with three libraries of 8'949,334 paired readings (2x150bp). A deficit of heterozygotes was observed in all three populations. Higher allelic richness was observed in populations of the Upper Gulf of California. These two populations showed higher values of observed (Ho) and expected heterozygosity (He), inbreeding coefficients (Fis), and private alleles. The paired analysis of Fst indicated significant differences between all populations. Greater genetic differences were detected between Puerto Peñasco and Bahía Magdalena, while San Felipe and Bahía Magdalena had the lowest differentiation. Molecular variance analysis (P = 0.0001) showed that most of the observed variation in allele frequencies was within populations (96%), followed by variation among populations (4%). Thirty-five outlier loci were detected and compared with the GenBank databases using BLAST. No significant similarity was found with any sequence reported at the time. Based on the analysis of allele frequencies, a SET for molecular traceability of Panopea globosa is being developed.

COLD CHAINS FOR FARMED OYSTERS PRODUCED IN THE CHESAPEAKE BAY AND MODELED *VIBRIO PARAHAEMOLYTICUS* GROWTH

David C. Love[1,2], Robert M. Lane[3], Kate Clancy[1], Benjamin J.K. Davis[4], Jillian P. Fry[1,2,5], Jamie Harding[1], and Bobbi Hudson[6*]

[1]Johns Hopkins Center for a Livable Future, Johns Hopkins University, Baltimore, Maryland, USA

[2]Johns Hopkins University, Department of Environmental Health and Engineering, Bloomberg School of Public Health, Baltimore, Maryland, USA

[3]Virginia Tech, Virginia Seafood Agriculture Research and Extension Center, Hampton, Virginia, USA

[4]Johns Hopkins University, Department of Epidemiology, Bloomberg School of Public health, Baltimore, Maryland, USA

[5]Johns Hopkins University, Department of Health, Behavior and Society, Bloomberg School of Public Health, 624 N. Broadway, Baltimore, Maryland, USA

[6]Pacific Shellfish Institute, Olympia, Washington, USA

bobbi@pacshell.org

Temperature controlled supply chains (cold chains) require an unbroken chain of refrigeration to maintain product quality and safety. This study assessed the performance of cold chains for farmed oysters produced in the Chesapeake Bay and sold live to the half-shell market in surrounding states. A total of 156 temperature sensors were added to oysters and oyster boxes on farms and removed once the products reached food retailer and restaurants. The study ran from February to September 2017 and generated 5,250 hours of temperature sensor data. Twenty-six interviews were performed with producers, freight carriers, wholesalers, food retailers and restaurants to further understand how cold chains function. Cold abuse was occasionally an issue for supply chains in cooler months. In summer months, 5 of 25 shipments had internal oyster temperatures above 50 °F for over 1 hr. The highest internal oyster temperature recorded in any shipment was 54.5 °F. We modeled the effects of temperature fluctuations on *Vibrio parahaemolyticus* and

found moderate bacterial growth before oysters were under temperature control, but cold chains prevented further growth and allowed for a moderate drop-off in abundance. The highest estimated risk of Vibriosis was 0.06 cases per 100,000 servings. The findings improve understanding of cold chain performance for shellfish, V. *parahaemolyticus* growth in supply chains, and can aid in industry and regulatory policy development.

OYSTERS SHOW ENHANCED GROWTH IN EELGRASS: DOES DIET EXPLAIN THE DIFFERENCE?

Alexander T. Lowe[1]* and Micah Horwith[2]

[1]University of Washington, Department of Biology, 24 Kincaid Hall, Seattle, Washington 98195 USA

[2]Washington Department of Natural Resources, 1111 Washington St., Olympia, Washington 98504 USA

alowe70@uw.edu

Recent anthropogenic effects on coastal estuaries, including ocean acidification and productivity changes, have raised concerns over the future of seagrass and ecologically and economically important bivalves. The potential for phytoremediation of ocean acidification by seagrass has gained recent attention. Additionally, seagrass can alter sedimentation and food availability in ways that influence suspension-feeding bivalves. Because these influences are occurring simultaneously, studies are needed that evaluate the relative influence of these hypothesized mechanisms. Over two years, effects of eelgrass on two species of oysters were investigated through a coordinated field experiment that measured shell and soft tissue growth, stable isotope and fatty acid biomarkers of food availability, and sedimentation concomitant to monitoring of environmental conditions inside and outside of eelgrass beds. Hatchery-produced Olympia and Pacific oysters were deployed into eelgrass and unvegetated habitats at five sites in Washington state for periods ranging from 40 to 80 days in 2016 and 2017. Both Olympia and Pacific oysters repeatedly exhibited greater growth in eelgrass. Stable isotope and fatty acid biomarkers will be used to evaluate the relative influence of food availability on habitat-specific growth differences.

MONITORING EELGRASS RESPONSES TO AQUACULTURE ACTIVITIES AND DEVELOPMENT OF IMPROVED MONITORING TOOLS

Sarah Lummis[1*], Kristy Kroeker[1], Sarah Newkirk[2], Kirk Klausmeyer[2], Serena Lomonico[2], Robert Jones[3], John Finger[4], and Terry Sawyer[4]

[1]University California, Santa Cruz, Ecology and Evolutionary Biology Department, Institute of Marine Sciences, 100 Shaffer Rd, Santa Cruz, California 95064, USA

[2]The Nature Conservancy, California Oceans Program, 201 Mission Street, 4th Floor, San Francisco, California 94105, USA

[3]The Nature Conservancy, Global Marine Program, 4245 North Fairfax Drive Suite 100, Arlington, Virginia 22203, USA

[4]Hog Island Oyster Company, 20215 Shoreline Highway, Marshall, California 94940, USA

slummis@ucsc.edu

One factor limiting the growth in areas of potential shellfish aquaculture cultivation is a lack of understanding regarding the impacts of aquaculture operations on ecosystems. Eelgrass, protected at both the state and federal level as essential fish habitat, is found in many estuaries where aquaculture activities occur. These systems are of particular concern due to their role as a habitat forming species and nursery for a wide array of fish and invertebrates; however, it is challenging to monitoring eelgrass systems, particularly at a landscape scale, which increases the difficulty of understanding the affects of aquaculture activities on their overall extent and health. UC Santa Cruz, The Nature Conservancy, and Hog Island Oyster Company are developing new tools to monitor eelgrass-aquaculture interactions and better understand the extent of aquaculture impacts on eelgrass ecosystems. The project includes two core objectives: 1) develop an accessible UAV-based methodology to monitor eelgrass-aquaculture interactions; 2) experimentally test impacts of oyster aquaculture on adjacent eelgrass communities and the local environment following a Before-After-Control-Impact (BACI) design in Tomales Bay California. Although this study is ongoing, presented here are initial results and developed monitoring methods. To ensure applicability and dissemination of results, the project is advised by staff from NOAA Fisheries West Coast Region and the California Department of Fish and Wildlife. Ultimately, this collaboration will contribute to both an improved process-based understanding and novel monitoring tools.

BAY SCALLOP LARVAL SWIMMING BEHAVIOR IN RESPONSE TO TEMPERATURE, SALINITY, AND LIGHT

Samantha G. Lynch[1*]and Joseph Caracappa[2]

[1]Rutgers, The State University of New Jersey, 14 College Farm Road, New Brunswick, New Jersey 08901 USA

[2]Rutgers University, Haskin Shellfish Research Laboratory, 7959 Miller Ave, Port Norris, New Jersey 08349 USA

s.gilbert@rutgers.edu

Bay scallops (*Argopecten irradians*) are a relatively short-lived bivalve species historically found along the North American eastern seaboard. A mesocosm study was conducted to better understand how the swimming behavior of bay scallop larvae is influenced by environmental conditions. The swimming behavior of bay scallop larvae was observed in response to light, temperature, and salinity. Late-stage scallop veliger larvae (10 days old) were exposed to three temperature conditions: cold (15°C), temperate (23°C), and hot (30°C). To evaluate the effect of salinity on swimming behavior, temperature was held constant at 23°C and veligers were exposed to either varying salinities (20, 25, and 30). The effect of light on bay scallop swimming response was evalu-

ated under temperate conditions (23°C, salinity of 30) by exposing larvae to either white or red light. High definition video cameras with macro-lenses were used to record the swimming behaviors of individual larvae. These videos were digitized, and the swimming trajectories of individual larvae were mapped. Behavioral metrics quantified in this study include net vertical velocity, helical trajectories, and sinking rates. These data will be used to identify patterns in swimming responses under environmentally relevant conditions. Characterizing the swimming behavior of bay scallop veliger larvae is a fundamental step to inform future larval dispersal models, and ultimately to better understand population connectivity.

A LIFE IN FLUX: EFFECTS OF FLUCTUATING TEMPERATURES, AIR EXPOSURE, SALINITY, SUSPENDENDED PARTICULATE MATTER (SPM), AND TURBIDITY ON OSTREID HERPES VIRUS-1 MICROVAR EXPOSED *CRASSOSTREA GIGAS* (VIVALDI PROJECT)

Sharon A. Lynch*, Erin Molloy, Ciara Mcdonald, Kathryn Cox, and Sarah C. Culloty

University College Cork, School of Biological, Earth and Environmental Sciences, Aquaculture and Fisheries Development Centre and Environmental Research Institute, Ireland

s.lynch@ucc.ie

The Pacific oyster (*Crassostrea gigas*) is commonly cultured in the intertidal zone and is tolerant of a range of environmental conditions, which makes this species an ideal candidate for culture; however, daily fluctuating temperatures, salinity, suspended particulate matter (SPM) and turbidity imposed by tidal exchange, in particular in spring and autumn months when sudden and dramatic increases or decreases in air temperature and precipitation events can occur, may catch the *C. gigas* "off-guard" thus making them more susceptible to pathogens and disease. The objectives of this study were to investigate the effects of fluctuating temperature, air exposure, reduced salinity, suspended particulate matter (SPM), and turbidity on oyster performance, immune response and ostreid herpesvirus-1 microVar (OsHV-1 μVar) development in *C. gigas*. Laboratory trials to simulate potential conditions at Irish culture sites were carried out. In one trial, two extreme temperature treatments were conducted over three days to simulate the effects of a sudden heat wave (30°C air temperature) in late spring and a polar snap (0°C air temperature) in late autumn, while the seawater temperature would be at 15°C. In a second simulation, a sudden heavy precipitation event with land run off from the surrounding catchment area, with different turbidity levels ("low", "medium" and "high"), was carried out. Results indicate that *C. gigas* do respond at an individual and cellular level to sudden short-term fluctuations, with some conditions having a greater impact on *C. gigas* and its recovery and on viral development, more than others.

UNDER THE RADAR: EMERGING *HAPLOSPORIDIA* SPP. IN WILD COMMON COCKLE, *CERASTODERMA EDULE,* AND MUSSELS, *MYTILUS* SPP., AT PACIFIC OYSTER, *CRASSOSTREA GIGAS,* CULTURE SITES

Sharon A. Lynch*, Sara Lepée Rivero, Richard Kelly, Emma Quinn, Aoife Coughlan, and Sarah C. Culloty

University College Cork, School of Biological, Earth and Environmental Sciences, Aquaculture & Fisheries Development Centre and Environmental Research Institute, Ireland

s.lynch@ucc.ie

The frequency of emerging infectious diseases (EIDs) in marine ecosystems is increasing due to increasing rates of environmental change, caused by changing climates and anthropogenic activities. Such phenomena may provoke previously non-problematic marine parasites to emerge, which may appear for the first time or existed previously but have extended their geographical and host range. *Haplosporidia* single cell parasites are a major concern for aquatic animal health, in particular in bivalve molluscs, as they have been responsible for some of the most significant marine epizootics on record. In this study, the common cockle *Cerastoderma edule* (*C. edule*), mussels *Mytilus* spp. and the Pacific oyster *Crassostrea gigas* (*C. gigas*) from three Irish locations (*C. gigas* culture and non-culture sites) were screened for *Haplosporidia* spp. by polymerase chain reaction (PCR) using multiple molecular markers. The DNA of three emerging *Haplosporidia* spp. was detected, isolated and confirmed by Direct Sanger sequencing in surfaced *C. edule* while a single species was detected in the blue mussel *Mytilus edulis*. Of interest, the *Haplosporidia* spp. were not detected in the cohabiting *C. gigas* on oyster trestles. This finding may indicate that the *Haplosporidia* spp. are host specific and 'host partitioning' was occurring. The effects of these *Haplosporidia* spp. on the *C. edule* and *Mytilus* spp. populations is currently unknown. The findings of this study highlight the diversity of emerging *Haplosporidia* spp. that may be present in coastal marine environments but remain undetected, even in well-studied commercial shellfish species such as cockles and mussels.

BACTERIOPHAGES SIGNIFICANTLY REDUCE LARVAL OYSTER MORTALITY CAUSED BY *VIBRIO CORALLIILYTICUS*

David Madison[1]*, Chris Langdon[1], Claudia Hase[1], Gary Richards[2], Michael Watson[2], Nitzan Soffer[3], Manrong Li[3], and Alexander Sulakvelidze[3]

[1]Oregon State University, Hatfield Marine Science Center, 2030 SE Marine Science Dr., Newport Oregon 97365 USA

[2]Oregon State University, College of Veterinary Medicine, 700 SW 30th Street Corvallis, Oregon 97331 USA

[3]USDA Agricultural Research Service, USDA, ARS James Baker Center, Rooms 28-31 Dover, Deleware 19901 USA

[4]Intralytix, Inc., The Columbus Center, 701 E. Pratt Street, Baltimore, Maryland 21202 USA

david.madison@oregonstate.edu

The pathogenic bacterium, *Vibrio coralliilyticus* (Vcor), has plagued Pacific North West (PNW) shellfish hatcheries, causing unpredictable and severe mortalities of larval Pacific oysters *Crassostrea gigas*. Outbreaks can dramatically reduce seed availability for farmers. Bacteriophages (phages) are being studied as an environmentally friendly means of increasing larval survival by controlling Vcor populations. Phages are viruses that selectively attack and destroy bacteria. They are believed to be the main regulators of bacterial populations in nature. Phages are very specific and each phage will only attack and lyse specific strains of a single bacterial species or a small number of very closely related species. The USDA ARS has isolated several phages that attack either Vcor RE98 or Vcor RE22 - two strains of Vcor that are known larval pathogens in PNW hatcheries.

Experiments carried out by Oregon State University have shown that approximately 99% of Pacific oyster larvae die within 48 hours of exposure to a concentration of 10^4 Vcor RE98 cells per mL; however, addition of a cocktail of RE98-specific phages at a concentration of 10^7 plaque-forming units (PFU) per ml eliminated mortality of 2-day old larvae exposed to those same Vcor conditions and even increased the number of larvae that metamorphosed and settled compared to the larvae only controls. These results indicate that phages have the potential to be used as a powerful tool for reducing larval oyster mortality due to Vcor infections.

AN INTERTIDAL HOST-PARASITE SYSTEM: PREDICTING SOME OF THE EFFECTS OF CLIMATE CHANGE

Luísa Magalhães[1,2]*, Xavier de Montaudouin[2], Etelvina Figueira[1], and Rosa Freitas[1]

[1]Departamento de Biologia & CESAM, Universidade de Aveiro, 3810-193 Aveiro, Portugal

[2]Université de Bordeaux, EPOC, UMR 5805 CNRS, 2, rue du Pr Jolyet, F-33120 Arcachon, France

luisa.magalhaes@ua.pt

Seawater temperature rise and increased input of freshwater into the oceans, resulting from atmospheric carbon dioxide build-up, are among the most important climate change related factors affecting costal marine ecosystems. These changes are likely to impact many biotic interactions, including host–parasite interactions which are particularly dependent on temperature conditions.

For the Ria de Aveiro coastal lagoon (Portugal), by the end of the century, projections describe an increase of water temperature by 2°C and a decrease of precipitation and average water discharges. In this way, in the present study we tested the hypothesis that *Cerastoderma edule* exposure to different pH, salinity and temperature levels, as proxy for climate change, modified the infection success of the trematode parasite *Himasthla elongata*. Accordingly, a series of laboratory experiments were conducted by exposing cockles to *H. elongata* cercariae, in distinct experimental conditions, differing in terms of seawater pH, salinity and temperature, during 96 h. At experiment completion, success of infection and biochemical responses of cockles were analysed.

The results showed that 1) the cercariae infection success increased with water acidification and higher temperature, while different salinities showed no influence and 2) cockles biochemical responses differed when each stressor (parasitism or climate change variables) was acting alone in comparison to the combination of parasitism with each of the three variables tested. The present findings emphasize the increased impact of parasites on cockle populations in a global warming scenario.

PREDICTING ADAPTIVE RESPONSES TO OCEAN CHANGE: IMPLICATIONS FOR AQUACULTURE

Donal T. Manahan

University of Southern California, Department of Biological Sciences, Los Angeles, California 90089-0371 USA

manahan@usc.edu

In this presentation, approaches to improve predictions of adaptive responses and resiliency limits to ocean change will be discussed in the context of marine aquaculture. Predicting how marine organisms may respond to rapid anthropogenic change is a major challenge in environmental science. Given the near-infinite combinatorial possibilities and interactions of biotic and abiotic processes, it remains difficult to design biological experiments to predict adaptive responses and potential resiliency to environmental change. Bioenergetic modeling, based on analyses of biochemical strategies that maintain homeostatic stability, provides a useful framework for assessing the capacity of organisms to respond to compounding stressors. Since genetic variance in response to environmental change is clearly evident, any predictive analysis requires a merging of experimental approaches from environmental science, genetics, and physiology. Specifically, this integrative approach requires an understanding of the capacity for trade-offs in allocation of cellular energy to support specific homeostatic responses, the mechanisms underlying metabolic limits of biologi-

cal resilience, and the identification of "tipping point" biomarkers. Such analyses offer new insights to assess the ability of organisms to cope with environmental stress under defined (laboratory) and unknown (field) conditions. Identifying the biological bases of superior fitness has obvious practical implications for future breeding programs in aquaculture to improve stress resistance and yield.

THE CASE OF THE "MISSING" ARCTIC BIVALVES AND THE WALRUS, THE BIGGEST [IGNORED] CLAM FISHERY ON THE PLANET

Roger Mann[1*], Eric N. Powell[2], and Daphne M. Munroe[3]

[1]Virginia Institute of Marine Science, The College of William and Mary, P.O. Box 1346, Gloucester Point, Virginia 23062 USA

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

[3]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Ave., Port Norris, New Jersey 08349 USA

rmann@vims.edu

Although the Arctic marine ecosystem is recognized as rich in benthos, quantitative records of the biomass of long-lived, large, sedentary infaunal bivalves on the Arctic shelf are rare. Bivalves are pivotal to both benthic-pelagic coupling and carbonate cycling. The latter is of particular relevance in a period of seasonal ice retreat, fresh water release into associated surface waters, decreasing water pH, and possible undersaturation of Arctic waters with aragonite. Employing population estimates and predation rates for the Atlantic walrus (*Odobenus rosmarus rosmarus*), annual consumption of bivalves in the region of active foraging is conservatively estimated at 2 x 10^6 tonnes. Predation loss to other apex predators such as bearded seals is discounted. This is a "fishery" that exceeds by nearly two orders of magnitude the collected annual harvests of clam species in US federal waters. Assuming values of clam natural mortality comparable to that of Atlantic surf clams and a P:B ratio of 0.1, the standing stock and "live" carbonate reservoir represented on the Arctic shelf is estimated at 2 x 10^7 tonnes. This substantial biomass is subject to significant underestimation using common benthic biomass sampling tools and protocols. Accurate estimates of the biomass and thereby, the carbonate budget, of large Arctic shelf clam species is critical to understanding the stability of associated shelf communities with warming of these high latitude systems and their associated tendency towards aragonite undersaturation.

OYSTER SHELL BUDGETS IN THE CHESAPEAKE BAY: A SUMMARY FROM LONG-TERM SURVEY DATA

Roger Mann[1*], Melissa Southworth[1], James E. Wesson[2], Mitch Tarnowski[3], and John Thomas[1]

[1]Virginia Institute of Marine Sciences, The College of William and Mary, P.O. Box 1346, Gloucester Point, Virginia 23062 USA

[2]Virginia Marine Resources Commission, Newport News, Virginia 23607 USA

[3]Maryland Department of Natural Resources, 580 Taylor Avenue, Annapolis, Maryland 21401 USA

rmann@vims.edu

Sustainable oyster management plans must be sensitive to the dynamics of both live oysters and the underlying shell that forms reef habitat. The dynamics over time of oyster and shell differ in that shell degradation continues in the absence of live oysters. Local variations in recruitment, growth and mortality rates, and size and shape of oysters all contribute to estimation of shell addition to the benthos. Taphonomic and burial processes contribute to shell loss. A review of oyster survey data for both Maryland and Virginia from 2006-2016 presented the opportunity to estimate spatial and temporal variation in shell budgets at a riverine or regional level, and thereby assess which regions are self-maintaining and which require regular repletion to maintain oyster populations.

LACCASE-SILICA NANOPARTICLE CONJUGATES CAN EFFICIENTLY REDUCE THE EARLY MATURATION RISK DUE TO BISPHENOL A (BPA) IN FEMALE *OREOCHROMIS MOSSAMBICUS* AND ITS TOXIC LOAD FROM THE CONTAMINATED EFFLUENT

Abhijit Manna[1]* and Chinnaiah Amutha[2]

[1]Madurai Kamaraj University, Department of Animal Behaviour and Physiology, Madurai 625 021, India

[2]Madurai Kamaraj University, School of Biological Sciences, Madurai 625 021, India

environmentalgenomics.warren@gmail.com

Purified intracellular laccase from *Trametes versicolor* was conjugated with synthesized silica nanoparticles (200 nm). The data obtained from isothermal titration calorimetry (ITC) indicated that the exothermic nature of conjugation was stable due to moderate positive and negative values of entropy and enthalpy, respectively. The in-silico approach (molecular docking) revealed that BPA can be attached to the laccase enzyme at a specific binding pocket, along with similar types of moderate thermodynamic parameters obtained from ITC. Histopathology and ESI-MS analysis clearly indicate that early maturation of the fingerling (*Oreochromis mossambicus*) ovary, along with the necrosis of hepatocytes and the BPA deposition in the liver can be significantly reduced by the immobilization of laccase on silica nanoparticles, compared to free laccase. A significant reduction of vitellogenin protein expression levels (an ovary maturation factor) in fingerling stages, due to immobilized laccase was determined using FPLC and ELISA. The

decreasing vitellogenin gene expression level was also determined using q-PCR, which was correlated with the significant reduction of early maturation in the ovaries (fingerling stage) using laccase–nanoparticle conjugates. ESI-MS and fluorescence quenching assays using rhodamine-B were used to ascertain the effective reduction of BPA concentration from the industrial effluent.

CONSERVATION PALEOBIOLOGY AS A TOOL TO SUPPORT OLYMPIA OYSTER RESTORATION

Julieta C. Martinelli[1,2]* and Jaqueline L. Padilla-Gamiño[1]

[1]University of Washington, School of Aquatic Fishery Sciences, Seattle, Washington 98105 USA

[2]Centro de Estudios Avanzados en Zonas Aridas, CEAZA, Coquimbo, Chile

julimar@uw.edu

Historical baselines are fundamental to inform and monitor restoration efforts, and to interpret long-term changes in marine ecosystems; however, the validity and reliability of historical baselines can be compromised if the ecosystem has already been degraded and/or modified by anthropogenic activities. In Washington State, restoration of native oysters is limited by shifting baselines and the lack of information of Olympia oyster populations before they collapsed in the late 1800s due to over-exploitation. Conservation Paleobiology is an emerging multidisciplinary field that aims to use recent fossil and archeological records to develop historical baselines and support conservation and restoration strategies. This presentation will explain that data obtained from Quaternary assemblages can be used to increase our understanding on what healthy oyster beds looked like in the past. Preserved oyster beds can help us learn more about community-level processes such as biotic interactions and habitat provision to other organisms. Furthermore, important metrics for oyster restoration such as reef height, oyster density, and size frequency distributions can also be quantified from preserved oyster beds. At the individual level, oyster shells function as archives of water temperature, salinity, and pH at the time organisms were alive and depositing their shells. Better integration of historical ecological baselines and increased collaboration between paleobiologists, ecologists and managers will help to improve the planning, design and implementation of biological conservation and restoration efforts of Olympia oysters.

DETERMINING PRESENCE OF MICROPLASTICS IN SHELLFISH FROM PUGET SOUND, WASHINGTON, USA

Julieta C. Martinelli[1,2]* and Jaqueline L. Padilla-Gamiño[1]

[1]University of Washington, School of Aquatic Fishery Sciences, Seattle, Washington 98105 USA

[2]Centro de Estudios Avanzados en Zonas Aridas, CEAZA, Coquimbo, Chile

julimar@uw.edu

Marine plastic pollution is a serious threat to marine life with long term impacts to ecosystems and organisms. Marine environments around the world ranging from isolated islands to populated estuaries are exposed to plastic contaminants. Over time, some of these plastics break into smaller pieces, or microplastics (< 5 mm). These particles can float in the ocean, flow through rivers and accumulate in sand. Washington State is home to Puget Sound, the second largest estuary in the United States. Puget Sound supports populations of filter feeders such as oysters, which can easily capture and accumulate microplastics from the surrounding water. Previous studies have shown that microplastics are present in Puget Sound beaches, suggesting that shellfish may also be exposed to these contaminants. In this research, the abundance and type of microplastics in Pacific oysters *Crassostrea gigas* (n = 240) from 12 wild populations in Puget Sound was quantified. Bivalve tissue was digested with hydrogen peroxide, and the resulting solution was filtered with a 5µm membrane. The filter membrane was examined under a microscope to count and visually identify the microplastics retained. Microplastics were also analyzed with a Scanning Electron Microscope, and with a micro-Fourier transformed infrared spectroscope to detect microplastic composition and determine possible sources. The findings from this study will help to better understand the abundance and distribution of microplastics in ecological and commercial important species in Washington State and introduce mitigation strategies to ensure shellfish health for current and future generations.

DEVELOPMENT OF DIAGNOSTIC PCR ASSAY TO DETECT APICOMPLEXAN PARASITE IN ATLANTIC SEA SCALLOPS (*PLACEOPECTEN MAGELLANICUS*) WITH GRAY MEAT DISEASE

Ava A. Mastrostefano*, Abigail Scro, Kiserian Jackson, and Roxanna Smolowitz

Roger Williams University, Aquatic Diagnostic Laboratory, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

amastrostefano599@g.rwu.edu

In 2004, gray meat disease was found in Atlantic sea scallops (*Placopecten magellanicus*) in the Nantucket Lightship closed area, just south of Georges Bank. Previously seen in Nova Scotia and mid-Atlantic areas, the disease is characterized by weak, gray adductor muscles instead of the firm, white muscle found in healthy scallops. The adductor muscle is harvested and marketed as a high value, edible product. Adductor muscles with gray meat disease are of poor quality and cannot be sold, resulting in a biomass loss of nearly US$100 million ex–vessel in 2007 (Levesque et al., 2016). The cause of the disease is currently unknown, but previous research suggests that an apicomplexan parasite, found in Icelandic scallops (*Chlamys islandica*) exhibiting gray meat disease, has a major role in the disease seen in *P. magellanicus*.

Scallop adductor muscle samples were collected from areas just south of George's Bank from 2015 to 2017. These samples are be-

ing used to develop a successful diagnostic method to detect the apicomplexan parasite in *P. magellanicus.* Because the organism is not in culture, positive controls will be verified using histological examination. Homogenization methods were established to prepare the samples for DNA extraction. A PCR assay is being developed using previously published primers to detect the apicomplexan parasite. The PCR data will be cross referenced with histological examination from all collected animals to understand the relationship between the presence and abundance of the parasite in the adductor muscle samples and the grossly observable gray appearance of the muscle.

QUANTITATIVE METHODS FOR MEASURING MITOTIC, MEIOTIC, AND DIFFERENTIATION ACTIVITY WITHIN GAMETOGENESIS OF TRIPLOID *CRASSOSTREA VIRGINICA*

Joseph L. Matt* and Standish K. Allen, Jr.

Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center, 1375 Greate Road, Gloucester Point, Virginia 23062 USA

jlmatt@vims.edu

Triploidy reduces, but does not completely arrest, gametogenesis in many species of shellfish, including the commercially important oyster species *Crassostrea virginica*. Compared to the uniform nature of gametogenesis in diploids, gametogenesis in triploid *C. virginica* is abnormal and highly variable among individuals, both in the extent of follicle development and the production of gametes. Significant detail is therefore likely lost when stages of gametogenic development in triploids are classified using traditional criteria for diploid oysters, as has been done in early observations of triploid *C. gigas.* Even triploid-specific qualitative classifications likely have major limitations in detailing the true nature of triploid gametogenesis. To capture the full extent of the variation in gametogenesis of triploid *C. virginica*, methods for collecting quantitative data from histological cross sections were developed. The methods, which differed based on sex, separately quantified two aspects of gametogenic development suspected to be acting independently in triploid oysters: gonia proliferation, controlled by mitotic activity, and gamete production, a result of successful meiotic divisions and/or differentiation. Mitotic activity was measured in both sexes as the extent of gonia proliferation in relation to the incipient gonad area. In males, meiotic activity was determined in individual follicles as the proportion of successful meiotic divisions out of the total possible. Differentiation in females was determined as the proportion of gonia that developed into oocytes. The methods are expected to yield novel insight into triploid gametogenesis, including the expected indiscrete variation in development and lack of relationship between follicle coverage and gamete development.

OBSERVATIONS OF GAMETOGENESIS IN *CRASSOSTREA VIRGINICA* ASSOCIATED WITH TRIPLOID-SPECIFIC SPRING MORTALITIES ON COMMERCIAL FARMS IN THE CHESAPEAKE BAY

Joseph L. Matt*, Eric Guévélou, and Standish K. Allen, Jr.

Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center, 1375 Greate Road, Gloucester Point, Virginia 23062 USA

jlmatt@vims.edu

Unusual spikes in mortalities of cultured *Crassostrea virginica* in late spring have been reported from farms in the Chesapeake Bay over the last several years. None of the usual suspects (i.e. disease, poor husbandry) seem responsible, and empirical evidence suggests that triploids are more susceptible. Both the timing of the mortalities and recent observations of relatively high fecundity in some triploids grown on commercial farms have made gametogenic processes in triploids a suspect. To investigate the role of gametogenesis in spring mortality of triploids, various strains of triploids and diploid controls were deployed to previously affected commercial farms as well as to a control site with no history of spring mortality, and sampled regularly from February to August of 2016. Triploid and diploid samples were examined using histology from a site where triploid-specific spring mortality occurred, as well as from the control site where there was little mortality. Diploids at the affected site had accelerated gametogenic development compared to diploids at the control site, reaching spawning condition weeks earlier. Gametogenesis in triploids was abnormal and variable. No obvious difference was observed in gametogenesis between triploids regularly sampled at the two sites, however a higher percentage of female triploids with elevated fecundity were found in moribund triploids sampled during the mortality event (26%) compared to live triploids sampled at the same time (8%). Gametogenenic processes may be important in triploid spring mortalities, as unusual physiological manifestations may occur while triploids are in the process of producing a significant amount of eggs.

ART, SCIENCE, AND HUMOR: THE IMPORTANCE OF EFFECTIVE COMMUNICATION

Jason McDermott

Computational Biology and Bioinformatics Group, Pacific Northwest National Laboratory, Richland, Washington 99352 USA

Jason.McDermott@pnnl.gov

Scientific results are too often poorly communicated in the scientific literature and at conferences; however, it is essential that science is communicated in an effective and engaging way to the lay public as well as to other scientists. The addition of art and humor to science can be an effective method for communication of complex ideas. Through framing complex ideas as approachable metaphors a broader audience can be reached at a deeper level.

Dr. Jason McDermott is a computational biologist who also is the artist behind RedPen/BlackPen, a webcomic that addresses the triumphs and tribulations of scientific and academic life. He will

talk about his experience in merging more art and humor with his science and outline some methods for expanding the use of art and humor in your own work.

COMPARING PREDATION IMPACTS OF NATIVE AND INVASIVE CRABS USING A BIOENERGETICS APPROACH

P. Sean McDonald[1]*, Kirstin K. Holsman[2], and David A. Armstrong[3]

[1]University of Washington, Program on the Environment, BOX 355679, Seattle, Washington 98195 USA

[2]National Marine Fisheries Service, Alaska Fisheries Science Center, NOAA, 7600 Sand Point Way N.E., Building 4, Seattle, Washington 98115 USA

[3]University of Washington, School of Aquatic and Fishery Science, BOX 355020, Seattle, Washington 98195 USA

psean@uw.edu

Evaluating the potential impacts of invasive species is difficult without extensive empirical studies, thus researchers frequently make qualitative predictions based on impacts observed elsewhere. Such speculation has been rampant as invasive European green crab, *Carcinus maenas*, has spread northward along the Pacific coast of North America. In some areas green crabs have become abundant but impacts have not been fully addressed. The aim of the present work was to examine the potential predation impact of green crab relative to native crabs under observed conditions in Salish Sea estuaries using bioenergetics models. These models, which consider consumption, metabolic costs, and growth, were parameterized through a combination of existing data from published studies, laboratory feeding trials, and field studies. In particular, model estimates were compared for green crab, Dungeness crab (*Cancer* [*Metacarcinus*] *magister*), and graceful crab (*C.* [*M.*] *gracilis*). Model scenarios provide a range of relative prey consumption rates, which may be useful to managers when evaluating interventions. Results indicate that shifts in composition and abundance of crab predators in susceptible habitats may alter pressure on prey populations. Implications for Salish Sea pocket estuaries are discussed.

TEMPERATURE EFFECTS ON THE BIOENERGETICS OF DUNGENESS AND GRACEFUL CRABS, WITH IMPLICATIONS FOR MANAGEMENT

P. Sean McDonald[1]*, Kirstin K. Holsman[2], Grace Workman[3], and David A. Armstrong[3]

[1]University of Washington, Program on the Environment, BOX 355679, Seattle, Washington 98195 USA

[2]National Marine Fisheries Service, Alaska Fisheries Science Center, NOAA, 7600 Sand Point Way N.E., Building 4, Seattle, Washington 98115, USA

[3]University of Washington, School of Aquatic and Fishery Science, BOX 355020, Seattle, Washington 98195 USA

psean@uw.edu

Dungeness crabs (*Cancer* [*Metacarcinus*] *magister*) are culturally and economically important in Washington State. Yet there exists little information that could be used to assess potential climate effects on populations. For one thing increasing water temperatures associated with climate change might impact crab distribution. Dungeness crabs are most abundant in coastal waters and deeper, cooler areas of central and northern Puget Sound. In contrast, a congener, the graceful crab (*C.* [*M.*] *gracilis*), is abundant in relatively shallow, warm waters of South Puget Sound and some embayments. The aim of the present study was to evaluate the effect of temperature on crab bioenergetics. Feeding trials were conducted using crabs of roughly equal size fed known quantities of prey across a range of temperatures. Similarly, in order to determine size-specific consumption rates, feeding trials were conducted at the optimal foraging temperature for a wide size range of crabs. Consumption rates from feeding trials were fit to size- and temperature- specific algorithms using maximum likelihood estimates that also incorporate previous data. Consumption estimates were compared for the species and the impact on crab bioenergetics and implications for management was considered. While Dungeness crab presently outgrow and possibly outcompete graceful crab, as water temperatures increase the latter may expand their distribution, potentially occupying areas presently used by the former. Such a shift may have management implications, as well as widespread economic and ecological impacts.

MENTAL MODELING AND PARTICIPATORY SCIENCE TO INVESTIGATE PRIBILOF ISLAND BLUE KING CRAB

P. Sean McDonald[1]*, Jonathan Reum[2,3], Kirstin K. Holsman[2], William Christopher Long[4], David A. Armstrong[3], Janet Armstrong[3], and Matt Sedlacek[1]

[1]University of Washington, Program on the Environment, BOX 355679, Seattle, Washington 98195 USA

[2]National Marine Fisheries Service, Alaska Fisheries Science Center, NOAA, 7600 Sand Point Way N.E., Building 4, Seattle, Washington 98115 USA

[3]University of Washington, School of Aquatic and Fishery Science, BOX 355020, Seattle, Washington 98195 USA

[4]National Marine Fisheries Service, Alaska Fisheries Science Center, NOAA, Kodiak Fisheries Research Center, 301 Research Court, Kodiak, Alaska 99615 USA

psean@uw.edu

Fisheries management can be both complex and contentious, particularly for data-poor stocks. A mental modeling approach can be applied where quantitative data are scarce and/or interdisciplinary questions require input of disparate information sources. Moreover, mental models are well suited for collaborative science because expert opinion and local and traditional ecological knowledge can be integrated and visualized. In the present study, stake-

holder meetings were used and mental models were formalized to explore issues in a coupled human-marine ecosystem involving Pribilof Island blue king crab (PIBKC). In the Pribilof Islands, protections for overfished PIBKC impact management of other fisheries and consequently human use of the nearshore environment. Meeting participants were asked to construct mental models of the PIBKC human-ecological system to understand how stakeholders' perceptions of key ecological, human, and environmental variables influencing the lack of PIBKC stock recovery. Additionally, pre- and post-meeting surveys of the participants were conducted. Results show some similarities in the way stakeholders perceive the ecosystem but the number of linkages differs widely among individuals. Surveys indicate that stakeholders responded positively when contributing toward group dynamics and felt a stronger personal connection to the issue. Overall, the integration of participatory science in the PIBKC discussion can provide positive benefits to management and help guide future research to support recovery of the species.

TESTING FITNESS CONSEQUENCES OF DOMESTICATION SELECTION AT THE LARVAL STAGE IN EASTERN OYSTERS

Katherine McFarland[*1,2], Louis Plough[1], Michelle Nguyen[1], and Matthew Hare[2]

[1]University of Maryland, Center for Environmental Science, Cambridge, Maryland 21613 USA

[2]Cornell University, Department of Natural Resources, Ithaca, New York 14850 USA

mcfarland.316@gmail.com

Selective breeding of oysters in the aquaculture industry has succeeded at improving the product, increasing profits, and boosting economies where the industry is growing. Because some artificially selected traits seem desirable in restoration contexts, selective breeding continues to be suggested in the literature as a potentially efficacious approach to population supplementation. One concern is that many unintended traits can change quickly during artificial selection simply due to inadvertent domestication, and little is understood about the fitness effects of these changes in the wild. For example, hatchery produced oysters are fed *ad libitum* during larval culture, potentially selecting for larval traits that reduce starvation resistance. To test this hypothesis, larvae were produced from wild Choptank River, MD broodstock and from a cross between two longstanding selected lines (CROSSbreed x DEBY; to reduce potential inbreeding effects). At day 7, a 10-day starvation treatment was imposed followed by a recovery period in which *ad libitum* feeding was resumed, all compared to a consistently *ad libitum* set of controls. Following starvation, wild larvae had higher survivorship than aquaculture larvae (21 ± 2% and 8 ± 3%, respectively), suggesting that domestication selection may reduce the ability of larvae to withstand periods of starvation. Preliminary measurements of larval respiration at the end of the starvation period also showed consistent differences between wild and aquaculture cohorts, which further points to physiological differences underlying variation in starvation tolerance. Ongoing work will assess transcriptomic differences between cohorts and treatments using RNA-seq to determine genetic effects of domestication selection.

BIVALVE—SEAGRASS INTERACTIONS: AN INTRODUCTION TO THE SESSION

Katherine A. McGraw[1*] and Brett R. Dumbauld[2]

[1]NOAA Restoration Division, 1315 East West Hwy, Silver Spring, Maryland 20910 USA

[2]USDA-ARS, Hatfield Marine Science Center, 2030 SE Marine Science Dr, Newport, Oregon 97365 USA

Kay.McGraw@noaa.gov

Seagrasses and bivalves are found on all U.S. coasts and provide many ecosystem benefits where they exist, including nutrient recycling, habitat (e.g., for salmon and other fish) and food provision for numerous species; however, they have also been depleted because of environmental degradation, development, eutrophication, fishing gear, and diseases. Bivalves and seagrasses also interact in a mutualistic way in many cases. For example, oyster reefs may enhance seagrass cover in some areas by reducing turbidity and providing nutrients for the seagrasses via benthic-pelagic coupling; thus oyster reefs are being incorporated into some "living shorelines" projects to enhance seagrass growth. Some mussel species have also been shown to have beneficial effects on seagrass community development. Shellfish aquaculture also interacts with seagrass resulting in competing interests between the shellfish industry and managers who seek to expand seafood production and regulators who seek to protect and conserve seagrasses. These and other related topics will be covered in presentations in the Seagrass-Bivalve session.

OLYMPIA OYSTERS—PAST, PRESENT, AND FUTURE

Katherine A. McGraw[1]* and Betsy Peabody[2]

NOAA Restoration Division, 1315 East West Hwy., Silver Spring, Maryland 20910 USA

Puget Sound Restoration Fund, 382 Wyatt Way NE, Bainbridge Island, Washington 98110 USA

Kay.McGraw@noaa.gov

The Olympia oyster (*Ostrea lurida* Carpenter, 1864) is the only native oyster on the west coast of the United States, with a range from Baja, California to British Columbia, Canada. Once plentiful throughout this range, the species was harvested by Native American tribes for thousands of years; but, subsequent to European settlement, it was overexploited to almost commercial extinction by the 1920s. Cultivation of Olympia oysters in dikes by shellfish growers in south Puget Sound during the early 1900s was successful until the establishment of pulp mills in that area. Effluent from the mills further decimated populations there. Following introduction of the non-native Pacific (Japanese) oyster, *Crassostrea gigas*

(Thunberg, 1793) in the 1930s, it supplanted the Olympia oyster as the primary commercial species. In addition, several non-native oyster predators and parasites were imported with the *C. gigas* oyster seed from Japan. Thereafter, interest in research and cultivation of Olympia oysters waned for several decades; however, efforts to restore this species have increased dramatically in the last 20 years, accompanied by more research and peer-reviewed publications, state shellfish initiatives, monitoring guides, restoration projects, and shellfish hatcheries designated for restoration efforts. Growing recognition that Olympia oysters are still present throughout their historic range has also helped expand restoration. Now people in all west coast states and British Columbia are involved in restoration and research efforts involving *Ostrea lurida*, and plans are being formulated to develop a coast-wide network of restoration practitioners, shellfish scientists, aquaculturists, and educators. This session will include a brief historical perspective of Olympia oysters, presentations about restoration techniques, genetics, ecology, hatchery production, and an update on the formation of the Baja to B.C. Olympia oyster network.

FACTORS THAT AFFECT THE VERTICAL DISTRIBUTION OF OLYMPIA OYSTER LARVAE IN FIDALGO BAY, WASHINGTON, USA

Brooke A. McIntyre[1*], Erika McPhee-Shaw[2], Marco Hatch[2], and Shawn M. Arellano[1]

[1]Western Washington University, Shannon Point Marine Center, 1900 Shannon Point Rd., Anacortes, Washington, 98221 USA

[2]Western Washington University, Department of Environmental Science, 516 High Street, Bellingham, Washington 98225 USA

mcintyb@wwu.edu

Collaborative restoration efforts for the native Olympia oyster, *Ostrea lurida*, are underway in the Salish Sea because restoring viable, self-sustaining populations has high ecological and social value. Olympia oysters rely on their free-swimming planktonic larvae to disperse between sites. Larvae actively control their vertical position in the water column with swimming and sinking behaviors, affecting which current regimes carry them and ultimately determine dispersal patterns and population connectivity. This study investigates the effects of several abiotic and biotic factors that influence the vertical distribution of Olympia oyster larvae in Fidalgo Bay, a Washington state priority restoration site. On four consecutive days in July 2017, larvae were pumped, counted, and measured from several depths over ebb and flood tides in combination with temperature and chlorophyll measurements. In addition, an upward-facing Acoustic Doppler Current Profiler was deployed near the sampling location to measure current velocities in the main channel of the Bay. Generalized linear mixed modeling was used to determine which factors (temperature, chlorophyll concentration, current velocity, and larval size) impacted both larval abundance and the weighted mean depth at which the larvae resided. Results from this study can be used to inform a biophysical model to simulate larval transport and dispersal patterns from the Fidalgo Bay restoration site to aid restoration efforts.

COMPARING NATIVE AND NON-NATIVE ESTUARINE SPECIES: DO MORE TOLERANT SPECIES HARBOR MORE GENES TO COMBAT CLIMATE CHANGE STRESS?

Stacey L. McIntyre*, Joshua P. Der, Danielle C. Zacherl, and Ryan P. Walter

California State University, Fullerton, Department of Biological Science, 800 N State College Blvd., Fullerton, California 92831 USA

staceymc@csu.fullerton.edu

The genetic basis of organismal stress tolerance remains poorly understood but is an important consideration for effective species conservation and management. In Southern California, restoration efforts aimed at increasing the abundance of native Olympia oysters (*Ostrea lurida*) are challenged by the presence of an introduced non-native, the Pacific oyster (*Crassostrea gigas*). Establishing a record of molecular responses to environmental stress in both species may prove valuable in developing effective restoration strategies that maximize native oyster recovery while controlling non-native expansion. Using RNA-sequencing, gene expression profiles of temperature and salinity stressed oysters were compared. Overall, the non-native oyster exhibited a three-fold greater number of differentially expressed genes than the native oyster (104 for *O. lurida* and 350 for *C. gigas*; FDR<0.001) representing a more complex physiological response and possibly a "more equipped species" for coping with changing environmental conditions. The results from this study will further the understanding of molecular mechanisms underlying genomic adaptation between co-occurring native and introduced species.

FRESHWATER MUSSEL SHELLFISHING AS EVIDENCE OF CULTURAL CONTINUITY AND DIVERGENCE DURING THE LATE PREHISTORIC IN WISCONSIN

Rachel C. McTavish

University of Wiscosin-Milwaukee, Department of Anthropology, 3413 N, Downer Ave, Milwaukee, Wisconsin 53211 USA

mctavis2@uwm.edu

The role of shellfish for Late Prehistoric Oneota groups in Wisconsin has previously been extrapolated from the La Crosse locality, in western Wisconsin, owing to the substantial amount of published data on the topic (e.g., Theler 1985, 1993, 1994). New data from the southeastern region of Wisconsin, in the Lake Koshkonong locality allows for the examination of the differential role of shellfishing as it relates Oneota subsistence-settlement and dietary patterns, particularly as the use of freshwater mussel shells

provides evidence of differential cultural practices and influences by contemporaneous groups.

The presented comparative analysis is an integral step towards understanding Western and Eastern Wisconsin Oneota groups use of shell as a raw material for tool manufacture and its dietary contributions. This presentation aims for the integration of freshwater mussel data to connect to larger anthropological themes. As such, data are discussed in the context of environmental adaptations and varying degrees of documented socio-political conflict in the region.

ASSESSMENT OF INTERACTIONS BETWEEN SALMON HABITAT RESTORATION ACTIONS AND SHELLFISH RESOURCES

Marlene Meaders* and Paul Schlenger

Confluence Environmental Company, 146 N Canal St, Seattle, Washington 98103 USA

marlene.meaders@confenv.com

River deltas and marine nearshore environments are important habitats for salmon and shellfish. Given the overlapping locations of these economically and culturally important resources, changes made to improve conditions for salmon can positively or negatively affect growing conditions for shellfish, such as oysters and clams. The potential interactions between salmon habitat restoration efforts and shellfish resources in Hood Canal have emerged as a key consideration for salmon restoration planning. As projects get larger, and include more of a habitat mosaic, potential conflicts between user groups in the nearshore are becoming evident. To improve our understanding of the potential interactions, and identify ways to reduce the potential for conflict, the Hood Canal Coordinating Council assessed how salmon habitat projects may be affecting tribal, state, private commercial, and native shellfish resources. The assessment included a literature review and interviews with representatives from a diverse range of interests on this topic. The assessment report provided a state of the knowledge on the potential interactions, guidance for salmon habitat project development in areas with shellfish resources, and recommendations of monitoring parameters to fill data gaps and/or inform discussions during project planning. This is the initial effort in understanding this issue, which will hopefully develop and evolve along with salmon restoration activities. The presentation will also include an indication of whether this effort has been helpful for current salmon restoration planning in Hood Canal.

COMPARATIVE HABITAT USE OF ESTUARINE HABITATS WITH AND WITHOUT OYSTER AQUACULTURE: CHALLENGES, PARTNERSHIPS, AND INITIAL LESSONS

Marlene Meaders*, Phil Bloch, and Chris Cziesla

Confluence Environmental Company, 146 N Canal St, Seattle, Washington 98103 USA

marlene.meaders@confenv.com

Shellfish aquaculture, native eelgrass, and mudflat habitats have co-existed in Humboldt Bay, California, for at least the last 60 years of commercial shellfish production, and for more than 100 years since the first attempts to introduce shellfish in 1896. The goal of the project is to provide research on the environmental impacts of aquaculture facilities by furthering the understanding of how fish and invertebrate communities are affected by the presence of cultch-on-longline oyster aquaculture in comparison to areas without oyster aquaculture in Humboldt Bay. The first year of sampling has brought together challenges with effectively sampling habitat *in situ* but within a set unit area. Paired habitats were sampled using modified fyke net enclosures that are 30 feet by 30 feet (or 0.02 acres). In addition, important benthic invertebrate prey resources show wide variability throughout Humboldt Bay, depending on habitat type, geographic location in the bay, and shellfish aquaculture presence or absence. Lessons learned include how to deploy enclosures in a dynamic environment, the best ways to sample bottom fish that burrow into soft sediment, how to get meaningful data to address changes in the benthic community, and how to bring together a diverse group of individuals. The lessons learned from 2017 were used to improve upon the sampling methods for the final events in 2018. The presentation will be sure to display the range of environmental conditions during the field sampling portions of the study, including the joys of sampling in the Humboldt mud.

ENGAGING FISHERMEN TO ADDRESS DATA GAPS AND EVOLVE MANAGEMENT OF THE QUAHOG (*MERCENARIA MERCENARIA*) IN NARRAGANSETT BAY

Anna Malek Mercer[1], Dale Leavitt[2], Conor McManus[3], and Thomas Heimann[1*]

[1]Commercial Fisheries Research Foundation, 61B East Farm Road, Kingston, Rhode Island 02881 USA

[2]Roger Williams University, Department of Biology, Marine Biology and Environmental Science, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

[3]Rhode Island Department of Environmental Management, Marine Fisheries, 3 Fort Wetherill Road, Jamestown, Rhode Island 02835 USA

theimann@cfrfoundation.org

The quahog (*Mercenaria mercenaria*) fishery is the most valuable fishery in Narragansett Bay, with a dockside value over $5 million. The complex population and fishery dynamics of this species in combination with aggregated distribution patterns make

it difficult to accurately assess the population and thus, properly manage the resource. This work pilots a novel technique that involves commercial shellfishermen using a tablet app to collect quahog data via bullrake sampling year-round, focusing on regions of Narragansett Bay not assessed by the Rhode Island Department of Environmental Management (RI DEM) hydraulic dredge survey. The catch efficiency of bullrake sampling and the RI DEM hydraulic dredge survey are calibrated via in-situ SCUBA observations, enabling integration of project data with the existing dredge survey time series. Preliminary results suggest that quahog density varies at a suite of spatial scales as a result of complex environmental conditions. Furthermore, bullrake sampling appears to document higher quahog densities than the hydraulic dredge survey by accessing different areas and habitats within Narragansett Bay. A variety of alternative stock assessment approaches that incorporate the spatial and seasonal dynamics of the quahog resource are currently being explored. Results of these alternative models will be compared to the traditional quahog stock assessment and used to refine reference points and management measures. Ultimately, this work fosters a transparent and accurate quahog management system by providing commercial shellfishermen an opportunity to actively participate in the scientific and management process.

UPDATE ON TWO ENIGMATIC DISEASES (*PERKINSUS QUGWADI* AND *FRANCISCELLA HALIOTICIDA*) AFFECTING THE HEALTH OF CULTURED YESSO SCALLOPS (*PATINOPECTEN YESSOENSIS*) IN BRITISH COLUMBIA, CANADA

Gary R. Meyer[1]*, Naoki Itoh[2], Geoff Lowe[1], and Eliah Kim[1]

[1]Pacific Biological Station, Department of Fisheries and Oceans, 3190 Hammond Bay Road, Nanaimo, British Columbia V9T 6N7, Canada

[2]The University of Tokyo, Laboratory of Fish Diseases, Graduate School of Agricultural and Life Sciences, Tokyo 113-8657, Japan

Gary.Meyer@dfo-mpo.gc.ca

Both *Perkinsus qugwadi* (SPX) and *Francisella halioticida* have sporadically caused disease and mortality among cultured Yesso scallops in British Columbia, Canada. The protozoan parasite, *P. qugwadi* caused significant mortalities during the late 1980s and early 1990s; however, the prevalence of infection decreased dramatically following 1995 and was not problematic again until the fall of 2011 when it was again detected in association with mortalities. To gain a better understanding of the biology of this parasite and to obtain material for development of in-vitro culture techniques, experimental stocks of scallops were out-planted in 2016 and 2017 at Kanish Bay, the location where *P. qugwadi* has historically been most problematic; however, to date *P. qugwadi* has not been detected in the sentinel scallops nor from eDNA samples, further adding to the enigmatic nature of this parasite. The intracellular Gram-negative bacterium, *Francisella halioticida*, was identified as the putative cause for disease and mortality affecting up to 40% of the scallops from one location during the fall of 2015. *In situ* hybridization assays conducted on archived samples from 3 different locations dating back to 1995 also indicated that *F. halioticida* was the most probable cause of the lesions observed in these cases. During recent testing of scallops collected from three locations the prevalence of lesions and infection with *F. halioticida* has ranged from 0 to 10%. Characterization of isolates obtained from these scallops and results from a laboratory challenge designed to assess the transmission and pathogenicity of *F. halioticida* will be discussed.

LIVELIHOOD DIVERSIFICATION AND IMPLICATIONS IN EXTENSION PLANNING

Adriane K. Michaelis[1]*, Donald W. Webster[2], and L. Jen Shaffer[1]

[1]University of Maryland, Department of Anthropology, 1111 Woods Hall, 4302 Chapel Lane, College Park, Maryland 20742 USA

[2]University of Maryland Extension, Wye Research & Education Center, 124 Wye Narrows Dr., Queenstown, Maryland, 21658 USA

amichael@umd.edu

Maryland aquaculture extension programs target current and potential shellfish growers to strengthen the state's expanding industry. It is important in program planning to understand how growers incorporate aquaculture into existing livelihood strategies. Patterns of livelihood diversification -- wherein an individual participates in multiple income-generating activities -- are present in small-scale inshore fisheries worldwide and are an integral part of the Maryland seafood industry.

This study details livelihood diversification in Maryland oyster aquaculture, with emphasis on whether aquaculture has replaced a previous source of income, and if so, what that might mean for the state's public fisheries. Outcomes are the goal of extension planning, particularly as programs attempt to integrate commercial watermen into aquaculture. Understanding how aquaculture is likely to fit into watermen's existing livelihood strategies yields more effective programming as well as greater participation.

Results indicate that patterns of incorporation exist relative to aquaculture lease type; water column leases tend to be replacement income, whereas submerged land or bottom leases are additional income and are taken on largely by commercial watermen. For watermen who have replaced activity in other fisheries, many have reduced or eliminated participation in the crab fishery but are still active in the wild harvest oyster fishery. These patterns may imply challenges associated with each type of lease, particularly for watermen, as well as suggesting that growth of oyster aquaculture in Maryland has not yet led to reduced fishing pressure in the wild oyster harvest.

UNDERSTANDING THE MOLECULAR BASIS OF PATHOGENESIS OF WHITE SPOT SYNDROME VIRUS (WSSV) USING COMPARATIVE TRANSCRIPTOMICS IN THE PACIFIC WHITELEG SHRIMP (*PENAEUS VANNAMEI*) AND EUROPEAN SHORE CRAB (*CARCINUS MAENAS*)

Rebecca S. Millard[1*], Bas Verbruggen[1], Lisa K. Bickley[1], Kelly S. Bateman[2], Grant D. Stentiford[2], Charles R. Tyler[1], Ronny van Aerle[2], and Eduarda M. Santos[1]

[1]Biosciences, College of Life and Environmental Sciences, Geoffrey Pope Building, University of Exeter, Exeter, United Kingdom, EX4 4QD

[2]European Union Reference Laboratory (EURL) for Crustacean Diseases, Centre for Environment, Fisheries and Aquaculture Sciences (Cefas), Barrack Road, The Nothe, Weymouth, Dorset, United Kingdom, DT4 8UB

rm527@exeter.ac.uk

White spot syndrome virus (WSSV) is the major pathogen of shrimp culture, causing global annual losses in the region of $1B USD. Understanding host-pathogen interactions is crucial for the development of disease treatments and sequencing techniques are increasingly being employed to address this challenge.

This study aims to identify the molecular pathways associated with susceptibility to WSSV in the Pacific whiteleg shrimp (*Penaeus vannamei*). To do so, the temporal transcriptional changes in response to WSSV infection, and the role of microRNAs in regulating host and pathogen gene expression will be established. These data will be compared with an existing dataset on the temporal transcriptional and microRNA expression changes in a crustacean (European shore crab, *Carcinus maenas*) infected with WSSV that is highly resistant to the disease. In this way, the ability to identify individual genes and pathways associated with susceptibility and resistance to WSSV is expected.

To address this objective, shrimp were divided into two treatment groups and injected with either SPF- (specific pathogen free) or WSSV-shrimp homogenates. The gills from four shrimp from each treatment were sampled from 3-36h post-injection. Total RNA was extracted (n=48) and mRNA libraries (Illumina) and small RNA libraries (Nextflex) were prepared and sequenced. These datasets are currently being analysed to identify individual genes, miRNAs and pathways that are modified as a result of WSSV infection. Through comparison with the resistant shore crab dataset, mechanisms of susceptibility and resistance, and potential gene targets for disease prophylactics in the future are hoped to be identified.

POPULATION GENETICS, BIOGEOGRAPHY, AND PHYLOGENETICS OF *VIBRIO PARAHAEMOLYTICUS* FROM NORTH AMERICA USING WHOLE GENOME SEQUENCE DATA

John J. Miller[1,2], Catharina H. M. Lüdeke[3,4], Bart C. Weimer[5], and Jessica L. Jones[3]*

[1]FDA, Division of Mathematics, College Park, Maryland, USA

[2]Oak Ridge Institute for Science and Education, Oak Ridge, Tennessee, USA

[3]FDA, Division of Seafood Science and Technology, Gulf Coast Seafood Laboratory, Dauphin Island, Alabama, USA

[4]University of Hamburg, Hamburg School of Food Science, Hamburg, Germany

[5]University of California of Davis, Institute for Veterinary Medicine, Davis, California, USA

Jessica.Jones@fda.hhs.gov

Infections caused by *Vibrio parahaemolyticus* (*Vp*) are the most common seafood-borne illnesses reported in the United States and are frequently associated with consumption of shellfish. To investigate differences in *Vp* populations, draft genomes of 132 clinical and oyster *Vp* isolates from across North America were sequenced. Population genomics and biogeography analysis demonstrated that the majority of oyster isolate sequence types (STs) were identified from a single harvest location; however, four STs were identified in multiple harvest locations. STRUCTURE identified three clusters containing multiple STs with Fst values above 0.2, implying some level of population structure along the Gulf and Atlantic Coasts, with Gulf Coast sites generally having a greater diversity of *Vp* than other locations. When examining the isolates' phylogenetic relationship, 12 large strongly supported clades (bootstrap ≥70) were identified. Of those, six were comprised of either clinical or oyster isolates, while six were composed of a mix of the two isolate sources. In addition, three STs (3, 36, 65) were identified in clinical isolates, most likely from northern latitudes, but not represented by any oyster isolates in this collection. These results support the previously documented genomic diversity of *Vp*, but indicate geographical specificity and clinical predominance which may be informative to risk modeling efforts.

ALIGNING BIOLOGY, ASSESSMENT, AND MANAGEMENT OF BLUE CRAB IN CHESAPEAKE BAY

Thomas J. Miller*, Michael J. Wilberg, Dong Liang, and Geneviève M. Nesslage

Chesapeake Biological Laboratory, University of Maryland Center for Environmental Science, 146 Williams Street, Box 0038, Solomons, Maryland, USA

miller@umces.edu

Blue crab (*Callinectes sapidus*) supports an iconic and valuable fishery in the Chesapeake Bay. Over the last 25 years efforts to align biological knowledge with stock assessment and management

approaches have resulted in improved stock conditions. These efforts have sought to recognize and include the importance of saltatory growth, sex-specific life history variation and reproductive ecology, and have resulted in transition from simply yield per analyses to sophisticated sex-specific, stage based assessment models and the adoption of female-based conservation management. The changes that have occurred are reviewed, but the focus will be on current research to improve reliability of survey indices, evaluate the importance of sperm limitation, and understand drivers of recruitment variability. This presentation will show how (i) geostatistical approaches can provide robust estimates of uncertainty of population abundance, (ii) life table analysis indicates little concern over sperm limitation and (iii) probability network models can evaluate the importance of drivers of recruitment variation.

IMMUNOLOGICAL RESPONSE OF *CRASSOSTREA VIRGINICA* LARVAE TO PROBIOTIC *BACILLUS PUMILUS* RI06-95

Tejashree Modak*, David Nelson, David Rowley, and Marta Gomez-Chiarri

University of Rhode Island, 120 Flagg Rd, Kingston, Rhode Island 02881 USA

tejashree@uri.edu

The eastern oyster, *Crassostrea virginica,* is an ecologically and economically important species. The rearing of oyster larvae in hatcheries can be impacted by mortalities caused by bacterial pathogens such as *Vibrio*. Probiotics are an inexpensive, practical, and natural method of disease control. Pretreatment of larval oysters in hatcheries with probiotic *Bacillus pumilus* RI06-95 has been shown to significantly decrease mortality caused by experimental challenge with *Vibrio coralliilyticus* RE22. The aim of this study is to understand the mechanism of action of the probiotic leading to improved larval survival and how pre-exposure to a probiotic may change larval immune responses to a pathogen. Larval *Crassostrea virginica* were exposed to the probiotic daily for 16 days post fertilization in a hatchery setting. To test the efficacy of probiotic, a laboratory pathogen challenge assay was performed on day eight. Transcriptomes from samples collected on days 5, 12 and 16 were compared to understand the effect of probiotic treatment on larval gene expression. Probiotic treated larvae on day eight showed an increase in percent survival (28 ± 6 %) as compared to untreated larvae after a challenge with *V. coralliilyticus* RE22. A PCA analysis of the transcriptomes showed an effect of treatment and time. Comparison of gene expression between control and treatment showed some differentially expressed immune related genes (CLEC4E*,* caspase 7, TNFAIP3) along with several uncharacterized genes. Gene enrichment shows enrichment in oxidation-reduction processes. These transcriptomic comparisons provide an evidence of gene modulation by probiotic treatment as a potential mechanism to provide protection.

EFFECTS OF PREDATION AND SUBSTRATE CHOICE ON RIBBED MUSSEL RECRUITMENT FOR LIVING SHORELINE APPLICATIONS

Joshua A. Moody* and Danielle Kreeger

Partnership for the Delaware Estuary, 110 S. Poplar St. Ste 202, Wilmington, Delaware 19801 USA

jmoody@delawareestuary.org

Ribbed mussels are one of the functional dominant species in eastern USA salt marshes, providing many ecosystem services such as stabilizing substrates and enhancing vegetative growth. As of 2012, the Delaware Estuary was losing approximately one acre per day of coastal wetlands, resulting in reduced ribbed mussel populations along the shoreline. There is growing interest in living shorelines to protect and restore coastal marshes, and since 2008, the Partnership for the Delaware Estuary has implemented and sustained 14 active treatments. Ribbed mussel recruitment into these projects has been variable across space and time. The goal of this study was to test whether mussel recruitment in living shorelines can be enhanced by substrate choice and/or predator exclusion.

Two multi-factor experiments were conducted in triplicate at two locations in two representative rivers of the Delaware Bay, New Jersey, USA. The first experiment evaluated the effects of predation at three positions relative to the vegetated marsh edge. The second experiment assessed interactive effects between predatory exclusion and various substrates including: oyster shell; oyster castles; *Spartina alterniflora* plugs; and coir fiber. Recruitment of ribbed mussels was significantly lower along surfaces exposed to predation than along surfaces where predation was inhibited, independent of position. Additionally, materials that did not provide interstitial recruitment space had significantly higher recruitment rates when predation was inhibited, whereas materials with interstitial space saw no difference in recruitment rates across predation levels. These results indicate that material selection and predator exclusion can affect ribbed mussel colonization in living shorelines projects.

TRIBAL SHELLFISH HARVEST MANAGEMENT ON PRIVATELY OWNED TIDELANDS IN WASHINGTON STATE

Jeff Moore*, Viviane Barry, and Elizabeth Unsell

Suquamish Tribe, Fisheries Department, 18490 Suquamish Way, Suquamish, Washington 98392 USA

Jmoore@suquamish.nsn.us

Shellfish are a valuable resource for many tribal communities in western Washington, both economically and culturally. Treaty tribes are guaranteed a 50% share of naturally occurring shellfish on tidelands located within their Usual and Accustomed fishing grounds and stations. The shorelines of Puget Sound are a mosaic of mostly relatively small (less than one acre) tideland parcels. Unlike the shorelines of most states, the majority of these tidelands are privately owned.

Successful management of Treaty shellfish on private tidelands presents many challenges. Water quality issues, harvest practices,

and differing perspectives, interests, and perceptions among tribes, shellfish companies, growers, local and state government agencies, and individual tideland owners all converge on these small tidelands. These factors, and more, must be considered and a harvest management plan developed for each private tideland.

The Suquamish Tribe is committed to providing opportunities for its tribal members to exercise their Treaty harvest rights now, and in the future. With this goal in mind, the Tribe has developed harvest management strategies that are both dynamic and robust in addressing the many challenges associated with Treaty harvest on private tidelands. The Tribe has also partnered with various agencies and individuals to protect and enhance shellfish resources. As a result, tribal members have experienced increased cultural, ceremonial, subsistence, and commercial harvest opportunities. The community has also benefited from improvements to water quality, increased shellfish productivity, and a growing positive relationship with the Tribe.

HAEMOCYTES FROM *CRASSOSTREA GIGAS* AND OSHV-1: A PROMISING *IN VITRO* SYSTEM TO STUDY HOST-VIRUS INTERACTIONS

Benjamin Morga*[1], Nicole Faury[1], Stéphane Guesdon[1], Bruno Chollet[1], and Tristan Renault[2]

[1]IFREMER, Laboratoire de Génétique et Pathologie des Mollusques Marins, Avenue de Mus de Loup, 17390 La Tremblade, France

[2]Ifremer, Département Ressources Biologiques et Environnement, Nantes, France

benjamin.morga@ifremer.fr

Since 2008, mass mortality outbreaks associated with the detection of particular variants of OsHV-1 are reported in *Crassostrea gigas* spat and juveniles in several countries. Some recent studies reported information on viral replication during an experimental infection. Viral RNA detection was noticed in spat mantle 4h post-virus suspension injection. Moreover, an *in situ* hybridization approach showed that OsHV-1 mRNAs were mainly present in the connective tissue of gills, mantle, adductor muscle, digestive gland, and gonads following the injection of the virus suspension in the hemolymphatic sinus of the adductor muscle. Viral DNA and RNA were also detected in the haemolymph and hemocytes suggesting that the virus could circulate through the circulatory system; however, it is unknown if the virus is free in the haemolymph, passively associated at the surface of hemocytes or if it is able to replicate inside these cells inducing or not virion production.

In the present study, haemocytes from the hemolymphatic sinus of the adductor muscle of healthy *C. gigas* spat were collected and put *in vitro* in contact with a viral suspension. Results showed that viral RNAs were detectable one hour after contact and the number of virus transcripts increased across the time of contact in association with an increase of viral DNA detection. These results suggested that the virus is able to initiate replication rapidly inside haemocytes maintained *in vitro*. These *in vitro* trials were also used to carry out a dual transcriptomic study. Additionally, transmission electron microscopy examination was carried out and did not allow the detection of viral particles. The expression of some host immune genes and 15 viral genes were concomitantly analyzed. Results showed an up regulation of oyster genes currently studied during OsHV-1 infection. All the results suggested that the *in vitro* model based on the use of haemocytes can be a valuable model opening new perspectives in terms of better understanding host – pathogen interactions.

DOES FIRST BARRIER PASSAGE SHUNT MATTER IN DISEASE REPRODUCTION? UPDATE FROM OSHV-1 – *CRASSOSTREA GIGAS* MODEL

Benjamin Morga*[1], Sandy Picot[1], Nicole Faury[1], Lionel Dégremont[1], Tristan Renault[2], Coralie Lupo[1], and Marie-Agnès Travers[1]

[1]IFREMER, SG2M-LGPMM, Laboratoire de Génétique et Pathologie des Mollusques Marins, Avenue de Mus de Loup, 17390 La Tremblade, France

[2]Ifremer, Département Ressources Biologiques et Environnement, Nantes, France

benjamin.morga@ifremer.fr

Since 2008, mass mortality outbreaks associated with the detection of particular variants of Ostreid herpesvirus type 1 (OsHV-1) are reported in *Crassostrea gigas* spat and juveniles in several countries. This disease has become a major threat for a sustainable oyster industry. Ostreid herpesvirus type 1 (OsHV-1), the causative agent of major economic losses in the Pacific oyster industry, is a member of the family Malacoherpesviridae from the order Herpesvirales.

Many research groups initiated studies to decipher the interaction mechanisms between the virus and the oyster. The major limitation of this model is the absence of virus cultivation protocols, mostly linked to the absence of cellular culture model in mollusc; however, through partial "purification" the infectivity of variants was demonstrated in oysters by intramuscular injection. The first investigation on the direct transmission through seawater has been done before 2008 in larval stage. Based on this, an experimental laboratory-based infection protocol has been developed at juvenile stage to better understand the transmission routes and the infection kinetics of the herpesviruses OsHV-1. Cohabitation of naïve juvenile oysters with injected oysters with a viral suspension has demonstrated that seawater can act as a medium in the horizontal transmission of OsHV-1. Although this protocol reproduces better the natural way of infection, the viral exposure dose of the naïve oysters cannot be controlled.

Thus, a new infection protocol based on immersion into titrated contaminated seawater was developed. This new protocol was compared with usual protocol consisting in injecting oysters with a viral suspension. Using different oyster families, it was demonstrated that both protocols revealed similar contrasted phenotypes with high virus loads; however, a dose effect was only visible in immersion protocol. This methodological update gives further understanding of the transmission dynamics of OsHV-1 among oysters, in prospects for its spread control.

GROWTH, MORTALITY, AND YIELD OF FARMED SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) IN MAINE USING THE EAR-HANGING METHOD, AND INFLUENCES OF SUBSTRATE AND DEPTH ON YIELD OF SCALLOP SPAT COLLECTORS

Dana L. Morse[1*], Melissa Britsch[2], Nathaniel Perry[3], and Hugh S. Cowperthwaite[4]

[1]Maine Sea Grant and University of Maine Cooperative Extension, Darling Marine Center, 193 Clark's Cove Road, Walpole, Maine 04573 USA

[2]Darling Marine Center, 193 Clark's Cove Road, Walpole, Maine 04573 USA

[3]Pine Point Oyster Company, 10 Pine Ridge Road, Cape Elizabeth, Maine 04107 USA

[4]Coastal Enterprises, Inc., 30 Federal St., Brunswick, Maine 04011 USA

The ear-hanging method for scallop production has produced positive early results in coastal Maine waters, with reasonable growth rates and survival. This developing industry sector is dependent on wild spat collection for the source of seed, using Japanese-style spat collectors. Yields for spat collectors have are also encouraging, but materials costs are high, with producers consequently seeking equally-effective, cheaper options. This ongoing experiment examines: growth, survival and yield of ear-hung scallops on six sites in coastal Maine; the use of alternate materials as settlement substrate in scallop spat collectors; and the influence of depth on spat bag returns. The experiment also investigates the effect of different drilling locations near the hinge, on subsequent growth and survival. To date, standard agricultural nettings are as effective as the more-costly industry standard ("Netron") in terms of spat collection production, and that mid-depth in the water column produces the highest yields. Collectors set highest in the water column collected sufficient numbers of scallops, but also had the highest number of blue mussels (*Mytilus edulis*), which can damage post-set scallops through byssal attachment and smothering, and which complicate the spat-sorting process that begins nursery-phase culture. Growth rates for shell heights range from 0.05mm/day (0.7"/year) to over 0.12mm/day (1.7"/year), analyses for meat yields by shell height are ongoing.

AQUACULTURE IN SHARED WATERS - AN AQUACULTURE TRAINING PROGRAM DESIGNED TO EXPLORE THE INTEGRATION OF FISHING AND FARMING IN MAINE

Dana L. Morse[1*], Chris Bartlett[2], Nick Battista[3], Sebastian Belle[4], Caitlin Cleaver[5], Hugh S. Cowperthwaite[6], Chris Davis[7], Teresa Johnson[8], and Natalie Springuel[9]

[1]Maine Sea Grant and University of Maine Cooperative Extension, Darling Marine Center, 193 Clark's Cove Road, Walpole, Maine 04573 USA

[2]Maine Sea Grant/University of Maine Cooperative Extension, P.O. Box 278, 141 Water St., Eastport, Maine 04631 USA

[3]Island Institute, 386 Main Street, Rockland, Maine 04841 USA

[4]Maine Aquaculture Association, 103 Water Street #2, Hallowell, Maine 04347 USA

[5]University of Maine, School of Marine Sciences, 360 Aubert Hall, Orono, Maine 04469 USA

[6]Coastal Enterprises, Inc., 30 Federal St., Brunswick, Maine 04011 USA

[7]Maine Aquaculture Innovation Center, Darling Marine Center, 193 Clark's Cove Road, Walpole, Maine 04573 USA

[8]University of Maine, School of Marine Sciences, 200 Libby Hall, Orono, Maine 04469 USA

[9]Maine Sea Grant, College of the Atlantic, 105 Eden St., Bar Harbor, Maine 04609 USA

dana.morse@maine.edu

The increase of marine aquaculture is not unique to Maine, but given the state's high dependence on commercial fishing, and the deep connection between coastal life and commercial fishing, changes to the fishing industry here especially strong implications; the fishery for lobster (*Homarus americanus*) is the most valuable in the nation, and Maine lands 80% of the lobster in the US. Further, lobsters make up ~75% of the value of all marine landings in Maine. Increasingly over the last 5-8 years, more Maine fishermen are considering aquaculture as a way to maintain income diversity.

Aquaculture in Shared Waters is an education/training program targeting fishing families, to advance working waterfront diversification, and minimize user conflicts. The program provides classroom teaching, applied educational materials, and extended technical support to participants, and begins to build the professional network that every new producer needs for business success. Since 2013, there have been five rounds of training, with two emerging for 2018. Approximately 100 individuals have completed the course, with about 30 now engaged in aquaculture or new seafood business. The program is tightly tied to social science research, to learn more about course delivery, changes in knowledge and perception, and effectiveness of materials. AQSW has inspired similar efforts in the state, and has been a venue to increase the integration between fishing and farming. Research to date indicates that participants value the training, they find it helpful in preparing them for an aquaculture business, and that applied, hands-on learning opportunities are most effective.

DENSITY-DEPENDENT CAPTURE EFFICIENCY OF A SURVEY DREDGE AND ITS INFLUENCE ON THE STOCK ASSESSMENT OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) IN DELAWARE BAY

Jason M. Morson[1]*, Daphne M. Munroe[1], Kathy A. Ashton-Alcox[1], Eric N. Powell[2], David Bushek[1], and Jennifer Gius[1]

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

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

jmorson@hsrl.rutgers.edu

A reliable measure of gear capture efficiency is required to calculate unbiased estimates of population size and fishing mortality from survey data in a stock assessment; however, capture efficiency can vary spatially and temporally due to changes in abundance, stock area, the environment, and the sampling gear itself. Therefore, periodic reassessment of this parameter is necessary to ensure that the catchability coefficients being applied accurately reflect the capture efficiency of the survey sampling gear, especially when catchability is being estimated outside of the stock assessment model. Using data from field experiments conducted in 1999, 2000, 2003, and 2013, spatial and temporal variability in capture efficiency was evaluated for a commercial dredge used to conduct a fishery-independent survey of the eastern oyster (*Crassostrea virginica*) population in Delaware Bay, USA. A spatial gradient in capture efficiency was detected, but no temporal trend. Capture efficiency was a function of the density of oysters in the sampled area. This is likely the first time density-dependent capture efficiency has been identified for a sessile invertebrate stock survey. Since density dependence in capture efficiency leads to hyperstable catch-per-unit-effort, caution is advised when deriving oyster abundance from dredge survey catch-per-effort data, especially at low oyster density and when high spatial resolution estimates of survey dredge capture efficiency are not available.

MONITORING HAB TOXINS USING SPATT PROXY FOR SHELLFISH MANAGEMENT

Steve L. Morton*[1], Bennie Haynes[1], Zhihong Wang[1], Theresa Hattenrath[2], Christopher Gobler[2], and Tod Leighfield[1]

[1]NOAA/NOS/NCCOS, HAB Monitoring and Reference Branch, 219 Fort Johnson Road, Charleston, South Carolina 20412 USA

[2]Stony Brook University, School of Marine and Atmospheric Sciences, Southampton, New York 11968 USA

steve.morton@noaa.gov

The range, frequency, and intensity of harmful algal blooms have increased in recent decades. HAB species that produce biotoxins are a growing societal concern in many coastal regions due to their impacts on human health and the economy of shellfisheries. Paralytic shellfish poisoning (PSP) and diarrhetic shellfish poisoning (DSP) are globally significant human health syndromes that are caused by ingestion of toxins produced by the dinoflagellates *Alexandrium* and *Dinophysis*. This study evaluates approaches for monitoring toxins associated with recurrent toxin-producing *Alexandrium* and *Dinophysis* blooms on Long Island, NY, USA. Within contrasting locations, the dynamics of *Alexandrium* and *Dinophysis* cell densities, toxins in plankton, and toxins in deployed blue mussels (*Mytilus edulis*) were compared with passive solid-phase adsorption toxin tracking (SPATT) samplers filled with two types of resin. Multiple species of wild shellfish were collected during *Dinophysis* blooms and used to compare toxin content using two different toxin analysis assays. DSP toxins measured in the shellfish proxy were significantly correlated with total DSP toxins in wild shellfish. Blue mussels (*Mytilus edulis*) and ribbed mussels (*Geukensia demissa*) were found to accumulate DSP toxins above federal and international standards (160 ng g^{-1}) during *Dinophysis* blooms while Eastern oysters (*Crassostrea virginica*) and soft shell clams (*Mya arenaria*) did not. This study demonstrated that SPATT samplers coupled with PP2A technology could be used to provide early warning of DSP, but not PSP, events for shellfish management.

IMPLEMENTING A SIZE RESTRICTION TO OFFSET IMPACTS FROM SIZE-SELECTIVE HARVESTING OF GIANT RED SEA CUCUMBERS

Karl W. Mueller

Lummi Natural Resources Department, LIBC, 2665 Kwina Road, Bellingham, Washington 98226 USA

KarlM@lummi-nsn.gov

Size-selective harvesting of the giant red sea cucumber (*Parastichopus californicus*) in the San Juan Islands, Washington has led to a change in body size of *P. californicus*, both landed and in the wild, since commercial fisheries (trawl and diver-harvested) for the species began in the 1970s. While it is possible that recent fishery-dependent data reflect the size, distribution, and abundance of small animals within easy grasp of commercial harvest divers, the preponderance of fishery-independent data supports the premise of a 20–30% reduction in size of *P. californicus* over the years. Harvesting increasingly smaller individuals has long-term consequences for the giant red sea cucumber population in the San Juan Islands. Evolutionary changes in growth, size at maturity, and reproductive capacity are all documented outcomes of size-selective harvesting. Moving forward, treaty tribal and non-tribal natural resource authorities, i.e., the co-managers of *P. californicus* fisheries in Washington State, must consider the potentially detrimental consequences of not taking action on this management issue. One simple, intuitive management tool to offset the effects of size-selective harvesting would be to implement a size restriction for the giant red sea cucumber. This presentation introduces a novel way to implement a minimum size limit for the species and provides the proof of principle that underwater harvesters could comply with the restriction. Implementing the restriction will minimize evolutionary changes to growth and size at maturity, and will reduce the possibility of harvesting a giant red sea cucumber before it has spawned at least once during its lifetime.

COMPARING FISH AND CRAB USE OF THE BOUNDARY BETWEEN TWO TYPES OF PACIFIC OYSTER AQUACULTURE AND EELGRASS IN WILLAPA BAY, WASHINGTON, USA

Kelly Muething[1]* and Brett Dumbauld[2]

[1]Oregon State University, Strand Agriculture Hall, 170 SW Waldo Pl, Corvallis, Oregon 97331 USA

[2]Hatfield Marine Science Center, 2030 SE Marine Science Dr, Newport, Oregon 97365 USA

muethink@oregonstate.edu

Estuaries provide productive habitat but are also subject to a variety of human pressures, making them highly-contested space. Pacific oyster (*Crassostrea gigas*) aquaculture has been practiced for almost 100 years and commonly occurs in intertidal areas in US West Coast estuaries where native eelgrass (*Zostera marina*) is also present. Seagrasses provide valuable nursery habitat for many commercially-harvested species (e.g. salmonids, English sole, and Dungeness crab) and have recently garnered more conservation interest because they are declining in many locations. To help inform management decisions, questions were addressed regarding the use of both aquaculture and eelgrass beds as habitat. Specifically, there was interest in quantifying and distinguishing whether the edge between these two habitats functioned differently. Due to a recent shift towards off-bottom culture methods, in part to protect seagrasses, this comparison was made in both long-line and on-bottom aquaculture. Both direct (underwater video) and indirect (e.g. predation tethering units) measures of fish and invertebrate community composition and behavior were used to quantify effects along a transect that ran between the two habitats in each type of aquaculture. Preliminary results suggest that most species use longline oyster and eelgrass habitats similarly with minimal edge effect while habitat use was more distinct between on-bottom oyster and eelgrass habitats. This is consistent with an expected increase in fish and crab abundance with the amount of vertical structure within a habitat. This work could provide valuable insight to managers and permitting agencies as they consider requests to expand culture operations.

HORSESHOE CRAB PASSAGE THROUGH RACK-AND-BAG OYSTER FARMS

Daphne Munroe, David Bushek*, Patricia Woodruff, and Lisa Calvo

Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, New Jersey 08349 USA

bushek@hsrl.rutgers.edu

Concern has been raised about the ability of horseshoe crabs (*Limulus polyphemus*) to traverse intertidal rack-and-bag oyster farms, and how farms may change shorebird foraging activity. During the 2016 horseshoe crab spawning season, experiments conducted in Delaware Bay (New Jersey, USA) assessed crab ability to move among oyster farms and access landward nesting grounds, and surveyed distribution of dislodged eggs upon which many shorebirds feed. Experiments included (1) testing rack heights for impairment of crab passage, (2) repeated crab census on paired farm/control sites, (3) assessing distribution and stranding of crabs on nesting beaches with and without farms, and (4) a spatial survey of dislodged eggs along the wrack zone. All crabs, regardless of size, passed beneath racks 10 cm (4 inches) tall or more, indicating that the regulated rack height of 30.5 cm (12") is abundantly precautious to allow crab movement beneath racks. Farm/control census of crabs remaining on farms during low tide observed 853 crabs total, with no evidence of differing crab numbers among farmed and control transects. Only two of 853 (<0.5%) crabs were obstructed by farm gear, and more crabs were present on nesting beaches inshore of farms compared to adjacent farm-free areas. The proportion of crabs flipped (stranded) at low tide within nesting habitats was constant regardless of farm presence. Dislodged eggs in the wrack zone were observed most frequently in the center of the survey area, and were not concentrated near farms suggesting that in 2016, shorebird foraging opportunities were not coincident with farm locations.

LEVELS OF *VIBRIO* SPP. AFTER DESICCATION AND RE-SUBMERGENCE OF OYSTERS STORED IN THREE COMMON GEAR TYPES IN ALABAMA

Whitney A. Neil[1]*, Victoria L. Pruente[2], Byron Webb[3], William C. Walton[2], and Jessica L. Jones[1]

[1]Gulf Coast Seafood Laboratory, U.S. Food and Drug Administration, 1 Iberville Drive, Dauphin Island, Alabama 36528 USA

[2]Auburn University Shellfish Lab, 150 Agassiz St., Dauphin Island, Alabama 36528 USA

[3]Alabama Department of Public Health, 250 N. Water Street, Mobile, Alabama 36602 USA

Whitney.neil@fda.hhs.gov

The marine bacteria, *Vibrio parahaemolyticus* (Vp) and *Vibrio vulnificus* (Vv), can cause gastrointestinal illness in humans after consumption of raw or undercooked shellfish. Both Vp and Vv grow quickly in warm temperatures, so oyster farmers must consider the effect that routine handling practices, such as desiccation to reduce biofouling, have on *Vibrio* levels. A recent study in Alabama (AL) indicated that elevated *Vibrio* levels from desiccation of oysters in an Adjustable Longline System (ALS) returned to baseline after a seven day re-submergence. The current goal was to determine if a seven day submergence time is suitable for oysters desiccated in OysterGro (OG) floating cages and bottom cages (BC).

Four trials were conducted in AL during the fall of 2017. Oyster samples from each gear type (ALS, OG, and BC) were collected prior to desiccation, after a 24 hour desiccation, and after a seven day re-submergence in their respective gear. Control samples were collected from each gear type. Duplicate samples were analyzed using MPN-Real-time PCR.

After a seven day re-submergence, mean *Vibrio* levels in control and desiccated oysters, respectively, were 3.3 and 4.1 log MPN/g

(Vp) and 4.2 and 3.7 log MPN/g (Vv) in ALS; 3.3 and 4.0 log MPN/g (Vp) and 4.1 and 3.6 log MPN/g (Vv) in OG; and 4.3 and 4.1 log MPN/g (Vp) and 4.2 and 4.0 log MPN/g (Vv) for BC. None of these differences were statistically significant. These preliminary data suggest that a seven day re-submergence time may be suitable for desiccated oysters in multiple gear types.

NAVIGATING THE COMPLEXITY OF AQUACULTURE PERMITTING: UNDERSTANDING HOW THE PIECES FIT TOGETHER THROUGH TWO CASE STUDIES

Amanda Nichols* and Catherine Janasie

University of Mississippi, National Sea Grant Law Center, P.O. Box 1848, University, Mississippi 38677 USA

alnichol@olemiss.edu

Federal permitting issues often pose problems for shellfish aquaculturists in coastal areas. Navigating these difficulties is complicated and oftentimes requires specialized expertise to achieve success. This presentation will provide an overview of two case studies examining the intersection of federal law and aquaculture permitting.

The first case study focuses on the Endangered Species Act (ESA). Passed by Congress in 1973, the ESA is a broad mandate for species and habitat protection, and the statute's provisions could have major implications for aquaculture operations. This presentation will provide an overview of the Red Knot listing to illustrate how a threatened bird species impacted the federal permitting of aquaculture operations on the New Jersey coastline. Both Section 7 consultation, which applies to the actions of federal agencies, and Section 9 take, which applies to the actions of any person, came into play.

The second case study examines the impact of Nationwide Permit 48, reauthorized by the U.S. Army Corps of Engineers in 2017. NWP 48 permits commercial shellfish aquaculture activities predicted to have minimum individual and cumulative impacts. However, regions and states can control the extent to which the NWP is implemented in particular geographic areas—allowing for individualization that can make aquaculture permitting confusing and complicated from place to place.

A NOVEL LOW-VOLUME PORTABLE PUMP SYSTEM FOR SAMPLING LARVAL SHELLFISH IN SHALLOW, TURBULENT, 'DIRTY' ENVIRONMENTS

Owen C. Nichols* and Christine A. Hudak

Center for Coastal Studies, 5 Holway Avenue, Provincetown, Massachusetts 02657 USA

nichols@coastalstudies.org

The East Harbor coastal lagoon system in Truro, Massachusetts (MA), has been artificially isolated from Cape Cod Bay since 1868, when its inlet was filled by a causeway. A drainage system was installed in 1894 to allow rainwater to escape. The lack of tidal flow caused salinity and water quality to decline over the last century. Following a severe oxygen depletion event and fish kill, the clapper valves in the drainage pipe were opened in 2002, allowing limited tidal exchange with Cape Cod Bay. Since the restoration of tidal flow, native fauna have reestablished in East Harbor, including horseshoe crabs (*Limulus polyphemus*) and several species of bivalves, notably the soft-shell clam (*Mya arenaria*), northern quahog (*Mercenaria mercenaria*), and blue mussel (*Mytilus edulis*). To evaluate the degree to which East Harbor maintains self-sustaining marine benthic invertebrate populations and supplies larvae to adjacent coastal waters, a pilot study of planktonic larval dynamics was begun in 2016. Comparison of plankton samples collected at the drainage pipe during ebb and flood tides can be used to determine the amount and direction of net larval flux between the East Harbor system and Cape Cod Bay; however, zooplankton sampling in shallow, turbulent, 'dirty' environments is fraught with challenges, rendering quantitative sampling using traditional methods difficult. A novel low-volume portable pump sampler was developed and tested for this application in summer 2017. Preliminary comparisons indicated that samples obtained with the pump system were similar in species composition and size frequency to those obtained with a traditional conical net.

BABYSITTING BABY SQUID: *IN SITU* MONITORING OF LONGFIN INSHORE SQUID EGG DEPOSITION AND EMBRYONIC DEVELOPMENT

Owen C. Nichols[1,2]*, Katie Groglio[3], and Ernie Eldredge[4]

[1]Center for Coastal Studies, 5 Holway Avenue, Provincetown, Massachusetts 02657 USA

[2]University of Massachusetts-Dartmouth, School for Marine Science and Technology, 836 South Rodney French Boulevard, New Bedford, Massachusetts 02744 USA

[3]Harvard University, Northwest Building, Room B239, 52 Oxford Street, Cambridge, Massachusetts 02138 USA

[4]Chatham Fish Weirs Enterprises, 3 Champlain Road, Chatham, Massachusetts 02633 USA

nichols@coastalstudies.org

Knowledge of squid early life history is relatively poor despite its importance for fisheries management. The longfin inshore squid (*Doryteuthis pealeii*) is a commercially important species harvested extensively along the northeastern U.S. continental shelf. In order to understand the effects of fishing and environmental variability on *D. pealeii* in an inshore spawning ground (Nantucket Sound, MA), egg deposition and embryonic development were monitored *in situ* at commercial fish weirs in spring and summer 2008-2016. Logbooks were maintained in which catch (including the presence of egg masses) and effort data for each weir were recorded daily. Seawater temperature was recorded using data loggers affixed to the weirs. Newly deposited egg masses were transferred to a mesh enclosure on an opportunistic basis and placed immediately adjacent to the weir to permit semiweekly retrieval and sampling. Samples (five randomly chosen 'fingers' excised from a mass) were

chilled and transported to a nearby wetlab for microscopic examination to determine embryonic development stage. Hatch timing was determined via direct observation of paralarvae emerging from egg masses and development time was calculated as the number of days between egg mass deposition and hatching. The timing and duration of egg mass deposition varied between years. Embryonic development time of 15 egg masses ranged from 12-34 days and generally decreased at warmer temperatures. *In situ* observations were consistent with the findings of laboratory studies of *D. pealeii* and other loliginid squids.

CHAIN REACTION? DEVELOPMENT AND TESTING OF A MODIFIED SEA SCALLOP DREDGE TO REDUCE FLATFISH BYCATCH

Owen C. Nichols[1]*, Michael V. Pol[2], David M. Chosid[2], and Beau Gribbin[3]

[1]Center for Coastal Studies, 5 Holway Avenue, Provincetown, Massachusetts 02657 USA

[2]Massachusetts Division of Marine Fisheries, 1213 Purchase Street, New Bedford, Massachusetts 02740 USA

[3]High Pressure Fisheries, PO Box 1851, Provincetown, Massachusetts 02657 USA

nichols@coastalstudies.org

Bycatch of heavily exploited flatfish stocks, particularly yellowtail flounder (*Limanda ferruginea*), threatens access to the northeast U.S. sea scallop (*Placopecten magellanicus*) fishery by triggering accountability measures such as area closures if annual catch limits are exceeded. Due to the variable nature and small scale of the Gulf of Maine scallop fishery, a simple, easily-applied dredge modification holds promise as a flatfish bycatch reduction measure. Based on underwater observations of flounder behavior by local (Provincetown, MA) fishermen, a sea scallop dredge was modified with easily removable 'tickler' chains to stimulate flatfish to swim out of the dredge's path. This simple 'TickleDredge' design was developed and tested on board a commercial scallop fishing vessel in the southern Gulf of Maine during 2016 and 2017. Both real-time and recorded underwater video proved particularly valuable for refining the size and arrangement of the tickler chains as well as optimal towing speed and scope for testing. Comparisons of paired tows indicated slight increases in catch of scallops as well as some flatfish and non-target species with the TickleDredge modification, but no significant differences in catch between modified and standard dredges were observed. Overall rates of bycatch were low.

PUBLIC HEALTH AND PERSONAL LIVELIHOODS: A CASE STUDY OF OYSTERS AND NOROVIRUS IN HAMMERSLEY INLET, PUGET SOUND

Marisa R. Nixon

Washington State Department of Health, 243 Israel Road SE, Tumwater, Washington, 98501 USA

marisa.nixon@doh.wa.gov

Hammersley Inlet in Washington State is a highly productive growing area for oysters that provide an important source of income, employment and recreation in the region. In late winter and early spring 2017, Hammersley Inlet was implicated in a shellfish-transmitted norovirus outbreak that resulted in growing area closures and recalls, significantly impacting small, local shellfish farmers.

The Washington State Department of Health (DOH) undertook a multi-faceted investigation to examine the event and its impacts. From a technical perspective, in order to better understand local dilution rates and the accumulation of viral pathogens in shellfish, DOH and several partners completed a hydrographic dye study of waste water treatment plant (WWTP) effluent in Hammersley Inlet in November 2017. Shellfish staged in the study area also had their tissue tested for several pathogens, including norovirus.

This technical study was augmented by interviews with local shellfish farmers to inform an economic impact assessment and livelihood characterization of the shellfish industry in the area affected by the outbreak, closures and recalls. Moving forward, increasing pressure from human development and changing environmental conditions may affect the likelihood of norovirus infection in shellfish, which could prove detrimental to the local economy. This research has implications for shellfish sanitation policy as it pertains to norovirus, and for the way that local communities may need to adapt their livelihoods around long-term public health concerns.

A TOOL FOR SEED STOCK MANAGEMENT IN COMMERCIAL OYSTER NURSERIES

Ana Nobre[1]*, Filipe Soares[2], João G. Ferreira[2], François Hubert[3], and Luisa M.P. Valente[1,4]

[1]CIMAR/CIIMAR—Centro Interdisciplinar de Investigação Marinha e Ambiental, Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos, S/N, 4450-208 Matosinhos, Portugal

[2]DCEA, Fac. Ciências e Tecnologia, Universidade Nova de Lisboa, Qta Torre, 2829-516 Monte de Caparica, Portugal

[3]Bivalvia-Mariscos da Formosa, Lda. Piscicultura da Meia-Légua. Cova da Onça - Caixa Postal 491ª, 8700-177 Olhão, Portugal

[4]ICBAS - Instituto de Ciências Biomédicas de Abel Salazar, Universidade do Porto, Rua Jorge Viterbo Ferreira 228, 4050-313 Porto, Portugal

nobreamd@gmail.com; anobre@ciimar.up.pt

Models designed to provide practical guidance about food limitation in oyster nurseries can support seed stock management; however, most of the available shellfish models are developed for adult oysters and seldom target farmer, the end-users of these models. The goal of this work is to present a nursery model application for seed stock management, which is available online for widespread use at http://seaplusplus4.com/oysterspatbud.html. This approach applies to nurseries, including floating upwelling systems (FLUPSY) or land-based tanks, and is implemented for the Pacific oyster (*Crassostrea gigas* Thunberg). The model was evaluated with published experimental dataset and was further tested to simulate the application of a general rule of thumb regarding spat holding capacity for a given nursery. The model can be used by Pacific oyster farmers to improve the application of general rules of thumb and estimate stock biomass to hold in their nursery as a function of typical external food concentrations. Herein is illustrated the application of this model to a nursery located in a Southwestern European coastal lagoon.

INDEX SITE SURVEYS FOR OLYMPIA OYSTERS (*OSTREA LURIDA*) IN BRITISH COLUMBIA—2009 TO 2017

T.C. Norgard[1], M.I. Bigg[2*], S.E.M. MacConnachie[3], J.L. Finney[4], and G.E. Gillespie[5]

[1]Fisheries and Oceans Canada, Offshore Marine Protected Areas, Marine Spatial Ecology and Analysis Section, 3190 Hammond Bay, Road, Nanaimo, B.C. Canada, V9T 6N7

[2]Fisheries and Oceans Canada, Aquatic Resources Research and Assessment Division, 3190 Hammond Bay Road, Nanaimo, B.C. Canada, V9T 6N7

[3]Fisheries and Oceans Canada, Aquatic Ecosystem and Marine Mammal Science, 3190 Hammond Bay Road, Nanaimo, B.C. Canada, V9T 6N7

[4]Fisheries and Oceans Canada, GIS Data Program, 3190 Hammond Bay Road, Nanaimo, B.C. Canada, V9T 6N7

[5]Fisheries and Oceans Canada (Retired), 3190 Hammond Bay Road, Nanaimo, B.C. Canada, V9T 6N7

michelle.bigg@dfo-mpo.gc.ca

The Olympia oyster (*Ostrea lurida* Carpenter, 1864) was designated a species of Special Concern by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) in 2000 and listed as Special Concern under the Canadian Species at Risk Act (SARA) in 2003. A management plan was developed and posted to the SARA Public Registry in 2009; one of the objectives was to ensure maintenance of the relative abundance (density) of Olympia oyster at index sites between 2008 and 2013. In 2009 a Science Advisory Report was completed on the establishment of index sites. Fourteen index sites were chosen to monitor changes in relative abundance spanning the majority of the Olympia oyster range in Canadian waters. All fourteen sites have been surveyed at least twice and most have been surveyed three times since 2009. At each site the density, length frequency and calculation of bed area have been completed. Relative densities ranged from 507 ± 74.1 oysters m^{-2} at Port Eliza Beach 3 in 2013 to 0.6 ± 0.4 at Bacchante Bay in 2012. Densities varied across sites and years, but in most cases differences in survey design preclude meaningful discussion of differences or trends in density. These surveys will serve as baseline information in future examination of variability and trends in density at Olympia oyster index sites in British Columbia.

A HIERARCHICAL BAYESIAN SURPLUS PRODUCTION MODEL FOR BLUE CRAB (*CALLINECTES SAPIDUS*) IN THE NORTHERN GULF OF MEXICO

Megumi Oshima* and Robert Leaf

The University of Southern Mississippi, Division of Coastal Sciences, School of Ocean Science and Technology, Mississippi, USA

Megumi.oshima@usm.edu

Assessment of stocks such as blue crab (*Callinectes sapidus*) in the northern Gulf of Mexico (nGOM) can be challenging because age structured approaches cannot be used. To overcome this and data availability challenges, a surplus production model was constructed for the gulf-wide stock evaluated in a Hierarchical Bayesian (HB) framework which provides a way to incorporate abundance dynamics from data rich regions. The HB framework allows the inclusion of prior information and hyperparameters to facilitate estimation of parameters to explicitly model uncertainty. The objectives of this study were to develop a HB surplus production model for assessing the nGOM blue crab stock, evaluate the sensitivity of the model to the inclusion of fishery independent indices of abundance, and determine harvest strategies consistent with proposed fishery reference points. Commercial landings and fishery-independent survey data from the five Gulf States were incorporated. State-specific hyperparameters - population growth rate, carrying capacity, and catchability - were estimated and median values were used to determine fishery reference points, maximum sustainable yield (MSY), and associated biomass (B_{MSY}) and fishing mortality rate (F_{MSY}). Alternative model runs were conducted to evaluate the sensitivity of parameter estimates to the inclusion of indices of abundance. Lastly, model predictive power was assessed by projecting stock abundances under a suite of catch scenarios. Overall, this model can be used to assess the blue crab population at state and Gulf-wide scale, as well as inform future management decisions by identifying areas of greater uncertainty and evaluating the impact of including particular survey data.

CRACKING THE SHELL: AN INVESTIGATION OF SHELL REPAIR IN THE OYSTER, *CRASSOSTREA VIRGINICA*

Alyssa Outhwaite[1]*, Douglas C. Hansen[2], and Karolyn M. Hansen[1]

[1]University of Dayton, Department of Biology, 300 College Park, Dayton, Ohio 45469 USA

[2]University of Dayton, Research Institute, 300 College Park, Dayton, Ohio 45469 USA

outhwaitea1@udayton.edu

Molluscan shell formation has been an intriguing phenomenon for decades and current research efforts represent a paradigm shift in how oyster shell formation occurs. The matrix mediated model relies on bulk secretion of organic and mineral precursor components into the extrapallial space, while the cellular mediated model includes cells and vesicles as transport vectors for organic and mineral components. The current research focuses on the potential role of hemocytes in moving organic and mineral components to the shell formation front. A protein biomarker, the amino acid L-3,4-dihydroxyphenylalanine (L-DOPA), is unique to the proteins involved in insoluble organic matrix formation. Tracking the location and temporal occurrence of L-DOPA-containing proteins reveals the potential role in shell repair.

Three notch-repair experiments were conducted: a short-term 36 hour notch-repair study, a mid-term seven day notch-repair study, and a long-term eight week notch-repair study. At discrete time intervals, selected oyster compartments of hemocytes, mantle tissues, hemolymph, and nascent shell were sampled to determine the spatial and temporal distributions of the DOPA biomarker. Preliminary results show an increase in DOPA concentration in hemolymph from 0 to 48 hours. Conversely, hemocytes show a decrease in DOPA over time, with the greatest amount of DOPA present at 0 hours and a subsequent decrease over the course of repair. These results suggest that hemocytes are selectively shuttling and releasing protein resources to areas of shell repair and provide additional support for the cellular mediated shell formation model, where hemocytes play an active role in materials transport.

LOCATION, LOCATION, LOCATION: POPULATION DIFFERENCES IN RESPONSE TO OCEAN ACIDIFICATION IN BLUE MUSSELS

Dianna K. Padilla[1*], Nils Volkenborn[2], Samuel Gurr[2], Lisa Milke[3], Shannon Meseck[3], Allison Rugila[1], Dylan Redman[3], Mark Dixon[3], David Veilleux[3], Alyssa Liguori[1], and Maria Rosa[1]

[1]Stony Brook University, Department of Ecology and Evolution, Stony Brook, New York 11794-5245 USA

[2]Stony Brook University, School of Marine and Atmospheric Sciences, Stony Brook, New York 11794-5000 USA

[3]NOAA/NMFS, 212 Rogers Ave., Milford, Connecticut, 06460 USA

Dianna.Padilla@stonybrook.edu

Recent information suggests that bivalve molluscs are particularly sensitive to the impacts of ocean acidification (OA); however, it is not known whether differences among local environmental conditions has selected for animals with different sensitivities to stressors, or whether responses to environmental stressors are phenotypically plastic, allowing animals with broad physiological tolerances to be robust to environmental stress. Traditional metrics of the effects of stress integrate over long periods of time (e.g., growth), are a snapshot of animal state (e.g., condition index), or require isolation of animals from their environment (respiration rate); however, infrared and Hall-Effect sensors allow monitoring heartbeat and valve gaping (time spent filtering) with high temporal resolution over extended periods of time, allowing detection of immediate metabolic and behavioral responses to changes in environmental conditions. Blue mussels, *Mytilus edulis*, were collected from sites around Long Island Sound (LIS) with different water quality conditions to test whether mussels from more stressful environments are more resilient to the impacts of OA. Mussels from different populations showed different stress responses to OA (manipulating aragonite saturation). Mussels from eastern and western LIS had elevated heartbeat rates in response to OA, while animals from central LIS showed no response to even extreme OA conditions, suggesting site-specific resilience to the environmental stress of OA.

THE EFFECT OF HIGH SALINITY ON THE ABUNDANCE, ANTIBIOTIC RESISTANCE, AND GENETIC DIVERSITY OF *VIBRIO PARAHAEMOLYTICUS* IN AN OYSTER RELAY STUDY

Salina Parveen[1*], Sara Elmahdi[1,2], Michael Jahncke[3], John Jacobs[4], and John Bowers[5]

[1]University of Maryland Eastern Shore, Department of Agriculture, Food and Resource Sciences, Princess Anne, Maryland 21853 USA

[2]University of Hail, Department of Clinical Nutrition, Hail, KSA 2440 Saudia Arabia

[3]Virginia Tech., Virginia Seafood Agricultural Research and Extension Center, Hampton, Virginia 23669 USA

[4]National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Cooperative Oxford Lab, Oxford, Maryland 21654 USA

[5]U.S. Food and Drug Administration, College Park, Maryland 20740 USA

sparveen@umes.edu

The estuarine bacterium, *Vibrio parahaemolyticus* (*Vp*), is naturally occurring and the leading cause of seafood-associated infections in the USA. Though multiple-antibiotic resistant *Vp* has been reported, resistance patterns in *Vibrios* are not as well documented as other food-borne bacterial pathogens. Salinity relaying (SR) is a Post-Harvest Processing treatment to reduce the abundance of *Vp* in shellfish harvested during warmer months. The purpose of

this study was to evaluate the abundance, antimicrobial susceptibility (AMS), and genetic diversity of *Vp* in oysters during an oyster relay study. Several SR trials (salinity ranging from 29-34 ppt.) were carried out in on-shore closed recirculating tanks and in the Chesapeake Bay. After 7, 14 and 21 days of relaying, oysters were analyzed for *Vp* using Multiplex Real Time PCR. A total of 296 isolates recovered from oysters before and during the 21 day relaying study were tested for AMS to 20 different antibiotics using micro broth dilution and Pulsed-Field Gel Electrophoresis (PFGE) was used to study the genetic profiles of *Vp*. The initial levels of *Vp* ranged from 3.70 to 5.64 log MPN/g with 1-3 log reductions after relaying. More than 30% and 8% of *Vp* isolates were resistant to at least one and multiple antimicrobials, respectively. All isolates demonstrated high genetic diversity, even among those isolated from the same site and having a similar AMS profile. No significant effect of the high salinity on AMS or PFGE profiles of *Vp* was observed.

EFFECTS OF CONTROLLED, LARGE-SCALE REMOVAL OF *ZOSTERA JAPONICA* ON ESTUARINE FAUNA

Kim Patten* and Scott Norelius

Washington State University, Long Beach Research and Extension Unit, 2907 Pioneer Road, Long Beach, Washington 98630 USA

pattenk@wsu.edu

Manipulative experiments were done to evaluate the ecological impacts of large-scale removal of Japanese eelgrass (*Zostera japonica*) from tideflats of Willapa Bay, Washington. Completely randomized replicated paired plots (0.2 to 2.0 ha in size) were established using herbicide to remove *Z. japonica*. Treated and untreated tideflats were compared over three years for differences in populations of ichnyofauna, avifauna, and macrofauna. Plots where *Z. japonica* had been removed had seven times the density of ESA-listed green sturgeon (*Acipenser medirostris*) foraging pits compared to plots with *Z. japonica*. Based on kick net transect surveys, there were no consistent differences between paired sites with and without Z. *japonica* for small bottom-feeding forage fish, shrimp (*Crangon septemspinosa*), or Dungeness crab (*Cancer magister*). Avifauna were assessed by bird, fecal droppings and/or feeding pit density. Dabbling ducks tended to forage more in *Z. japonica* plots than on plots where it was removed, but there was no trend for shorebird usage. There were no treatment effects on the populations of Mollusca and Arthropoda; however, Annelida benthic fauna counts were higher in sediment with *Z. japonica* than where it was removed. Greater than 90% of the annelid population in *Z. japonica* sites consisted of the invasive Japanese polydorid tube worm, *Pseudopolydora paucibranchiata.* Removal of Z. *japonica* did not affect Manila clam (*Venerupis philippinarum*) recruitment, but increased total clam yield and size at harvest.

UNUSUAL 2017 MICROALGAL BLOOM HAS RIPPLE EFFECTS ON THE BIVALVES OF HOOD CANAL

Blair M. Paul* and Seth K. Books

Skokomish Nation, Department of Natural Resources, N. 541 Tribal Center Road, Skokomish, Washington 98584 USA

bpaul@skokomish.org

Visitors to the Hood Canal during the summer of 2017 saw an unusual sight, turquoise water that looked more tropical in color than those typically seen in a temperate water body. Even life-long residents of the area do not remember ever seeing the canal look so striking. It was clear something was happening in the water that was different. By taking water samples and identifying what algae was growing, a reason for the color was determined, but what effect would it have on the shellfish resources so many depend on for sustenance and income? All anyone could do was watch as the impacts unfold in whatever way they would play out. This session will chronicle the events that were observed in 2017 in the Hood Canal related to the Coccolithophore bloom and observations from researchers, biologists, tribal fishermen, shellfish growers, and citizens who participated in the observation systems in place. These observations will be framed in relation to whether the microalgae were good, bad, or indifferent to the food web that feeds the abundant shellfish of the Hood Canal.

OYSTER RESTORATION IN HARRIS CREEK, MARYLAND: A PROGRESS REPORT

Kennedy T. Paynter, Drew Needham, and Audrey McDowell

University of Maryland, Marine Estuarine Environmental Sciences, College Park, Maryland 20742 USA

paynter@umd.edu

A large-scale oyster reef restoration effort was undertaken in Harris Creek, a small tributary in the mesohaline region of Chesapeake Bay in 2011. After an initial population survey, a plan for reconstruction of historic oyster reefs in Harris Creek was developed and has been implemented over the last six years. Juvenile oysters (spat) settled on shell in the University of Maryland oyster hatchery were used to "plant" oysters in high densities on various historical reef locations. In some areas, where sediment had covered the original benthic shell substrate, alternate substrates such as granite rubble were used to stabilize the bottom. Between 2011 and 2016, 2.334 billion spat on shell were planted on 90 unique sites across 13 historic oyster bars covering approximately 140.9 hectares. For the 2012 year class, 2.13% of the oyster spat planted were still alive in 2015, were 99 mm in shell height, and present on restored reefs at densities of 35 oysters/m^2. A robust natural spat set was detected in 2016 at densities upwards of 10/m^2. It is unknown if these spat were the product of restored broodstocks in the Creek, settled from native broodstocks in the area as a result of restoration or are simply part of a natural cycle. In addition, a robust benthic community of oyster reef related species recruited to the restored sites.

RECRUITMENT PATTERNS OF OLYMPIA OYSTER, *OSTREA LURIDA* (CARPENTER 1864), IN THE GORGE WATERWAY—ENHANCEMENT FROM NEW BRIDGE PILINGS

Ben Pearse*, Laura Kravac, Sarah Schroeder, Heather Wright, Joachim Carolsfeld, and Louise Page

434 Russel Street, Victoria, BC V9A 3X3, Canada

btpearse@gmail.com

The Olympia oyster, *Ostrea lurida*, is the only native oyster in British Columbia and is listed as a species of Special Concern under the Species At Risk Act. Historically, Olympia oysters were used as a food source for First Nations, but were virtually wiped out by 1920 due to their popularity during the gold rush and the introduction of other oyster species. The Gorge Waterway is a restricted flow tidal inlet in Victoria, British Columbia, with a resilient native oyster population. Despite being at the centre of the oyster market, the Gorge Waterway has retained an anomalously large population of Olympia oysters. Spat recruitment dynamics have been monitored for the last four years, including during construction of a bridge with textured concrete pilings to foster oyster settlement. Significant settlement of oysters on these pilings since 2014 of up to 1,100 adult oysters per m^2 and an estimated 150,000 total oysters, has led to peak spatfalls in 2015, 2016, and 2017 of up to 46,000 spat per m^2 – comparable to the highest on the Pacific Coast. Nevertheless, long-term survival is low, with nearly 80% of oysters on the bridge now deceased. The Gorge Waterway is potentially a substantial natural hatchery of native oysters. We are seeding reefballs to transfer to outer harbor locations for a pilot transfer.

THE CORE AND ACCESSORY GENOME OF *VIBRIO PARAHAEMOLYTICUS*, A PATHOGEN OF PENAEID SHRIMP

Sarah Mae U. Penir[1,2,*] and Cynthia P. Saloma[1,2]

[1]National Institute of Molecular Biology and Biotechnology, University of the Philippines Diliman, Quezon City, Philippines

[2]Philippine Genome Center, University of the Philippines System, Quezon City, Philippines

smupenir@gmail.com

Shrimp/prawn are among the major export commodities of the Philippines. One well-documented pathogen of penaeid shrimp is *Vibrio parahaemolyticus*, a Gram-negative, halophilic bacterium with a single polar flagellum. Most environmental or seafood-isolated strains of *V. parahaemolyticus* are not pathogenic, but some strains become capable of causing diseases due to the presence of certain virulence factors. In order to gain insight on the pathogenicity of the strains of the bacterium, pangenome analysis was implemented on the assembled whole-genome sequences of 137 *V. parahaemolyticus* isolates collected from the hepatopancreas of penaeid shrimp obtained from both outbreak (AHPND, luminescent vibriosis, WSSV-positive, outbreaks of unknown etiology) and non-outbreak sites in 12 Philippine provinces. A total of 2,333 core genes encoded in 2.30 Mb of sequence are conserved in all ten reference whole genomes of the species. *In silico* subtractive hybridization of the core genes on the draft genomes of the 137 isolates and 10 additional shrimp-associated *V. parahaemolyticus* strains reveal a large collection of 31,000 protein-coding accessory genes (present in 5% - 95% of the isolates). Obtained genomic information was compounded with epidemiological data to generate knowledge on the occurrence, and regional and local transmission patterns of shrimp-isolated *V. parahaemolyticus*. A thorough understanding of the nature of the genome of *V. parahaemolyticus* will pave the way for the establishment of effective shrimp disease management interventions, such as the development of fast and affordable detection tools, which can preclude further severe losses in shrimp production.

A REVIEW OF RECENT FISHERY-INDEPENDENT MONITORING DATA FOR BLUE CRABS IN THE GULF OF MEXICO: THE DISCONNECT BETWEEN SETTLEMENT AND SUBSEQUENT JUVENILE ABUNDANCE

Harriet Perry[1]*, Lillian Collins[1], John Anderson[1], Donald Johnson[1], Guillermo Sanchez-Rubio[1], Rick Burris[2], and Tom Wagner[3]

[1]Gulf Coast Laboratory, Research 703 East Beach, Ocean Springs, Mississippi 39564 USA

[2]Mississippi Department of Marine Resources, 1141 Bayview Avenue, Biloxi, Mississippi 39530 USA

[3]Texas Parks & Wildlife Department, 702 Navigation Circle, Rockport, Texas 78382 USA

harriet.perry@usm.edu

Data from a fishery-independent study of blue crab (*Callinectes sapidus*) settlement are reviewed to examine the relationship between recruitment, measured as settlement, and subsequent abundances of juvenile blue crabs. Megalopal settlement data are derived from a series of collections taken in the years 1991-2001, 2010, 2012, and 2014-2016 in the Biloxi and Belle Fountaine areas of Mississippi Sound. Published data attribute fluctuations in numbers of settling megalopae to variations in seasonal wind forcing or basin-scale events associated with Loop Current (LC) intrusions and spin-off of warm core eddies. Huge increases in settlement occurred in the fall of 2016. Average daily settlement in October of that year exceeded 1,500 megalopae per day with a yearly average of 652 per collector. Next highest yearly averages occurred in 1991 with 655 megalopae/collector in August and a yearly average of 295. In all other years, average annual catch was below 55 megalopae/collector. The large settlement events in 2016 did not result in increased numbers of juvenile crabs in fishery-independent seine and trawl monitoring samples.

FILTER-FEEDING BIVALVES CAN ENHANCE *ZOSTERA MARINA* REPRODUCTIVE OUTPUT

Bradley J. Peterson*, Lisa J. Jackson, and Bradley T. Furman

School of Marine and Atmospheric Sciences, Stony Brook University, New York 11790 USA

Bradley.Peterson@stonybrook.edu

The presence of suspension-feeding bivalves associated with seagrass beds are known to increase porewater nutrients, which can be used by seagrass to enhance vegetative leaf growth. To test for a morphological response of seagrass reproductive shoots to bivalve presence, five small patch replicates (<2.0 m^2) were selected within a developing *Zostera marina* meadow for each of six treatments including fertilizer addition, live hard clams, clam shell, clam shell and fertilizer, mussels, and ambient. Fertilizer stakes consisted of a nutrient N:P:K ratio of 15:3:3 and were placed in the sediment in the late fall 2013, early spring, and mid-summer. Live hard clams and shells were placed in the patches at four times the density of the fertilizer in late fall. Mussel spat naturally settled in the patches in spring 2013, grew to adult sizes and migrated to sediment by late fall that year. In June 2014, at three consecutive week time-points, ten flowers per patch were collected and morphometrics analyzed as well as the stage of ovary development. Flower morphology influencing seed output was altered, indicating bivalves' natural presence in seagrass meadows could result in hot spots of reproductive success with important ecological consequences for meadow development, maintenance and stability.

EFFECT OF ANOXIA ON THE VIRULENCE OF *VIBRIO CORALLIILYTICUS* AND ITS IMPACT ON THE MORTALITY AND IMMUNE FUNCTION OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Britney L. Phippen[1*], Anna V. Ivanina[1], Inna M. Sokolova[2], and James D. Oliver[1]

[1]University of North Carolina at Charlotte, Department of Biological Sciences, 9201 University City Blvd, Charlotte, North Carolina, 28223 USA

[2]University of Rostock, Department of Marine Biology, Pressestelle 18051 Rostock, Germany

bphippen@uncc.edu

The extent of the coastal dead zones is increasing with global warming which can increase oyster vulnerability to potential pathogens. An important coral pathogen, *Vibrio coralliilyticus* has recently been shown to also cause infection of fish and shellfish, including eastern and Pacific oyster larvae. Thus, its effects on adult oysters under anoxic conditions was examined including host mortality, immune response, and expression of genes involved in virulence and intracellular signaling by the pathogen. The combination of *V. coralliilyticus* and anoxia resulted in 100% mortality after six days of exposure, with the first deaths occurring after just three days. In contrast, 100% of oysters survived 18 days of exposure to anoxia or bacterial stress alone. Concomitant anoxia and pathogen stress resulted in a significant increase in the hypoxia inducible factor-1α, lectin, and key antioxidant enzymes in oyster immune cells. In *V. coralliilyticus,* anoxia exposure led to a significant increase of the expression of multiple virulence factors including zinc-metalloprotease, type-two and type-six secretion systems, and genes involved in both AI-2 and AI-3 pathways of quorum sensing. Other putative virulence factors (hemolysin and flagella biosynthesis) were increased under normoxia. This indicates that different virulence factors are activated in normoxia and anoxia possibly contributing to differential mortality of the hosts. Overall, we have shown the importance of *V. coralliilyticus* as a potential pathogen for adult oysters and indicate that anoxia may increase virulence of this bacterium via increased intracellular signaling, thereby enhancing host morbidity and mortality.

LEGAL REQUIREMENTS FOR THE USE OF WATERFRONT INFRASTRUCTURE BY SHELLFISH GROWERS IN RHODE ISLAND: CHALLENGES FOR INDUSTRY SUSTAINABILITY

Read Porter

Roger Williams University School of Law, Marine Affairs Institute / Rhode Island Sea Grant Legal Program, 10 Metacom Ave., Bristol, Rhode Island 02809 USA

rporter@rwu.edu

Shellfish growers require waterfront infrastructure for a variety of reasons, including for launching vessels, preparing and storing gear, loading and unloading product, and growing seed to a size suitable for growout. Inability to access this infrastructure poses a real threat to the economic sustainability of existing farms as well as to the expansion of aquaculture in Rhode Island.

This presentation will consider two ways in which laws and regulations may impede shellfish grower access to waterfront infrastructure. First, it will present research on restrictions on the use of public boat launches for commercial use. Imposition of such restrictions, which are common in other coastal states, could leave some Rhode Island growers without the ability to access their sites or require substantially longer transit times. This study will present a multi-state review of state laws on use of public boat launches to inform Rhode Island policy development.

Second, the presentation will consider the impact of state and local land use law on the availability of shellfish nursery facilities (notably FLUPSYs) in marinas. Nursery structures are a critical resource for growers and in Rhode Island are often located in marinas or dock complexes; however, these facilities may not wish to remain open to use by growers. This case study will discuss state coastal zone regulations and local ordinances that may affect whether and how growers can use these areas.

THE WARMING OF THE NORTHWEST ATLANTIC AS RECORDED BY THE OCEAN QUAHOG, *ARCTICA ISLANDICA,* WITH A NOTE ON CLIMATE CYCLES

Eric N. Powell[1*], Sara Pace[1], Roger Mann[2], and J.M. Klinck[3]

[1]Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, Mississippi 39564 USA

[2]Virginia Institute of Marine Science, Rt. 1208 Greate Road, Gloucester Point, Virginia 23062 USA

[3]Old Dominion University, Center for Coastal Physical Oceanography, Norfolk, Virginia 23529 USA

Eric.N.Powell@usm.edu

Ocean quahogs, the longest-lived, common non-colonial marine animal, support an important commercial fishery on the northeastern continental shelf. Both geographic and temporal differences (on a scale of decadal or longer) in growth rates exist throughout the range of the stock. Average growth rates increased significantly with birth year at a New Jersey and a Long Island site, both located in the southwestern portion of the stock, since initial colonization in the late 1700s, likely in response to increasing bottom water temperatures. That is, growth rates vary temporally with birth date, with younger animals growing over twice as fast in recent decades than those born decades previously, whereas at more northern sites off southern New England and on Georges Bank, changes in growth rates through time are limited. The fact that ocean quahogs record the rise in ocean temperatures after the Little Ice Age southeast of southern New England, yet demonstrate no evidence of such a rise in the southern New England and Georges Bank region, would suggest a differential response of ocean circulation and its control of bottom water temperature between the northern and southern portions of the Mid-Atlantic Bight over the last 200+ years. Besides a long-term rise in temperature, ocean quahogs record cyclic variations related to the Atlantic Multidecadal Oscillation and the North Atlantic Oscillation, suggesting that these animals are a repository of information on the evolution of oceanic bottom water temperatures on the Mid-Atlantic continental shelf since the end of the Little Ice Age.

EXPRESSED EXOME CAPTURE SEQUENCING (EECSEQ): A METHOD FOR COST-EFFECTIVE EXOME SEQUENCING OF NON-MODEL ORGANISMS

Jonathan B. Puritz[1,2]* and Kathleen E. Lotterhos[1]

[1]Northeastern University, Marine Science Center, 430 Nahant RD. Nahant, Massachusetts 01908 USA

[2]University of Rhode Island, Department of Biological Sciences, 120 Flagg RD, Kingston, Rhode Island 02881 USA

j.puritz@uri.edu

Exome capture is an effective tool for surveying the genome for loci under selection; however, traditional methods require *a priori* knowledge of exon sequences from an annotated genome and/or transcriptome. Here, a new method that creates cDNA probes from expressed mRNA is presented, which is then used to enrich genomic DNA for expressed exon sequences. The new method eliminates the need for costly probe design and synthesis. Four adult eastern oysters (*Crassostrea virginica*) were heat shocked at 36°C for one hour and four control oysters kept at ambient temperature. Stranded mRNA libraries were prepared for two exposed and two control individuals and pooled. Half of the combined library was used for probe synthesis and half was sequenced to evaluate the efficiency of capture. Genomic DNA from all eight individuals was enriched via captured probes, and sequenced directly. EecSeq had an average capture sensitivity of 86.8% across all known exons and over 99.4% sensitivity for expressed exons (i.e. exons with detectable levels of mRNA expression). For all mapped reads, over 47.9% mapped to exons and 37.0% mapped to expressed targets, which is similar to the success of capture in other species where probes were designed from genomic resources. EecSeq displayed even coverage within exons (i.e. no "edge effects") and coverage uniformly distributed across exon GC content. Across six replicate pools, 5,951 SNPs with a minimum average coverage of 80X were discovered, with 3,508 SNPs appearing in exonic regions. EecSeq provides comparable, if not superior, performance compared to costly, traditional methods.

TRANSCRIPTOMIC RESPONSES TO DERMO DISEASE IN SUSCEPTIBLE AND RESISTANT EASTERN OYSTERS

Dina A. Proestou[1]*, Kathryn Markey Lundgren[1], Jessica Moss Small[2], and Standish K. Allen Jr.[2]

[1]USDA ARS National Cold Water Marine Aquaculture Center, Shellfish Genetics Laboratory, Kingston, Rhode Island 02881 USA

[2]Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center, Gloucester Point, Virginia 23062 USA

dina.proestou@ars.usda.gov

Dermo resistance has long been a priority for eastern oyster breeding programs, yet the lack of simple methods to directly measure resistance limits genetic improvement of the trait. Laboratory challenge experiments were conducted to identify Dermo-resistant and -susceptible phenotypes among selectively-bred oyster families. Five oysters per treatment from each of three phenotypically divergent families were sampled at multiple time points over the course of the experiment to characterize parasite load trajectories and gene expression profiles. Indexed TruSeq libraries were constructed, pooled, and sequenced on the Illumina HiSeq, resulting in between 20 and 30 million reads per individual. Following QC, transcript abundances were quantified by mapping reads to the reference eastern oyster genome. Differences in gene expression between families, among treatments within a family, and within exposed treatments over time were evaluated using DESeq2. The largest number of differentially expressed genes (>2000) was detected in unexposed oysters from the different families. Four times more genes responded to exposure in the most resistant family

compared to the most susceptible family, with the most significantly differentially expressed transcripts associated with the negative regulation of peptidase activity and proteolysis. In addition, differences in gene expression profiles between exposed and control treatments were most pronounced at seven days post exposure. Using transcriptome data to further characterize Dermo-resistant and –susceptible phenotypes will be discussed.

EFFECTS OF TUMBLING AND REFRIGERATION ON THE ABUNDANCE OF *VIBRIO VULNIFICUS* AND *VIBRIO PARAHAEMOLYTICUS* IN CULTURED OYSTERS (*CRASSOSTREA VIRGINICA*)

Victoria L. Pruente[1,2*], William C. Walton[1], Jessica L. Jones[2]

[1]Auburn University, School of Fisheries, Aquaculture, and Aquatic Sciences, 203 Swingle Hall, Auburn, Alabama 36849 USA

[2]Gulf Coast Seafood Laboratory, U.S. Food and Drug Administration, 1 Iberville Drive, Dauphin Island, Alabama 36528 USA

vlp0006@auburn.edu

Off-bottom oyster aquaculture involves routine handling that exposes oysters to elevated temperatures. This can cause growth of *Vibrio parahaemolyticus* (*Vp*) and *V. vulnificus* (*Vv*), which are bacteria that are a public health concern when oysters are consumed raw. In this study, the effects of two common types of handling (tumbling and refrigeration) were examined on *Vibrio* levels in oysters both initially and after resubmersion. Both tumbling (tumbled, T; or not, NT) and refrigeration (refrigerated overnight, R; or not, NR) for four different experimental treatment combinations (TR, TNR, NTR, NTNR) were tested during a 24-hr removal from the water. Then, the recovery of *Vp* and *Vv* levels during a 14 day resubmersion period was examined. A set of non-treated oysters that remained submerged throughout the study was tested to monitor ambient *Vibrio* levels. Preliminary data revealed that *Vp* and *Vv* levels in non-refrigerated oysters (TNR, NTNR) significantly increased from ambient levels (4.0 and 4.1 log MPN/g respectively) immediately post-treatment (*Vp*: 5.4 and 5.3 log MPN/g, *Vv*: 5.1 and 5.5 log MPN/g respectively), while levels in refrigerated oysters (TR, NTR) significantly increased after one day of re-submersion (*Vp*: 5.2 and 5.5 log MPN/g, *Vv*: 5.2 and 5.5 log MPN/g, respectively). These data indicate that *Vibrio* levels in the treated oysters recovered to levels similar to ambient (*Vp*: 4.4 log MPN/gram, *Vv*: 4.8 log MPN/g) after 4 days of re-submersion. These results could help regulators make informed public health decisions regarding farmed oysters.

MOLECULAR AND MORPHOLOGICAL ANALYSIS OF BIVALVE SHELL BORERS OF THE GENUS *POLYDORA* FROM THE EASTERN UNITED STATES

Paul D. Rawson*, Lauren Rice, and Sara M. Lindsay

Univesity of Maine, School of Marine Sciences, Orono, Maine 04469 USA

prawson@maine.edu

Marine polychaetes in several genera, including *Polydora*, *Pseudopolydora,* and *Boccardia*, are known to excavate burrows in the shells of bivalves and other molluscs. While fascinating to natural historians because of their unique burrowing habits, worms that inhabit the shells of commercially important shellfish are considered pest species because their burrowing activity can negatively impact shellfish appearance, and severe infestations can lead to shellfish mortality. Using a combination of morphological analyses and sequencing of mitochondrial COX1 and nuclear 18S rRNA genes, the taxonomic affinity of polydorids sampled from the shells of scallops and oysters cultured at five shellfish farms located from Alabama to Maine were examined. It was found that the most common polydroid from these five farms was *Polydora websteri* and it was nearly identical at both genetic markers to *P. websteri* from Asia and Australia. Samples of worms fitting the description of *P. neocaeca* were obtained from both scallops and oysters at one site in Massachusetts. Morphological and molecular analyses suggest that *P. neoceaca* from this site is identical to *P. haswelli*, a species previously described from Japan. These same analyses provide evidence that worms sampled from one farm in Maine are identical to *P. onagawaensis*, another species first described from northeastern Japan. Taken together, the results of this study support the conclusions of Sato-Okoshi and others that shell-boring polychaetes in the genus *Polydora* have been inadvertently transported worldwide as a consequence of the movement of non-native commercially important shellfish.

IMPACTS OF TWO HARMFUL ALGAL BLOOM SPECIES ON DIPLOID AND TRIPLOID LARVAL AND JUVENILE OYSTERS

Kimberly S. Reece[1]*, Patrice L.M. Hobbs[1], William M. Jones III[1], Gail P. Scott[1], Thomas M. Harris[1,2] and Wolfgang K. Vogelbein[1]

[1]Virginia Institute of Marine Science, Department of Aquatic Health Sciences, The College of William and Mary, 1375 Greate Road, Gloucester Point, Virginia 23062 USA

[2]Vanderbilt University, Chemistry Department, 7330 Stevenson Center, Nashville, Tennessee 37235 USA

kreece@vims.edu

Late summer blooms of *Alexandrium monilatum* and *Margalefidinium* (formerly *Cochlodinium*) *polykrikoides* have been particularly intense and widespread throughout lower Chesapeake Bay in recent years. Reports of oyster mortalities, particularly of young animals, from local aquaculturists during and immediately following these blooms have prompted laboratory studies with diploid and triploid *C. virginica* larvae and spat. Laboratory bioassays have demonstrated acute dose dependent toxicity of York River *A. monilatum* to both larvae and spat, and of *M. polykrikoides* to larvae. Diploid and triploid animals responded similarly to both HAB spe-

cies. In all laboratory bioassays control mortality was less than 3%. Exposure to *M. polykrikoides* concentrations >1,000 cells/mL resulted in 80-100% larval mortality after 72-96 hr, while no mortality was observed in spat after 96 hr of exposure to *M. polykrikoides* at concentrations up to ~5,000 cells/mL. Exposure to *A. monilatum* at concentrations >1,000 cells/mL caused 80-100% larval mortality after 48 hr and 100% mortality at all concentrations after 72 hr. Oyster spat exposed to *A. monilatum* concentrations >800 cells/mL suffered 80-100% mortality after 72 hr. The toxin goniodomin A, produced by *A. monilatum*, was isolated from York River water samples collected during blooms and was found to cause rapid mortality (i.e. within 24 hours) in larval oysters at a concentration of 1 µg/mL. At a concentration of 0.1 µg/mL 100 % mortality was observed after 72 hr. Controlled laboratory and field studies are being done with juvenile and adult oysters to complement these small-scale bioassays.

INTERACTIVE TALK: DEVELOPING A SHELLFISH HATCHERY BIOSECURITY CERTIFICATION PROGRAM

Robert Rheault[1]*, David Bushek[2], Lisa Calvo[2], Ryan Carnegie[3], Karen Hudson[3], and Lori Gustafson[4]

[1]East Coast Shellfish Growers Association, 1623 Whitesville Rd., Toms River, New Jersey 08755 USA

[2]Rutgers University, Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, New Jersey 08349 USA

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

[4]Centers for Epidemiology and Animal Health, USDA APHIS Veterinary Services, 2150 Centre Ave, Building B, Mail Stop 2E6, Fort Collins, Colorado 80526 USA

bob@ecsga.org

A series of facilitated workshops supported by National Sea Grant, several state Sea Grant offices and the USDA APHIS Veterinary Services identified the development of a hatchery certification program as a key need to facilitate transfers of shellfish seed. Hatchery certification is a strategic action that can reduce the need for expensive surveillance and costly batch certifications while providing the biosecurity necessary to minimize disease transfer risk. Developing a viable hatchery certification system will increase regulatory confidence and promote industry growth. The concept of convening a Hatchery Certification Working Group to develop a hatchery certification program was universally accepted by industry and regulators alike. The goal is to develop protocols that are both protective of resources (cultured and wild stocks) and practical for both users and regulators. To that end, a working group was created and the group seeks input to identify needs and concerns as they work to create a viable program for implementation in the near future. In this interactive session, supported by NOAA Sea Grant 2017 Aquaculture Initiative, attendees will be introduced to the problem and the progress to date, then surveyed to identify concerns, oversights, weaknesses and alternatives. Presenters also seek to gauge the overall acceptance of implementing such a program from regulatory, industry and academic perspectives.

MAINTAINING LIVELIHOODS AND CULTURAL IDENTITY THROUGH TRIBAL SHELLFISH AQUACULTURE

Ralph Riccio*, Kelly Toy, Jim Parsons, and Kurt Grinnell

Jamestown S'Klallam Tribe, 1033 Old Blyn Highway, Sequim Washington 98382 USA

rriccio@jamestowntribe.org

Salmon and shellfish have been a mainstay of the Pacific Northwest Tribes for thousands of years and continue to be a crucial part of Tribal culture and economy. Obstructed water ways, degraded water quality, increased harvest pressure and poaching have substantially reduced fishery resources available to Pacific Northwest Tribes. While wild harvest opportunity continues to decline, aquaculture provides a way for Tribes to maintain their livelihood and cultural identity. Supplementation of wild salmon runs and enhancement of wild shellfish populations with hatchery produced offspring have become standard practices to provide consistent opportunities for both tribal and state harvesters alike; however, enhancement of wild populations alone is not economically feasible to sustain tribes, motivating many tribes to put effort into seafood farming. The Jamestown S'Klallam Tribe has been involved with modern aquaculture since 1990 and has steadily grown to include oyster and geoduck farms as well as the establishment of shellfish hatcheries in Washington and Hawaii. The hatcheries produce oyster seed to stock the Tribal oyster farm in Sequim Bay, as well as for commercial sale to tribal and non-tribal shellfish growers. The Jamestown S'Klallam Tribe is producing two premium oysters on the farm for local and national markets, while also prioritizing enhancement of tribal tidelands by out-planting clam and oyster seed for commercial tribal harvest. The Jamestown S'Klallam Tribe's unwavering focus on shellfish aquaculture is bolstering opportunity for the Tribe and its citizens.

USING NEXT GENERATION SEQUENCING TO IDENTIFY POTENTIAL LOCAL ADAPTATION TO SALINITY IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, ALONG THE LOUISIANA GULF COAST

Scott M. Riley[1], Morgan W. Kelly[1], Jerome F. La Peyre[2], and Megan K. La Peyre[3]

[1]Louisiana State University, Department of Biological Sciences, Baton Rouge, Louisiana 70803 USA

[2]Louisiana State University Agricultural Center, School of Animal Sciences, Baton Rouge, Louisiana 70803 USA

[3]U.S. Geological Survey, Louisiana Fish and Wildlife Cooperative Research Unit, 124 School of Renewable Natural Resources, Louisiana State University Agricultural Center, Baton Rouge, Louisiana 70803 USA

srile14@lsu.edu

Salinity plays a key role in controlling the distribution of eastern oysters, *Crassostrea virginica*, a keystone species that provides food, shelter, and nursery habitat for numerous species in Louisiana estuaries. Climate change induced precipitation patterns along with human freshwater diversion processes alter the frequency, location, and volume of freshwater inflow to estuaries, impacting salinity regimes where oysters thrive. To improve accuracy of predicted responses of *C. virginica* to altered salinity regimes, oyster populations were tested to see whether they are locally adapted to salinity. First, restriction site associated DNA sequencing was used to identify potential genetic variants, single nucleotide polymorphisms (SNPs), in four populations of oysters with varying salinity: Vermilion Bay (low salinity), Sister Lake (mid-salinity), Lake Fortuna (mid-salinity), and Calcasieu Lake (high salinity). Second, local adaptation to salinity was tested in a one-year reciprocal transplant experiment (three populations at three field sites) of juvenile oysters. Mortality data show definite differences as a function of transplant site. After seven months of deployment, the Grand Isle (high salinity) deployment site shows the highest mortality across all three source populations, whereas the Sister Lake (mid-salinity) deployment site showed the lowest mortality. Preliminary sequence data show outlier loci between two populations. It is expected to see additional differences in SNP frequencies among the populations with additional sequencing. A lab experiment showed that oysters from a high salinity died faster at high salinity exposure (without acclimation). Identifying markers associated with salinity tolerance will assist in the selection of breeding stocks for use in restoration or aquaculture.

DIFFERENTIAL EXPRESSION OF APOPTOSIS PATHWAY GENE FAMILIES IN RESPONSE TO IMMUNE CHALLENGE IN *CRASSOSTREA GIGAS* AND *CRASSOSTREA VIRGINICA*

Erin M. Roberts* and Marta Gomez-Chiarri

University of Rhode Island, Department of Fisheries, Animal, and Veterinary Science, 120 Flagg Rd., Kingston, Rhode Island, 02881 USA

erin_roberts@my.uri.edu

The eastern oyster, *Crassostrea virginica,* and Pacific oyster, *C. gigas*, are affected by disease outbreaks which threaten industry sustainability and ecosystem function. Oysters rely on a complex innate immune system characterized by several significantly expanded innate immune gene families. The genetically controlled pathway of programmed cell death, apoptosis, plays significant roles in immunity. Expansion of gene families involved in apoptosis is confirmed in *C. gigas* and supported by *C. virginica de novo* transcriptomic studies. The role of apoptosis in disease resistance in these species is unknown. This study utilized the recently available *C. virginica* genome to perform differential gene expression analysis on publically available transcriptomes of oysters challenged with a variety of stimuli, including Oyster Herpesvirus OsHV-1, several *Vibrio* spp., *Micrococcus luteus*, *Alliroseovarius crassostreae* CV919-312 (cause of Roseovarius Oyster Disease), and the probiotic bacterium *Bacillus pumilus* RI-695. Intra-species analysis reveals unique apoptosis pathway responses between challenges, and changes in functionally enriched pathways identified by Gene Set Enrichment Analysis. Bacterial challenge significantly enriched metabolic processes and chromosomal maintenance genes. Viral challenge significantly enriched signal transduction and apoptosis inhibitors, with Inhibitor of Apoptosis 2 (IAP2) and suppressor of cytokine signaling two most significantly differentially expressed. Transcripts from the expanded families IAP and GTPase of the Immune Associated Proteins (GIMAP) show distinct patterns of expression depending on the nature of the immune challenge. Cross-species comparison of apoptosis pathway expression indicates promising genetic targets for pathway manipulation under disease challenge and potential candidates for disease resistance markers.

IMPACTS OF TWO HARMFUL ALGAL BLOOM SPECIES ON OYSTERS CULTURED IN LOWER CHESAPEAKE BAY

Clara L. Robison*, Wolfgang K. Vogelbein, William G. Reay, Ryan B. Carnegie, Juliette L. Smith, and Kimberly S. Reece

Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, Virginia 23062 USA

clrobison@vims.edu

Understanding impacts of harmful algal blooms (HAB) is crucial for managing important resource species such as the eastern oyster, *Crassostrea virginica*, in Chesapeake Bay (CB). Besides potential toxic effects, blooms may incur physiological challenges associated with reduced feeding, or with bloom-associated hypoxia. Two toxigenic dinoflagellates, *Margalefidinium* (formerly *Cochlodinium*) *polykrikoides* and *Alexandrium monilatum*, bloom sequentially most summers in lower CB. These blooms have increased in density and distribution in recent years, raising concerns particularly about effects on shellfish aquaculture. Previous research indicated that oysters may close and cease feeding to avoid exposure to *A. monilatum*; however, it is unknown whether intertidal oysters, particularly juveniles with more limited energy reserves, are being forced to filter during blooms due to increased respiratory and nutritional demands during their more limited periods of immersion, and whether these factors make oysters more susceptible to detrimental effects. To address these questions, two size classes of juvenile oysters were deployed subtidally and intertidally in 2017 at two HAB-endemic sites in lower CB and a third, reference site seldom impacted. Oyster growth rate, mortality, condition index, and histopathology were monitored throughout the bloom season, and oysters were sampled for quantification of phy-

cotoxin concentration in tissues. Algal concentrations in the water were monitored, and temperature, salinity, and dissolved oxygen were measured continuously. Although significant oyster mortality was not observed, results indicated reduced growth of experimental animals during the bloom period. Further analyses are underway to help resolve whether other sub-lethal bloom impacts on oysters may have occurred.

EFFECTS OF SURFACE SURFACTANTS ON PARTICLE CAPTURE, EFFICIENCY, AND CLEARANCE RATES OF THE BLUE MUSSEL (*MYTILUS EDULIS*)

Maria Rosa*[1], J. Evan Ward[2], Yoselin Flores[3], Katie Sierra[4], and Brian Torres[5]

[1]Stony Brook University, Department of Ecology and Evolution, Stony Brook, New York 11794 USA

[2]University of Connecticut, Marine Sciences Department, Groton, Connecticut 06340 USA

[3]University of Illinois, Department of Biological Sciences, Chicago, Illinois 60607 USA

[4]Northport Senior High School, Northport, New York 11768 USA

[5]Brentwood High School, Brentwood, New York 11717 USA

maria.rosa@stonybrook.edu

The capture of particles by bivalve molluscs is dependent on particle encounter and retention on the gill filaments, with several factors influencing this process. Generally, smaller particles (i.e., 0.1 to 4 µm) are more difficult for most bivalves to capture, but species-specific differences in gill structures can mediate capture efficiencies. Over the past 30 years, different types of microspheres have been used to examine aspects of particle capture and ingestion by bivalves. Critics have posited that manufactured particles may contain surfactants, chemicals commonly used in the manufacturing of plastics to reduce surface tension, which could produce spurious capture and ingestion rates. The goal of this work was to experimentally assess whether the presence of different types of surfactants on manufactured polystyrene particles can result in altered capture efficiencies (CE) and clearance rates (CR) in the blue mussel *Mytilus edulis.* The effects of three different types of common surfactants (Sodium dodecyl sulfate, Benzalkonium chloride, and Triton-x) and a control (no surfactant) were tested. Polystyrene microspheres were incubated at a saturating solution (0.2 mg/ml) of each surfactant prior to use. There was no effect of surfactant treatment on CR. Treatment with Triton-X significantly lowered CE for all microspheres tested (3, 6, 10 µm), but there were no significant differences in CE for the other types of surfactants tested compared to the control treatment. These data add to our understanding about particle handling by bivalves, and suggest that residual amounts of surfactants found on commercially available microspheres have little effect on feeding processes.

AN 'OMICS' APPROACH TO UNDERSTAND OYSTER-OSHV-1 INTERACTIONS

Umberto Rosani[1]*, Miriam Abbadi[2], Stefania Domeneghetti[1], and Paola Venier[1]

[1]University of Padova, Department of Biology, 35121 Padua, Italy

[2]Istituto Zooprofilattico Delle Venezie, 35020 Legnaro, Italy

umberto.rosani@unipd.it

The family of double-stranded DNA, *Malacoherpesviridae,* includes viruses able to infect marine molluscs, detrimental for the aquaculture production worldwide. Due to the uniqueness of the evolutionary race between these viruses and their mollusc hosts, little is known about the origin of *Malacoherpesviridae*, their biology, and molecular steps crucial for pathogenicity. Therefore, innovative research approaches are urgently needed in support to the aquaculture expectations.

An omics approach has the potential to finely resolve host-pathogen interactions, especially when new data derive from complementary technologies and targeted functional testing. Transcriptomics, in particular dual RNA-seq of OsHV-1-infected oysters, has revealed common virus expression patterns denoting the burst of viral proteins in the lytic phase as well as the oyster countermeasures to the viral infection. For instance, the expression patterns of viral ORF107 and ORF104, still functionally unknown, candidate them as key viral proteins for additional studies. Refinements of RNA library preparations further support the OsHV-1 genome annotation and also the search of small RNAs. Complementary to transcriptomics, shotgun DNA sequencing of infected oysters farmed in Italy allowed the whole-genome resolution of a new OsHV-1 variant. Among other genome features, the presence of several single nucleotide polymorphisms suggest them as driving factors of the differential pathogenicity of OsHV-1 strains.

DISCARD MORTALITY OF SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) FOLLOWING CAPTURE AND HANDLING IN THE SEA SCALLOP DREDGE FISHERY

David B. Rudders[1], Sally A. Roman[1]*, Ryan J. Knotek[2,5], James A. Sulikowski[3], John A. Mandleman[2], and Hugues T. Benoît[4]

[1]Virginia Institute of Marine Science, 1375 Greate Road Gloucester Point, Virginia, USA

[2]John H. Prescott Marine Laboratory, New England Aquarium, Central Wharf, Boston, Massachusetts, USA

[3]University of New England, Marine Science Center, 11 Hills Road, Biddeford, Maine, USA

[4]Gulf Fisheries Centre, Fisheries and Oceans Canada, Moncton, NB E1C 9B6, Canada

[5]University of Massachusetts Boston, School for the Environment, Boston, Massachusetts, USA

saroman@vims.edu

Discarding of sea scallops (*Placopecten magellanicus*) in the Northeast U.S. sea scallop fishery occurs during the capture handling process (CHP). The study provides an estimate of short-term

discard mortality (DM) for scallops. Sea trials were completed in 2015 onboard commercial fishing vessels in the Mid-Atlantic and Georges Bank. A subset of scallops was monitored in a deck tank system to determine time of mortality. A vitality assessment consisting of assessing shell damage (SD) and response to stimuli was completed after the CHP to determine the health/vigor of scallops. SD and stimuli responses were grouped into health indicator classifications (HIC). Kaplan-Meier analysis and survival mixture models (SMM) were used to estimate survival and the effects of other variables on survival. The estimated survival rate was 81 percent, although survival varied significantly among HIC groups. SMMs indicated HIC, SD, exposure time and bottom type contributed to increased DM.

INVESTIGATION OF THE SCALLOP NEMATODE, *SULCASCARIS SULCATA*: DISTRIBUTION, SEASONALITY, SHEDDING, TRANSMISSION, THERMAL TOLERANCE, AND HOST IMPACT

David B. Rudders[1]*, Sally Roman[1], Robert Fisher[1], David Bushek[2], Daphne Munroe[2], Eleanor Bochenek[2], and Emily McGurk[2]

[1]Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, Virginia, USA

[2]Rutgers University, Haskins Shellfish Laboratory, Port Norris, New Jersey, USA

rudders@vims.edu

The Atlantic sea scallop, *Placopecten magellanicus,* is one of the most valuable fisheries along the east coast of the United States. In spring 2015, a high frequency of scallops landed from recently opened mid-Atlantic management areas exhibited exterior adductor muscle lesions. Similar reports occurred in May 2003, but those quickly waned whereas the 2015 reports expanded. Morphological and molecular evidence identified an ascarid nematode worm (*Sulcascaris sulcata*) as the cause; a species that utilizes benthic molluscs as intermediate hosts and marine turtles (loggerhead (*Carretta caretta*) and green (*Chelonia mydas*)) as definitive hosts.

During 2016 and 2017, the basic biology and ecology of the parasite was investigated using a region-wide resource assessment survey as a research platform. Results support the life cycle reported in the literature with approximately 29% of lesions containing a larval nematode. Larger scallops were more likely to have more lesions and more nematodes. Ancillary observations indicated infected scallops had a higher mortality rate that increased with the number of lesions observed. Direct transmission was not observed among live scallops nor from shucked meats even though nematodes extracted from lesions survived for weeks at ambient collection site temperatures up to room temperature. Nematodes died within a few hours at 37°C and within seconds above 50°C. Over the two-year study period, the parasite continues to be observed with a moderate spatial expansion. While many questions remain unanswered, biological and environmental conditions appear to have created a situation that supports the persistence of *S. sulcata* in the mid-Atlantic Bight.

PRESENT STATUS OF MANGROVE ECOSYSTEMS IN MEXICO, WITH NOTES ON THEIR KNOWLEDGE AND CONSERVATION CHALLENGES, REGARDING NATURAL AND ANTHROPOGENIC IMPACTS

Arturo Ruiz-Luna* and César A. Berlanga-Robles

Laboratorio de Manejo Ambiental, Centro de Investigación en Alimentación y Desarrollo (CIAD), A.C. Mazatlán, Sinaloa, Mexico

arluna@ciad.mx

Mangroves are present in all the seventeen Mexican coastal states, ranging from 30 to almost 200,000 hectares by state, amounting together >775 000 hectares, that make Mexico one of the top five countries in mangrove extent. There have been a lot of irregularities in the historic mangrove cover assessment, but the use of remote sensing and GIS techniques in recent dates, situates Mexican mangroves as some of the less deteriorated, with losses of 0.26% by year since 1980, compared with the world rate (1.38% since 2000). Official data also reveal that only 2.4% of the current extent is seen as deteriorated. Despite this, there is a generalized concern on mangrove conservation, and public and private agencies to give support to research projects, mostly focused on inventorying and monitoring issues. It has been documented that global change and some economic activities are endangering the mangrove cover, but unlike many other regions in the world, shrimp aquaculture is not the main cause of mangrove deforestation in Mexico, while agriculture and extensive cattle breeding, as well as urban growth, together with the sea rise level, have been signaled as the main menaces for this cover. Unfortunately, mangrove reforestation and restoration practices have failed or succeeded only at very low-scale, maintaining mangrove protection plans as the most effective conservation strategy.

OLYMPIA OYSTER PRODUCTION AND RESEARCH AT THE KENNETH K. CHEW CENTER FOR SHELLFISH RESEARCH AND RESTORATION

Stuart K. Ryan*[1,2], Ryan N. Crim[1,2], Brian Allen[1,2], and Betsy Peabody[1,2]

[1]Puget Sound Restoration Fund, 382 Wyatt Way NE, Bainbridge Island, Washington 98110 USA

[2]Kenneth K. Chew Center for Shellfish Research and Restoration, 7305 Beach Dr. E., Port Orchard, Washington 98366 USA

Stuart@restorationfund.org

In May of 2014, The Kenneth K. Chew Center for Shellfish Research and Restoration was dedicated at the NOAA Manchester Research Station. Operated by the Puget Sound Restoration Fund (PSRF), the facility was built as a joint venture between the PSRF and NOAA. Since then, PSRF has produced over 8 million genetically diverse Olympia oyster seed and spat-on-shell for restoration. Additionally, PSRF, University of Washington, NOAA and other partners have studied the effects of ocean acidification, genetic diversity, broodstock conditioning, and grow-out methods for Olympia oysters. This presentation will cover the methods, successes, failures and lessons learned from 4 years of growing Olympia oysters and the results of some of these studies.

EVALUATION OF MARINE BACTERIA THROUGH *IN VITRO* AND *IN VIVO* ASSAYS AND THEIR POTENTIAL USE AS FEED ADDITIVE AND PROBIOTIC AGENT AGAINST PATHOGENIC *VIBRIO PARAHAEMOLYTICUS* (AHPND) IN WHITE SHRIMP, *LITOPENAEUS VANNAMEI*

Ricardo Sánchez-Díaz[1,2*], Rosa A. Ocampo-Ayala[1], Diana P. Herrera-Patiño[1], Zinnia J. Molina-Garza[2], Lucía E. Crúz-Suárez[3], Bruno Gómez-Gil[4], Lucio Galavíz Silva[2], and José C. Ibarra-Gámez[1]

[1]Instituto Tecnológico de Sonora, Departamento de Ciencias Agronómicas y Veterinarias; 5 de Febrero # 818 Sur Col. Centro CP 85000, Cd. Obregón Sonora, México

[2]Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Laboratorio de Patología Molecular; Pedro de Alba, San Nicolás de los Garza, Nuevo León, México

[3]Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Programa Maricultura; Pedro de Alba, San Nicolás de los Garza, Nuevo León, México

[4]CIAD, Mazatlán Unit for Aquaculture and Environmental Management, AP 711, Mazatlán, Sinaloa, México

ricardos_d@hotmail.com

Recently, Asian and Mexican shrimp farming are facing the acute hepatopancreatic necrosis disease (AHPND), which causes 80-100% mortality in shrimp, resulting in large economic losses. The potential of marine bacteria as bioactive producers or probiotics is an alternative to control aquatic diseases. The aim of this study was to evaluate antagonistic activity of marine bacteria, and determine the survival of shrimp *L. vannamei* fed with a diet covered with bacteria, prior to challenge with AHPND pathogenic *V. parahaemolyticus*.

Marine heterotrophic bacteria were collected from the coast of Sonora, Mexico. *In vitro* antagonism was evaluated by cross streak, double layer and broth co-culture, with AHPND pathogenic *V. parahaemolyticus* strains MC32, B25, E14V2; and ATCC 17802. Five isolates were selected, characterized and identified (16S rRNA) as: 36R, 42 and 13L, Gram (+) spore forming rods, belonging to *Bacillus* genus; 36Y and 02Y, Gram (–) rods, related to *Pseudoalteromonas.* None of them produced chitinases. During 21 days shrimp were fed with bacterial covered diet, in six treatments by triplicate with eight shrimp (1.6 g) in 30 L aquaria. Pathogenic strain MC32 was used for immersion challenge (1.4 x 10^8 UFC/mL). The cumulative mortality was recorded: T1-36R (45%), T2-13L (54%), T3-36Y (54%), T4-Mix 136R-13L (25%), C+ (88%), C- (4%); statistically significant differences were found between treatments (ANOVA, $p<0.05$). The pathogen was confirmed by real-time PCR and histopathology. Shrimp fed with bacteria demonstrated improvement in survival compared with control.

This *Bacillus* and *Pseudoalteromonas* could be an effective probiotic or biocontrol agent against harmful bacteria in shrimp culture.

THE EFFECTS OF TAURINE ON MANGANESE ACCUMULATIONS IN GILL OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Rafael Santos[1]*, Emmanuel Agyei[2], Elvin Griffith, Jr.[3], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New Yorik 11235 USA

[2]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

[3]Notre Dame High School, 1 Notre Dame Way, West Haven, Connecticut 06516 USA

rafaelsantos2194@gmail.com

Taurine is a neuroprotective against some neurodegenerative diseases. Manganese causes Manganism, which often is confused with Parkinson's disease. Manganism has no effective treatment. The eastern oyster, *Crassostrea virginica*, has a serotonergic-dopaminergic innervation of gill lateral cells (GLC). Manganese disrupts the dopaminergic innervation and taurine protects against this disruption. We hypothesize taurine reduces manganese accumulations in gill or enhances manganese removal from gill. This was tested by treating gills 2 days with taurine, manganese, or taurine and manganese (500 µM each) and analyzing samples by Atomic Absorption Spectroscopy. Manganese treatments caused higher manganese accumulations compared to controls or taurine treatments. Co-treated with taurine and manganese had no significant difference in manganese accumulations compared to manganese treatments alone suggesting taurine does not block manganese accumulation into gill. To determine if taurine removes manganese from gill, gills were treated 2 days with manganese (500 µM), rinsed, then treated 2 days with taurine or EDTA (0.5 to 2.5 mM each). EDTA was effective at removing manganese from gill (80% compared to controls). Taurine treatments were effective to a lesser degree, removing 25%. The study shows while taurine did not prevent manganese accumulations, it did remove manganese, similar to how chelating agents treat metal toxicity. Considering taurine is a natural biological component and shows success as a protective agent in other neurodegenerative diseases, more studies are needed to determine if taurine would be an effective and safer therapeutic agent for clinical treatment of Manganism.

A PRELIMINARY ASSESSMENT OF THE ECONOMIC IMPACT ASSOCIATED WITH THE RECREATIONAL SCALLOP SEASON IN HERNANDO COUNTY, FLORIDA

Brittany J. Scharf[1]*, Charles Adams[2], and Stephen P. Geiger[3]

[1]University of Florida, Florida Sea Grant, 16110 Aviation Loop Drive, Brooksville, Florida 34604 USA

[2]University of Florida, Florida Sea Grant, Building 803 McCarty Drive, Gainesville, Florida 32611 USA

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

bhallscharf@ufl.edu

Recreational scalloping has become an increasingly popular activity within the Big Bend region and Hernando County is the southern extent of healthy, harvestable bay scallop populations. A previous study found that the recreational scallop fishery generated numerous jobs and $1.6 million in economic impact to the economy of neighboring Citrus County. State resource managers and County administrators expressed a need to know how the recreational scallop fishery impacts local economies. Surveys were developed by Florida Sea Grant to estimate the expenditures associated with a recreational scallop fishing trip. These surveys were administered either by in-person interviews at boating ramps, via on-line completion, or by postal mail-back. A total of 264 surveys were completed. The surveys collected information on numbers of harvesters, resident vs non-resident status, expenditures and where those expenditures occurred, week-day vs weekend activity. The Florida Fish and Wildlife Conservation Commission simultaneously collected information on recreational effort via flyovers and additional ramp surveys. The data sets provide an estimate of the total number of recreational scallop trips that launched from Hernando County, as well as the total amount of associated expenditures. That information was entered into the University of Florida IMPLAN model, which provided an estimate of the economic impact to the Hernando County economy associated with recreational scalloping. Such information will help managers better understand the benefits this popular activity generates on a local and state basis. Data will also aid estimates of mortality, which will be useful in managing harvest.

SHELLFISH LEASING AND PERMITTING WORKSHOP: CASE STUDIES FOR OVERCOMING COMMON LEGAL BARRIERS

Lisa Schiavinato

California Sea Grant, UC San Diego, Scripps Institution of Oceanography, 9500 Gilman Drive, MC #0232, La Jolla, California 92093-0232 USA

lschiavinato@ucsd.edu

Legal and permitting issues are consistently ranked as a critical impediment to domestic aquaculture development. The shellfish industry is growing in coastal areas, which are home to more than half of the population of the continental United States. A variety of legal conflicts can arise as states seek to encourage the development and expansion of shellfish aquaculture. The regulatory landscape facing the aquaculture industry can also be confusing and complicated.

In 2017, the National Oceanic and Atmospheric Administration funded a multi-institutional, national collaboration to examine impediments to shellfish aquaculture across the United States. In this session, project partners will share preliminary research findings and facilitate a dialogue to inform research and outreach efforts. Specifically, this session will include: 1) a general overview of legal challenges to shellfish aquaculture operations; 2) presentations of multiple national and state case studies covering topics such as nationwide permits, the Endangered Species Act, public access, managing use conflicts, and the challenges of operating in federal waters; and 3) a roundtable discussion where participants will be able to ask panel members questions, provide feedback, and identify potential interest areas that may warrant further attention.

The goal of this project is to equip scientists, management officials, industry members, and other interested parties with the knowledge needed to anticipate and overcome regulatory barriers to shellfish aquaculture. Participation in this session will help presenters create a "toolbox" of resources identifying common issues and solutions that those parties can utilize—advancing aquaculture on the state and local levels as a result.

VIBRIO PARAHAEMOLYTICUS MANAGEMENT FOR OYSTERS IN MASSACHUSETTS

Christopher A. Schillaci[1,2], Stephen Jones[1], Cheryl Whistler[3], and Diane Regan[2]

[1]University of New Hampshire, Department of Natural Resources and the Environment, 46 College Rd, 208 Rudman Halln Durham New Hampshire, USA

[2]Massachusetts Division of Marine Fisheries, 251 Causeway St Boston, Massachusetts, USA

[3]University of New Hampshire, Department of Molecular, Cellular, and Biomedical Sciences, 46 College Rd, 208 Rudman Hall, Durham, New Hampshire, USA

chris.schillaci@gmail.com

To meet National Shellfish Sanitation Program and federal Food and Drug Administration standards pertaining to the harvest and handling of oysters and *Vibrio parahaemolyticus* (*Vp.)* the Massachusetts Division of Marine Fisheries (DMF) and Massachusetts Department of Public Health (DPH) adopted control measures in 2012 intended to deter the post- harvest growth of *Vp.* in oysters. Historically *Vp*. cases in Massachusetts (MA) have been rare and the relatively cool waters and high salinities in MA harvest areas have not been considered particularly conducive to high levels of *Vp.* in shellfish. As a result of increased oyster production, warming air and water temperatures, and the introduction of a highly pathogenic strain of *Vp.* into MA waters this is no longer true. Since 2011 MA has experienced a significant increase in the occurrence of *Vp.* illness related to the consumption of raw oysters resulting in harvest area closures, recalls and considerable economic loss to the oyster industry. Field studies were conducted to validate existing *Vp*. control measures and aquaculture industry practices in MA to determine their impact on *Vp.* levels in oysters. Environmental conditions were also reviewed, background *Vp.* levels, harvest practices, and production levels in areas implicated in *Vp*. cases in efforts to develop proactive management strategies for *Vp* in Massachusetts.

PACIFIC RAZOR CLAM AND DUNGENESS CRAB FISHERY MANAGEMENT CHALLENGES ON THE WASHINGTON COAST

Ervin Joe Schumacker

Quinault Department of Fisheries, Quinault Indian Nation, P.O. Box 189, Taholah, Washington 98587 USA

jschumacker@quinault.org

The Quinault Indian Nation, located on the coast of Washington State, manages and co-manages shellfish resources including economically and culturally important fisheries for Pacific razor clams (*Siliqua patula*) and Dungeness crab (*Metacarcinus magister*). The fisheries for both of these species are dependent on natural spawns and survival and recruitment of young animals into the fishery. Recent changes in environmental conditions including large storm events, seasonal hypoxia and ocean acidification combined with increasing predation by sea otters (*Enhydra lutis*) and, most recently, gray whales (*Eschrichtius robustus*) are impacting populations of both species and challenging biologists to better understand sources of mortality at an ecosystem level. A large area of the Washington coast, once highly productive Dungeness crab habitat, is now considered a "crab desert" by fishermen and razor clam populations in the same area have recently suffered extremely large juvenile mortality events.

Information on tribal fishery management, recent population data and environmental conditions will be presented. Ongoing projects including seasonal hypoxia research, ocean acidification research and predator observations will also be discussed. The presentation is meant to encourage discussion of current and potential future challenges to west coast shellfish management.

THE ABUNDANCE AND OCCURRENCE OF VIBRIO IN CULTURED OYSTERS GROWN AT VARIOUS DEPTHS WITHIN THE WATER COLUMN

Abigail K. Scro*, M. Victoria Agnew, and Roxanna Smolowitz

Roger Williams University, Aquatic Diagnostic Laboratory, 1 Old Ferry Rd, Bristol, Rhode Island 02809 USA

ascro@rwu.edu

Global warming is quickly increasing the average water temperatures of Narragansett Bay and coastal ponds of Rhode Island (RI). As the RI estuary and marine waters continue to warm over the coming years, it is probable that the abundance of *Vibrio parahaemolyticus* (Vp) and *Vibrio vulnificus* (Vv) will also increase. *Vibrio* are gram-negative, halophilic bacteria that are found naturally in the marine environment. While Vp and Vv are not pathogenic for oysters, they can affect humans who consume raw or undercooked oysters. Although methods are currently in use in RI to manage *Vibrio* levels, it is probable that other types of management methods can be developed and used in aquacultured and fished oysters to further minimize the threat to human health. Rhode Island oyster aquaculture is predominated by subtidal culture; however, the depth of the water column over the oyster cultured on the bottom varies not only with the tidal cycle, but with the location of the farm. Many farms are also using floating bags as a culture method, but oysters in floating bags experience a different environment than oysters grown just off the sediment. This project aimed to determine the differences between Vp/Vv abundance and occurrence in cultured oysters grown in intertidal, shallow and deep water environments, as well as in surface bags over the same sample sites during the course of two years (2016-2017) in five locations in Rhode Island. Preliminary findings from this study will be presented.

HABITAT COMPLEXITY MEDIATES PREDATOR-BIVALVE INTERACTIONS IN CHESAPEAKE BAY

Rochelle D. Seitz[1]* and Cassandra N. Glaspie[2]

[1]Virginia Institute of Marine Science, The College of William & Mary, PO Box 1346, Gloucester Point, Virginia 23062, USA

[2]Oregon State University, 104 Nash Hall, Corvallis, Oregon 97331, USA

seitz@vims.edu

In Chesapeake Bay, the soft shell clam *Mya arenaria* exhibits population declines when predators are active, and it can persist at low densities. In contrast, the hard clam *Mercenaria mercenaria* has a stable population and age distribution. The potential for habitat and predators to drive densities and distributions of bivalves was examined in field caging and laboratory mesocosm experiments. In the field, clams exposed to predators experienced 76.3% greater mortality as compared to caged individuals, and blue crabs were likely responsible for most of the mortality of juvenile *M. arenaria*. In mesocosm experiments, *M. arenaria* had lower survival in sand and seagrass than in shell hash or oyster shell habitats. Crabs often failed to consume one or more prey items in seagrass, shell, and oyster shell habitats, suggesting that more-complex habitat such as seagrass may serve as a low-density refuge for *M. arenaria*. Predator search times and encounter rates declined when prey were at low densities, likely due to the added cost of inefficient foraging causing crabs to give up; this effect was more pronounced for *M. arenaria* than for *M. mercenaria*. Higher survival rates were observed for *M. mercenaria* than *M. arenaria* in mesocosm experiments, likely because predators feeding on *M. mercenaria* spent less time foraging than those feeding on *M. arenaria*. The soft shell clam may retain a low-density refuge from predation even with the loss of structurally complex habitats, though a loss of habitat refuge may result in clam densities that are not sustainable. A better understanding of density-dependent predator-prey interactions is necessary to conserve marine resources.

THE COSTS OF REGULATORY COMPLIANCE ON WEST COAST SHELLFISH FARMS: EFFECTS AND IMPACTS ON PRODUCERS

Jonathan van Senten* and Carole R. Engle

Virginia Tech Seafood AREC, 102 S. King St., Hampton, Virginia 23669 USA

jvansenten@vt.edu

Through the end of 2016, a survey to assess the costs and impacts of regulations affecting shellfish aquaculture on the west coast was conducted. While producers widely acknowledged the importance of regulations, specifically with regards to environmental protection and food safety; many also reported indirect costs of regulatory compliance in their business. Results from the study are now available, and there are several economic effects that were observed during interviews and from data analysis that are worthy of note. These included significant impacts to business development and planning resulting from permit and licensing delays, with 25% of respondents reporting to wait a year or more for a permit to be approved or processed; some delays lasting up to 20 years. Cash flow interruptions from missed planting or harvest windows; with small scale producers being particularly vulnerable to cash flow interruptions. Increased legal fees and administrative costs, and lost sales or missed opportunities for expansion and diversification; 40% of respondents indicated they were unable to expand their operations, despite increased demand for shellfish. In addition to these impacts, some producers also reported lost investment capital due to regulatory uncertainty, and the labor challenges of ensuring regulatory compliance as a small business.

POPULATION GENOMICS AND PHYLOGEOGRAPHY OF THE OLYMPIA OYSTER

Katherine Silliman[1]*and Doug Eernisse[2]

[1]University of Chicago, Committee on Evolutionary Biology, 1025 E. 57th Street, Chicago, Illinois 60637 USA

[2]California State University, Department of Biological Sciences, 800 N. State College Blvd., Fullerton, California 92831

ksilliman@uchicago.edu

Understanding the evolutionary processes that cause populations to diverge genetically and phenotypically is crucial to predicting how species will respond to rapid global environmental change. The Olympia oyster, *Ostrea lurida*, is patchily distributed from California to the central coast of Canada, extending over strong environmental clines and mosaics that are typically considered necessary for local adaptation to occur. Before testing hypotheses of adaptation, however, the underlying demographic population structure must be described. This pattern could be consistent with a null model of no significant population structure, a continuous isolation-by-distance (IBD) model, or contain regional blocks of genetic similarity separated by barriers to gene flow. Adult Olympia oysters were sampled across 20 sites from Klaskino Inlet, Vancouver Island (50° 17' 55") to San Diego Bay, CA (32° 361' 9"), as well as 15 individuals from the sister species, *O. conchaphila*. DNA from these samples were used to construct reduced representation Genotype-by-Sequencing libraries (GBS) and genotype thousands of single nucleotide polymorphisms (SNP). Principal component analysis, model-based approaches (e.g. Structure), and TreeMix indicate significant population structure at a regional level, as well as evidence for "human-assisted" migration. Using EEMS (Estimated Effective Migration Surfaces) to visualize spatial population structure, we have identified geographic regions with reduced gene flow. Although this method cannot distinguish between different scenarios that could produce the observed spatial structure, it supports the rejection of both a continuous IBD model and the null model of no significant genetic structure.

VARIATION IN RESPONSE TO OCEAN ACIDIFICATION AMONG OLYMPIA OYSTERS FROM CALIFORNIA, OREGON, AND BRITISH COLUMBIA

Katherine Silliman[1]*, Sean Bennett[2], and Steven B. Roberts[3]

[1]University of Chicago, Committee on Evolutionary Biology, 1025 E. 57th Street, Chicago, Illinois 60637 USA

[2]Division of Human Biology, Fred Hutchinson Cancer Research Center, Seattle, Washington 98105 USA

[3]University of Washington, School of Aquatic and Fishery Sciences, 1122 Boat Street, Seattle, Washington 98105 USA

ksilliman@uchicago.edu

Over the next century, rapid environmental change due to anthropogenic stressors is likely to be a serious concern for many marine species. Calcifying invertebrates in particular are expected to be impacted by ocean acidification- the reduction in ocean pH due to the uptake of anthropogenic CO_2. The Olympia oyster (*Ostrea lurida*) is patchily distributed from California to the central coast of Canada, extending over an environmental "mosaic" of pH regimes. Whether this tolerance is primarily due to plasticity, local adaptation, or balanced polymorphism is largely unknown. Previous work on *O. lurida* in California and Puget Sound has indicated that populations can diverge in heritable fitness-related traits on spatial scales as small as 20 km. Genomic data suggests that the demographic population structure of Olympia oysters consists of seven broad geographic regions. In order to better understand the spatial scale of adaptation in this species and characterize variation in response to ocean acidification, oysters from three different regions were brought together for a common garden experiment (San Francisco, CA, Coos Bay, OR, and Ladysmith Harbour, BC). After acclimating to common conditions for nine months, oysters from each population were exposed to two different pH levels (7.4 and 7.8) for seven weeks in the fall of 2016. Tissue samples (gills, mantle, and adductor muscle) were taken from oysters prior to reducing the pH, after 36 hours, and after seven weeks in order to compare gene expression responses from both an acute and a prolonged acidification stress.

SHELLFISH DISEASE WORKSHOP – MANAGING YOUR FARM TO REDUCE THE RISK

Roxanna Smolowitz and Dale Leavitt

Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

rsmolowitz@rwu.edu

Risk of disease is a constant threat to shellfish farmers across the industry. This workshop will provide growers with information to aid in their defense against losing shellfish to disease. Material covered during the workshop will include the anatomy/physiology of bivalves, some of the more important diseases of oysters and clams found in the U.S., what to do if a disease is suspected, and means of biosecurity to reduce the risk of disease initiating. Participants will learn basic anatomy and physiology of bivalve through a hands-on dissection of clams and oysters. After dissection, there will be an introduction to important diseases of bivalves, including dermo and associated diseases (*Perkinsus marinus* and *P. olseni*), Multinucleated Sphere Unknown (MSX – *Haplosporidium nelson*), Ostreid Herpes Virus 1 (OsHV-1), Quahog Parasite Unknown (QPX) and Transmissible Tumor. The workshop will conclude with a discussion of how to respond should one suspect a disease is developing on their farm; the timing of monitoring, sample collection and shipping; testing methods for disease diagnosis; and biosecurity practices for the farm.

A DYNAMIC MODEL FOR MANAGEMENT OF OYSTER NURSERIES

Filipe M. Soares[1]*, Ana M. Nobre[2], and François Hubert[3]

[1]Universidade Nova de Lisboa, DCEA, Faculdade de Ciências e Tecnologia, Quinta da Torre, 2829-516 Monte de Caparica, Portugal

[2]CIMAR/CIIMAR — Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos, S/N, 4450-208 Matosinhos, Portugal

[3]Bivalvia-Mariscos da Formosa, Lda. Piscicultura da Meia-Légua. Cova da Onça - Caixa Postal 491ª, 8700-177 Olhão, Portugal

fmrc.soares@gmail.com

Ecological models have been used for shellfish aquaculture management (e.g. site selection, production optimization, among others), either at the ecosystem (bay, estuary, or related sub-units) or local scale (farm), and have proven to be powerful tools to be used by farmers and aquaculture consultants. Those models focus on the grow-out phase, lacking modelling approaches applicable at nurseries.

Herein, a dynamic model for management of oyster commercial nurseries is presented. The model main outputs are targeted to provide useful information to farmers or aquaculture consultants, namely: (i) oyster spat growth and body weight evolution over time, (ii) food availability within the farming system over time, and (iii) stock biomass over time. All the model developments were based on scientific knowledge, and validation was carried out with three experimental data sets from the literature, showing significant ($p<0.05$) agreements ($r = 0.895$, $n = 7$; $r = 0.997$, $n = 6$; $r = 0.976$, $n = 4$) between the simulated and observed oyster biomass. Herein the authors illustrate the model application in a commercial nursery. A set of what-if scenarios relevant to the farm were run with the model. The model outputs supported the quantification of the impact of key-factors for the production optimization, guiding the operational management.

DIFFERENCES IN MITOTIC INSTABILITY BETWEEN CHEMICAL AND MATED TETRAPLOID LINES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Joana Teixeira de Sousa* and Standish K. Allen Jr.

Virginia Institute of Marine Science, Aquaculture Genetics and Breeding Technology Center, Gloucester Point, Virginia 23062, USA

jtsousa@vims.edu

The creation of tetraploid brood stock to support the commercial production of triploids has become a successful technique in aquaculture of the eastern oyster, *Crassostrea virginica*. It is well known that triploid oysters have several advantages for oyster culture, such as reduced gonadal development, allowing for higher growth rates and superior market quality during the reproductive season. In order to produce tetraploids, chemical triploids are grown for 2-3 years in order to obtain exceptional triploids that produce eggs, which will be used to induce "chemical" tetraploids (4C). These tetraploids grow for 1-2 years and can be bred to themselves, creating mated tetraploids (4M). As novel genetic constructs, tetraploids undergo chromosome loss. This chromosome loss seems to be of little consequence to commercial triploids but for propagation of tetraploid lines over time, chromosome loss is problematic. The objective of this study was to document differences in chromosome loss between 4C and 4M tetraploids available in the breeding program of Aquaculture Genetics and Breeding Technology Center. The 4C line (4C XBSL is a founder tetraploid line (F_0) from 2013 and the 4M – a tenth generation line, 4MGEN from 2014 (F_{10}). Levels of aneuploidy were significantly different between the two lines, with the chemical tetraploids having the highest levels (58.5%) compared to the mated ones (39.5%). Moreover, 4C individuals tended to have more chromosome clumps in their cells, which is compatible with the hypothesis of ongoing chromosome loss. Understanding the nature of chromosome loss is essential for the ABC tetraploid breeding strategy.

PROTEOMICS REVEALS GEODUCK PHYSIOLOGICAL RESPONSE TO ENVIRONMENTAL CHANGE

Laura H. Spencer*[1], Micah Horwith[2], Alex Lowe[3], Emma Timmins-Schiffman[4], Brook L. Nunn[4], and Steven Roberts[1]

[1]University of Washington, School of Aquatic and Fishery Sciences, 1122 NE Boat St, Seattle, Washington 98105 USA

[2]Washington State Department of Natural Resources Aquatics Program, 1111 Washington St., SE Olympia, Washington 98504 USA

[3]University of Washington, Department of Biology, 24 Kincaid Hall Seattle, Washington 98195 USA

[4]University of Washington, Department of Genome Sciences 3720, 15th Ave NE Seattle Washington 98195-5065 USA

lhs3@uw.edu

The Pacific geoduck (*Panopea generosa*) is the largest clam native to the Pacific Northwest and is a burgeoning aquaculture species due to growing export demands from Asia. In Washington State, geoduck support important commercial fisheries via farmed and wild populations in Puget Sound and Willapa Bay. As a sedentary, calcifying bivalve occupying mostly subtidal sediment, geoduck are likely to be impacted by climate stressors, which have already been documented as trending towards warmer, more acidic marine conditions. In summer 2016 we outplanted sibling juvenile geoduck in four sites throughout Washington State, each site containing cohorts placed inside and outside eelgrass beds. Geoduck were enclosed to minimize predation, water chemistry was continuously monitored, and after four weeks of exposure geoduck gill tissue was taken for protein analysis. Specifically, shotgun then targeted proteomic analyses were performed and revealed expression pattern associated with local conditions and growth patterns. Together these results demonstrate protein profiles can provide valuable information on local conditions including how environmental change can influence bivalve physiology.

GENETIC CHARACTERIZATION OF WILD AND HATCHERY-PRODUCED *OSTREA LURIDA* IN PUGET SOUND, WASHINGTON, USA

Laura H. Spencer*[1], Brent Vadopalas[1], Crystal Simchick[2], Ryan Crim[3], Frederick W. Goetz[2], and Steven Roberts[1]

[1]University of Washington, School of Aquatic and Fishery Sciences, Seattle, Washington USA

[2]Environmental and Fisheries Sciences Division, Northwest Fisheries Science Center, National Marine Fisheries Service, NOAA, Port Orchard, Washington, USA

[3]Puget Sound Restoration Fund, Bainbridge Island, Washington, USA

lhs3@uw.edu

Efforts to restore the Olympia oyster (*Ostrea lurida*) along its historic distribution in the Puget Sound, Washington (WA) include population enhancement with hatchery-produced seed. Recent genotype-by-sequencing data suggest genetically distinct populations between sub-basins, and very high allelic diversity, with over 10,000 single nucleotide polymorphism (SNP) loci. In an effort to minimize genetic selection within the hatchery, current practices include collecting broodstock annually, breeding via mass spawn within genetically distinct populations, collecting brooded larvae over an extended period of time, and measuring genetic diversity. Results from 2010 and 2011 microsatellite data informed these hatchery practices. This project examines new data from 2014 and 2015 cohorts, focusing on patterns of allelic diversity between wild broodstock and the hatchery-produced F1 individuals. These results and future annual genetic testing will continue to inform hatchery practices for restoration groups and commercial aquaculture facilities that produce this native oyster.

DUNGENESS CRAB TRAP CATCH EFFICIENCY RELATED TO ESCAPE RING LOCATION AND SIZE

George Stearns[1]*, Robert Conrad[2], David Winfrey[1], Nancy Shippentower-Games[1], and Deanna Finley[1]

[1]Puyallup Tribe of Indians, 3009 East Portland Avenue, Tacoma, Washington 98404

[2]Northwest Indian Fisheries Commission, 6730 Martin Way East, Olympia, Washington 98516

george.stearns@puyalluptribe.com

The Dungeness crab *Metacarcinus magister* (*Cancer magister*) supports a commercially important fishery along the West Coast of the United States. Only male crabs above a certain size limit may be retained (i.e., legal-size males). Escape rings are used in traps to create circular holes that facilitate the release of both females and undersized males (sublegal crabs). Sublegal crabs that are retained in a trap can suffer stress, injury, and mortality. In this experiment, both the location and size of the escape ring were modified in an effort to reduce retention rates of sublegal crabs. Four different trap configurations were used: (1) a standard trap without escape rings (control configuration); (2) an unmodified trap with two 4.25-in-diameter escape rings on top (standard configuration); (3) a standard trap with one 4.25-indiameter escape ring placed in each corner adjacent with the bottom (modified 4.25-in configuration); and (4) a trap with two 4.5-in-diameter escape rings on top and one 4.5-in-diameter escape ring placed in each corner adjacent with the bottom (modified 4.5-in configuration). Two different catch statistics were compared among trap configurations: catch of legal-size= males and catch of sublegal crabs. No statistical difference was observed in the catch of legal-sized males in any trap configuration. Compared with the standard configuration, the two modified configurations caught significantly fewer sublegal crabs. Catches of sublegal crabs were not statistically different between the modified 4.25-in and modified 4.5-in configurations.

TRENDS IN OYSTER-ASSOCIATED MICROBIAL TRANSCRIPTOMES

Rebecca J. Stevick[1*], Anton F. Post[2], and Marta Gómez-Chiarri[3]

[1]University of Rhode Island, Graduate School of Oceanography, 220 S Ferry Rd, Narragansett, Rhode Island 02882 USA

[2]Florida Atlantic University, Harbor Branch Oceanographic Institute, 5600 US-1, Fort Pierce, Florida 34946 USA

[3]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, 120 Flagg Rd, Kingston, Rhode Island 02881 USA

rstevick@my.uri.edu

Transcriptomic analysis is often used to determine an organism's genetic response to varying environmental conditions. Although trends are seen in the oyster's response to environmental cues, there is also an abundance of sequencing reads in oyster transcriptomes derived from oyster-associated microbes, including parasites, bacteria, and viruses. These "un-mapped" reads have been largely ignored, but acclimation in the oyster microbiome may ultimately benefit the host. These microbial reads, combined with specific gene expression patterns in host transcriptomes, could also serve as markers of the health status of the host. In order to determine the suitability of mining short read archive (SRA) sequences from oyster transcriptomes to explore the responses of oyster-associated microbial communities, ~15,000 bacterial and viral genomes were indexed and used as a reference for the assembly of quality-controlled transcriptomes present in the oyster SRAs. The coverage and expression of these bacterial genomes was calculated and compared between samples. Preliminary analysis of 16 transcriptomes from two separate experiments (larval and juvenile eastern oysters *Crassostrea virginica* exposed or not to bacterial challenges) shows that bacterial reads account for 30-70% of the raw reads. Within these transcriptomes, there are distinct differences between life stage (larvae versus juveniles) and treatment (control versus bacterial challenge). Specific pathways related to denitrification, metabolism, and virulence will be queried within these microbial reads. This early-stage project will determine the suitability of mining host SRAs to elucidate the function of the oyster core microbiome and microbes specific to age, tissue type, disease status, and environmental parameters, among others.

BACTERIAL COMMUNITY DYNAMICS IN AN OYSTER HATCHERY IN RESPONSE TO PROBIOTIC TREATMENT

Rebecca J. Stevick[1*], Saebom Sohn[2], Tejashree Modak[2], David Nelson[3], David Rowley[4], Roxanna Smolowitz[5], Anton F. Post[6], and Marta Gómez-Chiarri[3]

[1]University of Rhode Island, Graduate School of Oceanography, 220 S Ferry Rd, Narragansett, Rhode Island 02882 USA

[2]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, 120 Flagg Rd, Kingston, Rhode Island 02881 USA

[3]University of Rhode Island, Department of Cell and Molecular Biology, 120 Flagg Rd, Kingston, Rhode Island 02881 USA

[4]University of Rhode Island, College of Pharmacy, 120 Flagg Rd, Kingston, Rhode Island 02881 USA

[5]Roger Williams University, Feinstein School of Social and Natural Sciences, 1 Old Ferry Rd, Bristol, RI 02809 USA

[6]Florida Atlantic University, Harbor Branch Oceanographic Institute, 5600 US-1, Fort Pierce, FL 34946 USA

rstevick@my.uri.edu

Larval oysters in hatcheries are susceptible to diseases caused by marine bacterial pathogens, including *Vibrio* spp. The daily addition of probiotic *Bacillus pumilus* RI06-95 to water in rearing tanks leads to increased larval survival to challenge with *Vibrio coralliilyticus*. It was proposed that the presence of probiotics may change how the larvae respond to pathogens, regulate their environment, and recruit beneficial microbes. During three separate trials spanning the 2012-2015 growing seasons, larvae, tank biofilm, and rearing water samples were collected from control and probiotic-treated tanks in an oyster hatchery at timepoints between Day 0 (spawning) and Day 12. DNA was extracted from 0.22 µm water filters, larvae, and biofilm swabs, and then prepared for sequencing. All samples were analyzed using 16S rDNA sequencing of the V3-V4 or V6 regions and direct taxonomic classification, in order to determine the microbial community. There were significant differences in microbial composition over time and between sample sources, but no major effect of probiotics on the overall rearing water bacterial communities (Bray-Curtis k=2, 95% confidence); however, probiotics increased niche selection of certain bacteria from the water in the oyster larvae, and a significantly higher proportion of *Oceanospirillales* spp. and *Bacillus* spp. was detected in the treated rearing water. Co-occurrence network analysis suggests that the overall probiotic effect on the rearing water is mediated through select associated taxa. This research reveals interactions between probiont and microbial communities in oyster hatcheries, and how new probiotic formulations may be designed.

ESTIMATING SEASONAL GROWTH IN SEA SCALLOPS USING ISOTOPIC DATA IN A CHANGING ENVIRONMENT

Kevin D.E. Stokesbury* and Susan Inglis

University of Massachusetts Dartmouth, School for Marine Science and Technology, 706 South Rodney French Boulevard, New Bedford, Massachusetts, USA 02744-1221

kstokesbury@umassd.edu

The North Atlantic marine environment in changing rapidly, raising concerns about the negative effects on the sea scallop (*Placopecten magellanicus*) fishery, which has recently experienced unprecedented rebuilding. Through the use of spatial and temporal management strategies, large recruitment events have been protected until the scallops reach a harvestable size contributing

to the rebuilding of these stocks; however, growth and mortality rates for these recruitment events are not well defined, occurring from several sources and vary spatially. In support of this spatial management plan a large experiment was conducted from 2001 to 2007 in which 130,000 scallops were, measured, individually tagged and release at specific locations correlating with management access areas on Georges Bank and in the Mid-Atlantic. The fishing industry recapture and returned about 10% of the scallop shells along with the vessel position. Several of the returned scallops were at large for more than two years. These 52 scallop shells provide a unique opportunity for isotopic analysis as two specifics sites on the shell have known dates, the release and return. Shell carbonate powder was collected every 0.5-1.0 mm along the shell. These 2,763 carbonate samples were processed by the University of Michigan Isotope Laboratory and reported depletion of ^{18}O (parts per thousand ‰) relative to the Peedee belemnite carbonate standard. Using available oceanographic data, the seasonal growth patterns were determined by area. This growth information may be used as a baseline to understand variations on scallop growth as the marine environment changes.

THE RAMIFICATIONS OF MISMATCHING SPATIAL ROTATIONAL MANAGEMENT WITH LIFE HISTORY AND POPULATION TRAITS: AN EXAMPLE IN THE SEA SCALLOP FISHERY

Kevin D.E. Stokesbury*, Emily Keiley, Daniel Georgianna, N. David Bethoney, and Susan Inglis

University of Massachusetts Dartmouth, School for Marine Science and Technology, 706 South Rodney French Boulevard, New Bedford, Massachusetts, USA 02744-1221

kstokesbury@umassd.edu

Mismatching spatial rotational management with life history and population traits of the target species can have long reaching economic consequences. An example of this occurred in the sea scallop (*Placopecten magellanicus*) fishery of the eastern United States. In this fishery there are several large Marine Protected Areas, including Closed Area I, which contain portions of the historic scallop fishing ground. Closed Area I was intensely surveyed in 1999 and a triangular area, covering about 700 km^2, was incorporated into the Amendment 10 rotational plan allowing the scallop fishery limited access, depending on exploitable biomass. A proposal to expand this access area in 2004 to include a large portion of the fishing grounds to the south of the original boundary was denied due to process by a Federal court decision; the change needed to be made in a full rule rather than a framework. As a result the area expansion was delayed until 2011. When the area opened the expected harvest was not achieved, and fishermen reported large amounts of "grey meat" scallops. Many vessels were unable to complete their allotted trips and these continue to be carried forward. Here the shifts in abundance and biomass of sea scallops within the access and closed areas, the occurrence of grey meats, and the impacts it has had on the economics and management of the sea scallop fishery are examined to determine the ramification of this bureaucratic delay.

DEVELOPING RESILIENCE TO OCEAN ACIDIFICATION IN RED ABALONE AQUACULTURE

Daniel S. Swezey[1,3]*, Sara E. Boles[1, 2], Kristin M. Aquilino[1], Haley K. Stott[3], Doug Bush[3], Tessa M. Hill[1,5], Brian Gaylord[1,7], Cynthia A. Catton[1,4], Laura Rogers-Bennett[4,6], Andrew Whitehead[2], and Eric Sanford[1,7]

[1]University of California, Davis, Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, California, 94923, USA

[2]University of California, Davis, Department of Environmental Toxicology, 1 Shields Ave, Davis, California 95616, USA

[3]The Cultured Abalone Farm, 9580 Dos Pueblos Canyon Road, Goleta, Califorina 93117, USA

[4]California Department of Fish and Wildlife Marine Region, Bodega Marine Laboratory, 2099 Westshore Road, Bodega Bay, California 94923 USA

[5]University of California, Davis, Department of Earth and Planetary Sciences, 1 Shields Ave, Davis, California 95616, USA

[6]University of California Davis, Karen C. Drayer Wildlife Health Center and Bodega Marine Laboratory, Bodega Bay, California 94923, USA

[7]University of California, Davis, Department of Evolution and Ecology, 1 Shields Ave, Davis, California 95616, USA

dswezey@culturedabalone.com

The pH of the global ocean is decreasing due to absorption of anthropogenic CO_2 emissions, a process termed ocean acidification (OA). Recent research has demonstrated that most commercially harvested shellfish are sensitive to OA, with consequences including reductions in growth, calcification, reproduction and survival. The hypothesis that differences in regional oceanography could select for variation in OA tolerance among populations of red abalone (*Haliotis rufescens*) was examined, and laboratory experiments were conducted to investigate the sensitivity of red abalone to OA.

Offspring used in experiments were derived from broodstock sourced from two populations; the Mendocino coast, a region of California that experiences low ocean pH values and high levels of upwelling activity, and The Cultured Abalone Farm, a commercial aquaculture venture located near Santa Barbara, California whose broodstock animals are sourced from various coastal locales in Southern California. Offspring from both populations were reared from embryos to post-settlement juveniles under both contemporary ocean pH values (8.1 pH, 400 µatm CO_2) and low-pH conditions predicted for the future (7.6 pH, 1200 µatm CO_2), which also occur currently during episodic upwelling in northern California.

Under low-pH conditions, significant increases in mortality were observed in the Santa Barbara population, but not in offspring sourced from Mendocino. Within the vulnerable Santa Barbara population, certain maternal lineages were more resilient to low-pH stress than others. The heritability of these differences is now being investigated through trials on second generation offspring, with the goal of identifying adaptive genetic variation for use in future abalone aquaculture.

EUROPEAN GREEN CRAB IN BRITISH COLUMBIA: TRACKING THE SPREAD OF A HIGH-RISK INVADER

Thomas W. Therriault*, Vanessa Hodes, Tammy Norgard, Lyanne J.F. Curtis, and Graham E. Gillespie

Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, British Columbia, Canada

thomas.therriault@dfo-mpo.gc.ca

The European green crab, *Carcinus maenas*, is a high-risk global invader that arrived in British Columbia (BC) in the late-1990s. Since the early 2000s the Department of Fisheries and Oceans Canada (DFO) has been tracking the occurrence and changing distribution of this species throughout BC's coastal waters. The standardized monitoring program uses Fukui traps deployed in the intertidal zone where green crab in BC are known to preferentially inhabit. Since the start of this program, approximately 18,000 traps have been deployed at almost 3,000 locations throughout the province. In general, most established populations are restricted to inlets/sounds on the West Coast of Vancouver Island; however, significant range extensions were noted for emerging green crab populations in the Central Coast (2011 in Gale Passage and 2016 in Higgins Passage) and the Salish Sea (2012 in Sooke Basin). The northward spread of green crab is consistent with natural dispersal from southern populations while the movement into the Salish Sea appears to have been human-mediated. Following initial reports of green crab in Puget Sound, intensive fall trapping surveys were initiated in 2016 to better understand the unique invasion dynamics associated with this incursion into the Salish Sea. The first Canadian detection of green crab outside of Sooke Basin within the Salish Sea was in 2017 at Becher Bay (10 km south of Sooke). Since green crab may not be established broadly within the Salish Sea continued monitoring and intervention is suggested and potential control options will be discussed briefly.

ASSESSMENT OF THE DISTRIBUTION SHIFT AND RANGE EXPANSION OF THE ATLANTIC SURFCLAM, *SPISULA SOLIDISSIMA*, USING A SPATIAL DISTRIBUTION FUNCTION MODEL

Jeremy Timbs[1*], Roger Mann[2], and Eric Powell[1]

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

[2]Virginia Institute of Marine Science, College of William & Mary, 1208 Greate Road, Gloucester Point, Virginia 23062 USA

Jeremy.Timbs@usm.edu

The Atlantic surfclam (*Spisula solidissima*) is a commercially important species whose population has progressively moved offshore since the early 1970s. This movement has been documented in the literature but not approached through modeling the movement spatially over time. A Spatial Distribution Function (SDF) model-based approach was used to evaluate the Atlantic surfclam distribution over the course of the ~30 years of assessment data. The data were divided into size classes (lower boundary: 64, 80, 93, 104, 120) and by region (Delmarva, New Jersey, Long Island, Southern New England, Georges Bank) to evaluate temporal shifts in the center of gravity and range expansion of surfclams. New Jersey and Long Island showed a range expansion while the other regions remained fairly constant over time. The total area occupied by the surfclams in Delmarva has remained constant by a range shift occurring with a loss of surfclams nearshore and an increase in surfclams offshore. The Delmarva and New Jersey regions have shifted northeast while the Long Island, Southern New England, and Georges Bank regions have shifted south and southwest over the course of the stock assessment surveys. These results further support the movement of Atlantic surfclams offshore. This movement offshore could be attributed to the rise in bottom water temperatures especially in the Delmarva region which has seen a large reduction in nearshore surfclams.

IDENTIFYING ENVIRONMENTAL DRIVERS OF *ALEXANDRIUM* HARMFUL ALGAL BLOOMS IN SOUTHEAST ALASKA

Elizabeth D. Tobin[1,3*], Cody Crumpton[2], Chelsea Wallace[2] and Ginny L. Eckert[1]

[1]University of Alaska Fairbanks, College of Fisheries and Ocean Science, 17101 Point Lena Loop Rd, Juneau, Alaska 99801 USA

[2]University of Southeast Alaska, Department of Biology and Marine Biology, 11066 Auke Lake Way, Juneau, Alaska 99801 USA

[3]Jamestown S'Klallam Tribe, Natural Resources, 1033 Old Blyn Hwy, Sequim, Washington 98382 USA

edtobin@alaska.edu

Paralytic Shellfish Poisoning (PSP) in Alaska is a persistent problem that threatens human health and the availability of commercially and culturally important shellfish resources. Regular out-

breaks of PSP caused by the saxitoxin-producing marine alga, *Alexandrium* sp., make recreational and subsistence shellfish harvest unsafe and impose economic hardships. Despite these long-recognized impacts, limited research has been done to understand the ecological mechanisms that drive toxic *Alexandrium* blooms in Alaska.

The objectives of this study were to identify *Alexandrium* bloom initiation sites and environmental factors that support toxic blooms in Southeast Alaska. To accomplish this, an intensive benthic survey was completed in regions of northern Southeast Alaska with historically high levels of PSP. High abundances of overwintering *Alexandrium* cysts ("seed beds") were found throughout the region and in close proximity to well-known shellfish harvest areas. Environmental time series data collected from Auke Bay in Juneau, AK from 2008-2016 was analyzed to identify bloom-supporting conditions. *Alexandrium* cells were present across a range of sea surface temperatures (7-15°C) and salinities (7-30 psu), yet accelerated cell growth ("bloom") occurred within an optimal temperature/salinity window. *Alexandrium* cell abundance and particulate saxitoxin concentrations were strongly correlated, indicating that cells consistently produce toxins under growth-supporting conditions. No single environmental factor was identified in driving bloom events, rather several interacting conditions appear to support the development of toxin-producing *Alexandrium* blooms. Improved understanding of these environmental drivers of *Alexandrium* harmful algal blooms can help build predictive capacity in the timing, distribution and impacts of PSP in Alaska.

FIRST RECORDS OF THE GENUS *AZADINIUM* (DINOPHYCEAE) FROM PUGET SOUND, WASHINGTON STATE

Vera L. Trainer[1*], Joo-Hwan Kim[2], Brian D. Bill[1], Nicolaus Adams[1], Urban Tillmann[3], Bernd Krock[3], and Neil Harrington[4]

[1]NOAA, Northwest Fisheries Science Center, Seattle, Washington 98112 USA

[2]Hanyang University, Seoul 133-791, South Korea

[3]Alfred Wegener Institute, Am Handelshafen 12, D-27570 Bremerhaven, Germany

[4]Jamestown S'Klallam Tribe, 1033 Old Blyn Hwy, Sequim, Washington 98368 USA

vera.l.trainer@noaa.gov

Lipophilic toxins, in particular those associated with diarrhetic shellfish poisoning (DSP), are an emerging threat to shellfish harvesting in Washington State (WA). While Washington was the first state to implement the routine testing of shellfish for DSP toxins in 2012 after the occurrence DSP in Sequim Bay, WA in 2011, there continue to be occasional reports of DSP-like illnesses likely tied to the consumption of shellfish from Puget Sound. To address these illnesses of unknown etiology, a Monitoring and Event Response to Harmful Algal Blooms project was begun in 2015 to identify whether species of the genus *Azadinium* were present in Puget Sound. This small dinoflagellate, in particular *A. poporum*, *A. spinosum,* and *A. dexteroporum*, have been shown in other parts of the world to produce azaspiracids, lipophilic toxins which can produce DSP-like symptoms. The presence of the genus *Azadinium* was confirmed in whole water samples collected from several Sound Toxins sites in Puget Sound based on the use of molecular probes. The establishment of *Azadinium* cultures from sediment samples from Puget Sound including *A. obesum*, *A. cuneatum*, *A. poporum*, and *A. dalianense* will be reported. The production of a new azaspiracid, named AZA-59, was confirmed by liquid chromatography mass spectroscopy in several isolates of *A. poporum*. This first confirmation of the presence of the genus *Azadinium* in Puget Sound and the first report of azaspiracid on west coast of the U.S., underlining the potential risk of azaspiracid shellfish poisoning in this region.

PSEUDO-NITZSCHIA EARLY WARNING BULLETIN INCREASES CLAMMING OPPORTUNITIES ON PACIFIC NORTHWEST OUTER COAST BEACHES

Vera L. Trainer[1], Ryan M. McCabe[2], Barbara M. Hickey[3], Parker MacCready[3], Matthew Hunter[4], Stephanie Moore[5], Gregory J. Doucette[6], Neil S. Banas[7], and Zach Forster[8*]

[1]NOAA, Northwest Fisheries Science Center, Seattle, Washington USA

[2]University of Washington, Joint Institute for the Study of Atmosphere and Ocean, Seattle, Washington, USA

[3]University of Washington, School of Oceanography, Seattle, Washington, USA

[4]Oregon Department of Fish and Wildlife

[5]University Corporation for Atmospheric Research

[6]National Centers for Coastal Ocean Science, NOAA/NOS, Charleston, South Carolina, USA

[7]Strathclyde University, Glasgow, Scotland

[8] Washington Department of Fish and Wildlife, Nahcotta, Washington, USA

zachary.forster@dfw.wa.gov

The 2015 coastwide bloom of toxic *Pseudo-nitzschia* resulted in over $125 million losses to shellfish harvesters and contributed to the deaths of marine mammals. With little warning, an emergency closure of the recreational razor clam fishery in Washington State resulted in the destruction of toxic razor clams dug earlier that day. This event reinforced the need for shellfish managers to receive timely information to conduct safe and efficient fisheries. Toward this end, a Pacific Northwest Harmful Algal Bloom (PNW HAB) Bulletin provides forecasts intended to help resource managers from Neah Bay to Newport target beachside monitoring of toxicity levels in shellfish and fine-tune decisions regarding beach closures. This forecast system will include sampling by the Makah Tribe in a documented offshore HAB hotspot at two-week intervals. These offshore HAB data will be combined with other information sourc-

es: beachside monitoring by Olympic Region HAB partners and Oregon Department of Fish and Wildlife, the LiveOcean forecast model, and near real-time data from an offshore biological sensor (the Environmental Sample Processor). The first PNW HAB Bulletin in May 2017, gave Washington State shellfish managers the confidence to increase the daily limit from 15 to 25 razor clams to take advantage of record numbers of clams available for harvest. This increased limit resulted in record number of one-day digger trips and over $5.3 million injected into the local economy. Future PNW HAB Bulletins will help coastal managers make rapid, informed decisions about seafood safety and is planned to transition to operations starting in 2019.

COMPARISON OF GENETIC VARIATION AND INBREEDING AMONG THREE LINES OF HATCHERY-REARED *CRASSOSTREA VIRGINICA* BROODSTOCK

Robin L. Varney* and Ami E. Wilbur

University of North Carolina Wilmington, Shellfish Research Hatchery, CREST Research Park, 5600 Marvin K. Moss Lane, Wilmington, North Carolina 28409 USA

varneyr@uncw.edu

The eastern oyster, *Crassostrea virginica*, is an ecologically and economically important marine bivalve along the east coast of North America. Severe declines in natural populations of *C. virginica* due to overfishing, habitat loss and disease have led to increased restoration efforts. Expansion of the oyster aquaculture industry has enhanced efforts to restore natural populations, as well as produced genetically improved oyster lines through hatchery production. Loss of genetic diversity and inbreeding depression are potential negative effects of using hatchery-reared lines as broodstock in oyster aquaculture. This study assessed the genetic effects of breeding practices on three lines of hatchery-reared *C. virginica*, derived from wild North Carolina oyster populations. Utilizing 22 microsatellite loci, the genetic properties of 15 breeding populations from three generations of broodstock were estimated and compared. Parentage assignment was performed on each population of hatchery-reared progeny to evaluate reproductive success of mating pairs and inbreeding between siblings. Although few instances of direct inbreeding occurred between siblings, a trend of increasing genetic relatedness was observed with decreasing allelic richness over subsequent generations.

GROWTH MODELING IN TWO POPULATIONS OF *P. GLOBOSA* FROM THE UPPER GULF OF CALIFORNIA: INTEGRATION OF INDIVIDUAL GROWTH PROFILES AND JUVENILE DATA TO TERMINAL SIZE-AT-AGE

Karla Daniela Vega-Collazo*, Sergio Scarry González-Peláez, José Angel Hidalgo-de-la-Toba, J. Jesús Bautista-Romero, and Daniel B. Lluch-Cota

Centro de Investigaciones Biológicas del Noroeste. Av. Instituto Politécnico Nacional 195.

Col. Playa Palo de Santa Rita Sur, La Paz, B.C.S., México 23096

karla.auster@gmail.com

The individual growth modeling of long lived geoducks has been changed since the use of a single von Bertalanffy growth model to multimodel inference (MMI) approach as a method to improve the descriptions of growth patterns; however, a sampling bias towards larger size classes could affect the model estimations. Here the individual growth for the geoduck, *Panopea globosa,* in two populations from the upper Gulf of California region, San Felipe (n =148) and Puerto Peñasco (n= 123), was modeled using three different data sources: individual growth profiles (IGP), juvenile data, and terminal length-at-age data. The integrated information was used in six growth models -Von Bertalanffy, Generalized Von Bertalanffy (GVB), Gompertz, Logistic, Johnson and Richards- using a MMI and fitted with a maximum likelihood function. A model selection through Akaike information criterion selected the GVB as the best candidate growth model, showing that the asymptotic shell length estimated for San Felipe was 144.99 mm meanwhile for Puerto Peñasco it was 159.83 mm. These values are different from previous estimates, especially for San Felipe population, where the reported asymptotic length was 60.2 mm higher. These results showed that the integration of IGP and juvenile data improved the growth modeling and allow describing the whole ontogenic growth pattern in *P. globosa* populations. Finally, the age structure (unimodal structure for San Felipe and multimodal structure for Puerto Peñasco) suggest different recruitments patterns, thus different management policies should be applied.

EFFECT OF OCEAN ACIDIFICATION ON PACIFIC OYSTER (*CRASSOSTREA GIGAS*) REPRODUCTION

Yaamini R. Venkataraman* and Steven B. Roberts

University of Washington, School of Aquatic and Fishery Sciences, 1122 NE Boat St, Seattle, Washington 98105 USA

yaaminiv@uw.edu

It is crucial to consider multigenerational impacts of ocean acidification and how this will affect ecologically and commercially relevant species like the Pacific oyster (*Crassostrea gigas*). To assess how ocean acidification affects adult and larval *C. gigas*, adult oysters were first exposed to either ambient or low pH conditions for seven weeks. Gonad maturation at was assessed using histology. Oyster were then conditioned and spawned to create four larval families based on parental exposure: low-low, low-ambient, ambient-low, and ambient-ambient. Differential mortality was assessed over the course of a 17-day larval period. In addition, global DNA methylation analysis and gene expression analysis was performed. There was a substantial influence of acidification on gametogenesis. A sex-specific broodstock response was also observed, where females exposed to low pH conditions produced fewer larvae. These combined data suggest there is an impact of ocean acidification on reproductive development and larval output, potentially

explained by differential gene methylation patterns. This study will also provide information necessary for understanding how larval *C. gigas* can inherit methylation patterns, and how these patterns can affect performance at developmental bottlenecks.

OLIGOMERIZATION PATTERNS OF PIRA AND PIRB CAUSING ACUTE HEPATOPANCREATIC NECROSIS DISEASE (AHPND) AND ITS INTERACTION WITH THE MEMBRANE COMPONENTS OF THE EPITHELIAL CELLS OF THE SHRIMP HEPATOPANCREAS

Marcelo Victorio-De Los Santos[1*], Alejandra Hernández-Santoyo[2], and Sonia Soto-Rodriguez[1]

[1]Centro de Investigación en Alimentación y Desarrollo, Av. Sábalo Cerritos S/N A.P. 711

Mazatlán, Sinaloa, México

[2]Departamento de Química de Biomacromoléculas, Instituto de Química, Universidad Nacional Autónoma de México

marcelo.victorio@estudiantes.ciad.mx

The Acute Hepatopancreatic Necrosis Disease (AHPND) is an emerging infectious disease of shrimp caused by specific strains of *Vibrio parahaemolyticus* (Vp AHPND+), which contains PirA and PirB toxins encoded in the pVA1 plasmid. PirA and PirB have been shown to cause the typical histological lesion of AHPND in infected shrimp. Presently, it is unknown how the intoxication takes place and what are the toxins role during the disease. Do they act in a complex A/B form or in a protein-protein polymerization way? Given what little information exists about this, it is important to study the interaction between the PirA and PirB toxins and the epithelial cells of the hepatopancreas, which, once elucidated, alternatives ways to control the shrimp intoxication could be developed.

The interaction between individual toxins (PirA-PirA, PirB-PirB and PirA-PirB) was investigated, as well as the potential binding site to a receptor on the membrane of the epithelial cells in *Litopenaeus vannamei* hepatopancreas. *In vitro* assays showed different oligomerization patterns of the toxins, generating up to tetramers of both the PirA/PirB complex and PirB/PirB. It suggests that the mechanism of infection may include the oligomerization of the complex or PirB oligomerization alone. Efforts are underway to identify the membrane receptor, trying to understand the molecular mechanism used by the toxins.

LETHAL AND SUB-LETHAL EFFECTS OF THE POLYFLUORINATED COMPOUND, GENX, ON THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Uma Volety[1], Ai Ning Loh[2], Leo Soudant[3], Melissa Lenentine[2], Cailin Harell[2], Philippe Soudant[4], and Aswani Volety[2*]

[1]Roland-Grise Middle School, 4412 Lake Ave, Wilmington, North Carolina 28403 USA

[2]University of North Carolina Wilmington, 601 S. College Rd, Wilmington, North Carolina 28409 USA

[3]Lycée Vauban, Rue de Kerichen, 29200 Brest, France

[4]Laboratoire des Sciences de l'Environnement Marin (UMR 6539, LEMAR), IUEM/UBO, Technopole Brest Iroise, Plouzané, France

voletya@uncw.edu

GenX is a polyfluorinated compound that was created by DuPont to make Teflon. GenX, a polyflourinated compound (PFC) was created to replace the more toxic perfluorooctanoic acid, (PFOA). Recent results suggest that GenX has been contaminating water supply in the rivers and estuaries in southeastern North Carolina for over 20 years. PFOA and PFC have been shown to have negative impacts on humans as well as marine organisms. This project examined the effects of GenX on the filtration, growth, and mortality of juvenile oysters (18-27 mm). Juvenile oysters were exposed to 0, 1, 10, and 100 parts per billion (ppb) for four weeks and length of the oysters and clearance rates measured after two and four weeks of exposure. While there was no effect of GenX on the growth or mortality of oysters, oysters exposed to 100 ppb had significantly lower clearance rates compared to controls and other concentrations. Investigations of the bioaccumulation of GenX as well as examining the cellular responses of GenX oysters in oysters are underway.

SUMMER MORTALITY IN FARMED TRIPLOID AND DIPLOID OYSTERS, *CRASSOSTREA VIRGINICA,* IN THE NORTHERN GULF OF MEXICO

Pandora C. Wadsworth* and William C. Walton

Auburn University School of Fisheries, Aquaculture and Aquatic Sciences, Auburn University Shellfish Laboratory, 150 Agassiz Street, Dauphin Island, Alabama, 36528 USA

pzw0014@auburn.edu

After unusually high mortality of farmed oysters at commercial farms in Alabama during the summer of 2016, this study was started to determine whether summer mortality was site-specific and dependent on ploidy. Growth and survival were evaluated in paired triploid and diploid *Crassostrea virginica* deployed for 11 months at four sites adjacent to commercial oyster farms in Alabama. The results were supplemented with growth and mortality rates of triploid oysters at four commercial farms along the northern Gulf of Mexico (LA, AL, FL). Similar to 2016, mortality at the experimental sites peaked during the summer and triploid oysters experienced significantly higher mortality than diploid oysters at three of four sites (site x ploidy, $p < 0.05$). Cumulative mortality reached 100% for triploid baskets (n = 4 ploidy/site) at two experimental sites and reached 90-100% at two commercial farms. Shell height, whole wet weight, dry tissue weight and dry shell weight were significantly different across sites and ploidy ($p < 0.05$), but not site x ploidy ($p > 0.05$). The presence and intensity of *Perkinsus marinus* was consistent with past studies in Alabama and was significantly different across sites and ploidy ($p < 0.05$), but not site x ploidy (p

> 0.05). While prolonged low salinity and high water temperatures help explain mortality at two of the sites, these factors alone do not explain the differences at all sites. The results draw attention to the need for a better understanding of the triggers of summer mortality in triploids.

A REVIEW OF RECENT FISHERY-INDEPENDENT AND FISHERY-DEPENDENT MONITORING DATA FOR BLUE CRABS IN THE GULF OF MEXICO SPECIFIC TO MANAGEMENT OF THE RESOURCE

Tom Wagner[1]*, Harriet Perry[2], Lillian Collins[2], John Anderson[2], Rick Burris[3], Joel Anderson[4], Zachary Olsen[5], Carey Gelpi[6], and Darin Topping[7]

[1]Texas Parks & Wildlife Department, 702 Navigation Circle, Rockport, Texas 78382 USA

[2]Gulf Coast Laboratory, Research 703 East Beach, Ocean Springs, Mississippi 39564 USA

[3]Mississippi Department of Marine Resources, 1141 Bayview Avenue, Biloxi, Mississippi 39530 USA

[4]Texas Parks & Wildlife Department, Perry R Bass Marine Fisheries Research Station, 3864 FM 3280, Palacios, Texas 77465 USA

[5]Texas Parks & Wildlife Department, 6300 Ocean Drive, Unit 5845, Corpus Christi, Texas 78412 USA

[6]Texas Parks & Wildlife Department, 601 Channelview, Port Arthur, Texas 77640 USA

[7]Texas Parks & Wildlife Department, 702 Navigation Circle, Rockport, Texas 78382 USA

Tom.Wagner@tpwd.texas.gov

Recent data from a variety of fishery-independent studies suggest further examination of the impact of current management strategies on the blue crab resource. The 2015 Blue Crab Fishery Management Plan (BCFMP) and the 2013 Gulf Data, Assessment, and Review (GDAR) provide comprehensive assessments of the fishery and serve as a framework for re-interpretation of historic data in light of current research and the integration of new studies. Information from the BCFMP and GDAR documents are summarized and relevant new data presented. Fishery-independent and fishery-dependent data for the Blue Crab (*Callinectes sapidus*) from long-term and recent monitoring programs conducted by Gulf of Mexico state management agencies and scientific laboratories are summarized, with the specific goal of comparing long-term changes in the fishery across the Gulf of Mexico. Fishery-independent data from 1984 through 2016 from the five Gulf States were collected using trawls in state inshore waters. Fishery-dependent data include commercial hard crab landings and ex-vessel value reported to the National Marine Fisheries Service, and catch-per-unit effort (CPUE) data collected by the states through their respective Trip Ticket Programs. Data from a 2007-2016 fishery-dependent survey of Mississippi commercial blue crab fishermen were summarized to determine CPUE. Blue crab fishery management regulations are presented for each of the five Gulf States. Trends in fishery-independent and fishery-dependent data are evaluated in light of current management strategies.

THE GULF OF MEXICO SHELLFISH INITIATIVE: A REGIONAL APPROACH

Bethany A. Walton[1]*, LaDon Swann[2], and William C. Walton[3]

[1]University of Southern Mississippi, Mississippi-Alabama Sea Grant Consortium, 703 East Beach Drive, Ocean Springs, Mississippi 39564 USA

[2]Auburn University Marine Extension and Research Center, 118 North Royal Street, Suite 800, Mobile, Alabama 36602 USA

[3]Auburn University Shellfish Laboratory, 150 Agassiz Street, Dauphin Island, Alabama 36528 USA

bethany.walton@usm.edu

The intention of the Gulf of Mexico Shellfish Initiative (GoMexSI) is to protect and enhance shellfish resources in a way that creates sustainable water-dependent jobs while improving the water quality of numerous US Gulf of Mexico estuaries, through long-term regional planning for the wise and sustainable use of shellfish resources. To accomplish this, a planning team has gathered input from stakeholders from across the US Gulf of Mexico to identify common goals among the states, as well as those which are unique to each state. Within each state, shellfish stakeholders are being engaged to determine state-specific action items (objectives) to accomplish the goals of GoMexSI.

Over the last year, at least one stakeholder meeting per state in the region was held, with multiple meetings in Florida and Texas during the summer and fall of 2017. These meetings, coordinated with local Sea Grant and Extension personnel, were facilitated to maximize input from stakeholders. In addition to these meetings, an online survey was distributed to the public in summer 2017 and has obtained over 100 responses so far. Stakeholder meeting feedback and survey responses are being analyzed and summaries will be presented.

MOLECULAR EVOLUTION OF I84 PROTEASE INHIBITOR FAMILY IN CHINESE RAZOR CLAMS AND PHYLUM MOLLUSCA

Xiarong Wang[1,2], Qinggang Xue*[2], Xiaowei Mao[1,2], Yinghui Dong[2], Chenhua Li[1], Zhihua Lin[2]

[1]Ningbo University, School of Marine Sciences, Ningbo, Zhejiang 315010, China

[2]Zhejiang Wanli University, Key Laboratory of Aquatic Germplasm Resource of Zhejiang, Ningbo, Zhejiang 315100, China

qxue@zwu.edu.cn

The I84 protease inhibitor family in the MEROPS classification system consists of novel proteins that inhibit certain serine proteases and are believed to play a role in mollusk host defense. Five family members, 3 (cvSI-1, cvSI-2 and cvSI-3) from the eastern oyster *Crassotrea virgincia* and 2 (scSI-1 and scSI-2) from the Chinese

razor clam *Sinonovacula constricta*, have been identified. In the present research, we studied the gene structure and genetic polymorphisms of scSI-1 and scSI-2. Our results showed that both scSI-1 and scSI-2 genes had 2 exons and 1 intron, but the length of exons and introns differed between the 2 genes. Resequencing the coding regions of the 2 genes in 100 clam individuals from 2 geographic populations identified 9 and 2 single nucleotide polymorphisms (SNPs) respectively in scSI-1 and scSI-2. Seven of the scSI-1 SNPs and all the scSI-2 SNPs were nonsynonymous, suggesting that the genes have been evolving under positive selection. We also measured using real-time PCR the expression of scSI-1 and scSI-2 genes during *Sinonovacula constricta* larva development. It was found that the expression of both genes elevated significantly in D-stage larvae, but the expression level of scSI-1 decreased while that of scSI-2 continued to increase in juvenile clams. In addition, we searched the sequenced genome of mollusk species and EST sequence databases and phylogenetically analyzed the homologous sequences of the I84 family. This research provided valuable insight into the molecular evolution of the novel protease inhibitor family in *Sinonovacula constricta* and the Phylum Mollusca.

DEVELOPING AN EFFECTIVE TRANSFECTION PROTOCOL FOR GENE EDITING IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*

Zhenwei Wang[1,2*] and Ximing Guo[1]

[1]Rutgers University, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, New Jersey, 08349 USA

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

zw233@hsrl.rutgers.edu

Genetic improvement of oysters has so far relied on selective breeding, polyploidization or marker-assisted selection. With the advent of genomics, functional genes underlying economically important traits are being identified, which opens the door to genetic improvement by gene editing. Clustered Regularly Interspersed Short Palindromic Repeats-Cas9 (CRISPR/Cas9) can provide effective gene editing and create heritable changes without introducing foreign genes as in recombinant-DNA based genetic modifications. Gene editing by CRISPR/Cas9 requires efficient plasmid transfection, which remains a challenge in many invertebrates. The objective of this study is to develop an effective transfection protocol for gene editing by CRISPR/Cas9. The transfection reagent Superfect (Sigma) is used to treat sperm, eggs or both for transfecting a green fluorescence protein (GFP) plasmid. After treating the sperm and/or eggs, fertilization was conducted to create four groups: 1) treated eggs and untreated sperm; 2) treated eggs and treated sperm; 3) untreated eggs and treated sperm; and 4) untreated eggs and untreated sperm. Transfection success was determined by observing GFP expression or green fluorescence under a fluorescence microscope at 30 and 72 hours post-fertilization. Successful transfection of GFP was observed in groups 1 (40%) and 2 (22%) but not in groups 3 and 4, suggesting that treating eggs is more effective than treating sperm. Dead larvae exhibited the strongest fluorescence signals, indicating that over-expression of GFP may be toxic to oyster larvae. This study provides a simple and effective transfection protocol which paves the way for gene editing by CRISPR/Cas9 in oysters and other bivalve molluscs.

CAPTURE AND INGESTION OF NANOPARTICLES BY BIVALVES: IMPLICATIONS FOR BIOACCUMULATION AND TOXICITY

J. Evan Ward[1]*, John Doyle[2], Vena Haynes[1], and Bridget Holohan[1]

[1]University of Connecticut, Department of Marine Sciences, Groton, Connecticut 06340 USA

[2]Gloucester Marine Genomics Institute, 6 Rowe Square, Gloucester, Massachusetts 01930 USA

Evan.ward@uconn.edu

Particle ingestion is a direct route for uptake of anthropogenic contaminants by bivalves. The feeding processes of these animals are constrained by functional mechanisms, and most bivalves capture particles <1 µm at efficiencies of < 25%. Such limitations have implications for ingestion of nanoparticles (NP) which are operationally defined as <0.1 µm. In aquatic environments, however, most particles are not monodispersed but form homo-agglomerations and hetero-aggregations (i.e, marine snow) that are micrometers in size. Determining the tendency of NP to form homo-agglomerates and be incorporated into marine snow is important for an understanding of NP ingestion and bioaccumulation. In the laboratory, four different types of NP were delivered to two species of bivalves: the mussel, *Mytilus edulis*, and oyster, *Crassostrea virginica*. NP differed in composition and size, and included two types of nano-titania (n-TiO_2) and two types of nano-polystyrene (n-Poly). NP were delivered to bivalves either incorporated in marine snow (laboratory generated) or freely suspended at a concentration of 1 mg/L. The lowest incorporation efficiency was found for n-Poly (16% - 58%), whereas n-TiO_2 was incorporated in marine snow at higher efficiencies (70% - 97%). When delivered n-TiO_2 and 50-nm n-Poly, the percentage of NP ingested per hour by both species was independent of form of delivery (NP in marine snow = freely suspended). For 100-nm polystyrene, both species ingested significantly more NP when particles were incorporated in marine snow. Results demonstrate that for some NP, formation of homo-agglomerations produce masses large enough to be captured and ingested by bivalves.

INGESTION, BIOACCUMULATION, AND DEPURATION OF MICRO- AND NANO-PLASTIC PARTICLES BY MARINE BIVALVES

J. Evan Ward*, Vena Haynes, Bridget Holohan, and Kayla Mladinich

University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Road, Groton, Connecticut 06340 USA

Evan.ward@uconn.edu

Plastic debris is introduced into the oceans through anthropogenic waste. Larger plastics are broken down into microplastic (MPP) and nanoplastic particles (NPP) via weathering and UV degradation, thus exposing coastal organisms to these pollutants. Studies have shown that MPP and NPP negatively affect marine animals on an organ and cellular level. Despite the potential for exposure and toxicological effects, the uptake and accumulation of MPP and NPP by benthic animals, such as suspension-feeding bivalves, is largely unexplored. This study examined the ingestion and depuration of fluorescent polystyrene MPP and NPP by the blue mussel, *Mytilus edulis*. Particles were aged in filtered seawater for three days prior to use in exposure experiments. Mussels were exposed to a 0.1 mg/L/hr concentration of either MPP or NPP for two weeks and then allowed to depurate for one week in filtered seawater. Mussels were fed a standard microalgal diet throughout the three-week experiment. Feces were collected daily and replicate mussels sampled and frozen at the end of each week for later analysis. Tissue and feces samples were analyzed via a scanning fluorescence spectrophotometer and concentration of plastic quantified. Results from this study will allow us to develop biokinetic models of uptake and accumulation of MPP and NPP in bivalves, and help elucidate the potential for these materials to be passed to higher trophic levels including humans.

COAST-WIDE OLYMPIA OYSTER NETWORK: RESILIENT NATIVE OYSTERS FROM BRITISH COLUMBIA, CANADA TO BAJA CALIFORNIA, MEXICO

Kerstin Wasson[1]*, Danielle Zacherl[2], and Chela Zabin[3]

[1]Elkhorn Slough National Estuarine Research Reserve, 1700 Elkhorn Road, Royal Oaks, California 95076 USA

[2]California State University Fullerton, Box 6850, Department of Biological Science, Fullerton, California 92834 USA

[3]Smithsonian Environmental Research Center, 3152 Paradise Drive, Tiburon California 95050 USA

kerstin.wasson@gmail.com

Olympia oyster conservation and restoration practitioners, scientists, aquaculturists, and other stakeholders are coming together to develop a shared vision of resilient Olympia oyster populations, performing key ecosystem functions, in bays and estuaries stretching from British Columbia, Canada to Baja California, Mexico. On behalf of a 15-person Steering Committee with representatives across the range of the species, the results of first steps that have been taken to develop a coast-wide Olympia oyster network will be shared.

In Fall 2017, a survey of 37 people working with Olympia oysters was conducted. One objective was to begin to develop a database of information about where monitoring, restoration, and aquaculture are occurring along the coast. Highlights of this new database will be shared, and further participation invited.

A second objective of the survey was to obtain feedback on the concept of developing a coast-wide network, and to identify priority activities and who would want to work on them. A summary of the feedback received and the ranking of priorities will be presented, and potential next steps proposed.

The rationale behind this coast-wide network is that local work on Olympia oysters can be strengthened by sharing information across sites and jointly raising the profile of Olympia oyster conservation and restoration on the Pacific coast. Participants hope to exchange lessons learned from restoration, develop shared monitoring protocols and databases, and produce outreach materials together. Anyone interested in this topic is invited to join the workshop discussion held later on this day.

WORKSHOP: BUILDING A COAST-WIDE OLYMPIA OYSTER NETWORK

Kerstin Wasson[1,2], Chela J. Zabin[3,4], Danielle C. Zacherl[5], Edwin D. Grosholz[4], Betsy Peabody[6], and Kay McGraw[7]

[1]Elkhorn Slough National Estuarine Research Reserve, 1700 Elkhorn Rd, Royal Oaks, California 95064 USA

[2]University of California, Ecology and Evolutionary Biology, 100 Shaffer Road, Santa Cruz, California 95060 USA

[3]Smithsonian Environmental Research Center, 3152 Paradise Drive, Tiburon, California 94920 USA

[4]University of California, Davis, Department of Environmental Science and Policy, 1 Shields Ave., Davis, California 95616 USA

[5]California State University, Department of Biological Science, Fullerton, California 92834 USA

[6]Puget Sound Restoration Fund, 382 Wyatt Way NE, Bainbridge Island, Washington 98110 USA

[7]Office of Aquaculture, NOAA, Rm 12317, 1315 East West Hwy, Silver Spring, Maryland 20910 USA

kerstin.wasson@gmail.com

The purpose of this workshop is to foster increased collaboration among scientists, educators, shellfish growers and restoration practitioners to support conservation and restoration of Olympia oysters across the range of the species from Baja California, Mexico to British Columbia, Canada. This workshop complements the Olympia oyster presentation session and is organized with support of a 15-person steering committee dedicated to developing an Olympia oyster network.

The majority of the session will be spent in groups, organized by topic areas, with participants choosing which to join. Groups will exchange information, brainstorm priorities for the future, and identify action items for the coming year. At the end, we will come together to share results. Tentative topic areas and potential discussion questions include the following, but are open to modification by participants:

- ***Community engagement***: How can we better educate the public about Olympia oysters in the context of healthy coastlines, and involve them in restoration efforts and community science?
- ***Restoration/conservation***: How can we support and expand existing efforts to protect and bring back sustainable oyster populations along the species range? Would shared protocols, photoguides or databases be helpful?
- ***Aquaculture***: Can commercial production be integrated with a sustainable restoration and conservation approach?
- ***Science*****:** What are the critical gaps in our understanding of the conditions that limit oyster populations? Which environmental stressors, including those related to climate change, pose the greatest threat? How can we identify the most appropriate sites and methods for restoring oysters and their functions in coastal ecosystems?

OLYMPIA OYSTER RECRUITMENT DYNAMICS FROM SOUTHERN CALIFORNIA TO BRITISH COLUMBIA

Kerstin Wasson[1,2*], Brent B. Hughes[2], John S. Berriman[3], Andrew L. Chang[4,5,8], Anna K. Deck[5], Paul A. Dinnel[6], Charlie Endris[1], Michael Espinoza[3], Sarah Dudas[7], Matthew C. Ferner[5], Edwin D. Grosholz[8], David Kimbro[9], Jennifer L. Ruesink[10], Alan C. Trimble[10], Dick Vander Schaaf[11], Chela J. Zabin[4,8], and Danielle C. Zacherl[3]

[1]Elkhorn Slough National Estuarine Research Reserve, 1700 Elkhorn Rd, Royal Oaks, California 95064 USA

[2]University of California, Ecology and Evolutionary Biology, 100 Shaffer Road, Santa Cruz, California 95060 USA

[3]California State University, Department of Biological Science, Fullerton, California 92834 USA

[4]Smithsonian Environmental Research Center, 3152 Paradise Drive, Tiburon, California 94920 USA

[5]San Francisco State University, San Francisco Bay NERR, 3150 Paradise Drive, Tiburon, California 94920 USA

[6]Skagit County Marine Resources Committee, 1800 Continental Pl., Mount Vernon, Washington 98273 USA

[7]Vancouver Island University, 900 Fifth St., Nanaimo, BC, V9R 5S5 Canada

[8]University of California, Davis, Department of Environmental Science and Policy, 1 Shields Ave., Davis, California 95616 USA

[9]Northeastern University, Department of Marine and Environmental Sciences, Marine Science Center, Nahant, Massachusetts 01908 USA

[10]University of Washington, Department of Biology, Seattle, Washington 98195 USA

[11]The Nature Conservancy, 821 SE 14th Avenue, Portland, Oregon 97214 USA

kerstin.wasson@gmail.com

Repeated recruitment failure of Olympia oysters at one California estuary, Elkhorn Slough, motivated a coast-wide investigation of recruitment dynamics, to determine whether failure is common and whether it occurs synchronously among estuaries. Recruitment dynamics were investigated at 37 sites in eight estuaries along 2500 km of Pacific North American coastline. There was little evidence of synchrony among estuaries, and only limited synchrony of sites within estuaries, although some correlation with local upwelling strength. Recruitment was uncorrelated with oceanographic drivers including ENSO or PDO, which together suggests that recruitment rates are influenced by local oceanographic dynamics and estuarine processes, and not forces operating at broader regional scales. This highlights the importance of local wetland and watershed management for the demography of oysters. Estuaries with more homogeneous environmental conditions had greater synchrony among sites, which created potential failure estuary-wide when all sites had no recruitment in the same year. Environmental heterogeneity within estuaries may prevent estuary-wide recruitment failure, analogous to the portfolio effect for diversity. Recruitment failure was correlated with lower summer water temperature, higher winter salinity, and shorter residence time, indicative of stronger marine influence on estuaries. Recruitment failure was also more common in estuaries with where adult oysters occupied only small portions of the estuary. Thus, large networks of oyster populations have high conservation value, while estuaries without them would benefit from restoration efforts to increase the extent and connectivity of sites supporting oysters. This study is an example of the value of coast-wide collaborations to inform Olympia oyster restoration.

IF YOU BUILD IT, WHY DO THEY COME? AN INVESTIGATION INTO THE MOTIVATIONS OF VOLUNTEER OYSTER GARDENERS

Phillip "P.J." L. Waters, Jr.[1,2,3]*, William C. Walton[1,2], Daniel R. Petrolia[4], David L. Swann[1,3] and James E. Witte[5]

[1]Auburn University, Marine Extension and Research Center, 118 North Royal Street, Suite 800, Mobile, Alabama 36602 USA

[2]Alabama Cooperative Extension System, 118 North Royal Street, Suite 800, Mobile, Alabama 36602 USA

[3]Mississippi-Alabama Sea Grant Consortium, 118 North Royal Street, Suite 800, Mobile, Alabama 36602 USA

[4]Mississippi State University, Department of Agricultural Economics, Box 5187, Mississippi State, Mississippi 39762 USA

[5]Auburn University, Educational Foundations, Leadership, and Technology, 3006 Haley Center Auburn University, Alabama 36849 USA

waterph@auburn.edu

Volunteer Oyster Gardening Programs (OGP) work to combat habitat loss and provide experiential educational opportunities focused on the ecological and economical attributes of oysters. Across different states and regions, OGPs have three shared traits; (1) a goal of seeing local oyster populations returned to some healthier state; (2) heavy participation by volunteers and (3) limited resources, with a tremendous percentage of spent capital and temporal investment dedicated to identifying, training and maintaining their volunteer base to continue to support their objectives. For OGP managers, there is a need to identify the factors that attract and retain volunteers to an OGP program. A volunteer must perceive a value on a personal level and identify meaning behind their efforts to select joining or continuing in an OGP over alternative leisure time activities. To quantify volunteer motivation(s) to join and remain in their OGP, a survey was designed and administered to current and former OGP volunteers (n=237) of 10 programs in the United States during the Fall of 2017. Programs included five in the Gulf of Mexico (Texas, Mississippi, Alabama (2) and Florida) and five on the Atlantic Coast (Florida, Virginia (2) and Maryland (2)). The analysis will provide insight that programs can utilize to improve recruitment efficiencies and retention success, thereby reducing the time and capital requirements currently devoted to these critical aspects of OGP management. Further, the analysis may identify variations among OGPs and common themes between them related to influences on volunteer decision making. Data are currently being analyzed.

COMMERCIAL SCALE COMPARISON OF SELECTED WATER COLUMN OYSTER CULTURE GEAR TYPES AND NATIVE OYSTER STRAINS DEVELOPED FOR THE NORTH CAROLINA INDUSTRY

Chuck Weirich[1*], Ami Wilbur[2], and Dave Cerino[3]

[1]North Carolina Sea Grant, NCSU Center for Marine Sciences and Technology, 303 College Circle, Morehead City, North Carolina 28557 USA

[2]University of North Carolina-Wilmington Shellfish Research Hatchery, 5606 Marvin K. Moss Lane, Wilmington, North Carolina 28409 USA

[3]Carteret Community College Aquaculture Technology Program, 301 College Circle, Morehead City, North Carolina 28557 USA

chuck_weirich@ncsu.edu

North Carolina (NC) is currently experiencing rapid development of its oyster farming industry, primarily due to expansion of water column production of single oysters for the half-shell market using containerized gear. While there are a number of gear systems available, limited research has been conducted to compare gear types as a means of improving efficiencies and profitability of commercial operations. Another means to optimize production is via genetic improvement. In 2012, the UNCW Shellfish Research Hatchery initiated a breeding program aimed at developing selected strains of oysters native to NC. While significant progress has been made, there remains the need for evaluation of developed strains at different locations along the NC coast.

In 2016, a 12-month trial was initiated to compare four oyster culture gear types (floating bags, off-bottom cages, long-line baskets, floating cages) and four regional oyster strains on the basis of oyster survival and production indices. Gear units were stocked with seed (25-mm shell length) at approx. 25% of volume. Oysters from each gear unit at each site were counted quarterly to determine percent survival and a random sample of 20 individuals from each unit was obtained to assess growth, shell morphology, and condition. At the conclusion of the trial, the percentage of market (> 76-mm shell length) and sub-market size oysters present in each gear unit was also determined at each site. Final results of the trial will be presented. In addition, regional differences in oyster production with respect to culture gear and strain will be discussed.

EVERYTHING FROM SHELLS: GENETICS OF SHELL SHAPE AND COLOR IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Michael Whiteside*and Ximing Guo

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

mjw253@scarletmail.rutgers.edu

As the commercial production of the eastern oyster, *Crassostrea virginica*, increases, emphasis on characteristics desirable to both consumers and growers, such as external appearance, may become more important. Some oysters exhibit a hooked hinge area that binds to the left side, making them difficult to shuck and sell. Oyster seeds of a certain color can be used as markers for selected stocks. To determine if there is a genetic basis for shell shape and color, crosses were conducted using oysters with flat and hooked hinges, and, as a separate experiment, using oysters with differing pigmentation patterns.

For hooked crosses, two cohorts of oysters were selected and crossed amongst each other: one group with hooked hinges and one normal. The progeny from each cross were grown separately, and in the following year, the crosses were repeated using selected F1s, resulting in two generations of selection for normal and for hooked oysters. Four-month-old F2s were subsequently cut ventro-dorsally and the relative curvature of the right and left valves were measured using a computer program. Initial analyses indicate that hooked hinges have a strong genetic component.

For shell-color crosses, four shell-pigmentation types were described: fully pigmented, lightly pigmented, positively striped, and negatively striped; and crosses between each of the types were performed. The pigmentation types used to describe parents were then assigned to >100 of the progeny. The proportions of the pigmentation types in the progeny suggest types are under genetic control, with some following simple Mendelian inheritance and others appearing more complicated.

FORECASTING *VIBRIO PARAHAEMOLYTICUS* IN LONG ISLAND SOUND OYSTERS AND MANAGEMENT STRATEGIES FOR AQUACULTURE

Michael M. Whitney[1]*, Kristin DeRosia-Banick[2], and Steven R. Deignan-Schmidt[1]

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

[2]Connecticut Department of Agriculture, Bureau of Aquaculture, P.O. Box 97, 190 Rogers Ave., Milford, Connecticut 06460 USA

michael.whitney@uconn.edu

The marine bacterium, *Vibrio parahaemolyticus* (*Vp*), occurs naturally in brackish and saltwater environments, and tends to be more prevalent as water temperatures rise. Consumption of shellfish with high *Vp* levels can result in gastrointestinal human illnesses. Management response to *Vp*-related illness outbreaks includes closure of shellfish growing areas. Additional management strategies are informed by *Vp* forecasting systems and improved understanding of environmental conditions that are linked to human illnesses. Water quality observations, *Vp* measurements, and model forecasts are key components to effective management of shellfish growing areas. There remains a clear need for observational systems within the growing area themselves. These areas are offshore of coastal stations and typically inshore of the observing system moorings. New field observations in Long Island Sound (LIS) shellfish growing areas are described and their agreement with high-resolution satellite sea surface temperature data is discussed. A new dataset of *Vp* concentrations in shellfish tissue is used to determine the LIS-specific *Vp* vs. temperature relationship following methods in the FDA pre-harvest *Vp* risk model. This information is combined with output from a high-resolution hydrodynamic model of LIS to make daily forecasts of *Vp* levels. Past *Vp*-related illnesses are linked to the corresponding conditions at harvest to establish environmental triggers for post-harvest rapid cooling of oysters. Fewer *Vp*-related illnesses in recent years point to the success of these new management strategies that can increase the resilience of LIS aquaculture in a warming climate.

MICROALGAL BIOCHEMICAL COMPOSITION AND BIVALVE NUTRITION: HOW WE KNOW WHAT WE KNOW

Gary H. Wikfors

NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford, Connecitcut 06460 USA

Gary.Wikfors@noaa.gov

The year I turned one, Bob Guillard was hired by Victor Loosanoff in the Milford Lab and assigned the job of finding suitable microalgae for feeding larval shellfish. Several publications resulted showing that some microalgae supported higher survival and growth of larvae than others. The search for superior algal diets continued in Milford by Ravenna Ukeles and in Conwy, U.K. by P.R. Walne. The realization that these pioneers needed to isolate phytoplankton strains, develop protocols for microalgal culture and larval rearing and feeding, and resolve many paradoxes, e.g., how to compare algae with different cell sizes, makes it all the more amazing that they found many of the microalgal strains still in use. The next generation of researchers in several institutions took cues from agricultural animal science and investigated the biochemical basis of bivalve nutrition. We were hampered in following standard agricultural practice by the lack of a defined, non-algal diet in which specific biochemical components could be included or excluded. Accordingly, statistical methods, adding non-living components to microalgae, and culturing microalgae under different conditions to modify biochemical composition were employed. In Milford, these methods, breakthrough insights from others, and collaborations with biochemists and physiologists led to biochemical nutritional profiles for oysters and clams. Experiments comparing rations and regimes of high-quality microalgae led to feeding standards for hatchery and nursery culture that have been communicated to practitioners in annual Milford Microalgal Culture Workshops. While further scientific breakthroughs in bivalve nutrition are likely, implementation of existing knowledge in hatcheries continues.

"THE MILFORD METHOD": ORIGINS, EVOLUTION, AND APPLICATIONS

Gary H. Wikfors

NOAA Fisheries, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford, Connecticut 06460 USA

Gary.Wikfors@noaa.gov

"The Milford Method," is a phrase that came into being in the early 1960s to discriminate the use of selected microalgal strains to feed shellfish larvae from the previously-employed "Wells-Glancy Method," which was fertilization and blooming of natural plankton as feed. It is not possible to attribute the idea to one individual, but the "Lennon and McCartney" of bivalve aquaculture, "Loosanoff and Davis," in 1955 hired Robert R.L. Guillard, the first microalgal specialist to work in the Milford Laboratory, so the decision had been made to seek nutritionally superior microalgae. After Guillard confirmed that some microalgae were better feeds than others, he moved on and was replaced by Ravenna Ukeles, who oversaw nearly 30 years of research and development of the Milford Method in the institution for which it is named. Ukeles collected microalgal isolates from sources near and far, developed methods for the aseptic mass-culture of microalgae, conducted countless feeding experiments with shellfish larvae and juveniles, and developed a profile of a superior microalgal feed. When I arrived in Milford, "The Doc's" research had advanced to biochemical profiling of microalgae, and I was given this assignment. Details about the trajectory of shellfish nutrition research in Milford and other institutions

are presented in the special session at this conference honoring the memory of R.R.L. Guillard. Beyond the original impetus to feed shellfish larvae in a hatchery, The Milford Method continues to have wide application in crustacean and fish aquaculture, biofuels, and nutriceuticals, with microalgal strain selection a key element.

COLOURFUL SHELLS: THE EVOLUTION OF COLOUR IN MOLLUSCA

Suzanne T. Williams

Natural History Museum, Department of Life Sciences, Cromwell Rd, London SW7 5BD, United Kingdom

s.williams@nhm.ac.uk

In order to understand how shell colour can drive evolution in molluscs, we first need to 1) know more about how shell colour is distributed across taxonomic groups, 2) identify shell pigments and 3) link pigments to biochemical pathways. To address the first question, a total of 24 characters related to shell colour were recorded for the entire NHM dry bivalve collection and plotted onto a molecular phylogeny and analysed to determine whether phylogeny effects the taxonomic distribution of colour. To address the second question, high performance liquid chromatography was used to identify two pigments in the shell and coloured foot tissue of marine snails *Clanculus pharaonius* and *C. margaritarius*. Evidence from confocal microscopy analyses shows that the distribution of porphyrin pigments corresponds to the striking pink-red of *C. pharaonius* shells, and both pink-red and yellow-brown color of *C. margaritarius* shells. Porphyrin pigments were not found in a third species, *Calliostoma zizyphinum,* even though its shell colour was similar to the *Clanculus* species. In order to determine whether the snails are capable of producing the porphyrin pigments *de novo*, transcriptomes of the two *Clanculus* species and *Calliostoma zizyphinum,* as a negative control, were sequenced to identify genes associated with their synthesis and qPCR was used to compare expression levels of those genes. Genes necessary for the production of porphyrins were found in all three species, but gene expression levels results were consistent with synthesis of porphyrin pigments in mantle and coloured foot tissue only in *Clanculus* species.

POTENTIAL TRANSGENERATIONAL EFFECTS OF OCEAN ACIDIFICATION ON THE OLYMPIA OYSTER, *OSTREA LURIDA*: A THREE-PART EXPERIMENTAL STUDY

Bryanda J.T. Wippel*[1], Carolyn S. Friedman[1], Lisa Crosson[1], Molly Roberts[2], Robyn Strenge[1], Matt George[2], Emily Carrington[2], and Sam White[1]

[1]University of Washington, School of Aquatic and Fishery Sciences, Box 355020, Seattle Washington, 98195 USA

[2]University of Washington, Department of Biology, Box 351800, Seattle Washington, 98195 USA

bjtw@uw.edu

Ocean acidification (OA) is decreasing the pH of surface waters in Puget Sound, Washington, an area already prone to low pH from natural processes such as upwelling, freshwater inputs, and high respiration/decomposition rates. High rates of production and long residence times in Puget Sound can also lead to low dissolved oxygen (DO) levels (hypoxia) in some areas. Studies have shown the negative effects of these stressors on marine organisms, particularly calcifiers. In this study, changes in pH and oxygen in seawater affect adult fecundity and larval survival of the native Olympia oyster (*Ostrea lurida*) were examined. Through three discrete trials, the following trends were observed: Adult oysters conditioned at ~400 µatm released significantly more larvae than those conditioned at higher pCO_2 levels ranging from 1000 to 2475 µatm pCO_2. Larval survival decreased in two multi-stressor treatments when challenged with varying combinations of pCO_2 and DO. Offspring of parents conditioned under high pCO_2 experienced reduced survival when exposed to both high pCO_2 and low DO (14.7% survival). In addition, progeny of adults conditioned under low pCO_2 died when exposed to high pCO_2 and high DO (22% survival). These results suggest that elevated pCO_2 negatively affects fecundity in *O. lurida* but that the synergistic effects of high CO_2 and low DO on larval survival is more complicated than previously reported. Multigenerational, multi-stressor studies such as this are important in determining how species will respond to an environmental change in the ocean.

MOLECULAR CLONING, EXPRESSION PATTERN ANALYSIS, AND IN SITU HYBRIDIZATION OF A DMRT11E GENE IN THE ORIENTAL FRESHWATER PRAWN, *MACROBRACHIUM NIPPONENSE*

Wang Yabing, Fu Hongtuo[1,2], Qiao Hui[2], Sun Shengming[2], Zhang Wenyi[2], Jin Shubo*[2], Gong Yongsheng[2], Jiang Sufei[2], Xiong Yiwei[2], and Wu Yan[2]

[1]Wuxi Fisheries College, Nanjing Agricultural University, Wuxi 214081, PR China

[2]Key Laboratory of Freshwater Fisheries and Germplasm Resources Utilization, Ministry of Agriculture, Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, Wuxi 214081, PR China

jinshubo054@sina.com.cn

The *Dmrt* (*doublesex* and *mab-3* related transcription factor) gene family is widely conserved for its involvement in sex development from invertebrates to humans. This study isolated a full-length cDNA sequence encoding a DM-domain gene from the *Macrobrachium nipponense*, which was named *MnDmrt11E* according to the high similarities and close evolutionary divergence with arthropod *Dmrt11E*, and investigated its gene function. The full-length cDNA of *MnDmrt11E* was 2258 bp, consisting of a 5' UTR of 200 bp, a 3' UTR of 756 bp, and an ORF of 1629 bp encoding 542 amino acids. Amino acid alignments and structural prediction uncovered conservation and putative active sites of the DM domain. QPCR analysis showed the *MnDmrt11E* was highly expressed in the gonad in both males and females. Further in situ

hybridization analysis showed that *Dmrt11E* was mainly located in the oocytes of the ovary, and the spermatocyte of the testis. During embryogenesis, the mRNA expression of *MnDmrt11E* was higher at the cleavage stage than those of other stages. During the different stages of ovarian reproductive cycle, the *MnDmrt11E* expression reached the peak at OvaryIII and decreased to the lowest level at OvaryIV. These results indicating that *MnDmrt11E* probably plays important roles in embryonic development and sex maturity of *M. nipponense*. The complicated expression profiles of *Dmrt* family genes may provide clues of their rapid evolution and multi-functionality. This study will contribute to understanding mechanistic and evolutionary dynamics of *Dmrt* family genes in sex differentiation and embryogenesis.

EVAULATION OF SHORT-TERM REMOVAL EFFORT TO CONTROL THE EUROPEAN GREEN CRAB, *CARCINUS MAENAS*, POPULATION IN THE BROKEN GROUP ISLANDS, BRITISH COLUMBIA

Jennifer Yakimishyn* and Yuri Zharikov

Pacific Rim National Park Reserve of Canada, Parks Canada, P.O. Box 280, Ucluelet, British Columbia, Canada V0R 3A0

Jennifer.Yakimishyn@pc.gc.ca

The invasive European green crab, *Carcinus maenas,* was first detected in Barkly Sound, British Columbia in 1998. Since then, green crabs have expanded throughout Barkley Sound, including the Broken Group Islands (BGI) unit of Pacific Rim National Park Reserve (PRNPR). Green crab invasions in eastern Canada have resulted in losses of eelgrass habitat and clam fisheries. The expansion of green crab populations throughout the BGI, into sensitive eelgrass habitats, triggered a Before-After-Control-Impact (BACI) green crab removal study in three eelgrass meadows, monitored by Parks Canada. Two control sites, without crab removal, were compared to a single impact site with green crabs removed over six trapping days. Short- and long-term trapping effects were evaluated, a few days and then a month following the removal. Overall, there was no effect detected on green crab abundance at the removal site. Smaller green crabs were caught in the short-term, but the size effect was not apparent in the month following the removal efforts. The number of male green crabs decreased after removal efforts compared to control sites. Fukui traps were more effective at trapping green crabs than minnow traps, although minnow traps caught smaller crabs. Future efforts will explore trapping during months, and in areas, with higher green crab catch. Continued monitoring of eelgrass extent will also ensure early detection of habitat loss and trigger additional management actions.

BIOLOGICAL AND PHYSICAL OCEAN INDICATORS PREDICT THE SUCCESS OF THE INVASIVE EUROPEAN GREEN CRAB, *CARCINUS MAENAS*

Sylvia B. Yamada[1]*, Joel Prickett[2], Bree Yednock[3], Christina Geierman[3], Julia Indivero[3], Collin Williams[3], Andrea Randall[4], Bill Peterson[5], Jennifer Fisher[5], and Mike Kosro[6]

[1]Oregon State University, Integrative Biology, Corvallis, Oregon USA

[2]Oregon Department of Fish and Wildlife, 4907 3rd St. Tillamook, Oregon USA

[3]South Slough National Estuarine Research Reserve, Charleston, Oregon USA

[4] P.O. Box 6, Chinook, Washington USA

[5]NOOA-Fisheries, Northwest Fisheries Science Center, Newport, Oregon USA

[6]Oregon State University, College of Earth, Ocean and Atmospheric Sciences, Corvallis, Oregon USA

yamadas@science.oregonstate.edu

An introduced population of European green crabs was established in San Francisco Bay prior to 1989. Subsequently, their larvae were carried northward to Oregon, Washington, and British Columbia by the unusually strong Davidson Current during the winter of the 1997/1998 El Niño. After the arrival of the strong founding year-class of 1998, green crabs persisted in Oregon and Washington coastal estuaries at low densities, but only recruited significantly during 2005, 2006, 2015, 2016 and 2017.

It is hypothesized that larvae are delivered to Oregon and Washington estuaries during winters when (1) there is strong northward flow of coastal waters (2) the water is relatively warm (sea surface temperature >10°C), enabling larvae to complete their development, and (3) when coastal circulation patterns favor nearshore retention where larvae can then be carried by tidal currents into estuaries to settle. Indeed, strong year-classes of green crabs are correlated with anomalously warm winter water temperatures, positive Pacific Decadal Oscillation (PDO) and Multivariate ENSO (El Niño Southern Oscillation) indices, weak equatorward shelf currents during March and April, a late, delayed biological spring transition, and increased biomass anomalies of subtropical copepod. These conditions would also favor local larval production. During the persistent unprecedented warming that occurred from 2015 through 2017, green crab recruitment was the highest observed since 1998. Recently catches of adult crabs, in some sites, exceeded 10 per trap, a threshold at which they start exerting measurable damage to shellfish beds. Careful monitoring will continue to discern crab survival and whether ecological impacts occur.

UNCOVERING THE GENETIC BASES OF GROWTH HETEROSIS IN THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*

Xiaoshen Yin* and Dennis Hedgecock

University of Southern California, Department of Biological Sciences, 3616 Trousdale Pkwy, Los Angeles, California 90089-0371 USA

xiaoshey@usc.edu

Heterosis (hybrid vigor) has been widely observed in plants and animals, but debate over its genetic causes has lasted for more than a hundred years without resolution. Previous analyses of experimental crosses of inbred lines demonstrated growth heterosis in the Pacific oyster (Hedgecock & Davis, 2007 *Aquaculture*), but did not resolve long-standing alternative genetic hypotheses for it. To elucidate the genetic mechanisms of growth heterosis, Quantitative Trait Locus (QTL) mapping is conducted on six, inter-related F_2 families of Pacific oysters, using single nucleotide polymorphisms (SNP) detected by Illumina sequencing of reduced-representation genomic libraries (genotyping-by-sequencing, GBS). High-density linkage maps with an average interval between SNP of 0.65 cM provide frameworks for QTL mapping within each family. The growth phenotypes mapped are five live weights measured monthly over the second summer post-fertilization, the four growth increments between adjacent live weights, and deviations in intercepts and slopes of growth curves fitted to logarithm-transformed live weights. Twenty-eight minor and 16 major growth QTL mappings contribute to individual variation in single and multiple growth traits, respectively. Growth QTL mappings show overdominant, dominant, underdominant, and additive gene effects, but only non-additive effects can explain growth heterosis. Results simultaneously support alternative hypotheses for heterosis. In addition to genetic effects, environmental factors also play a role. The rate of logarithm-transformed live-weight increase from September to October is smaller than that from June to September, indicating that growth slows in response to lower fall temperatures. Interestingly, genotypes of superior individuals differ under low and high temperatures, suggesting genotype-by-environment interaction.

GENOME SEQUENCING AND POPULATION GENOMIC ANALYSES PROVIDE INSIGHTS INTO THERMAL ADAPTATION OF PACIFIC ABALONE

Weiwei You[1,2,3]*, Zekun Huang1[,2,3], Xuan Luo[1,2,3], and Caihuan Ke[1,2,3]

[1]State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen 361102, China

[2]College of Ocean and Earth Sciences, Xiamen University, Xiamen 361102, China

[3]Fujian Collaborative Innovation Center for Exploitation and Utilization of Marine Biological Resources, Xiamen University, Xiamen 361102, China

wwyou@xmu.edu.cn

Abalone is one of the most economically important marine gastropod species in the world. The temperate Pacific abalone, *Haliotis discus hannai*, is successfully domesticated on a large-scale and adapted to the subtropical area, spanning thermally divergent locations separated by 15° of latitude. The *de novo* whole-genome sequence of *H. discus hannai* and recognized lineage-specific characterization of abalone in the naturally extreme coastal water environment via comparative genomic analyses is reported. Notably, macrosynteny analysis reveals a striking result that 18-chosomosome karyotype of *H. discus hannai* was significantly conserved and presumed to be close to the ancient karyotype of Haliotidae. Whole-genome resequencing of 71 individuals from five representative populations uncovers population structure and provides support of the abalone "Pacific Rim" origin hypothesis. Selective sweep analysis identified candidate genes involved in important biological progress including calcification, apoptotic process and response to stimulus, which are implicated in thermal adaptation of abalone.

TEMPORAL AND SPATIAL VARIABILITY IN OYSTER PERFORMANCE IN RESTORATION PROJECTS IN SAN FRANCISCO BAY, USA

Chela J. Zabin[1,2] *, Geana Ayala[1], Stephanie Kiriakopolos[1], Marilyn Latta[3], and Edwin D. Grosholz[1]

[1]University of California, Davis, Environmental Science and Policy Department, 1023 Wickson Hall, One Shields Way, Davis California 95616 USA

[2]Smithsonian Environmental Research Center, 3152 Paradise Drive, Tiburon California 94920 USA

[3]California State Coastal Conservancy, 1515 Clay St., Oakland California 94612 USA

zabinc@si.edu

Olympia oysters (*Ostrea lurida*) are an important foundation species in estuaries on the west coast of North America, but since the mid-1800s populations have declined precipitously. Restoration efforts are increasing in California, but relatively little is known about factors that currently limit this species, how best to approach restoration in estuaries that have been highly modified, and how climate change may affect oysters. Data gathered from five years of monitoring two sites in the San Francisco Bay Living Shorelines Project suggest that factors that affect adult oyster population densities and distribution vary by site and time. In the first years of these projects, overall adult oyster densities were high at Site 1 and low at Site 2, mirroring differences in recruitment rates at these sites. At Site 1, initial oyster abundance was highest at lower tidal elevations, on north vs. south sides of structures, and on vertical vs. horizontal substrates, suggesting that heat stress, sedimentation and settlement patterns affected distribution. At Site 2, oysters were more abundant at higher tidal elevations, where they appear to have a partial refuge from predation from Atlantic oyster drills (*Urosalpinx cinerea*), which are not present at Site 1. In subsequent years, differences between tidal elevations disappeared at Site 1, possibly

due to competition for space with other species, and low recruitment appeared to be a major driving factor for an overall decline in adult densities there as well as at Site 2. Extreme low salinity in Year 5 also impacted both sites.

HOW LOW CAN THEY GO? DISTRIBUTIONS OF THE OLYMPIA OYSTER (*OSTREA LURIDA*) AND THE PACIFIC OYSTER (*CRASSOSTREA GIGAS*) AS A FUNCTION OF TIDAL ELEVATIONS AND IMPLICATIONS FOR RESTORATION

Danielle C. Zacherl[1*], Richard A. Torres, Jr.[1], Thomas A. Parker[1], Holly Henderson[2], and Nicole Tronske[3]

[1]California State University Fullerton, Box 6850, Department of Biological Science, Fullerton, California 92834 USA

[2]Merkel & Associates, Inc., 5434 Ruffin Road, San Diego, California 92123 USA

[3]California State Polytechnic University Pomona, Department of Biological Sciences, 3801 W. Temple Avenue, Pomona, California 91768 USA

dzacherl@fullerton.edu

Surveys of seawalls, fences, mudflats, and cobble fields throughout southern California (CA) bays confirmed the establishment of feral aggregates of non-indigenous Pacific oysters (*Crassostrea gigas*), which occur in zonation with native Olympia oysters (*Ostrea lurida*). It was observed that *C. gigas* achieved its maximum density above + 1.5 ft MLLW versus *O. lurida* at or below +0.5 ft MLLW. The mechanism generating this zonation pattern might be explained through differences in settlement, recruitment, and/or growth and survival across species. On a mudflat and a chain-link fence in San Diego Bay, and across tidal elevations from -1 to +3 ft. MLLW, settlement and recruitment for three consecutive reproductive seasons (2015-2017), and, survival and growth during summer 2015 was observed. Settlement of both species paralleled adult distributions. Recruitment, growth and survival patterns appear to simply reinforce the distributional pattern set at settlement. Recruitment onto restoration beds constructed across various tidal elevations in Alamitos Bay, CA and Newport Bay, CA mirrors predictions based upon zonation. It is predicted that constructing oyster beds at tidal elevations below +1 MLLW will maximize native performance and minimize non-indigenous oyster performance. These data establish a critical baseline for evaluating future changes in oyster density.

MOLECULAR MODELING AND CHARACTERIZATION OF A MUSSEL ADHESIVE PROTEIN (MEFP-5)

Kathryn Zimlich[1]*, Douglas C. Hansen[2], and Karolyn M. Hansen[1]

[1]University of Dayton, Department of Biology, 300 College Park, Dayton, Ohio 45469 USA

[2]University of Dayton Research Institute, 1700 South Patterson Blvd., Dayton, Ohio 45409 USA

zimlichk1@udayton.edu

The blue mussel, *Mytilus edulis,* secretes adhesive proteins to facilitate adhesion to a variety of substrates. Several *Mytilus edulis* foot proteins (MeFP) have been isolated and characterized. MeFP-5 is said to be the most adhesive of these proteins, and has a comparatively large molecular percentage of L-Dopa when examined against MeFP proteins 1-4 at over 25% L-Dopa, if full conversion from tyrosine occurs. The catechol functional group of L-Dopa complexes with Fe^{3+} to form organometallic linkages, but how L-Dopa in MeFP-5 is interacting with an iron oxide surface, and if the lysine amino acids adjacent to L-Dopa help to facilitate formation of the epoxy-like barrier on iron oxides, is unknown. This project focuses on evaluating the orientation of the catechol groups in L-Dopa through molecular modeling, generating a 3D model of magnetite as an example of an iron oxide surface, characterizing regions of MeFP-5 which are most likely to complex with Fe3+, and altering the amino acid composition of MeFP-5 to attempt to maximize adhesive properties and explore possibilities for creating a synthetic analog. Modeling is done in the programs ChemDraw® and Chem3D® (PerkinElmer) to analyze protein structure and the catechol positioning of L-Dopa within the protein MeFP-5. To validate and refine the model, experimental data of MeFP-5 adsorbed onto HY80 steel using Raman infrared spectroscopy have been used to determine what interaction the lysine and L-Dopa functional groups in MeFP-5 have on the steel surface. These data have been incorporated into the 3-dimensional model of the protein-metal interface.

MANGROVEENCODE (2017-2027: DEVELOPING TECHNOLOGIES FOR THE ASSESSMENT OF CO_2, MICROBIOME, ENDOCRINE DISRUPTING CHEMICALS (GLYPHOSATE, METALS), AND MICROBIAL TRANSGENE *BACILLUS THURINGIENSIS* IN MANGROVES SEDIMENT AND AGRICULTURAL SOIL OF SELECTED COUNTRIES

Liliana Zuniga[1]*, Daniela Espinoza[1], Arturo Ruiz-Luna[2], Cesar A. Berlanga-Robles[2], Bruno Gómez-Gil[2], Mira Maude Chouinard[3], Dina Morell[3], Modesto Ochoa[3], Miriam Alcívar-Arteaga[1], Gober Asunción[1], Mayra Galindo[1], Christian Saltos[1], Sofía Figueroa Zambrano[1], Johanna Alcivar Parrales[1], Acacia Alcivar-Warren[1,4], Jorge Echevarria[5], and Chika F. Ikeogu[6]

[1]The Mangrove Epigenome (mangroveENCODE) Project, Fundación para la Conservación de la Biodiversidad Acuática y Terrestre de Ecuador (FUCOBI), Quito, Ecuador

[2]Centro de Alimentacion y Desarrollo (CIAD), A.C., Unidad Mazatlan en Acuicultura y Manejo Ambiental, AP.711, Mazatlan, Sinaloa, Mexico 82000

[3]CODDEFAGOLF, Honduras

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

[5]Universidad de Tumbes, Tumbes, Peru

[6]Nnamdi Azikiwe University, Department of Fisheries and Aquaculture, Awka, Nigeria

fucobi@gmail.com

The long-term goal of The Mangroves Epigenome (mangroveENCODE) Project is to study the interactions of greenhouse gas fluxes, carbon sequestration and microbial communities in light of climate change and environmental degradation-related health issues. The plan is to obtain baseline information for future studies to test mechanism-driven hypotheses to examine the epigenetic mechanisms involved in the interactions of CO_2 with endocrine disrupting chemicals (EDC) and the microbiome of mangrove sediments and agricultural soil, using computational ecology tools.

The genetic and epigenetic modifications such as DNA (CpG) methylation in mangroves species from Brazil (*Laguncularia racemosa*) and China (*Ceriops tagal*) using Methyl-Sensitive Amplified Polymorphism (MSAP) and Illumina RNA-seq technologies, respectively, will be reviewed. Within-population diversity was significantly greater for epigenetic than genetic data in Brazil samples. Individuals with similar genetic profiles presented divergent epigenetic profiles that were characteristic of the population in a particular environment, suggesting that CpG-methylation changes may be associated with environmental heterogeneity. RNA-seq data from *C. tagal* plants suggest they could survive salt stress through biochemical modification.

A 2018 pilot study will be discussed to determine best technologies for epigenetic studies and for the assessment of the microbiome, CO_2, EDC (glyphosate, metals) and microbial transgene *Bacillus thuringiensis* in agricultural soil and sediment of mangroves and adjacent shrimp ponds of selected countries, for conservation of mangrove habitats. The final protocol to collect 1m sediment cores, administrative responsibilities and shipment of samples to the EDC-testing laboratories will be reviewed.

WHAT IS VIVALDI? A 4-YEAR EUROPEAN PROJECT AIMING AT PREVENTING AND MITIGATING FARMED BIVALVE DISEASES

Isabelle Arzul[1]*, Steve Feist[2], Antonio Figueras[3], Sylvie Lapègue[1], Christine Paillard[4], and Dolors Furones[5]

[1]Ifremer, SG2M-LGPMM, av de Mus de Loup, 17390 La Tremblade, France

[2]Cefas, Weymouth Laboratory, Barrack Road, The Nothe,Weymouth, Dorset. DT4 8UB, United Kingdom

[3]Consejo Superior de Investigaciones Científicas (CSIC) Instituto de Investigaciones Marinas, Rúa de Eduardo Cabello, 6, 36208 Vigo, Pontevedra, Spain

[4]Institut Universitaire Européen de la Mer, LEMAR, Technopôle Brest-Iroise - rue Dumont d'Urville - 29280 Plouzané France

[5]Investigacion y Technologia Agroalimentarias (IRTA), Crta. Poble Nou, km. 5'5 43540 Sant Carles de la Ràpita, Spain

Isabelle.Arzul@ifremer.fr

European shellfish farming enjoys a prominent position on a global scale. European production of shellfish relies mostly on mussels, oysters, and clams. In the last few years, the industry has been weakened by mortality events linked with various viruses (e.g. OsHV-1), bacteria (e.g. *Vibrio aestuarianus*) and parasites (e.g. *Marteilia cochillia*), which lead to great economic losses. It is in this context that the H2020-European VIVALDI project aims to improve the sustainability and competitiveness of the European shellfish industry by developing tools and approaches to prevent and mitigate bivalve diseases.

Started in April 2016, this 4-year project involves 21 partners. First results have been achieved in understanding the diversity of pathogens in bivalve populations and in their detection thanks to the elaboration of passive sensors. Mathematical models for the transmission of diseases and risk levels for farming are currently developed and will be helpful to better anticipate the emergence of disease.

Studies on the response of bivalves against diseases have contributed to identify key pathways (e.g. Warburg metabolism and autophagy) and novel important protein families. Microbiome is also deeply investigated during disease development mostly in *Crassostrea gigas* and *Mytilus* spp. Field experiments and monitoring are on going in different key sites on the European Atlantic and Mediterranean coasts and allow identifying biosecurity measures contributing to avoid disease and to decrease mortality outbreaks. Finally, in order to improve the dialogue among the parties affected by shellfish diseases and to disseminate results of the project, a mapping of stakeholders is currently under way.

GROWTH AND SURVIVAL OF HATCHERY PRODUCED EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) SPAT IN BOTTOM CAGES IN COATAL GEORGIA

Thomas H. Bliss*, Justin P. Manley, and Robert E. Hein

University of Georgia Marine Extension and Georgia Sea Grant, Shellfish Research Laboratory, 20 Ocean Science Circle, Savannah, Georgia 31411 USA

tbliss@uga.edu

The development of oyster aquaculture within Georgia is necessary to increase oyster production. Single oysters grown using aquaculture methods are in high demand, bring a better price than bulk oysters, are much easier to distribute, but current aquaculture methodology is not permitted in Georgia. To offer a consistent supply of single oysters from Georgia, there are two criteria that must be met; 1) access to hatchery produced oyster spat and 2) successful grow out methodology. In 2015, an instate oyster hatchery was set up at the University of Georgia Marine Extension and Georgia Sea Grant Shellfish Research Laboratory and 860,000 spat (6 mm) were distributed to commercial growers along the Georgia coast. An experimental grow-out trial was conducted using hatchery produced spat on commercial leases using bottom cages (Chesapeake Bay Oyster Company) to evaluate the growth, survival, and fan and cup ratios from March 2016-March 2017. In terms of growth, it was observed that oysters reached legal market size (50.8 mm) within one year of spawn and ideal market size of > 65 mm within 18 months. Oysters had an excellent cup ratio > 0.25, and had a survival rate of 57%. No difference was found in growth rate between different test sites. Therefore, oyster farmers can consistently produce single oysters from hatchery spat in bottom cages. Evaluation of triploid and diploid oysters in floating gear is currently underway, and we feel that once regulations change that oyster aquaculture will be quickly established.

PRELIMINARY FINDINGS OF A SURVEY FOR THE OYSTER PARASITES *BONAMIA* AND MSX IN TEXAS BAYS

Hailey M. Boeck*[1], Susan E. Laramore[2], David S. Portnoy[1], and John Scarpa[1]

[1]Texas A&M University – Corpus Christi, 6300 Ocean Drive, Corpus Christi, Texas 78412 USA

[2]Florida Atlantic University, Harbor Branch Oceanographic Institute, 5600 US 1, Fort Pierce, Florida 34946 USA

hboeck@islander.tamucc.edu

The Texas Parks and Wildlife Department restricts movement of eastern oysters (*Crassostrea virginica*) from one Texas bay system to another because of potential disease transfer and genetic differences in natural oyster stocks. Oyster diseases, such as Bonamiosis, which was found serendipitously in 2007 in Florida waters, and MSX have not been characterized in Texas bays. Therefore, it is prudent to examine *Crassostrea virginica* and other related species (e.g., *Ostrea equestris* and *Isognomon* sp.) periodically from different Texas bays for the presence of the causative agents of these diseases, i.e., *Bonamia* and *Haplosporidium nelsoni* (MSX). The causative agent of Dermo, *Perkinsus marinus,* is endemic in Texas and was also measured. One-hundred-fifty American oysters were collected during October to December 2016 from Copano Bay, San Antonio Bay, Matagorda Bay, Galveston Bay, and Sabine Lake. PCR analysis of tissues found no *Bonamia* in these oysters, but an average prevalence of 4.67% for MSX and 14.67% for Dermo. In addition, 89 historical eastern oyster tissue samples from 2010 and 2011 were assessed by PCR. Again, no *Bonamia* was found, but there was a 6.74% MSX prevalence and a 28.09% Dermo prevalence. MSX is endemic to the Northeastern U.S. seaboard and up until this point, the Gulf of Mexico has been considered free of this pathogen. Further research to confirm the MSX findings is necessary and will be completed using histological examination of oyster tissue and Sanger sequencing of isolated DNA.

REDUCING THE IMPACT OF PATHOGENS IN THE IRISH OYSTER INDUSTRY TO SUPPORT THE SUSTAINABILITY AND GROWTH OF THE SECTOR

B.E. Bookelaar[1]*, C.O'Toole[2], D. Cheslett[2], S.A. Lynch[1], and S.C. Culloty[1]

[1]Aquaculture and Fisheries Development Centre, School of Biological, Earth and Environmental Sciences & Environmental Research Institute, University College Cork, Cork, Ireland

[2]Marine Institute, Oranmore, Ireland

b.bookelaar@umail.ucc.ie

Pacific oysters, *Crassostrea gigas*, have been farmed in Ireland since 1970s and are of commercial importance; however, significant summer mortalities in Pacific oysters have been observed, associated with a complex aetiology, including interactions between the physical status of the host, environmental parameters and pathogens like OsHV-1 microVar (OsHV-1 μVar) and/or *Vibrio aesturianus* (*V. aes*). This research is part of the project, REPOSUS, a collaborative three-year project between University College Cork and the Marine Institute started in April 2015. The objectives are to acquire more knowledge how pathogens affect the Irish Pacific Oyster industry and to come up with new practical measures to support the sector. Field and laboratory trials were conducted to reveal a better understanding of "pathogen-host-environment interplay" of Irish Pacific oysters. Field trials took place at two main Irish oyster culture sites, both with history of OsHV-1 μVar and/or *Vibrio* spp. The role of other marine invertebrates found around oyster culture sites as a potential carrier, reservoir or alternative host of OsHV-1 μVar and the spread of diseases in marine invertebrate species within different ranges of oyster culture sites were studied.

Also, the effects of air exposure on performance and disease development of *C. gigas* were investigated. Laboratory experiments were performed to study viral transmission between species and to reveal the effects of seaweed species on pathology and immunology of naïve and pathogen exposed Pacific oysters. Molecular diagnostic screening was performed by standard (cPCR) and quantitative (qPCR) poly chain reaction, in situ hybridization (ISH) and direct sequencing.

HEALTH EVALUATION OF TRIPLOID AND DIPLOID EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) UNDER VARIOUS CULTURE CONDITIONS

Nicholas Brandimarte[1*], Susan Laramore[1], and Leslie N. Sturmer[2]

[1]Florida Atlantic University, Harbor Branch Oceanographic Institute, Center for Aquaculture and Stock Enhancement, 5600 US Highway 1 North, Fort Pierce, Florida 34946 USA

[2]University of Florida/IFAS, Shellfish Aquaculture Extension Program, Senator Kirkpatrick Marine Lab, 11350 SW 153rd Court, Cedar Key, Florida 32625 USA

nbrandim@fau.edu

This study assessed the health of naturally mated triploid (Louisiana tetraploid, Florida diploid) and Florida diploid eastern oysters, *Crassostrea virginica*, reared under commercial conditions (on-bottom, off-bottom) along the west coast of Florida. A total of 623 triploid and diploid oysters were examined from eight commercial sites (n = 60-105) in four west coast counties from oysters planted July 2016 and harvested April 2017. Collected oysters were weighed, measured and the presence of shell pests (i.e. *Polydora websteri*), and abnormalities noted. The presence of *Perkinsus marinus* was evaluated. Samples were examined histologically for the presence of other parasites (i.e. *Tylocephalum* sp.) and reproductive status.

Triploid oysters were larger (72.5-98.78 mm SH) than diploids (64.1-88.62 mm SH) at all sites. Triploid wet meat weights (7.63-14.72 g) were also greater than that of diploids (4.63-11.29 g) at all sites. Digestive tubule atrophy was higher for diploids (1.7-3.24) than triploids (1.5-2.48) at six of eight sites. Prevalence of *P. marinus* was generally low, but higher for triploid oysters (19.5%) than diploid oysters (12.2%) at six of eight sites. Infestation of the mudworm, *P. websteri* and boring sponge, *Cliona* sp., were more pronounced in triploids and diploids reared using on bottom culture techniques. Seasonal health differences are currently being evaluated for triploid and diploid oyster seed planted in March 2017 and harvested in November 2017.

CONTAMINANTS OF EMERGING CONCERN IN WILD EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) AND ENVIRONMENTAL SAMPLES FROM ESTUARIES IN GEORGIA, USA

David W. Brew* and Marsha C. Black

University of Georgia, Department of Environmental Health Science, Athens, Georgia, USA

dbrew@uga.edu

As coastal zone populations continue to increase, contaminants of emerging concern (CEC) in estuarine environments will be an increasingly complex problem facing estuarine organisms, including many economically important bivalve species. CEC can elicit a biological response at low ng/L - µg/L concentrations, putting organisms in these sensitive estuarine areas at risk to toxic effects from increased or prolonged exposures. CEC were quantified in tissue from wild eastern oysters (*Crassostrea virginica*), water, and sediment samples near Brunswick and Sapelo Island, Georgia. Sites were selected to provide a gradient of presumed exposures based on septic tank densities. Samples were analyzed for 30 CEC including selective serotonin reuptake inhibitors (SSRI), hormones, anti-epileptics, stimulants, antihistamines, analgesics, heart/cholesterol medication, personal care products, herbicides, and pesticides. Oyster samples were collected bimonthly from October 2013 - October 2015 and environmental samples were collected October 2014 - October 2015. Oyster tissue concentrations displayed strong seasonal trends. The highest mean tissue concentrations [± 95% confidence intervals] and highest frequency of chemical classes detected was during warmer months (October 2013, April, June, August, October 2014/2015). SSRI, analgesics, cholesterol medication, personal care products and hormones had the highest mean tissue concentrations (32.8, 30.4, 16.5, 15.2 and 9.5 ng/g, respectively). Water and sediment samples had generally lower mean concentrations (low ng concentrations) than oysters, with stimulants, analgesics, anti-epileptics, antihistamines, personal care products and herbicides being the chemical classes most frequently detected. Surprisingly, there were few statistical differences (based on 95% CI) among CEC concentrations between the Brunswick and the Sapelo Island samples.

IS NEGATIVE SENESCENCE A TACTIC IN THE LIFE HISTORY OF *PANOPEA GLOBOSA*? A CASE STUDY IN TROPICAL POPULATIONS

Liliana Carvalho-Saucedo*, Nurenskaya Vélez-Arellano, Sergio Scarry González-Peláez, and Daniel B. Lluch-Cota

Centro de Investigaciones Biológicas del Noroeste. Av. Instituto Politécnico Nacional 195 Col. Playa Palo de Santa Rita Sur. La Paz, México

carvalholiliana@ymail.com

It has been suggested that in bivalves, senescence begins immediately after reproductive maturation-*i.e.*, "the earlier this point

is reached, the sooner the senescence will begin", so that the age a bivalve will live after its first maturation should be directly proportional to the time it took to reach maturity. Regarding this, *Panopea globosa,* is a particularly long-lived species, which others have suggested as an indication of possible negative senescence. This possibility was evaluated in a sample of 30 organisms, in a population from Bahía Magdalena, B.C.S., Mexico located at the limit of temperate distribution of the species. While no relationship was found between female fecundity and age, an inverse relation was evident regarding Fulton's condition factor (*K*) as well as mantle contents of proteins, carbohydrates and lipids. It was observed in the mantle that as age increases, there was a potential decrease of: condition factor (r = 0.6532), content of proteins, carbohydrates and total lipids (r = 0.6780, 0.5814 and 0.6620, respectively). On the contrary, in the male mantle, an increase in (*K*) and in lipids was observed in individuals up to 20 years old, and later a decrease with age occurred, which suggests the non-senescence in males in the first years. Despite these results, what is found in temperate populations (case study II), points out the need to analyze whether the presence or absence of senescence in *P. globosa* is not associated with environmental differences in each region.

COOPERATIVE PARTNERSHIPS TO MAXIMIZE COMMERCIAL SHELLFISH PRODUCTION IN SOUTHWEST FLORIDA

Angela B. Collins[1]*, Bruce Barber[2], Barry Hurt[3], Chuck Adams[4], Curt Hemmel[2], and Aaron Welch III[2]

[1]University of Florida/IFAS Extension, Florida Sea Grant, Manatee County, 1303 17th Street West, Palmetto, Florida 34221 USA

[2]Gulf Shellfish Institute, 1905 Intermodal Circle, Suite 330, Palmetto, Florida 34221 USA

[3]Placida Gold Aquafarms, 144 Lake Sears Drive, Winter Haven, Florida 33880 USA

[4]University of Florida/IFAS Extension, Food and Resource Economics Department, PO Box 110240, Gainesville, Florida 32611 USA

abcollins@ufl.edu

Florida aquaculture ranks 7th in total domestic production, with annual sales exceeding $70 million. Southwest Florida is an important producer of farmed bivalves, and is also home to one of the most successful shellfish hatcheries in the southeast. The environmental benefits of farmed bivalves have been proven, and the economic impact of shellfish aquaculture continues to grow as seafood consumption increases and demand strains natural wild populations. Industry efforts to expand production can be enhanced by partnerships with Extension, who can assist with grant applications, research and the transfer of academic information.

In collaboration with the Southwest Florida Shellfish Association and the Gulf Shellfish Institute, multiple projects are currently underway to address regional, industry driven questions. These include 1) an investigation into solutions for specific larval shellfish pathogens in Tampa Bay, 2) extension efforts to assist industry with harmful algal bloom impacts upon shellfish production in southwest Florida, and 3) quantification of the economic impact harmful algal bloom related industry closures.

Extension partnerships allow for collaboration between scientists, managers and industry representatives to positively impact the growth of the industry and maximize environmental and economic benefits of shellfish production.

DEVELOPING AQUACULTURE TECHNIQUES FOR GIANT RED SEA CUCUMBERS IN PUGET SOUND: BROODSTOCK, LARVAE AND JUVENILE CULTURE

Ryan N. Crim[1,2]*, Stuart K. Ryan[1,2], Kendra Baird[3], Andy Suhrbier[4], and Paul Williams[5]

[1]Puget Sound Restoration Fund, 382 Wyatt Way NE, Bainbridge Island, Washington 98110 USA

[2]Kenneth K. Chew Center for Shellfish Research and Restoration, 7305 Beach Dr. E., Port Orchard, Washington 98366 USA

[3]Evergreen State University, 2700 Evergreen Park Way NW, Olympia, Washington 98505 USA

[4]Pacific Shellfish Institute, 509 12th Ave SE #14, Olympia, Washington 98501 USA

[5]Suquamish Tribe, 18490 Suquamish Way, Suquamish, Washington 98392 USA

ryan@restorationfund.org

The giant red sea cucumber, *Parastichopus californicus,* is an emerging aquaculture species with significant economic and ecological value for the North American west coast. In Washington State, *P. californicus* wild stocks have continually declined since their peak in 1991, despite reduced fishing pressures. Declining wild stocks and high commercial value make *P. californicus* an excellent candidate for aquaculture. In addition, sea cucumbers are detritivores and are thus of high interest for use in Integrated Multi-Trophic Aquaculture systems. Sea cucumber aquaculture has the potential to ameliorate negative environmental effects of existing aquaculture systems and reduce heavy fishing pressure on wild populations while providing an economic resource to coastal communities. Aquaculture research and development for this species has been in progress at the NOAA Kenneth K. Chew Center for Shellfish Research and Restoration since 2016. Research has focused on larval and early juvenile development. Several experiments have been conducted looking at optimizing temperature for larval and juvenile culture and effects of various microalgal diets on larval and juvenile development. The results of these experiments along with anecdotal information on broodstock handling and spawning techniques will be discussed.

RUDITAPES DECUSSATUS POPULATIONS IN EUROPE*:* EVIDENCE OF DIFFERENT INFECTION LEVELS OF *PERKINSUS* SP.WITHIN THE SAME POPULATION AND MORPHOLOGICAL CHARACTERIZATION

Andreia Cruz*, Ana Cerviño, Oscar Iglesias, Fiz da Costa, and Bernardo Carvalho

Oceano Fresco Lda, Edifício Mira Center, Centro de Ciência e Iniciativas Empresariais de Mira, Rua do Matadouro, 2º Piso, Lab. B2., Valeirinha, 3070-436 Mira, Portugal

andreia.cruz@oceano-fresco.pt

The European native clam species, *Ruditapes decussatus*, has high economical and gastronomic value. Populations of this species are being drastically reduced mainly due to over-exploration of natural clam beds, habitat contamination, significant temperature and salinity variations and pathologies caused by bacteria, virus and protozoa. The protistan parasites, *Perkinsus marinus* and *P. olseni* can infect bivalves worldwide. Infections with either *P. marinus* or *P. olseni* is frequently lethal, though an infected animal may live for several years before showing clinical signs of disease or abrupt mortality.

The aim of this study was to have knowledge of susceptible/resistance individuals within infected locations, by using a standard method – using Ray's fluid thioglycollate medium (FTM). Additionally, the morphology of the shell and of the siphons was evaluated in comparison to *Ruditapes philippinarum* species.

It was observed that: i) from the same location, different levels of *Perkinsus* sp. infection were detected in clams with similar size/age, what indicates that within the same population, there are individuals with different susceptibility/resistance for *Perkinsus*; ii) there are individuals that possess morphologic characteristics of the other species, i.e., individual characteristics of *R. decussatus* with *R. philippinarum,* and vice-versa, being an indication of hybridization between both species. This work can be a base for further studies to support *Ruditapes decussatus* breeding programs.

EFFECTS OF CAGE TYPE ON PARASITIC *POLYDORA* SP. INFESTATION OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Grant A. Diedrich* and Ami E. Wilbur

University of North Carolina Wilmington, Shellfish Research Hatchery, Department of Biology and Marine Biology, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, North Carolina, 28409 USA

gad7228@uncw.edu

Polydorid worms are well-known parasites of marine bivalves that chemically bore into the calcium carbonate shells of their hosts, forming burrows. The oysters respond by covering these burrows with additional nacre, creating the signature mud blister. Due to the unsightly nature and foul taste of the mud blisters if punctured, *Polydora* sp. potentially reduces the half-shell market value of farm-raised oysters.

As part of a larger study evaluating the effect of gear type on the growth, survival, and disease prevalence of oysters, we evaluated the degree of parasitic *Polydora* sp. infestation of oysters in four different shellfish aquaculture gear types (floating cages, flip bags, longline system and bottom cages) on two farms in southeastern North Carolina (UNCW's Aquaculture demonstration site and Chadwick Creek Oyster Co.). The prevalence and degree of infestation were determined using photo analyses. Percent coverage of mud blisters was quantified at the time of deployment (November, oysters 6 months old) as well as during the winter (three months post-deployment) and following fall (nine months post-deployment) seasons.

Prevalence was high (100%) at the start of the experiment. At three months, the infestations showed little change, but substantial increases were noted at nine months. Both gear type and location had effects on the degree on infection. The results of these analyses will be presented.

SPATIAL AND TEMPORAL PATTERNS OF NATURAL MORTALITY OF EASTERN OYSTER IN CHESAPEAKE BAY, MARYLAND DURING 1990-2015

Kathryn Doering[1*], Michael Wilberg[1], Dong Liang[1], and Mitchell Tarnowski[2]

[1]University of Maryland Center for Environmental Science, Chesapeake Biological Laboratory, P.O. Box 38, Solomons, Maryland 20688 USA

[2]Maryland Department of Natural Resources, 580 Taylor Ave. B-2, Annapolis, Maryland 21401 USA

kdoering@umces.edu

Understanding natural mortality rates is important for fisheries management because accurate estimates are required to develop reference points. One method for estimating the natural mortality rate of bivalves uses the number of articulated shells (shells attached by the hinge ligament) relative to the sum of live individuals and articulated shells; however, this approach relies on the assumptions that 1) articulated shells only persist in the environment for one year and 2) live individuals and articulated shells are equally vulnerable to the survey gear. These assumptions likely do not hold for eastern oysters, *Crassostrea virginica,* in Chesapeake Bay. Furthermore, the standard method only provides point estimates of natural mortality. The objective of this research was to use a new method of estimating natural mortality to investigate spatial and temporal patterns of natural mortality of eastern oysters in upper Chesapeake Bay. The new method corrects for assumptions of the standard method and estimates uncertainty in the natural mortality rates using a Bayesian approach. The new estimator was applied to

data collected during 1990-2015 by the Maryland Department of Natural Resources fall oyster survey for several regions. Regions had similar temporal trends, with variable mortality at the beginning of the time series and lower, more consistent natural mortality rates since 2003. The high mortality events coincided with high levels of disease. The use of this new method may provide more accurate estimates of natural mortality of eastern oysters in Chesapeake Bay and could be adapted to other bivalve populations with similar data availability.

IMMUNOHISTOFLUORESCENCE STUDY OF THE ACTIONS OF MANGANESE ON THE PHOSPHOLIPASE C AND IP3 RECEPTOR MECHANISMS OF DOPAMINE D2-LIKE POST-SYNAPTIC RECEPTORS IN *CRASSOSTREA VIRGINICA*

Mohamed Eid[1]*, Peter Amoako[1], Delilah Cummings[1], Maxine Jacobs[2], Margaret A. Carroll[1], and Edward J. Catapane[1]

[1]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

[2]Kingsborough Community College, 2001 Oriental Ave, Brooklyn, New York 11235 USA

meedeid@gmail.com

Manganese causes Manganism a Parkinson's-like disease. Reports postulate the neurotoxic mechanism is related to dopamine neuron dysfunction, not degeneration. Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine is cilio-inhibitory. Previous work showed the dopamine receptors are D2 type (D2DR) and manganese disrupts the cilio-inhibition of GLC cilia, suggesting D2DR is a site of action in manganese neurotoxicity. The D2DR pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC synthesizes inositol trisphosphate (IP3), which activates IP3 receptors (IP3R) increasing intracellular Ca^{2+}. PLC has not been well studied in bivalves, nor have effects of manganese on PLC or IP3R. It is hypothesized that PLC and IP3R are present in GLC, and if so, any effects of manganese will be determined. Gill sections were prepared with PLC and IP3R antibodies and viewed on a Leica microscope. All sections were photographed with the same camera setting. It was found that GLC displayed green fluorescence in cytoplasm and along cell membranes indicating the presence of PLC and IP3R. Gills threated with manganese had reduced PLC and reduced IP3R fluorescence compared to untreated cells. Zinc treated gills showed no differences. The study shows PLC and IP3R presence in GLC and that manganese did cause a small, significant reduction in PLC and IP3R fluorescence. This study provides new knowledge of manganese actions on D2DR pathway in bivalve gill. Future experiments will test if manganese negatively effects physiological actions of PLC and IP3R on GLC cilia activity.

THE DISTRIBUTION OF OCEAN QUAHOGS, ATLANTIC SURFCLAMS, AND THEIR SHELLS ON THE MID-ATLANTIC BIGHT CONTINENTAL SHELF

Anja Ewing[1*], Eric N. Powell[2], and Kelsey Kuykendall[2]

[1]University of Southern Mississippi, Gulf Park Campus, Long Beach, Mississippi 39560 USA

[2]Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, Mississippi 39564 USA

Anja.Ewing@usm.edu

The Atlantic surfclam, *Spisula solidissima*, and the ocean quahog, *Arctica islandica*, are commercially important bivalves in the Mid-Atlantic Bight. As a result of rising bottom water temperatures, the range of the surfclam has contracted offshore and towards the northeast. A range shift for the ocean quahog has not been documented by the National Marine Fisheries Service (NMFS) survey, which began in 1978; however, a recent analysis of ancillary survey data on Georges Bank suggests an offshore shift in range prior to initiation of this survey. Ancillary data collected from 1978-2011 by the NMFS include shells of both species. Death assemblages are repositories of information on the community history of site; their use in understanding community change unrecorded by survey is a growing research emphasis. The distributions of shells of these two species mark their historical footprint in the Mid-Atlantic Bight: comparison to their present distribution maps the degree to which their range has shifted over time. In particular, regions where clam shell is found without living clams mark earlier occupations now abandoned whereas regions where living clams are found without shells mark the regions of most recent colonization. The objective of this project is to combine information on the living clams and their death assemblages to track the shift in range in both species from the Chesapeake Bay to Georges Bank.

IS NEGATIVE SENESCENCE A TACTIC IN THE LIFE HISTORY OF *PANOPEA GLOBOSA*? ACASE STUDY IN TEMPERATE POPULATIONS

Alejandro Tomás Hernández-Muñoz, Daniel B. Lluch-Cota*, Liliana Carvalho-Saucedo, Nurenskaya Vélez-Arellano, Sergio Scarry González-Peláez, Fabiola Arcos-Ortega

Centro de Investigaciones Biológicas del Noroeste. Av. Instituto Politécnico Nacional 195 Col. Playa Palo de Santa Rita Sur. La Paz, México

dblluch@cibnor.mx

It has been suggested that in bivalves, senescence begins immediately after reproductive maturation-*i.e.*, "the earlier this point is reached, the sooner the senescence will begin": so that the age a bivalve will live after its first maturation should be directly proportional to the time it took to reach maturity. Regarding this, *Panopea globosa* is a particularly long-lived species, which others have

suggested as an indication of possible negative senescence. This possibility was analyzed in a sample of 30 organisms, in a population from Puerto Peñasco, Sonora, Mexico, located at the limit of temperate distribution of the species. In both sexes, an increase in lipid and protein in the gonad with age was found. In females the Fulton's condition factor (*K*) remains constant, suggesting a possible absence of senescence. While in males the (*K*) increases as the age elapses from 5 to 16 years, suggesting a period of negative senescence. Despite these results, what is found in tropical populations (case study I), points out the need to analyze whether the presence or absence of senescence in *P. globosa* is not associated with environmental differences in each region.

IMPACTS OF PAIRED OLYMPIA OYSTER (*OSTREA LURIDA*) AND EELGRASS (*ZOSTERA MARINA*) RESTORATION ON FISH AND INVERTEBRATE COMMUNITIES IN NEWPORT BAY, CALIFORNIA

Marjorie Howard[1]*, Christine Whitcraft[1], and Danielle C. Zacherl[2]

[1]California State University at Long Beach, Department of Biological Sciences, 1250 Bellflower Boulevard, Long Beach, California 90840 USA

[2]California State University Fullerton, Box 6850, Department of Biological Science, Fullerton, California 92834 USA

marjorieehoward@gmail.com

Efforts to restore the Olympia oyster (*Ostrea lurida*) are of high importance due to the substantial decline of the species as well as its ecological and economic importance. The construction of *O. lurida* beds may provide complex habitat for many species of fish and invertebrates, and enhance water clarity via filtration; however, previous studies have observed significant declines in abundance and diversity of benthic infauna immediately beneath restored beds due to an altered sediment-water interface. This loss has the potential to be counterbalanced by planting seagrass beds adjacent to constructed oyster beds, as the additional complex habitat provided by seagrass root systems is expected to increase infaunal abundance and diversity. Pairing oyster and seagrass restoration might create more diverse habitats for fish, also enhancing their abundance and diversity. Olympia oyster and eelgrass (*Zostera marina*) restoration were conducted, both paired and separately, at four sites within Upper Newport Bay, California. Each treatment plot was assessed both pre- and post-restoration for fish and infaunal community composition. Infauna were sampled by collecting sediment cores from both intertidal (oyster or control) and subtidal (eelgrass or control) plots of each treatment. Fish were monitored via a baited GoPro placed in subtidal plots of each treatment. Preliminary results show that the infaunal community exhibits site-specific changes in response to restoration, which will provide insight into the ideal conditions and locations for oyster and eelgrass restoration. The fish community was observed to utilize both complex habitats. Observed patterns of community change will be useful in informing future restoration efforts.

IS THE RNA BINDING PROTEIN CSDE1 REGULATING TRANSLATION DURING HYPOXIA IN MOLLUSCS?

Brandon Hsieh*, Carol Habib, and Maureen K. Krause

Hofstra University, Department of Biology, Hempstead, New York 11549-1140 USA

bhsieh1@pride.hofstra.edu

Hypoxia has major detrimental effects on marine bivalves, although individual species exhibit variability in their response to hypoxia. Within cells, the energetic crisis caused by reduced ATP production under hypoxia triggers translation repression, although a small number of critical mRNAs continue to be translated. RNA binding proteins including Cold Shock Domain Containing Protein E1 (CSDE1) are increasingly appreciated as regulators of translation during exposure to hypoxia and thermal stress. CSDE1 is a cytoplasmic RNA-binding protein known to play roles in the regulation of mRNA stability and translation, although its function in molluscs has not been explored. Here, bioinformatic and molecular biological approaches were used to examine the role of CSDE1 in translation regulation under hypoxia in scallops. Bioinformatics analyses of the newly published *Mizuhopecten yessoensis* scallop genome identified putative CSDE1 binding sites on target mRNAs associated with innate immunity, environmental stress, metal binding, cell cycle control and development. Many targets are homologs of established CSDE1 targets in vertebrates and some are upregulated in response to hypoxic stress. Quantitative PCR analyses reveal a significant increase in CSDE1 expression under hypoxia in bay scallops. In addition, Electrophoretic Mobility Shift Assays and RNA-pull down experiments were used to directly test whether recombinant affinity-tagged CSDE1 protein from *Argopecten irradians* binds to predicted target mRNAs. Collectively, these studies indicated that CSDE1 may be an important component of translation regulation during cellular stress such as hypoxia, and suggest the need for a comparative study of its role in bivalves with different hypoxia responses.

COCULTURE OF PROBIOTIC BACTERIA IN ALGAL FEEDSTOCKS FOR DISEASE MANAGEMENT IN BIVALVE HATCHERIES

Samuel Hughes[1]*, David Rowley[1], David Nelson[1], and Marta Gomez-Chiarri[1]

University of Rhode Island, Department of Fisheries, Animal Veterinary Sciences, 9 East Alumni Avenue, Kingston, Rhode Island 02881 USA

samuel_hughes@uri.edu

The use of probiotics for disease management in shellfish aquaculture shows great promise, based on their demonstrated effectiveness in reducing larval shellfish mortality in culture operations while providing a relatively inexpensive, easy to administer, and environmentally safe alternative to antibiotic usage. A current roadblock in the commercial implementation of probiotics in hatcheries is the cost of repeated (daily) additions of bacteria, which are necessary for larval mortality reduction. Bivalve hatcheries in-

clude microalgal culture operations as a food source for shellfish stocks. The objective of this project is to determine if a probiotic can grow and/or maintain a steady population size when grown in co-culture with microalgae with no negative impacts on algal growth. It is hypothesized that: 1) microalgal cultures can serve as an economical delivery vehicle of probiotics to bivalve stock; and 2) probiotics will prevent pathogen growth in algal culture. Co-incubation experiments of the microalgae *Pavlova pinguis* with the probiotic *Phaeobacter inhibens* S4 showed that, regardless of inoculation density, the probiotic maintained a density of about 10^5 colony-forming units per ml for up to 14 days with no inhibitory effect on the growth rate of the microalgae. Further research will test the effect of co-culture on probiotic activity. This research suggests that algal stocks can be used to deliver probiotics to shellfish larvae and enhances our understanding of algal/bacterial interaction in shellfish hatcheries.

AN ASSESSMENT OF SEASONAL GASTROPOD DISTRIBUTION AND DENSITY IN NEARSHORE HABITATS OF THE WEST FLORIDA SHELF

Steve Geiger[1], Sarah Stephenson[2], Britt Burke[3], Michael Poniatowski[1], Erica Levine[1], and Jennifer E. Granneman[1,4]*

[1]Florida Fish and Wildlife Research Institute, 100 8th Ave SE, St. Petersburg, Florida 33701 USA

[2]National Marine Fisheries Services, 263 13th Ave S, St. Petersburg, Florida 33701 USA

[3]Stock Enhancement Research Facility, 14495 Harllee Rd., Palmetto, Florida 34221 USA

[4]University of South Florida, 830 1st St. SE, St. Petersburg, Florida 33701 USA

Jennifer.Granneman@MyFWC.com

Population distribution and density are not known for many of the large, marine gastropods in Florida, even though many of these species perform critical functions within Floridian ecosystems. Although the demand for large marine gastropods appears to be climbing, regulations for gastropod harvest in Florida provide minimal protections and are not species-specific. The objective of this project was to establish baseline spatio-temporal data on the density and distribution of seven large, predatory marine snails in nearshore habitats of the West Florida Shelf. To obtain seasonal density estimates, underwater visual and tactile surveys were conducted quarterly within three habitats (seagrass, oyster reef and soft sediments) in the Tampa Bay estuary, using weighted transect lines. Snail densities were also estimated annually using underwater visual surveys in shallow seagrass beds in regions ranging from the Florida Keys north to St. Andrew Bay. Gastropod densities only varied significantly among seasons and years in Tampa Bay for two of the seven marine gastropods for which density estimates were obtained. However, gastropod distribution varied significantly among habitats and most species were closely associated with one habitat type. Although regional gastropod densities did not vary among years, there were significant and consistent differences in densities among regions. Although this study helped fill data gaps to provide managers with a more detailed status of large, predatory marine snails on the West Florida Shelf, future studies should investigate life history parameters of these organisms because gastropod age and size at maturity are not well understood.

MONITORING THE DISTRIBUTION AND ABUNDANCE OF INVASIVE EUROPEAN GREEN CRABS (*CARCINUS MAENAS*) IN THE SOUTH SLOUGH OF THE COOS ESTUARY, OREGON, USA

Julia Indivero[1,2]*, Bree Yednock[1], and Christina Geierman[2,3]

[1]South Slough National Estuarine Research Reserve, P.O. Box 5417, Charleston, Oregon 97420 USA

[2]Oregon Sea Grant, 1600 SW Western Blvd, Suite 350, Corvallis, Oregon 97333 USA

[3]North Bend High School, 2323 Pacific Street, North Bend, Oregon 97459 USA

julia.indivero@gmail.com

European green crabs (*Carcinus maenas*) have been found in the Coos Estuary in Oregon since 1998 and have consistently persisted at low levels. An estuary-wide survey during the summer of 2016 found the highest green crab abundance since their initial establishment in 1998. During the summer of 2017, sites within the South Slough National Estuarine Research Reserve were sampled as a follow-up to the 2016 survey. The aims of the study were to investigate: 1) the distribution and abundance of green crabs in South Slough compared to 2016 and to the rest of the Coos Estuary, 2) the size and age structure of the green crab population, and 3) the relative effectiveness of the two main types of traps (Fukui and minnow) used in green crab monitoring.

Green crab abundance in the Coos Estuary was four times greater than in 2016, with the increase predominantly located in the Upper Bay region. The population primarily consisted of the strong 2015 and 2016 classes, and the presence of 2017 young-of-the year crabs indicated that 2017 may additionally be a strong recruitment year. In our study, Fukui traps were significantly more effective than minnow traps, suggesting that they should be the primary method for eradication. Because of the successive strength of green crab recruitment over the past few years, eradication in the Coos Estuary may be necessary to prevent further establishment of green crabs in the system. Continued monitoring will further help assess ecological impacts on native shellfisheries and the larger ecosystem.

CORRELATION OF OYSTER DISEASE WITH ACCUMULATION OF *VIBRIO PARAHAEMOLYTICUS* IN OYSTER TISSUE

Kiserian Jackson*, Abigail Scro, and Roxanna Smolowitz

Roger Williams University, Aquatic Diagnostic Laboratory, 1 Old Ferry Rd, Bristol, Rhode Island 02809, USA

kjackson966@g.rwu.edu

As the average water temperature of Narragansett Bay and other coastal ponds in Rhode Island continue to increase due to climate change it is probable that the abundance of *Vibrio parahaemolyticus* (Vp) and *Vibrio vulnificus* (Vv) will increase as well. *Vibrio* are gram-negative bacteria that can accumulate in tissues of the eastern oyster (*Crasssostrea virginica).* While *Vibrio* is not pathogenic to the oyster it can cause gastroenteritis in humans that consume the raw oysters. Eastern oysters are commonly infected with three diseases: *Perkinsus marinus* (Dermo), *Haplosporidium nelsoni* (MSX), and *Haplosporidium costale* (SSO). These parasites can cause severe morbidity and mortality in cultured and wild oysters. Animals that are affected by any disease have a decreased immune functionality and it is probable that these diseased oysters are more likely to accumulate higher levels of Vp and Vv. To test this theory, oysters were collected from Roger Williams University during the summers of 2016 and 2017. Composites of 10 oysters were tested using multiplex qPCRs for Vp and Vv in conjunction with a second multiplex qPCR to determine the abundance of those three disease. Individuals were also tested in order to increase accuracy of the association because composites which produce averages may mask important relationships only identified in individual animals.

SPECTRAL SENSITIVITY OF SENSORY MOTOR INTEGRATION OF GILL LATERAL CELL CILIA IN THE BIVALVE MOLLUSC *CRASSOSTREA VIRGINICA*

Johanne Jean-Pierre[1]*, Reniece Buchanan[2], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New York 11235 USA

[2]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

johannejeanp@gmail.com

Gill lateral cells (GLC) of *Crassostrea virginica* are innervated by serotonin and dopamine nerves. Serotonin is cilio-excitatory and dopamine is cilio-inhibitory. Motor aspects of GLC innervation are well studied, but not the sensory side. Sensory cues, including light, were found to initiate a sensory-motor integration response between mantle rim tentacles or cerebral ocelli (with shells removed) and GLC cilia. GLC responded to light by slowing GLC cilia beating. It was hypothesized that light penetrates oyster shells and stimulates cerebral ocelli to initiate the motor response and if light does penetrate shells, certain wavelengths are more effective in stimulating sensory cells. To test this light transmittance through shells was measured using a spectrophotometer. Red light (650+ nm) was transmittance best through shells. Testing animal preparations showed white light shown though shells stimulated ocelli to slow down GLC cilis, while blue (405 nm), green (525 nm) and amber (591 nm) light did not. Red (680 nm) light shown on mantle rim tentacles and cerebral ocelli, with the shell in place, caused a sensory-motor response that slowed GLC cilia beating from a basal rate of about 15 beats/sec to zero over a 20 minute period. This study further demonstrates integration of photosensory signals in control of GLC cilia in the bivalve *C. virginica*, and adds new knowledge demonstrating a spectral sensitivity of sensory cells in cerebral ocelli and mantle rim tentacle involved.

A ROLE FOR PROTEIN KINASE C IN GILL LATERAL CELL ACTIVITY OF *CRASSOSTREA VIRGINICA*

Alexcia Johnson[1]*, Krystle Ernest[2], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New York 11235 USA

[2]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

alexciajohnson1997@gmail.com

Gill lateral cell (GLC) cilia of *Crassostrea virginica* are controlled by serotonergic-dopaminergic innervations. Dopamine causes cilio-inhibition, serotonin cilio-excitation. GLC dopamine postsynaptic receptors are D2-like (D2DR). The D2DR signaling pathway involves inhibition of adenylyl cyclase and activation of phospholipase C (PLC). PLC generates second messengers diacylglycerol (DAG) and inositol trisphosphate (IP3). IP3 binds to IP3 receptors causing release of intracellular calcium. DAG with calcium activates protein kinase C (PKC). While high cytoplasmic calcium slows GLC cilia beating, the role of PKC on GLC cilia has not been studied. It is hypothesized that PKC activation is involved in the cilio-inhibitory response caused by dopamine in *C. virginica*. The PKC activator SC9 [N-(6-Phenylhexyl)-5-chloro-1-naphthalenesulfonamide] and PKC inhibitor rottlerin were tested. Neither SC9 (10^{-6}–10^{-3}M) nor rottlerin (10^{-6}–10^{-4}M) applications to gill altered GLC cilia beating, nor did they alter cilio-excitatory actions of serotonin; however, rottlerin treated gills did not respond to dopamine, an SC9 did not alter the cilio-inhibitory effects of dopamine. These finding indicate PKC is involved in dopamine induced slowing of GLC cilia in *C. virginica.* Inhibiting PKC prevents actions of dopamine, while activating PKC by itself did not significantly alter cilia beating rates. The study suggests PKC plays a role in cilio-inhibition caused by dopamine, but alone PKC activation is insufficient to generate the cilio-inhibitory response and other aspects of the D2DR signaling pathway also must be involved. These findings are helpful in furthering the understanding of the D2DR mechanism of GLC and provides a foundation for further research.

ASSESSMENT OF THE GENETIC PARAMETERS FOR COPPER AND ZINC ACCUMULATION CAPABILITY IN THE OYSTER, *CRASSOSTREA ANGULATA*

Caihuan Ke [1,2,3]*, Yidi Wu[1,2,3], Bo Shi[1,2,3], Long Zhou[1,2,3], Chenyu Dong[1,2,3], and Weiwei You[1,2,3]

[1]State Key Laboratory of Marine Environmental Science, Xiamen University, Xiamen 361102, China

[2]College of Ocean and Earth Sciences, Xiamen University, Xiamen 361102, China

[3]Fujian Collaborative Innovation Center for Exploitation and Utilization of Marine Biological Resources, Xiamen University, Xiamen 361102, China

chke@xmu.edu.cn

Nowadays, the increasing heavy metal pollution in estuaries and coastal areas has posed critical threat to marine organisms, including oysters, which are one of the most commercially important marine shellfish worldwide. The Portuguese oyster, *Crassostrea angulata*, is the main cultivated oyster species in southern China. Oysters are considered as hyper-accumulators of copper (Cu) and zinc (Zn), and it has been proved that metals accumulation capability in oysters is a quantitative trait under genetic control. The genetic parameters of Cu and Zn accumulation capability and growth-related traits in *C. angulata* were estimated with a mixed-family method to determine the degree to which Cu and Zn accumulation is under genetic control. Moreover, the correlations between Cu/Zn and qualitative traits including glycogen and eight free amino acids were investigated to evaluate the trade-offs between Cu/Zn accumulation and performance. Results showed that the narrow-sense heritability estimated for Cu (0.19), Zn (0.32), shell width (0.24), shell depth (0.15) and dry meat weight (0.14) were moderate, while high for shell length (0.39) and live body weight (0.43). High genetic (0.80) and phenotypic (0.86) correlations were found between Cu and Zn, while correlations between metals and growth traits were lower (-0.01-0.436). Cu and Zn accumulation in *C. angulata* showed no significant influence on the qualitative traits measured, except for Tau which showed similar profiles with Cu and Zn, suggesting its important role in Cu/Zn accumulation. Results provide important information for effective selective breeding on *C. angulata* with specific Cu/Zn accumulation capability.

SCEMFIS 2017: A YEAR IN REVIEW

Kelsey M. Kuykendall[1*], Eric N. Powell[1], Roger Mann[2], and Karen Reay[2]

[1]Gulf Coast Research Laboratory, 703 East Beach Drive, Ocean Springs, Mississippi 39564 USA

[2]Virginia Institute of Marine Science, 1375 Greate Road, Gloucester Point, Virginia 23062 USA

Kelsey.kuykendall@usm.edu

The Science Center for Marine Fisheries (SCeMFiS) is a National Science Foundation (NSF) funded industry/university collaborative research center (I/UCRC) established in June 2013. SCeMFiS has two sites: The University of Southern Mississippi (USM) and Virginia Institute of Marine Science (VIMS). Since 2013, SCeMFiS has grown to include not only researchers from USM and VIMS, but also Cornell University, Rutgers University, University of Rhode Island, University of Maryland Center for Environmental Science, and The University of Massachusetts Dartmouth along with other U.S. and Canadian academics and consultants and fourteen industrial partners. SCeMFiS provides NSF sanctioned research to meet the needs of industry partners with the ultimate goal being sustainability of both the shellfish and fish stocks and their associated fisheries. Achievements for 2017 include presence at three national meetings with a total of nine contributions, nine peer reviewed publications with several publications in press, one graduate student receiving a Master's of Science from The University of Southern Mississippi, the first successful survey of the area east of Nantucket Shoals, and the recruitment of two research experience for undergraduates (REU) students. SCeMFiS is looking back at a successful year and forward to more progress in 2018 as more academics and industries become involved with the Center and its ongoing projects.

ASSESSMENT OF OYSTER (*CRASSOSTREA VIRGINICA*) HEALTH IN NATURAL VS RESTORED REEFS IN THE NORTHERN, CENTRAL, AND SOUTHERN INDIAN RIVER LAGOON (IRL), FLORIDA

Susan Laramore[1*], Elizabeth Urban-Gedamke[1], Carolyn Sinacore[1], Emily Davidson[1], Alycia Shatters[1], Erica Rose[1], Reika Yu[2], Jeffrey Beal[3], Emily Dark[4], and Matthew R. Anderson[4]

[1]Florida Atlantic University-Harbor Branch Oceanographic Institution, Center for Aquaculture and Stock Enhancement, 5600 US Hwy 1 North, Fort Pierce, Florida 34946 USA

[2]Boston University, 1 Silber Way, Boston, Massachusetts 02215 USA

[3]Florida Fish and Wildlife Conservation Commission-Estuarine Subsection, 5600 US 1 North, Fort Pierce, Florida 34946 USA

[4]Florida Department of Environmental Protection-Indian River Lagoon Aquatic Preserve Field Office, 3300 Lewis Street, Fort Pierce, Florida 34981 USA

slaramo1@fau.edu

The Indian River Lagoon (IRL) is a diverse estuary stretching 156 miles along the Florida Atlantic coast. Oyster (*Crassostrea virginica*) reef restoration has been implemented at various locations in the IRL to improve ecosystem health. Past monitoring efforts have focused on structural assessment rather than on organismal health.

The aim of this study was to compare the health of natural and restored oyster reefs in the IRL along a north to south gradient in

order to further inform future restoration efforts. Oyster reefs were monitored seasonally (n = 540/season; 1620 total) from three natural and three restored sites (n = 30/site) within three regions (north, central, south). Size, physiological condition, parasite and pest prevalence were compared.

Health indices varied regionally and seasonally. No difference was seen between natural and restored reefs in the north whereas natural reefs fared better in the central and southern IRL. Size was similar between region and reef type. Physiological condition was highest in the fall in all regions. Northern oysters exhibited poorest physiological condition. The prevalence and intensity of *P. marinus* was highest in the fall in the northern and central IRL, and in spring in the south. Northern regions had higher year-round *Perkinsus marinus* prevalence. Prevalence of *Bonamia* sp. was lowest in the north and not detected at any site in the fall. MSX was absent at all sites. Pest prevalence increased at all sites in spring. Pests were more prevalent in central and southern sites and at restored reefs.

OFF-BOTTOM CULTURE OF OLYMPIA OYSTERS

Jonathan S.F. Lee[1*], Ryan N. Crim[2], Brian L. Allen[2], Barry A. Berejikian[1], and Rick W. Goetz[1]

[1]Environmental and Fisheries Sciences Division, Northwest Fisheries Science Center, National Marine Fisheries Service, NOAA, 7305 Beach Dr E, Port Orchard, Washington 98366 USA

[2]Puget Sound Restoration Fund, 382 Wyatt Way NE, Bainbridge Island, Washington 98110 USA

Jon.Lee@noaa.gov

Most oyster culture research has focused on Pacific oysters (*Crassostrea gigas*), but diversification to other species would improve product assortment and increase resilience for industries and ecosystems. Compared to Pacific oysters, Olympia oysters (*Ostrea lurida*) are more resilient to ocean acidification, and thus may become more important on future shellfish farms in the Puget Sound. Olympia oysters once supported a thriving shellfish industry, but wild populations have been severely reduced. Interest in Olympia oysters has been limited because they are smaller and grow more slowly than Pacific oysters, but they may be well suited for the current half shell market. In order to achieve better growth and survival in Olympia oyster culture, an experiment was conducted to compare off-bottom to standard on-bottom juvenile culture methods for a winter season. The bag-on-bottom method, where bags lay directly on the beach, is the most common rearing method. Bag-on-rack and tray methods elevate the oysters above the beach ("off-bottom"), which may reduce sedimentation and provide improved water flow. Four different oyster densities (low, medium, high, extra-high) were also compared. Compared to the bag-on-bottom method, both off-bottom methods led to greater shell volumes, shell lengths, and survival by the end of the experiment. There were no significant differences between the two off-bottom techniques (bag-on-rack and tray). Density had a significant effect on shell volume and shell length. Density-dependent effects seemed to begin when density increased from medium to high, suggesting that the medium density is the optimal stocking density.

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF A SHELL-BORING MUDWORM *POLYDORA WEBSTERI* (POLYCHAETA: SPIONIDAE) FROM PUGET SOUND, WASHINGTON, USA

Heather M. Lopes[1]*, Julieta C. Martinelli[1,2], Jaqueline L. Padilla-Gamino[1], Lorenz Hauser[1], Isadora Jimenez-Hidalgo[1], Paul D. Rawson[3], Jason D. Williams[4], Teri L. King[5], and Chelsea L. Wood[1]

[1]University of Washington, School of Aquatic and Fishery Sciences, Seattle, Washington 98105, USA

[2] Centro de Estudios Avanzados en Zonas Aridas, CEAZA, Coquimbo, Chile

[3]University of Maine, School of Marine Sciences, Orono, Maine, 04469, USA

[4]Hofstra University, Department of Biology, Hempstead, New York 11549, USA

[5]Washington Sea Grant, Shelton, Washington 98584, USA

hlopes@uw.edu

Some spionid polychaetes can burrow into the shells of bivalves, creating unsightly mud blisters. Because they are unappealing to consumer and can burst, fouling oyster flesh, these blisters are an economic burden on affected oyster half-shell industries. Historical invasions by the spionid, *Polydora websteri,* have resulted in the collapse of aquaculture operations in Australia, New Zealand, and Hawaii, USA. Recent sightings of mud blisters on Pacific oysters (*Crassostrea gigas*) in Puget Sound, Washington, USA suggest that the area might be experiencing a spionid polychaete invasion. To determine whether *P. websteri* is the polychaete creating the mud blisters recently observed in Puget Sound, 170 Pacific oysters were obtained from six locations and examined for blisters and burrows. Polychaetes were extracted from the shells and vouchered for molecular analyses. Mitochondrial (cytochrome c oxidase I [COI] and cytochrome b) and nuclear (18S rRNA) genes for species-level identification was used. Positive identification of *P. websteri* found in the mud blisters of Puget Sound Pacific oysters will be the first confirmed sighting in Washington, USA. This study is the foundation for advising the Washington shellfish industry on strategies for mitigating the economic impacts of this invasive polychaete.

JUST A SNIPPET: HIGH RESOLUTION MELTING (HRM) ANALYSIS TO VALIDATE SNPS FOR THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Kathryn R. Markey Lundgren*, Brett Boudreau, and Dina A. Proestou

University of Rhode Island, USDA ARS National Cold Water Marine Aquaculture Center, Shellfish Genetics Laboratory, Kingston, Rhode Island 02881 USA

Kathryn.lundgren@ars.usda.gov

The eastern oyster, *Crassostrea virginica,* genome exhibits an exceptionally high level of polymorphism, yet relatively few single nucleotide polymorphism (SNP) markers are available for this species. This study outlines an approach to identify and validate SNP markers in the eastern oyster. Over 3000 putative SNPs were identified by mapping differentially expressed RNA transcripts derived from two oyster families to a high-quality transcriptome assembly. 358 putative SNPs were prioritized for SNP marker development and High Resolution Melting (HRM) genotyping assays were designed for 104 unique gene/SNP combinations. Twenty-three individuals sampled from seven selectively-bred oyster lines were screened in each assay. In total only 15% of the SNPs tested generated melting curves that were suitable for subsequent marker validation. 37 primers yielded no or poor amplification, 12 were monomorphic, and more than three genotypes were detected in 34. For the 21 SNPs where the HRM assay clearly discriminated two or three genotypes, amplicons associated with each distinct melting curve were cloned and sequenced to confirm allelic composition. Cloning and sequencing of amplicons with too many melting curves revealed additional SNPs in the short sequence. The confirmed SNPs are now being tested to evaluate their utility in differentiating among different populations/genetic lines of oysters. This study underscores the difficulties associated with developing SNP genotyping assays in highly polymorphic bivalve species.

AVIAN USE OF RESTORED EELGRASS MEADOWS AND OYSTER BEDS AS PART OF A LIVING SHORELINES PROJECT

Kiarra I. Lyons[1]*, Austin H. Xu[2], Danielle C. Zacherl[1], and William J. Hoese[1]

[1]California State University, Fullerton, Department of Biological Sciences, 800 N State College Blvd, Fullerton, California 92831 USA

[2]California State University, Los Angeles, Department of Biological Sciences, 5151 State University Dr, Los Angeles, California 90032 USA

kiarra.lyons@csu.fullerton.edu

Living shorelines restoration uses the infrastructure that some organisms create (e.g., oyster beds, eelgrass meadows) to reduce coastal erosion while simultaneously promoting ecological community diversity. Birds may benefit from living shorelines because restored habitat may increase the richness and density of prey species. This study examines bird use of constructed living shorelines at four sites prior to (January 2016 - March 2016) and after eelgrass and oyster restoration (May 2017 - ongoing) in Newport Bay, CA. Each site consists of a 130m long x 12m wide mudflat swath, divided into four randomized 20m long treatment plots (control, oyster, eelgrass, oyster-eelgrass) separated by 10m buffer zones. Bird use surveys consist of scan samples to quantify bird density and richness and focal samples to examine bird behavior at each site. It is predicted that post-restoration bird density and richness will increase in all restored treatments compared to control mudflat treatments. Data collection is ongoing. Sixty-seven surveys across all sites and treatments have been conducted with thirty-nine species observed; the most common species include willets, marbled godwits, and western and least sandpipers. Birds spend 70% of observed time foraging and do not favor any treatment. With only a few observations post-restoration, and thus low statistical power, density and richness do not differ across treatments, however trends show an increase in density and richness on all treatment plots, with highest richness on the oyster-eelgrass plots, compared to control plots. This project provides insight into the potential benefit of combining eelgrass and oyster restoration.

SEASONAL VARIATION OF TRANSCRIPTOMIC AND BIOCHEMICAL PARAMETERS OF *DONAX TRUNCULUS* RELATED TO ITS INFECTION BY THE TREMATODE PARASITE, *BACCIGER BACCIGER*

Luísa Magalhães[1,2]*, Xavier de Montaudouin[2], Simão Correia[1], Guillemine Daffe[2], Patrice Gonzalez[2], Etelvina Figueira[1], Jorge M.S. Gonçalves[3], and Rosa Freitas[1]

[1]Departamento de Biologia & CESAM, Universidade de Aveiro, 3810-193 Aveiro, Portugal

[2]Université de Bordeaux, EPOC, UMR 5805 CNRS, 2, rue du Pr Jolyet, F-33120 Arcachon, France

[3]Centro de Ciências do Mar - CCMAR, Universidade do Algarve, FCT, Campus de Gambelas, 8005-139 Faro, Portugal

luisa.magalhaes@ua.pt

The wedge clam (*Donax trunculus*) is widely distributed along moderately exposed beaches in the Atlantic coast, from France to Senegal. This species has high commercial importance, with the mean capture production of the last ten years of ca. 850 tonnes (50 % represented by Portugal captures). Populations of *D. trunculus* are modulated by several drivers such as tidal range, temperature, sediment grain size, fishing pressure, predation, and parasitism. Regarding parasitism, *D. trunculus* is the first intermediate host of *Bacciger bacciger* (trematode parasite) where the sporocysts develop. The sporocyst is the most damaging stage, reported as responsible of bivalve castration and flesh mass depletion.

In order to test the hypothesis that *B. bacciger* infection modified wedge clam health status, including its biochemical performance and gene expression, organisms were sampled every other month during one year in the Faro beach (Portugal south coast).

The results obtained revealed that *B. bacciger* prevalence ranged between 0 and 28 %, in May and July respectively. Overall, transcriptomic and biochemical results showed that *B. bacciger* induced in *D. trunculus* defence mechanisms against oxidative stress and increased the host metabolism and energy demand, especially in spawning and spent periods.

In conclusion, the present work showed that the markers used can provide additional and ecologically relevant information about, not only the environmental conditions that animals experience but also on the invasion effects of pathogens. These findings can help to predict organism's chances of reproduction and survival in their natural context, which can be applied in bivalve conservation and disease episodes management.

PRELIMINARY OBSERVATIONS REGARDING RIBBED MUSSEL (*GEUKENSIA DEMISSA*) SPAT PRODUCTION

Justin Manley*, Thomas Bliss, and Robert Hein

University of Georgia, Shellfish Research Laboratory, 20 Ocean Science Circle, Savannah, Georgia 31411 USA

manley@uga.edu

The Atlantic ribbed mussel, *Geukensia demissa* (Dillwyn, 1817), is naturally distributed along the Atlantic seaboard from the Gulf of St. Lawrence to northeastern Florida and is replaced by the Gulf estuarine ribbed mussel, *Geukensia granosissima* (Sowerby, 1914) in the Gulf of Mexico. Ribbed mussels are ideal species for restoration due to growth rate, dietary plasticity, geographical and tidal distribution, and environmental tolerances. Stable hatchery production of ribbed mussel spat for use in restoration/bioremediation efforts is important to planning projects that currently rely on sporadic natural recruitment. Development of basic hatchery protocols for consistent ribbed mussel spat production is necessary for executing restoration objectives. During August 2016 a small number (~10,000) of ribbed mussel spat were successfully reared to 4 mm at the University of Georgia shellfish hatchery from a limited spawn of 10 adult mussels. Mussel larvae were successfully reared through eyed and settlement stages in static culture using Shellfish Diet 1800 in accordance with feeding protocols established by Rikard and Walton (2012) for *Crassostrea virginica* larvae. Mussel spat was set on Manila rope, held in an upweller nursery, transferred to the field in 2 mm pearl nets, and cultured in 9 mm mesh aquaculture bags. Mussels attained a mean shell height of 38.37 ± 1.36 mm as of October 2017 approximately 12 months post-set. Preliminary observations regarding spawning, larval culture, setting, nursery maintenance, and field culture are discussed.

POTENTIALS OF MAJOR OYSTER PLASMA PROTEINS IN FUNCTIONING FOR METAL ION STORAGE AND TRANSPORTATION

Xiaowei Mao[1,2], Qinggang Xue*[2], Qifeng Xia[1,2], Xiarong Wang[1,2], Dengfeng Li[1], and Zhihua Lin[2]

[1]Ningbo University, School of Marine Sciences, Ningbo, Zhejiang 315010, China

[2]Zhejiang Wanli University, Key Laboratory of Aquatic Germplasm Resource of Zhejiang, Ningbo, Zhejiang 315100, China

qxue@zwu.edu.cn

Dominin and segon are the two most abundant proteins in the plasma of eastern oysters *Crassostrea virginica* and both are produced by the hemocytes. Dominin shares high sequence similarity with extracellular superoxide dismutase while segon represents a novel protein. Based on the measured metal contents, the two proteins are believed to serve as metal binding proteins and play a role in metal metabolism. In the present research, the possibility of dominin and segon homologues to function in metal ion storage and transportation was assessed in Pacific oysters, *Crassostrea gigas*. BLAST searches using dominin and segon as queries identified three dominin homologue genes, which included the previously reported CgEcSOD or cavortin, and 1 segon homologue gene in the Pacific oyster genome. To determine the capacity of these proteins to bind and carry metal ions, oysters were grouped and placed separately in natural seawater supplemented with $ZnSO_4$ at 60 mg/L and 100 mg/L and with $CdCl_2$ at 6 mg/L and 10 mg/L. Hemolymph and gill tissues were then sampled at different time points after metal ion exposure. Hemocytes and gill tissues were assayed for the expression of dominin and segon homologue genes using real-time PCR and plasma proteins of the related hemolymph samples quantified for the contents of zinc or cadmium ions using ICP-MS. Results of the research generated important information for assessing the function of the major plasma proteins of oysters in metal ion storage and transportation.

IN SITU FILTRATION RATES OF OLYMPIA OYSTER (*OSTREA LURIDA*) HABITAT AND PACIFIC OYSTER (*CRASSOSTREA GIGAS*) AQUACULTURE

Althea N. Marks* and Danielle Zacherl

University of California Fullerton, Department of Biology P.O. Box 6850 Fullerton, California 92834 USA

theamarks@csu.fullerton.edu

The filtration services of Olympia oyster (*Ostrea lurida*) habitat and Pacific oyster (*Crassostrea gigas*) aquaculture operations along the North American west coast have been little explored. *In situ* filtration studies can incorporate variable environmental conditions important to filtration as well as the contributions of other filter feeders living among oysters (i.e. mussels, tunicates, scallops, and sponges). This ongoing study is quantifying *in situ* filtration rates of two restored Olympia oyster habitats in Newport Bay, California

(CA) and San Francisco Bay, CA, two Pacific oyster aquaculture operations in San Diego Bay, CA and Morro Bay, CA, and natural Olympia oyster beds in the Pacific Northwest. Questions are: 1) How do filter feeder community composition and density affect filtration rates of oyster habitat? 2) How do water quality parameters affect oyster habitat filtration rates? 3) What are the filtration rates of *C. gigas* FLoating UPwelling SYstems operated by the Port of San Diego in San Diego Bay, CA and *C. gigas* floating long lines operated by Morro Bay Oyster Company in Morro Bay, CA? Two identical instruments are deployed upstream and downstream of the oyster habitat to measure temperature, salinity, turbidity, chlorophyll, and water velocity; filter feeder density is also measured. Each site will be measured four times over twelve months. Filtration rates are expressed in $Lhr^{-1}g^{-1}$ to compare to previous filtration studies and $Lhr^{-1}m^{-2}$ to calculate bay-wide filtration. This research bridges oyster-centric filtration studies with incorporation of aquaculture and restored oyster habitat into filtration models useful to resource management.

MARINE BIOTOXINS: DOMOIC ACID MONITORING ON THE OREGON COAST

Alexandria Marquardt[1*], Matthew Hunter[1], Steve Rumrill[2], Kelly Corbett[2], and Cyreis Schmitt[2]

[1]Oregon Department of Fish and Wildlife, 2001 Marine Drive, Astoria, Oregon 97103 USA

[2]Oregon Department of Fish and Wildlife, 2040 SE Marine Science Drive, Newport, Oregon 97365 USA

armarqua@calpoly.edu

Marine biotoxins, including domoic acid, are produced by phytoplankton during Harmful Algal Bloom (HAB) events along the west coast. Domoic acid (DA), produced by the diatom *Pseudo-nitzchia* spp. (*P-n*), is a potent neurological toxin that can accumulate in shellfish, forage fish, marine mammals, and humans. Elevated concentrations of domoic acid pose a significant risk to human health, and fishery closures have significant economic impacts to coastal communities. Unlike the bordering states, Oregon only has a rudimentary program to monitor biotoxin levels in shellfish and other living marine resources. The overall goal for this project was to: examine the scope and extent of historic and recent biotoxin testing in marine organisms along the Oregon coast and identify the need for additional programmatic development. This study focused on a suite of marine organisms not included in standard biotoxin testing programs for the measurement and analysis of domoic acid concentrations using Enzyme-Linked Immunosorbent Assays (ELISA) to identify relationships in trophic pathways. Findings show that during large, toxin-producing events, domoic acid can be found throughout the food web. Species not associated with DA (e.g. bay clams and mussels) were found with measurable accumulated toxins. For management, this indicates that during a bloom event there are multiple vectors for DA accumulation and toxin accumulation in higher taxa could be achieved through repeated low level exposure of non-DA associated species during a HAB event.

EFFECTS OF GENETIC DIVERSITY ON FITNESS-RELATED PERFORMANCE OF THE EASTERN OYSTER IN NATURE

Katherine McFarland[1,2] and Matthew Hare[1]

[1]Cornell University, Department of Natural Resources, Ithaca, New York 14850 USA

[2]University of Maryland, Center for Environmental Science, Cambridge, Maryland 21613 USA

mcfarland.316@gmail.com

In recruitment-limited areas it is common for population supplementation efforts and restoration projects to employ hatcheries to generate abundant seed oysters for planting. The literature contains examples of hatchery-induced genetic diversity bottlenecks based on comparing the wild brood stock to the resulting cohort. A cohort bottleneck occurs relative to the source population if relatively few brood stock individuals are spawned, or relative to spawning brood stock if reproductive contributions are skewed. These are known risks that can be managed to some extent. Much less information is available on the functional consequences in nature of low genetic diversity in hatchery cohorts. Recent work has demonstrated positive associations between genetic diversity metrics in spat and their survivorship and growth rate (Hanley et al. 2016). If there is a potential for hatchery bottlenecks to lower oyster performance or hardiness, it is important to know how strong the effect can be and whether it is context dependent (i.e., genetic by environment interactions). Here, strip-spawning was used to generate high- and low-diversity cohorts from a nested set of 24 and 6 moderate-salinity brood stock, respectively. Outplants to replicate cages at 11 sites throughout the Hudson River Estuary, NY, occurred in August 2016. At five sites the hatchery cohorts were compared to approximately same-age wild spat-on-shell. Survivorship and growth rate comparisons will be reported for the first year post-outplant, including an extremely wet, low-salinity Spring and Summer for some sites.

MONITORING OYSTER RESTORATION EFFORTS IN APALACHICOLA BAY, FLORIDA

Melanie L. Parker[1]*, Matthew Davis[2], Matthew LaGanke[2], Nicole Martin[2], Nicole Maloney[2], and Nick Tolopka[2]

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

[2]Florida Fish and Wildlife Conservation Commission, Apalachicola Field Lab, 350 Carroll Street, Eastpoint, Florida 32328 USA

melanie.parker@myfwc.com

Apalachicola Bay is one of the most productive estuarine systems in Florida. For decades, the Bay supported a successful commercial oyster fishery that accounted for over 90 percent of annual harvest in Florida; however, landings declined sharply in late 2012 and the fishery has since collapsed. Potential causes of this collapse include high predation and disease rates resulting from higher estuarine salinities and increased fishing pressure following the Deepwater Horizon oil spill in 2010. As a result, two projects focused on restoring oyster habitat in Apalachicola Bay were initiated in 2015. One aspect of these two restoration projects was to determine the most efficient method for increasing potential oyster habitat and resilience of the commercial fishery. To do this, two methods were used to cultch several acres with shell substrate: 1) shell was deployed by hand from commercial fishermen's boats and 2) shell was deployed by high-pressure water cannons from a shallow draft barge. In addition, cultch substrate was deployed at different densities (100, 200, 300, or 400 cubic yards per acre) at three sites in the bay. Surveys to determine live oyster density and size structure have been conducted two to four times per year at each site. Results at this point in the studies indicate that barge shelling larger areas increases retention of cultch material, and that no additional benefit is gained by cultching at densities greater than 300 cubic yards per acre.

CELLULAR BIOMARKER RESPONSES OF FRESHWATER BIVALVES TO CHLORPYRIFOS

Tuan K. Phan[1]*, Dane Thomason[1], Ed Johnson[2], Annie Jacob[2], Kimani Kimbrough[2], and Amy H. Ringwood[1]

[1]National Centers for Coastal Ocean Science, National Oceanic and Atmospheric Administration, Maryland USA

[2]University of North Carolina at Charlotte, Department of Biological Science, 9201 University City Blvd, Charlotte, North Carolina 28223 USA

tkpham@uncc.edu

Chlorpyrifos is the number one active ingredient used in many insecticides in the United States, mainly used for corn, soybean, and alfalfa agriculture. Very high concentrations of chlorpyrifos have found throughout the Great Lakes, especially along the Maumee River. Chlorpyrifos can have negative effects on freshwater ecosystems and organisms. Bivalves are valuable bioindicator organisms that can be used to characterize ecosystem health and monitor the effectiveness of remediation programs; however many North American freshwater bivalves are threatened or endangered so studies with abundant invasive freshwater species such as *Corbicula fluminea* and *Dreissena polymorpha* were used to assess chlorpyrifos toxicity. One part of these investigations was in situ caging studies of *C. fluminea* and *D. polymorpha* conducted by the National Oceanic and Atmospheric Administration (NOAA) as part of the Mussel Watch program in the Maumee River Basin in Lake Eerie, in collaboration with the Environmental Protection Agency (EPA). Cellular biomarkers (including acetlycholinesterase and glutathione) of sublethal toxicity of clams and mussels from these field studies as well as laboratory exposures of *C. fluminea* to environmentally relevant concentrations of chlorpyrifos were conducted at UNCC. Adverse effects in both bivalve species related to pesticide exposures, especially acetylcholinesterase, were observed. These studies will facilitate insights regarding the impacts and extent of chlorpyrifos on environmental health.

FIRST INVESTIGATION OF AUTOPHAGY MONITORING BY FLOW CYTOMETRY IN AN INVERTEBRATE ORGANISM, *CRASSOSTREA GIGAS*

Sandy Picot[1], Benjamin Morga[1*], Nicole Faury[1], Bruno Chollet[1], Lionel Dégremont[1], Marie-Agnès Travers[1], Tristan Renault[2], and Isabelle Arzul[1]

[1]Ifremer, Unité Santé Génétique et Microbiologie des Mollusques, Laboratoire de Génétique et Pathologie des Mollusques Marins, Avenue de Mus de Loup, 17390 La Tremblade, France [2]Ifremer, Département Ressources Biologiques et Environnement, Rue de l'Ile d'Yeu—BP 21105—44311 Nantes Cedex 3, France

benjamin.morga@ifremer.fr

Autophagy is a process that engulfs a portion of cytoplasm with components of the cell from proteins to whole organelles for their degradation by fusion with lysosomes. This mechanism permits to maintain cellular homeostasis and contributes to others roles including starvation adaptation, elimination of microorganisms, and cell death. This process exists from yeast to mammals. Recent results indicate that the autophagy pathway is functional in the mantle of the Pacific oyster, *Crassostrea gigas* (*C. gigas*); however, nothing is known about the autophagy pathway in haemocytes. Few methods have been developed to investigate the autophagy pathway in marine invertebrates, contrary to mammals. To study autophagy in haemocytes of cupped oysters, *C. gigas*, oysters were exposed to an autophagy inducer (Carbamazepine) and inhibitor (NH_4Cl) during 24 h to 48 h before collecting haemolymph from the adductor muscle. Flow cytometry and fluorescent microscopy approaches were developed and used to monitor autophagy in cells

in the different tested conditions. Complementary, transmission electron microscopy was used to describe ultrastructural alterations in haemocytes. Results demonstrated that flow cytometry and fluorescent microscopy are promising tools to study the autophagy pathway in bivalves and that the autophagy pathway is functional in the haemocytes of *C. gigas*.

MUD BLISTERS IN OYSTERS: RELATING WORM INFESTATION TO BLISTER STRENGTH

Rachel Pugh[1,2,3]*, Kelly Dorgan[3], Sarah Cole[3,4], and William C. Walton[5]

[1]Mississippi Gulf Coast Community College, 51 Main Street, Perkinston, Mississippi 39573 USA

[2]University of Southern Mississippi, 118 College Drive, Hattiesburg, Mississippi 39406 USA

[3]Dauphin Island Sea Lab, 102 Bienville Blvd, Dauphin Island, Alabama 36528 USA

[4]University of South Alabama, 307 N. University Blvd, Mobile, Alabama 36688 USA

[5]Auburn University Shellfish Lab, 150 Agassiz St, Dauphin Island, Alabama 36528 USA

rachelpugh1@gmail.com

The worm, *Polydora websteri*, a pest to farmed eastern oysters (*Crassostrea virginica*), creates mud-filled blisters in the oyster shell cavity. Blisters weaken the shell, are unappealing to consumers, and may decrease marketability of oysters. Oysters resist blisters by secreting new shell layers. This research examines the relationship between worm infestation and blister presence and breaking force to determine how closely worm infestation numbers reflect their damage to the oyster and therefore assess the effectiveness of the oyster's defense. Off-bottom triploid and diploid oysters were collected from three farms along the Alabama coast in June and July 2017. Worms were extracted. Shucking and blister breaking forces were measured using two custom-built instruments. The hypotheses were: (1) number of worms extracted would correlate with percent of shell area covered by blisters, (2) triploids would have less blister coverage than diploids due to higher growth rates, (3) blister breaking force would decrease as blister area increased, and (4) blister breaking force would be lower and blister area larger with darker blister color. Results show weak correlation between worms extracted and percent of shell area covered, indicating worm infestation cannot be used to determine blister numbers. Triploids have less percent shell area covered than diploids; triploids may have more efficient blister recovery. Blister breaking force and blister area were weakly correlated with blister color, suggesting blister recovery occurs more slowly than turnover rates of worm infestation. Farmers should treat oysters early and frequently to prevent blisters or allow long recovery times post-treatment to obtain clean shells.

INFLUENCE OF STOCK DENSITY ON REPRODUCTIVE CONDITION OF NORTHERN QUAHOGS FROM NARRAGANSETT BAY, USA

Shantelle Richards*, Matt Griffin, and Dale Leavitt

[1]Roger Williams University, Center for Economic and Environmental Development, 1 Old Ferry Road, Bristol, Rhode Island 02809 USA

srichards128@g.rwu.edu

Northern quahogs (*Mercenaria mercenaria*) are commercially important infaunal bivalve molluscs that are found throughout Narragansett Bay. Based on RI-DEM dredge surveys, it is most common to observe three to four quahogs per square meter within the upper sections of Narragansett Bay; however, in certain areas of the Bay characterized by being prohibited from commercial harvesting, *M. mercenaria* has been found to occur in densities up to or greater than an order of magnitude higher.

Recent studies suggested reproductive effort in northern quahogs from closure areas was significantly lower than in those from fished areas, suggesting reproductive condition may be density dependent. It was thought that a reduction in spawning effort may be due to a lack of food resource available to the larger population size, in combination with reduced water quality commonly found associated with prohibited waters.

The purpose of this study was to evaluate the reproductive condition in *M. mercenaria* collected from sites in Narragansett Bay with varying degrees of standing stock density. The hypothesis is that northern quahogs from areas of higher stock density demonstrate a decreased reproductive effort. Ten sites of varying northern quahog densities within Narragansett Bay were sampled biweekly through the 2013 reproductive season, where the stage of reproduction was assessed histologically. Biweekly assessment of reproductive condition suggested that areas of higher northern quahog density demonstrated a more disrupted annual reproductive cycle. Reduced reproductive effort with an asynchronous spawning cycle was prevalent in quahogs sampled from the highest density populations.

INHIBITION OF BIOFOULING AND BIOFILM GROWTH: THE EFFECT OF A CATIONIC PORPHYRIN ON *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION ON DIFFERENT SUBSTRATA

David Rivetti*, Nehaben Patel, Jayne B. Robinson, and Karolyn M. Hansen

University of Dayton, Department of Biology, 300 College Park, Dayton, Ohio 45469 USA

rivettid1@udayton.edu

Biofouling can have significantly detrimental impacts on aquaculture. Many current approaches to prevent biofouling, such as antifouling paints and coatings, release environmentally harmful chemicals and metals that negatively affect the growth of shell-

fish. As a result, control of biofouling presents a difficult and costly challenge to the aquaculture industry. Porphyrins are ringed, planar chemical compounds that are often used for sterilizing or cleaning an object or a surface. They occur naturally and also can be synthesized, as some porphyrins have even been used in photodynamic therapy. Cationic and zinc porphyrins have been used to both disrupt and prevent biofilm formation on various substrata, including glass, polyethylene, and stainless steel. As a result of their physical and chemical properties, biofilms are difficult to break down and remove from surfaces. Cationic porphyrins have the capacity to cause DNA damage in biofilms by intercalating between the base pairs of a DNA sequence, resulting in the breakage of the strand. Porphyrin treatment of *Pseudomonas aeruginosa* biofilms grown on glass, polyethylene, stainless steel, bone, and oyster shell (*Crassostrea virginica*) is being conducted to determine efficacy for inhibition and/or prevention of microbial fouling. Various concentrations of 5,10,15,20-tetrakis (1-methyl-pyridino)-21H,23H-porphine, tetra-*p*-tosylate (TMP) salt are used to determine disruption of *P. aeruginosa* biofilms grown on the substrates; porphyrin pretreatment of substrates is underway to determine inhibition of biofilm growth. Applications include reduction and/or prevention of biofilm growth and biofouling on a variety of substrates, including shells of live oysters.

CREATING FLOW REFUGIA IN THE TIDAL FRESHWATER DELAWARE RIVER TO AUGMENT AND RESTORE FRESHWATER MUSSEL POPULATIONS

S.A. Roberts[1,2*], J.A Moody[1,2], K. Cheng[1], and D.A. Kreeger[1,2]

[1]Partnership for the Delaware Estuary, 110 S Poplar St. Suite 202, Wilmington, Delaware 19801 USA

[2]Drexel University, Department of Biodiversity, Earth, and Environmental Science, 3201 Arch St. Suite 240, Philadelphia, Pennsylvania 19104 USA

sroberts@delawareestuary.org

Freshwater mussels (Order Unionoida) remain one of the most imperiled taxonomic groups in North America. Recent attention on population restoration and augmentation in tidal areas of the Delaware Estuary with historic populations has proven challenging as benthic conditions in urbanized areas may not provide readily suitable habitat. Lower benthic shear stress and increased sediment stability may promote mussel retention and recruitment; however, few studies have examined how such physical factors govern habitat suitability in tidal freshwater systems. In fall 2017, experimental structures comprised of salvaged logs and cobble were constructed along a shallow subtidal shoreline of the Delaware River where the preexisting mussel abundance was greatly reduced compared to a nearby reference site. The structures were oriented to stabilize sediments and reduce benthic shear stress while not interfering with seston delivery. Passive Integrated Transponder (PIT) tagged mussels were subsequently deployed into each structure and untreated controls. Mussel position, sediment grain size and organic content, and benthic shear force were monitored over the fall and winter 2017-18. Preliminary retention of mussels averaged 72%, suggesting that the structures may serve as refugia from high flow that typically mobilized the substrate. If confirmed with extended monitoring, these results should support design of living shoreline projects aimed at boosting populations of native unionids.

ONTOGENIC SHIFTS IN MICROALGAL HANDLING BY *CRASSOSTREA GIGAS* LARVAE

Maria Rosa* and Dianna K. Padilla

Stony Brook University, Dept. of Ecology and Evolution, Stony Brook, New York 11794-5245, USA

Maria.rosa@stonybrook.edu

Most molluscs, including bivalves and gastropods, have a very small (~100-300µm) planktonic feeding larval stage (veliger), with specialized structures for capturing planktonic microalgal food. Early work on veliger larvae has generally found no selection among microalgal species at this stage. Larvae undergo a radical metamorphosis that produces juveniles (~300-500µm) with structures similar to adults, but much smaller, and much less is known about feeding at this stage. The objective of this project was to test for differences among algal species in particle capture rates for developing veligers (week-old versus month-old larvae). Five different microalgal species were fed to *Crassostrea gigas* larvae individually and in combinations, and particle capture rates (PCR) measured. Larvae were also preserved for scanning electron microscopy of feeding structures through development. Early in development, PCR was most affected by the size of the microalgae (mechanical constraints). Some microalgae (e.g., *Rhodomonas* sp.) were cleared at lower rates regardless of veliger age. In food choice experiments veliger age affected which microalgal species were generally rejected or ingested. Results indicate that, across development, properties other than size may affect which microalgae are ultimately ingested.

THE EFFECTS OF TAURINE ON MANGANESE ACCUMULATIONS IN GILL OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*

Rafael Santos[1]*, Emmanuel Agyei[2], Elvin Griffith, Jr.[3], Margaret A. Carroll[2], and Edward J. Catapane[2]

[1]Kingsborough Community College, 2001 Oriental Blvd., Brooklyn, New Yorik 11235 USA

[2]Medgar Evers College, 1638 Bedford Ave, Brooklyn, New York 11225 USA

[3]Notre Dame High School, 1 Notre Dame Way, West Haven, Connecticut 06516 USA

rafaelsantos2194@gmail.com

Taurine is a neuroprotective against some neurodegenerative diseases. Manganese causes Manganism, which often is confused with Parkinson's disease. Manganism has no effective treatment.

The eastern oyster, *Crassostrea virginica*, has a serotonergic-dopaminergic innervation of gill lateral cells (GLC). Manganese disrupts the dopaminergic innervation and taurine protects against this disruption. We hypothesize taurine reduces manganese accumulations in gill or enhances manganese removal from gill. This was tested by treating gills 2 days with taurine, manganese, or taurine and manganese (500 µM each) and analyzing samples by Atomic Absorption Spectroscopy. Manganese treatments caused higher manganese accumulations compared to controls or taurine treatments. Co-treated with taurine and manganese had no significant difference in manganese accumulations compared to manganese treatments alone suggesting taurine does not block manganese accumulation into gill. To determine if taurine removes manganese from gill, gills were treated 2 days with manganese (500 µM), rinsed, then treated 2 days with taurine or EDTA (0.5 to 2.5 mM each). EDTA was effective at removing manganese from gill (80% compared to controls). Taurine treatments were effective to a lesser degree, removing 25%. The study shows while taurine did not prevent manganese accumulations, it did remove manganese, similar to how chelating agents treat metal toxicity. Considering taurine is a natural biological component and shows success as a protective agent in other neurodegenerative diseases, more studies are needed to determine if taurine would be an effective and safer therapeutic agent for clinical treatment of Manganism.

COMPARTMENTALIZATION AND TEMPORAL DISTRIBUTION OF L-DOPA-CONTAINING PROTEINS INVOLVED IN OYSTER SHELL FORMATION

Benjamin Schmeusser*[1], Alyssa Outhwaite[1], Donald J. Kleppel[1], David Rivetti[1], Douglas C. Hansen[2], and Karolyn M. Hansen[1]

[1]University of Dayton, Department of Biology, 300 College Park, Dayton, Ohio 45469 USA

[2]University of Dayton, University of Dayton Research Institute, 300 College Park, Dayton, Ohio 45469 USA

schmeusserb1@udayton.edu

Marine molluscs, such as the eastern oyster (*Crassostrea virginica*), produce structural proteins that are essential in adhesive strategies and shell biomineralization. The unique properties of these proteins derive from the amino acid composition. L-3,4-dihydroxyphenylalanine (L-dopa), which is a unique key amino acid in the cross-linking of these proteins, can be considered a biomarker for identification and localization of shell formation proteins. The focus of this research was to determine the compartmentalization of L-dopa-containing proteins involved in the process of biomineralization in *C. virginica* at different time points during a shell repair event. Three organismal compartments were identified as possible locations of L-dopa precursor proteins: hemocytes, cell-free hemolymph, and mantle tissue. Hemolymph was harvested from the adductor muscle of notched oysters and hemocytes were subsequently collected via hemolymph centrifugation. Mantle tissue was collected from specific locations. The product of repair, nascent shell deposited in the notch, was collected at discrete time points post-notching. Amino acid composition related to time since notching was determined via anion exchange HPLC with pulsed amperometric detection. Additionally, the Arnow Assay (specific for catechols) was used to stain for L-dopa in the samples. Preliminary data reveal increased L-dopa concentrations in hemocytes and hemolymph at 24-48 hours and 96 hours post notching, respectively, indicating a mobilization of resources for shell repair. These data support the hypothesis that L-dopa-containing proteins are involved in oyster shell formation and that they are distributed at discrete locations within the organism.

HOW OYSTERMEN AND FISHERMEN USE AND THINK ABOUT OYSTERS IN THE ST. AUGUSTINE REGION OF FLORIDA

Carrie Schuman[1,2] and Shirley Baker[1]

[1]University of Florida, Fisheries and Aquatic Sciences, 7922 NW 71st Street, PO Box 110600, Gainesville, Florida 32653 USA

[2]University of Florida, School of Natural Resources and Environment, 103 Black Hall, PO Box 116455, Gainesville, Florida 32611 USA

carrie.schuman@ufl.edu

Oysters provide a multitude of services that can be tied to human wellbeing including direct shellfish harvest and the support of healthy local populations of finfish; however, data regarding provision of harvest within Florida can be limited and low-resolution in quality. Management decisions in support of maintaining or improving oyster harvest and fishing opportunities can benefit from additional information regarding stakeholder behaviors, perceptions, and values.

The goal of this research was to examine how recreational and commercial oystermen and fishermen targeting finfish near oyster beds use and think about oysters within the St. Augustine area. Participants were identified by snowball sampling and engaged in one-on-one semi-structured interviews. They answered a series of questions designed to elicit information about: what makes a desirable oyster bed; how beds in the region are used temporally and spatially; how use has changed over time and perceived barriers to access; and what benefits oysters have beyond harvest.

The interviewer recorded participant responses with permission and transcribed the results while anonymizing the identity of the interviewee. In cases where recording did not occur, the interviewer took detailed notes. Notes and transcribed interviews were analyzed in MaxQDA using qualitative content analysis to identify core ideas among participant responses. Researchers further grouped responses into themes that were qualitatively compared within and between groups. Data and conclusions from this analysis are presented.

EMERGING PATTERNS OF LATE SUMMER HARMFUL ALGAL BLOOMS IN THE LOWER CHESAPEAKE BAY

Gail P. Scott*, William M. Jones III, and Kimberly S. Reece

Virginia Institute of Marine Science, Department of Aquatic Health Sciences, The College of William & Mary, 1375 Greate Road, Gloucester Point, Virginia 23062 USA

gpscott@vims.edu

Late summer blooms of *Alexandrium monilatum* and *Margalefidinium* (formerly *Cochlodinium*) *polykrikoides* have been particularly intense and widespread throughout the lower Cheseapeake Bay in recent years. Laboratory bioassays have demonstrated acute dose dependent toxicity of these species to oysters at different stages of development. Local oyster culturists have reported to researchers at the Virginia Institute of Marine Science numerous juvenile oyster mortality events during and immediately following these blooms at grow-out locations in natural estuarine habitats. This has led to increased efforts in tracking bloom activity. A York River bloom in 2007 marked the re-emergence of *A. monilatum* in the mid-Atlantic since a couple reports of blooms during the 1960s. Blooms of *Margalefidinium polykrikoides* have occurred almost annually in the York for decades and throughout the southern bay since the early 1990s. Until 2011, *A. monilatum* blooms were largely localized in and near the York River with cell counts reaching into the thousands of cells/mL. During blooms in 2012-2016, *A. monilatum* cells were found at increasing concentrations into the bay mainstem, in many lower bay estuaries, as well as to the south along the North Carolina Outer Banks. These more recent *A. monilatum* blooms were increasingly nearly monotypic with low diversity community structure and cell counts reaching into the hundred thousand cells/mL. A predictable population progression occurs in the York River with peak cell concentrations of *M. polykrikoides* followed one to two weeks later by peak concentrations of *A. monilatum*.

SPATIAL VARIATION IN OYSTER SHAPE IN THE CHESAPEAKE BAY: IMPLICATIONS FOR SHELL CARBONATE BUDGETS

Melissa Southworth[1*], Roger Mann[1], James E. Wesson[3], Mitch Tarnowski[2], Mark Homer[2], William Reay[1], and John Thomas[1]

[1]Virginia Institute of Marine Sciences, The College of William and Mary, P.O. Box 1346 Gloucester Point, Virginia 23062 USA

[2]Maryland Department of Natural Resources, 580 Taylor Avenue, Annapolis, Maryland 21401 USA

[3]Virginia Marine Resources Commission, Newport News, VA 23607 USA

melsouth@vims.edu

Spatial variation in shape in Chesapeake Bay oyster populations was examined to address two questions: how does shape influence estimates of shell production rates, and can variation in shape be ascribed to clines in one or more environmental variables? Oysters were collected as part of annual fall surveys (sample size n = 25 oysters >30mm SL) in 2011-2013 (Maryland) and 2011-2016 (Virginia) from 22 and 21 reefs respectively in the Maryland (MD) and Virginia (VA) portions of the Bay. Estimates were made of individual length (SL), biomass (B), dry tissue weight (W), and shell weight (SW), and the shape relationships examined by allometric plots. Variation was observed in the b value of SW versus SL plots (y ($SW = a \times SL^b$) coincident with the variation from long, thin shelled individuals through rounded individuals with shell that increased in thickness with age. The MD reefs present a general continuum of decreasing values of a, with increasing values of b, the latter gradually increasing from 2.177 (all years) to 2.952. In VA, b values varied from 2.73 to 3.28. High r^2 values for both individual and multi-year reef plots indicate consistency of shape. Distinct regions of common shape emerge. For example, the James River can be described by three common shaped areas. Spatial variation was examined in relation to long-term environmental monitoring data. A substantial portion of the variation can be associated with salinity, although the role of localized fine sediments (indicative of high fine suspended sediment loads) may predominate at low salinity.

DUNGENESS CRAB TRAP CATCH EFFICIENCY RELATED TO ESCAPE RING LOCATION AND SIZE

George Stearns[1]*, Robert Conrad[2], David Winfrey[1], Nancy Shippentower-Games[1], and Deanna Finley[1]

[1]Puyallup Tribe of Indians, 3009 East Portland Avenue, Tacoma, Washington 98404

[2]Northwest Indian Fisheries Commission, 6730 Martin Way East, Olympia, Washington 98516

george.stearns@puyalluptribe.com

The Dungeness crab, *Metacarcinus magister* (*Cancer magister*), supports a commercially important fishery along the West Coast of the United States. Only male crabs above a certain size limit may be retained (i.e., legal-size males). Escape rings are used in traps to create circular holes that facilitate the release of both females and undersized males (sublegal crabs). Sublegal crabs that are retained in a trap can suffer stress, injury, and mortality. In this experiment, both the location and size of the escape ring were modified in an effort to reduce retention rates of sublegal crabs. Four different trap configurations were used: (1) a standard trap without escape rings (control configuration); (2) an unmodified trap with two 4.25-in-diameter escape rings on top (standard configuration); (3) a standard trap with one 4.25-indiameter escape ring placed in each corner adjacent with the bottom (modified 4.25-in configuration); and (4) a trap with two 4.5-in-diameter escape rings on top and one 4.5-in-diameter escape ring placed in each corner adjacent with the bottom (modified 4.5-in configuration). Two different catch statistics were compared among trap configurations: catch of legal-size= males and catch of sublegal crabs. No statistical difference was observed in the catch of legal-sized males in any trap configuration. Compared with the standard configuration, the two modified configurations caught significantly fewer sublegal crabs. Catches of sublegal crabs were not statistically different between the modified 4.25-in and modified 4.5-in configurations.

APPLICATION OF TRIPLOIDY TO AN EMERGENT OYSTER CULTURE INDUSTRY ON THE FLORIDA WEST COAST: RESULTS OF GROWER TRIALS

Leslie N. Sturmer[1]*, Carter Cyr[1], Reggie Markham[1], Nicholas Brandimarte[2], and Susan Laramore[2]

[1]University of Florida/IFAS, Shellfish Aquaculture Extension Program, Senator Kirkpatrick Marine Lab, 11350 SW 153rd Court, Cedar Key, Florida 32625 USA

[2]Florida Atlantic University, Harbor Branch Oceanographic Institute, Center for Aquaculture and Stock Enhancement, 5600 US Highway 1 North, Fort Pierce, Florida 34946 USA

Lnst@ufl.edu

To address increased interest in oyster aquaculture on the Florida west coast, a demonstration project was initiated which allowed for evaluation of an oyster breeding process to local conditions. The objectives were to document production performance and assess the health of diploid and triploid oysters, *Crassostrea virginica,* under commercial conditions. Oysters were provided to eight shellfish growers in four coastal counties, each receiving 2,500 triploid and diploid seed (average shell height [SH]: 22 mm) in July 2016. Several culture systems used by growers also provided for evaluation of site and gear interaction on ploidy type. After eight months of culture, triploid oysters (grower averages: 64.6-97.7 mm SH) were larger than diploids (64.8-83.0 mm SH) at five of the six participating farms, while wet meat weights of triploids (grower averages: 5.5-13.7 g) were greater than diploids (4.4-6.6 g) at four of the six farms. Survival was commercially acceptable in floating bags and adjustable longline systems as opposed to bottom cages. Differences in shell shape and fouling were observed by ploidy type, gear type, and farm location. The parasite, *Perkinsus marinus,* was not prevalent in any of the samples at harvest, whereas infestation of the mudworm, *Polydora websteri,* was found in both diploid and triploid oysters cultured over the summer months. To evaluate seasonal differences, diploid and triploid oyster seed were planted in March 2017 with harvest anticipated after eight months. This project resulted in increased awareness of the benefits of triploidy and accelerated adoption of a new bivalve species for culture.

THREE YEARS OF DISEASE MONITORING DATA OF *CRASSOSTREA VIRGINICA* (EASTERN OYSTER) IN RHODE ISLAND AND SURROUNDING STATES AND IMPLICATIONS FOR AQUACULTURE AND A CHANGING ENVIRONMENT

Allison Surian*, Abigail Scro, M. Victoria Agnew, and Roxanna Smolowitz

Roger Williams University, Aquatic Diagnostic Laboratory, One Old Ferry Road, Bristol, Rhode Island 02809 USA

asurian706@g.rwu.edu

The Aquatic Diagnostic Laboratory at Roger Williams University receives eastern oyster samples for disease evaluation as a routine part of services offered by the laboratory. For the past three years, the laboratory has used a quantitative PCR (qPCR) method to determine abundance of parasite infections in submitted oysters. Evaluation of the data shows increases in the number of *Perkinsus marinus* (Dermo) parasites that correlates positively with oyster size, the culture location and season of the year. *Haplosporidium costale* (SSO) was identified in animals from Rhode Island and some reports of morbidity and mortality have been associated with the infection in the past. *Haplosporidium nelsoni* (MSX) infections are identified in several samples but do not appear to be in high abundance and no associated mortality has been reported. The laboratory qPCR monitoring data forms the basis for understanding parasite infection intensity currently and is being used for oyster management and transport determinations. It is probable there will be an increase in the abundance and severity of disease caused by Dermo, MSX, and SSO in the future as the northeast coastal waters warm. These data will establish a baseline that can be used to identify changes.

THE IMPACT OF ATMOSPHERIC RIVER EVENTS ON *OSTREA LURIDA* AND *CRASSOSTREA GIGAS* DENSITIES IN SOUTHERN CALIFORNIA ESTUARIES

Holly Suther*, Jacob Javier, Brittany Cook, Shannon Chou, Daniel Jaques, Amber Jolly, William Hoese, and Danielle C. Zacherl

California State University, Fullerton, 800 N State College Blvd, Fullerton, California 92831 USA

hollysuther@csu.fullerton.edu

U.S. west coast estuaries support diverse communities that can be negatively impacted by changes in water quality. Atmospheric river (AR) events, long, narrow corridors of water vapor delivering heavy precipitation, can reduce the water quality in estuaries to levels lethal to oysters. For example, native *Ostrea lurida* densities declined significantly in San Francisco Bay following an extreme AR event that decreased salinities for a lethal duration (< 6 salinity for > 8 days). This study focused on southern Californian estuaries that support native oysters, *O. lurida*, and non-native oysters, *Crassostrea gigas*. It was hypothesized that AR events would produce extreme drops in salinity for lethal durations, as in San Francisco Bay, and *O. lurida* would show greater density declines than *C. gigas*. Density was measured for both species in December/January and May 2017 at two sites each within Newport Bay (NB) and San Diego Bay (SD). Four AR events impacted NB and three impacted SD between December 2016 and May 2017. Salinity and pH dropped below tolerance levels for non-lethal durations in SD. *Crassostrea gigas* density declined significantly at three of four sites; however, *O. lurida* showed no density change. Native *O. lurida* may be more acclimatized to local AR events than recently introduced *C. gigas*, or *C. gigas* declines may be due to another unknown factor. San Francisco Bay may be more susceptible to AR impacts on oysters by experiencing more extreme ARs and having a larger watershed; both can lead to more significant impacts on estuarine water quality.

MORE THAN THE EYE CAN SEE: GROSS VISUAL AND RADIOGRAPHIC OBSERVATIONS OF SHELL-BORING PARASITES IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*, REVEAL DYNAMICS OF SHELL DAMAGE

Shelby Thomas*[1], Andy Kane[2], Ross Brooks[2], Felipe Sanchez[2], and Hanzhi Gao[2]

[1]University of Florida, School of Natural Resources and Environment, Aquatic Pathobiology, Laboratory, PO Box 110885, Gainesville, Florida 32611 USA

[2]University of Florida, Department of Environmental and Global Health, Aquatic Pathobiology, Laboratory, PO Box 110885, Gainesville, Florida 32611 USA

Shelby.thomas.21@ufl.edu

Shell-boring parasites on oyster reefs can reduce shell density and increase shell surface area, contributing to accelerated shell erosion. Discerning prevalence and severity of shell parasites as part of a basic health assessment in restoration monitoring is, therefore, an important factor that may affect long-term reef stability and restoration outcomes. This project examined the effectiveness of ranking the severity of parasite shell damage in eastern oysters based on typical gross visual examination versus diagnostic radiography. Oysters (n=347), representing all size classes, were sampled from Apalachicola Bay during June of 2016, and shells were evaluated grossly and from x-rays using an established, ranked severity score (0-5), based on percent area affected. Radiographic observations provided higher (i.e., better) parasite severity scores than gross visual observation scores using identical ranking criteria. Mean severity scores based on radiographic, visual internal and visual external shell observations for *Polydora* were 3.9, 1.6 and 1.0; for *Diplothyra* were 1.7, 0.7, and 1.2; and for *Cliona* were 2.3, 0.7 and 1.6, respectively. On average *Polydora* visual ranks were 2.4 ranks lower than radiographs, *Diplothyra* inside were 1.0 and outside 0.4 ranks lower than radiographs, and *Cliona* inside 1.6 and outside 0.7 ranks lower than radiographs. Through statistical analysis, a multiplier was developed from radiographic data to apply to what is observed visually, allowing for a more accurate prediction of shell damage to be made. This would enable researchers to analyze oysters visually and be able to have a better estimate of parasite severity though applying this multiplier.

INFECTION DYNAMICS OF AN ACANTHOCEPHALAN PARASITE, *PROFILICOLLIS BOTULUS,* IN THE GREEN CRAB, *CARCINUS MAENAS,* ON THE COAST OF MAINE

Tyler Van Kirk[1*], Ian Bricknell[1], Olivia Joyce[1], Allyson Redcay[1], Molly Westbrook[1], Caroline Spangenberg[2], Rebecca Lopez-Anido[3], and Liza Gallandt[3]

[1]University of Maine School of Marine Sciences, Aubert Hall Rm. 360, Orono, Maine 04469-5706 USA

[2]University of Maine School of Biology and Ecology, Murray Hall, Orono, Maine 04469-5751 USA

[3]Maine EPSCoR, Corbett Hall rm. 444, Orono, Maine 04469-5717 USA

tyler.d.van@maine.edu

The European green crab, *Carcinus maenas,* is invasive to the coast of Maine, and has been proposed as sustainable bait for the lobster industry. This species is also the intermediate host of the Acanthocephalan parasite, *Profilicollis botulus*, and little is known about the infection dynamics of this parasite on the coast of Maine, including the possibility of cross-contamination with other crucial species. More information will allow ecologists and policy-makers to better understand the impact of the parasite on the coast of Maine.

Crabs were collected from May 2017 through August 2017 from three alternating locations on the Maine coast and tested for parasite prevalence and intensity. Preliminary data analysis examined the influence of a variety of factors on parasite infection dynamics. Crab sex, color morph, carapace width, parasite presence, and number of parasites were recorded. Fisher's Exact Tests and Kruskal-Wallis Tests were used for preliminary comparison of prevalence among different sub-samples.

Overall prevalence for the summer of 2017 was 17% for the entire coast, a slight increase from 14% the previous summer. Prevalence was significantly higher in the southernmost bioregion of Maine at 32%, followed by the mid-coast at 13% and the northernmost location at 10%, suggesting a temperature effect. Prevalence was significantly higher than average in females, red color morphs, and berried females. Intensity was highest in the southernmost site with an average of five cysts per infection. These data support the hypothesis that a changing environment could significantly impact host-parasite dynamics of green crabs on the coast of Maine.

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

Robin L. Varney* and Ami E. Wilbur

University of North Carolina Wilmington, Shellfish Research Hatchery, CREST Research Park, 5600 Marvin K. Moss Lane, Wilmington, North Carolina 28409 USA

varneyr@uncw.edu

Populations of the eastern oyster, *Crassostrea virginica,* along the Atlantic coast of the United States have been severely impacted by a variety of parasites over the past 60 years. Prevalence and intensity of three *C. virginica* protozoan parasites – *Perkinsus marinus* (Dermo), *Haplosporidium nelsoni* (MSX), and *Bonamia* sp. – were monitored in wild and cultured oysters over a two-year period using quantitative PCR (qPCR). Starting in February 2016, samples of 100 wild oysters were collected monthly from Masonboro Sound, North Carolina (NC). A line (HC5-9) of cultured oysters was sampled prior to deployment on the farm in July 2016 and monthly thereafter. Prevalence of *P. marinus* and *H. nelsoni* in wild oysters varied widely over the two-year sampling period, with peaks in prevalence of both parasites in August 2017 (93% and

97%, respectively). *Bonamia* sp. was rarely detected in the wild oyster samplings, with peak prevalence observed in March 2016 (16%). Intensity of infection (estimated by Ct value) was greatest in late summer 2017 for *P. marinus* and in late spring 2017 for *H. nelsoni*. Cultured oysters initially tested negative for all three parasites, but by fall 2016 all three parasites were detected with low prevalence and intensity. Prevalence and intensity of *P. marinus* and *H. nelsoni* remained low throughout the winter months, but gradually increased through late spring and summer with peak prevalence of both parasites observed in August 2017 (86% and 98%, respectively). No significant correlation was observed between any environmental parameter examined (temperature, salinity, chlorophyll-α) and parasite prevalence.

WASHINGTON DEPARTMENT OF FISH AND WILDLIFE MANAGEMENT ACTIONS FOR EUROPEAN GREEN CRAB IN WASHINGTON WATERS

Richard H. Visser II* and Jesse M. Schultz

Washington Department of Fish and Wildlife, Aquatic Invasive Species Unit, 1111 Washington St SE, Olympia, Washington 98501 USA

Richard.Visser@dfw.wa.gov

European green crab (EGC), *Carcinus maenas,* are a Prohibited Level 1 species in the State of Washington, which means they pose a high invasive risk and are a priority for prevention and expedited rapid response management actions. EGC are known to be voracious predators on several species of shellfish (Cohen et al. 1995, DFO 2011) and the concern is that this threat could affect Washington waters and the Shellfish industry if unchecked. Although there have been small populations of EGC along Washington's outer coast such as in Wilapa Bay and Grays Harbor since 1997, these populations have remained small and have not become significantly harmful. It is only in the last two years EGC have spread to new locations in the Puget Sound where the risk of establishment, ability for sustainable reproduction, and potentially far greater resources impacts have raised alarms. The Washington Department of Fish and Wildlife (WDFW) is the lead entity for management of EGC and works closely with Washington Sea Grant, U.S. Fish and Wildlife Service, tribes, shellfish growers, and the Canada's Department of Fisheries and Oceans to assess risk and implement management actions. This coalition has been extremely effective in both early detection of new EGC settlements and rapid response in controlling those populations to prevent reproduction and further spread.

EFFECTS OF REDUCED PH ON GROWTH AND CHROMOSOME LOSS IN TETRAPLOID OYSTERS *CRASSOSTREA VIRGINICA*

Brittany M. Wolfe* and Ami E. Wilbur

University of North Carolina- Wilmington, Shellfish Research Hatchery, Department of Biology and Marine Biology, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, North Carolina 28409, USA

bmw1382@uncw.edu

Oyster aquaculture is increasingly supplying oysters for consumption, to some extent due to the decline of wild oyster stocks. Triploid oysters have become a staple in the oyster industry due to their faster growth and reduced gamete production, allowing them to be sold year-round. Triploids are produced by crossing a diploid oyster (two sets of chromosomes) with a tetraploid oyster (four sets of chromosomes) creating a triploid oyster (three sets of chromosomes). Tetraploid oysters are polyploid, meaning they possess more than two sets of chromosomes, and are essential to the production of triploid oysters. Chromosome instability is a fundamental aspect of polyploid and can be challenging for tetraploid breeding programs. This study investigates the potential impacts of environmental stress on reversion by exposing four tetraploid families (with three replicates) to three different pH treatments, ambient, 0.2 pH units below ambient, and 0.4 pH units below ambient. Mortality is being monitored daily, while growth will be assessed biweekly. Chromosomal loss will be assessed at the beginning and end of the experiment. Preliminary observations suggest that the family is having a greater influence on the mortality than the pH treatments. Data collection is ongoing, and the results will be presented.

THE EFFECT OF SEDIMENTATION ON OYSTERS ADJACENT TO EELGRASS MEADOWS

Victoria R. Wood[1]*, Juliann C. Vannordstrand[1], Christine Whitcraft[2], Joseph Carlin[3], Katie Nichols[4], and Danielle C. Zacherl[1]

[1]California State University, Fullerton, Department of Biological Science, 800 N. State College Avenue, Fullerton, California 92834 USA

[2]California State University, Long Beach, College of Natural Sciences and Mathematics, 1250 N. Bellflower Boulevard, Long Beach, California 90840 USA

[3]California State University, Fullerton, Department of Geological Sciences, 800 N. State College Avenue, Fullerton, California 92834 USA

[4]Orange County Coastkeeper, 3151 Airway Avenue, Costa Mesa, California 92626 USA

victoria.wood@csu.fullerton.edu

Oyster and eelgrass beds both provide ecosystem services including providing refuge from predation, offering complex, three-dimensional habitats, and providing shoreline resiliency by buffering erosion. The California native oyster, *Ostrea lurida*, and the native eelgrass, *Zostera marina*, have declined over the past two centuries on the west coast of the United States. As part of a Living Shorelines initiative to restore these important habitats while promoting shoreline resiliency, this study seeks to restore oysters and eelgrass alone and adjacent to one another, and assess if oyster response is affected by eelgrass due to eelgrass-induced sediment deposition.

Four treatment blocks were established with restored eelgrass, oyster, oyster/eelgrass, and control plots each at four locations in Newport Bay, California. Eelgrass and oyster responses were mea-

sured by assessing oyster spatfall and recruitment, and eelgrass blade density. Sediment characteristics were measured using sediment pins.

After five months of erosive conditions, sedimentation did not differ among treatments, but there was accumulated sediment only on eelgrass and oyster/eelgrass plots. There was higher oyster spatfall on oyster and oyster/eelgrass plots as compared to control and eelgrass plots during weeks of highest spatfall; however, this translated into higher recruitment only on the oyster plot compared to the control plot. Based on preliminary findings, restoring oysters and eelgrass in adjacent restoration plots might not yield the most effective outcomes for oysters, possibly due to eelgrass-induced sedimentation. These results will help direct future restoration initiatives involving oysters and eelgrass.

THE EFFECT OF GEAR TYPE AND MANAGEMENT STRATEGY ON THE ACQUISITION OF PARASITES BY CULTURED OYSTERS (*CRASSOSTREA VIRGINICA*)

Johanna K. Woods*and Ami E. Wilbur

University of North Carolina-Wilmington, Shellfish Research Hatchery, Department of Biology and Marine Biology, Center for Marine Science, 5600 Marvin K. Moss Lane, Wilmington, North Carolina, 28409 USA

jkw2295@uncw.edu

Parasites such as *Haplosporidium nelsoni* (MSX) and *Perkinsus marinus* (Dermo) have been an ongoing challenge for eastern oyster (*Crassostrea virginica*) aquaculture. Strategies including use of resistance lines of oysters have been presented as one way to mitigate the impacts. Another approach may be to utilize different gear and management strategies. This study monitored prevalence and intensity of *Haplosporidium nelsoni* and *Perkinsus marinus* in three different gear types (floating cages, flip bags and bottom cages) at three locations (Masonboro Sound, Cedar Island Bay, Roanoke Sound) in North Carolina. Each gear was replicated (n=3) at each site. Oysters in floating cages were exposed twice monthly for 12 hours, whereas oysters in the flip bags were constantly submerged in surface waters (<8 inches) and at depth in bottom cages. Oysters (n=25) were sampled at deployment (6 months post spawn) and at 3, 9, and 12 months post deployment, each sample was analyzed by quantitative PCR for the presence of the parasites. Initial prevalence of the parasites were modest (9±3% positive for *Haplosporidium nelsoni*, 21±7% positive for *Perkinsus marinus*), but increased substantially in some gears and on some farms over time. The results of these analyses will be presented.