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ABSTRACTS OF TECHNICAL PAPERS

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POSTERS

PERFORMANCES OF TWO DISEASE-TOLERANT OYSTER STRAINS IN THE PATUXENT RIVER, MARYLAND 2003-2007. George R. Abbe[1], Carol B. McCollough[2], Linda S. Barker[3], and **Christopher F. Dungan[2].** [1]Morgan State University Estuarine Research Center, St. Leonard, MD, 20685 USA; [2]Cooperative Oxford Laboratory, Oxford, MD 21654 USA; [3]Maryland Department of Natural Resources, Annapolis, MD 21401 USA.

Extreme mortalities occurred among a standard strain of specific-pathogen-free (SPF) *Crassostrea virginica* at three sites in the Patuxent River, Maryland during the 2000-02 drought, when salinities ranged from 12–16‰. These mortalities led to our search for improved performances from available disease-tolerant native oyster strains. SPF spat of disease-tolerant CROSBreed and DEBY strains, alongside a standard strain, were deployed in September 2003, at the same experimental sites, and sampled until September 2007. Salinities were below normal during the first two years, slightly above normal during the third and near normal during the fourth, but with a steady increase from May to September 2007. Mean 4-year growth was better for all strains combined at the mid-river (91.8 mm) and down-river (86.6 mm) sites, compared to upriver (75.7 mm), probably because of occasional marginal salinities upriver during the first 2 years. Four-year growth of DEBYs (93.3 mm) was better than for CROSBreeds (81.3 mm) or standards (68.9 mm) based on shell-height increases. After 4 years, both disease pressure from *Perkinsus marinus* and mortalities had increased. Mortalities across sites were greatest for CROSBreeds (32.7%), followed by standards (27.7%), and were lowest for DEBYs (17.3%). Overall, DEBYs outperformed both CROSBreeds and standards.

THE FINANCIAL COSTS ASSOCIATED WITH BIOFOULING CONTROL IN SHELLFISH CULTURE. Chuck Adams[1], Sandra E. Shumway[2], and **Robert Whitlatch[2].** [1]University of Florida; [2]University of Connecticut.

The costs associated with controlling biofouling in marine shellfish culture systems can be significant. This is particularly true for those systems which utilize the water column for the production process, such as rope, cage, and suspended net systems. This study examined the financial implications associated with bio-fouling in marine shellfish culture systems. A survey was conducted with commercial marine shellfish aquaculturists in the US. These operations predominantly culture clams, oysters, and mussels, and utilize a variety of culture methods. Survey recipients were asked to consider the financial implications of biofouling on their culture system. Survey recipients were asked to describe how biofouling affected their production, including impacts on growth rate, harvest size, yield, etc. Survey recipients were asked to provide an estimate of the annual costs associated with bio-fouling control. Similar questions were posed regarding the impact that bio-fouling has on the marketability of the harvested product. The responses provide insight into the differential effects that biofouling has on commercial shellfish culture operations, when considering species cultured, production method utilized, culture location, targeted market, and other factors. This information will be useful when considering the efficacy of future innovative methods for controlling biofouling in shellfish culture operations within the U.S.

COMPARISON OF GEOGRAPHIC INFORMATION SYSTEM (GIS) ANALYSIS OF PATENT TONG AND BAR CLEANING OYSTER POPULATION ESTIMATES IN THE UPPER CHESAPEAKE BAY. Steven Allen and **Kennedy T. Paynter Jr.** University of Maryland College Park, Biology Department, College Park, MD, 20742, USA.

The accuracy and comprehensiveness of oyster (*Crassostrea virginica*) population estimates in the Chesapeake Bay are of vital importance to current and future restoration efforts. In an attempt to lower transmission of disease, oyster bars are dredged prior to new plantings. Bar cleaning dredges provide an opportunistic prospect for ground-truthing GIS spatial analysis applied to patent tong survey estimates of oyster bar populations. Six oyster bars were surveyed using patent tongs before bar cleaning dredge efforts in 2006 and 2007. Patent tong data was interpolated using ArcGIS spatial analyst tool, to determine pre-dredge oyster bar populations. Number of oysters available for removal per bar was calculated from these estimates. GIS estimates were then compared to the actual number of oysters collected during the exhaustive dredgeing effort (uncorrected and effort-corrected by Leslie and DeLury models). Correlation between the patent tong/GIS and the DeLury bar-cleaning estimate was significant ($r = 0.8850$; $P = 0.0460$), as was the correlation between the patent tong/GIS and the raw number of oysters removed ($r = 0.8956$; $P = 0.0399$); a significant linear regression was created to predict bar population from the GIS estimate ($P < 0.05$). Our data suggest patent tong subsampling with concordant GIS analysis may be a powerful population estimation tool with proper calibration.

INTERTIDAL OYSTER HABITAT ASSESSMENT AND MANAGEMENT USING GIS, GPS AND REMOTE SENSING. William D. Anderson and **Guy M. Yianopoulos.** South Carolina Department of Natural Resources, Charleston, SC 29412 USA.

South Carolina's approximately 700,000 acres of wetlands and estuarine area support intertidal oyster (*Crassostrea virginica*) populations dispersed along shorelines, in feeder creeks and throughout expansive intertidal flat areas. Habitat propagation (cultivation and harvesting), restoration and closing areas to harvesting are most efficiently managed by GIS. In addition, GIS is used to maintain contemporary water quality cartographic data, shellfish management categories, generate commercial and recreational harvesting maps and identify optimum locations for habitat restoration.

Results of a state-wide intertidal oyster remote sensing project using 0.25 m^2 resolution multi-spectral digital imagery, *in situ* GPS, low altitude ground-truthing and how these components are integrated into the GIS is discussed. Contemporary habitat assessments, along with historical shellfish resource data (1890s and 1980s), are used to identify changes in the state's shellfish populations and monitor large-scale enhancement and restoration projects.

ABALONE VIRAL GANGLIONEURITIS IN SOUTH EASTERN AUSTRALIA—A WAKE UP CALL. **Peter Appleford[1], Mehdi Doroudi[2],** and **Paul Hardy-Smith[3].** [1]Department of Primary Industries, Fisheries Victoria, Melbourne, Victoria, 3000, Australia; [2]South Australian Research and Development Institute, Adelaide, South Australia, 5000, Australia; [3]Panaquatic Health Solutions Pty Ltd, Hawthorn, Victoria, 3122, Australia.

In December 2005 unusual mortalities were identified in farmed abalone in Victoria, south eastern Australia. The causative agent was found to be a herpes-like virus affecting the neural ganglion, abalone viral ganglioneuritis (AVG). Visually it results in curvature of the foot and swelling of the mouth area. In May 2006 AVG was identified in wild populations. Mortality levels typically range between 30% to 90%, varying between and within reefs. A "best fit" scenario indicated AVG was most likely introduced to the farms from wild stocks. Transmission studies found AVG was spread via direct contact and water, with infectivity readily reduced by dilution. In the field AVG travelled up to several kilometres indicating it was moving on agents in the water. Specific biosecurity protocols have been developed and implemented for all sectors, including recreational fishers. Allowable catch is being set using annual stock assessments with improved spatial modelling at the reef scale. Spatial closures and increased size limits are also being considered. Research efforts are focussing on biosecurity, stock rebuilding and epidemiology. This is a wake up call for fisheries and aquaculture in Australia.

VARIATIONS IN BAY SCALLOP (*ARGOPECTEN IRRADIANS*) STOCK DISTRIBUTION AND ABUNDANCE IN FLORIDA: TEMPLATE FOR RECOVERY. **William S. Arnold.** Florida FWCC Fish and Wildlife Research Institute, St. Petersburg, FL 33701 USA.

The past 50 years have been characterized by unprecedented human population growth and associated development along the coast of Florida. Resultant impacts on nearshore marine species such as the bay scallop (*Argopecten irradians*) are undeniable and to some extent irreversible. Prior to 1994, information on the status of bay scallop stocks in Florida were anecdotal at best, but since 1994 annual surveys have been conducted at a variety of locations within the remaining range of the species in Florida to characterize interannual fluctuations in distribution and abundance. Results of those surveys suggest that bay scallops are remarkably resilient to habitat and water quality alterations, and that complex ecological interactions synergistically contribute to the observed long-term collapse of local scallop populations. Identifying those key ecological interactions and their contribution to continued collapse of local populations provides opportunities for rebuilding those populations and thereby reinvigorating and stabilizing the overall metapopulation in Florida. In particular, it appears that a consistent lack of adequate larval supply to specific local populations, influenced by complex hydrodynamic patterns, prevents population resurgence at those locations. Restoration efforts focused on reestablishing larval supply are a viable option for rebuilding those local populations and thereby increasing metapopulation stability.

THE DELAWARE BAY SHELL PLANTING PROGRAM AFTER 3 YEARS: RECRUITMENT ENHANCEMENT AND CARBONATE BUDGET. **Kathryn Ashton-Alcox[1], Eric Powell[1], Jason Hearon[2], Russell Babb[2], Gulnihal Ozbay[3],** and **Richard Cole[4].** [1]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ 08349; [2]New Jersey Department of Environmental Protection, Bureau of Shellfisheries, Port Norris, NJ 08349; [3]Delaware State University, Department of Agriculture, Dover, DE 19901-2277; [4]Delaware Department of Natural Resources and Environmental Control. Division of Fish and Wildlife, Dover, DE 19901.

Three consecutive years of planting shell on the oyster beds of the Delaware Bay have proven very successful in two of the primary goals of any oyster restoration program: first, in enhancing recruitment of young oysters (spat) by supplying clean shell at the right time in carefully chosen places and second by the stabilization of the shell structure in those areas. In 2005 and 2006, shell plants contributed 14–58% of the recruitment on targeted New Jersey oyster beds. The ratio of spat to older oysters increased in these areas by factors of 1.1–2.4 over natural recruitment. Planted shell outperformed natural shell in recruitment rate when added in a timely fashion. In 2007, recruitment was high and later than normal resulting in planted shell recruitment approximating that of native shell. Thus, shell remains 'clean' for a limited time. Shell is not a permanent resource. The Delaware Bay oyster beds have experienced a period of declining surficial shell content as the loss of carbonate exceeds the addition from the reduced populations present. In the past three years, planted areas of the Bay have shown a net increase in shell, putting these beds back into carbonate balance.

INVESTIGATION OF *BONAMIA* SP. TRANSMISSION AMONG, AND INCIDENCE IN, *CRASSOSTREA ARIAKENSIS*. **Corinne Audemard[1], Ryan B. Carnegie[1], Kristina M. Hill[1], Charles H. Peterson[2],** and **Eugene M. Burreson[1].** [1]Virginia Institute of Marine Science, Environmental and Aquatic Animal Health, Gloucester Point, VA, 23062, USA; [2]University of North Carolina at Chapel Hill, Institute of Marine Sciences, Morehead City, NC 28557, USA.

Laboratory experiments in 2007 yielded new insights into the biology of *Bonamia* sp. infecting *Crassostrea ariakensis*. In one trial, naïve *C. ariakensis* developed *Bonamia* sp. infections after

exposure to infected *C. ariakensis*, suggesting that transmission may be direct as has been postulated for other *Bonamia* spp. In a second trial, we investigated *Bonamia* sp. incidence. Naive *C. ariakensis* were deployed in North Carolina, where *Bonamia* sp. is enzootic, and subsets were returned to ourquarantine laboratory after 4, 7, 14, 21 and 28 days exposure. Each subset was then placed with uninfected *C. ariakensis* to assess potential transmission and maintained under warm euhaline conditions for several weeks. Samples were preserved for PCR and histology both upon arrival at the laboratory and also at the end of the experiment. Although histology results are still being gathered, *Bonamia* sp. DNA was detected by PCR in oysters directly from the field after 2 weeks exposure. At the end of the experiment, however, *Bonamia* sp. could be detected by PCR (>30% prevalence) in samples returned at all time points, while cohabitating, previously unexposed *C. ariakensis* remained *Bonamia*-negative. These results highlight the remarkably rapid rate of *Bonamia* sp. infection acquisition by *C. ariakensis*.

DESCRIPTION OF THREE NEW PARASITIC WORMS ASSOCIATED WITH ABALONE SPECIES CULTURED IN CHILE AND WITH NATIVE MOLLUSCS. **Fabian Aviles B.** Aquagestión, Av. Parque Antonio Rabat Sur 6165, Vitacura, Santiago, Chile, 7660118.

This work is a review of three recent findings of parasite worms affecting the shells of abalone cultured in Chile (*Haliotis rufescens* and *H. discus hannai*) and other mollusks in Chile. One of the descriptions is the first report of the presence of sabellids from the genus *Oriopsis* forming tubes in the shells of Japanese abalone, *Haliotis discus hannai*, and the first record in shells of two species of Chilean native gastropods (*Fissurella* sp. and *Concholepas concholepas*). The main differences between this sabellid and *Terebrasabella heterouncinata* are described. The second work is the first report of polychaetes from the genus *Dodecaceria* forming galleries in the shell of the red abalone *Haliotis rufescens*. Previously, this Cirratulid was associated with the shells of the gastropod mollusks *Fissurella maxima* and *Concholepas concholepas*, in the bivalve *Aulacomya ater*, and in the shell of the barnacle *Austromegabalanus psittacus* in Chile. The last description is a record of phoronides (Phylum Phoronida) forming numerous quitinous tubes in the shells of the red abalone (*H. rufescens*). Only *Phoronis ovalis* has been previously recorded in Chile perforating the shell of Chilean abalone, *C. concholepas*, in samples from the coastal rocks of Mehuin, Valdivia (Arenas, 1972).

THE DELAWARE BAY OYSTER (*CRASSOSTREA VIRGINICA*) RESTORATION PROGRAM. **Russell M. Babb[1], Jason Hearon[1], Craig Tomlin[1], David Bushek[2], Kathryn Ashton-Alcox[2],** and **Eric Powell[2].** [1]New Jersey Department of Environmental Protection, Bureau of Shellfisheries, Port Norris, NJ 08349, USA; [2]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ, 08349, USA.

In 2007, natural oyster production on Delaware Bay seed beds increased in abundance for the first time since 2000, following years of exceptionally low recruitment. The potential for higher settlement continues to occur in the bay when suitable substrate is available. In 2003, the NJDEP conducted a pilot-scale program where spat was captured increasing early recruitment 75-fold and increased the industry TAC 26 percent. Based in large part on the success of this small project, federal funding support was secured by the Oyster Industry Revitalization Working Group (OIRWG) for activities in 2005, 2006 and 2007. Envisioned as a five-year program, years 1 and 2 resulted in a total of 780,000 bushels of shell being planted in the bay region. These shell plants accounted for more than 50 percent of the total recruitment in the bay regions where planting occurred. As a consequence, the NJ oyster allocation was the third largest since 1996. Year 3 resulted in greater than 675,000 bushels of shell being planted in NJ and DE waters. As of this writing, early monitoring indicates a significant setting event has occurred bay-wide.

TEN YEARS OF HACCP AND SHELLFISH: AND THE WINNER IS…. Nancy C. Balcom[1]. [1]Connecticut Sea Grant College Program, University of Connecticut, 1080 Shennecossett Road, Groton CT 06340 USA.

For more than ten years, The U.S. Food and Drug Administration (FDA) has required all domestic and imported fish and fishery products, including shellfish, to be processed under a Hazard Analysis and Critical Control Point (HACCP) program to minimize food safety risks to consumers. Shellfish sanitation, handling, and processing were already regulated under the National Shellfish Sanitation Program (NSSP), administered by the states in partnership with the FDA and the shellfish industry, as part of the Interstate Shellfish Sanitation Conference (ISSC). The ISSC adopted the "HACCP regulation" and incorporated it into the NSSP Model Ordinance. What has been the outcome? Results of a brief survey, undertaken to gather qualitative assessments of New England shellfish sanitarians, shellfish industry members, and HACCP instructors of the impact of HACCP programs on shellfish operations and shellfish regulators over the past ten years, will be discussed.

FROM ALLIGATOR WEED TO WAPATO: WILL INVASIVE CHANNELED APPLE SNAILS EAT US OUT OF HOUSE AND HOME? Shirley M. Baker[1], Frank Zimmanck[1], and **Patrick Baker[1].** [1]University of Florida, Department of Fisheries and Aquatic Sciences, Gainesville, Florida, 32653, USA.

The channeled apple snail, *Pomacea insularum*, is a common nonindigenous species in many parts of the world and is considered an important consumer of aquatic macrophytes. Twenty-two freshwater plant and alga species were presented to naïve *P. insularum*, in laboratory trials, using single-snail replicates and simultaneous no-snail control. *P. insularum* damaged at least half of the replicate plants for 16 species and, for 14 of these species, we were able to calculate ash-free dry weight-specific feeding rates of *P. insularum* on the plant species. The most heavily consumed species were two native taxa: frog's bit (*Limnobium spongia*, 0.744 $g \cdot g^{-1} \cdot d^{-1}$) and musk grass (*Chara* sp., 0.478 $g \cdot g^{-1} \cdot d^{-1}$). Other heavily consumed species included the nonindigenous torpedo grass (*Panicum repens,* 0.306 $g \cdot g^{-1} \cdot d^{-1}$) and hydrilla (*Hydrilla verticillata,* 0.292 $g \cdot g^{-1} \cdot d^{-1}$); and the native wapato (*Sagittaria latifolia,* 0.257 $g \cdot g^{-1} \cdot d^{-1}$) and southern naiad (*Najas guadalupensis*, 0.225 $g \cdot g^{-1} \cdot d^{-1}$). Nonindigenous water hyacinth (*Eichornia crassipes)* was consumed at a lower rate (0.053 $g \cdot g^{-1} \cdot d^{-1}$) while nonindigenous taro (*Colocasia esculenta*) and water lettuce (*Pistia stratiotes*) were not consumed at detectable levels. Our results indicate that in "natural" ecosystems with both native and nonindigenous plants, *P. insularum* cannot be relied upon as an agent for biological control of nonindigenous species and may heavily impact native aquatic plant species.

EFFICACY OF BAR CLEANING AS AN OYSTER DISEASE MANAGEMENT STRATEGY. Linda S. Barker. Maryland Department of Natural Resources.

Since 2001, the Maryland oyster reserve system has employed watermen to rehabilitate oyster bars by dredging existing shell, removing all possible oysters, then planting hatchery-produced spat-on-shell. By 2006, "bar cleaning" was considered suspect as a disease management strategy by the scientific and management communities and the public. Subsequent 2007 MD legislation mandated that MDDNR conduct a review.

Disease data indicate that cleaned bars do not show significantly different levels of dermo disease from untreated bars. Oysters planted on bar cleaned mid-river sites reached background disease levels within 1 year during the 1999–2002 drought. A 2007 study of paired sites (bar cleaned/not bar cleaned) with 2-year-old post-drought plantings showed no differences in dermo prevalence among sites or treatments.

Bar treatment records indicate that several principles of disease management were violated. (1) Bar cleaning was conducted as a "site" treatment, leaving areas with diseased mature oysters adjacent to cleaned areas. (2) Bar cleaned oysters were moved elsewhere in the same river (for future harvest), not removed from the system. (3) Poor/no records were kept of bar cleaning activities. (4) Although conducted as a disease management strategy, no scientifically-designed study or monitoring was conducted to validate effectiveness.

OYSTER REMOVAL EFFICIENCY OF DISEASE BAR CLEANING. Linda S. Barker. Maryland Department of Natural Resources, Annapolis, MD 21401.

Oyster removal data from four bars "disease bar cleaned" by professional watermen in the Chester and Choptank Rivers were analyzed to determine removal efficiency. In the bar cleaning process, oyster boats move in random patterns above the bar and use a power dredge to pull up existing shell. All possible oysters are removed and the shell is dumped overboard. The process continues until the dredge hauls contain little to no oysters. Leslie and DeLury models were used to estimate initial population, from which initial density and removal efficiency were calculated. Estimates of removal efficiency showed excellent agreement between models (minimum difference of 4%). The DeLury model provided more stable estimates of removal efficiency among bars (68–77%), typical of models that use logarithmic relationships. Results indicated that 18–29% of the stock remained on the infected bars after cleaning.

INTERSPECIFIC INTERACTIONS IN OYSTER REEF COMMUNITIES: THE EFFECT OF ESTABLISHED EPIFAUNA ON OYSTER LARVAL RECRUITMENT. Brian B. Barnes, M. W. Luckenbach, and **P. R. Kingsley-Smith.** Eastern Shore Laboratory, Virginia Institute of Marine Science, Wachapreague, VA 23480 USA.

Restoring degraded oyster reefs for fisheries and ecosystem services typically involves the addition of substrate for oyster settlement. These substrate additions are often carried out in coastal habitats where hard substrate is limiting, without consideration of how the colonization of these substrates by other organisms may affect oyster settlement and survival. Interspecific adult-larval interactions have been studied extensively in a variety of environments, generally revealing inhibition of larval settlement by adults. Most of the research involving epifauna, however, has been conducted on artificial plates, which show different settlement patterns to natural substrates.

We investigated the settlement of native (*Crassostrea virginica*) and non-native (*C. ariakensis*) oyster larvae in response to naturally-occurring epifauna on oyster shell substrate. Hatchery-reared larvae were exposed to reef-collected shells in a suite of laboratory microcosm experiments. The presence of adult bryozoans and boring sponges tended to slightly inhibit settlement. However, larval settlement was significantly facilitated by barnacle treatments: proportional to barnacle density for *C. ariakensis* larvae, yet density independent for *C. virginica* larvae. These species-specific differences merit further examination given proposals to introduce *C. ariakensis* to the Chesapeake Bay. The present study should be informative to oyster restoration managers deciding where substrate additions are most needed.

BENTHIC INVERTEBRATE COMMUNITIES ASSOCIATED WITH DEEP-WATER CRASSOSTREA GIGAS FARMS IN BRITISH COLUMBIA, CANADA. **P. A. G. Barnes** and **S. E. Switzer.** Centre for Shellfish Research, Malaspina University-College, Nanaimo, B.C. V9R 5S5, Canada.

The effects of biodeposition from two deep-water, suspended *Crassostrea gigas* farms in British Columbia were studied over a twelve-month period. The two farms were sited in areas with different hydrography and bathymetry but had oysters of comparable age. The effects of farm biodeposition on benthic faunal community composition, as well as the effects on sediment physical and geochemical parameters, were studied. At each of the sites, 7 stations (including 2 reference stations and 1 station under an oyster raft) were located along a transect that ran through the centre of the oyster farm, parallel to the dominant current direction. In addition to an initial hydrographic survey, 27 parameters were measured at the 7 stations at each site, on quarterly field trips; parameters included deposition rates, water column characters and benthic variables. The benthic faunal communities were studied using underwater video cameras and benthic grabs. The benthic invertebrate community at the raft station at each site showed no sign of faunal impoverishment. However, the benthic invertebrate community structure at the raft station was distinct from that at the other stations, due largely to the abundance of hard-substrate fauna. The role of biodeposition and benthic impact, related to deep-water *C.gigas* culture, in structuring benthic invertebrate communities is discussed.

FIELD TESTS TO EXAMINE THE INTERACTIVE EFFECTS OF ADULT CLAM DENSITY AND PREDATOR EXCLUSION ON JUVENILES OF THE SOFT-SHELL CLAM, *MYA ARENARIA*. **Brian F. Beal.** University of Maine at Machias, Environmental & Biological Sciences Division, Machias, Maine 04654 USA.

Two field experiments were conducted at an intertidal mudflat in Stockton Harbor, Stockton Springs, Maine (Penobscot Bay) during the summer and early fall of 2007 to assess the interactive effects of adult clam density and predator exclusion on the density and size-frequency distribution of wild juveniles of the soft-shell clam, *Mya arenaria*. The study site contained no native adult clams. The first experiment incorporated four treatments assigned randomly to large, 240-m^2 plots: no clams/netting absent; no clams/netting present; clams present/netting absent; clams present/netting present. Experimental animals ranged from 48–75 mm SL, and were seeded at a density of 35/m^2. After 103 days (July 15–October 25) core samples were taken from each of five replicate plots/treatment. Presence of adults had no effect on density of wild spat (2–15 mm SL); however, netting resulted in a 7-fold enhancement of wild spat compared to controls. Smaller, 1-m^2 plots (both open and netted), were used in the second experiment with adult clam densities at 0, 50, 100, and 200 m^{-2}. Core samples taken after 103 days demonstrated a significant (positive) effect of adult clam density ($P = 0.047$) on numbers of wild spat, and a 4-fold enhancement in netted vs. unnetted plots.

EXPERIMENTAL TRIALS ON THE NURSERY CULTURE, OVERWINTERING, AND FIELD GROWOUT OF CULTURED HARD CLAMS IN EASTERN MAINE. **Brian F. Beal[1], George Protopopescu[2], Katy Yeatts[2],** and **Joseph Porada[3].** [1]University of Maine at Machias, Environmental & Biological Sciences Division, Machias, Maine 04654, United States; [2]Downeast Institute for Applied Marine Research & Education, Beals, Maine 04611, United States; [3]Egypt Bay Sea Farms, Blue Hill, Maine 04614.

The first-ever field trials using cultured individuals of the northern quahog, *Mercenaria mercenaria*, were conducted in eastern Maine (Washington & Hancock county) in 2006–2007 to assess growth and survival in cold-water nursery and growout settings. Also, we examined the effects of intraspecific density on overwintering survival under flow-through conditions over 177 days. Nursery growout at Mud Hole Cove, Great Wass Island, Beals, Maine (July 5–6 to November 16, 2006) used 2 mm seed added to 1.1 m^2 wooden (floating) trays lined with nylon window screening at four stocking densities from 2,500–10,000 animals per tray ($n = 20$). Survival exceeded 99%; however, stocking density had a significant negative effect on final mean SL (8.4 ± 0.13 mm vs. 7.6 ± 0.22 mm). In November, animals were placed in soft bags constructed of window screening (masses = 0.6, 1.2, and 1.6 kg, or 3,400, 6,720, and 8,960 individuals/bag) and held until the following May. No shell growth occurred; however, survival rates were excellent (>95%). Individuals were planted (600 m^{-2}) at Trenton (Hancock; May 20, 2007) and Cutler (Washington; 19 June 2007) and the fate of these animals followed for 6-7 months. Final mean SL ranged from 15–18 mm.

SHELLFISH AT RISK: A GLOBAL ASSESSMENT OF DISTRIBUTION, CONDITION AND THREATS TO HABITAT-FORMING BIVALVES. **Michael W. Beck[1], Robert D. Brumbaugh[2], Alvar Carranza[3], Loren D. Coen[4], Omar Defeo[3], Hunter S. Lenihan[5], Mark W. Luckenbach[6], Caitlyn Toropova[1],** and **Jeffrey S. Vincent[7].** [1]The Nature Conservancy, University of California Santa Cruz, Long Marine Lab, Santa Cruz, CA 95060 USA; [2]The Nature Conservancy, University of Rhode Island Bay Campus, Narragansett, RI 02882 USA; [3]Marine Science Unit, Ecology Department, Faculty of Sciences, Igua 4225 Street, 11400 Montevideo, Uruguay; [4]Sanibel-Captiva Conservation Foundation, 900A Tarpon Bay Rd. Sanibel, FL 33957; [5]Donald Bren School of Environmental Science and Management, Bren Hall 3428, University of California, Santa Barbara CA 93106 USA; [6]Eastern Shore Laboratory, Virginia Institute of Marine Science, College of William and Mary, Wachapreague, VA 23480 USA; [7]Jackson School of Geosciences, University of Texas at Austin, University Station Box X, E0620 Austin, TX 78713-8924 USA.

Shellfish-dominated habitats are potentially the most impacted of all estuarine or marine ecosystems on the planet. Impacts and condition are most often reported on for individual bays, hindering the development of comprehensive management or restoration

strategies. A collaborative "Shellfish Reefs at Risk Assessment" was initiated to describe the global distribution, condition and most significant threats to native bivalves that provide structured habitat for other species. A global geospatial database was developed for key reef-building shellfish species, facilitating an assessment of condition and threats based on literature reviews and expert surveys. Preliminary returns reveal some important trends. Where data enabled a quantitative assessment of change in abundance or condition, more than half of respondents surveyed indicated recent declines (<50 years) of at least 90% for an array of species in North America, Europe and Australia. Fishing was the number one driver cited for this change, with water quality, diseases, invasive species, and habitat destruction also among the top five drivers. These factors were cited more than twice as frequently as any other factors examined. In the final phase, we are attempting to model current condition against threats such as population density, sediment inputs and pollutant loading at a global scale.

PRECISION AQUACULTURE: DETERMINING OPTIMUM SEEDING LEVELS. Peter Becker and **Carl Barringer.** Little Skookum Shellfish Growers LLC.

Little Skookum Shellfish Growers established the first West Coast hatchery seed based Manila clam farm, carefully monitoring the populations and production on a 2.19 ha bed over 30 years. Between 1982 and 1994, we maintained base line population diversity, size class structure of Manila clams prior to seeding and a harvest rate of between 40,000 kg/ha/yr and 45,000 kg/ha/yr, with an annual addition of 2×10^6 6–8 mm hatchery seed. After 1994, we instituted programs to determine the maximum rate of Manila clam seeding to achieve no net gain in the harvest and/or standing stocks on the beach while still maintaining biodiversity seen in 1977. We used two separate methods: empirical trial seeding and numerical modeling. Optimal empirical seeding rate for this bed is between 6×10^6 and 8×10^6 6–8 mm Manila clam seed planted in small batches of ~1 million between February and October for a harvest of 85–90,000 kg/ha/yr. Numerical modeling, built on previous studies, to verify the physiological requirements of this production rate and its approach to the carrying capacity of the system is presented. This technique can help establish optimal seeding levels for a commercially harvested shellfish beach while still maintaining sustainable mollusk population ecology.

BAY SCALLOP (*ARGOPECTEN IRRADIANS*) GENETIC POPULATION STRUCTURE IN THE FLORIDA GULF: METAPOPULATION DYNAMICS SHAPED BY OCEAN CURRENTS. Theresa M. Bert[1], Ami Wilbur[2], Seifu Seyoum[3], and **William Arnold[1].** [1]Florida FWC Fish and Wildlife Research Institute, St. Petersburg, Florida 33701, USA; [2]Univerisity of North Carolina, Dept. of Biology, Wilmington, North Carolina 28403, USA; [3]Georgia Institute of Technology, Atlanta, Georgia 30332, USA.

Bay scallops (*Argopecten irradians*) in the nearshore Gulf of Mexico off Florida belong to a different subspecies and have different population dynamics than bay scallops in the northwest Atlantic Ocean. Their genetic population structure reflects their distributional response to both regional and local current patterns and the degree of connectivity of suitable habitat. A relatively stable and abundant population exists off northwest peninsular Florida in an area of a permanent, seasonally variable oceanic gyre. More ephemeral and variable populations extend northwestward into the Florida panhandle and southward to the Florida Keys. The core population is genetically stable over time and is closely related to all populations in the Florida Gulf except the Florida Bay population, which is genetically unique and may be a distinct subspecies. Peripheral populations have statistically different genetic compositions over time and between locations—differences that are probably related to greater vagaries in ocean currents during recruitment times, the absence of stable local recruitment, and isolation of water bodies with suitable habitat. Except for the Florida Bay population, overall, bay scallops can be genetically homogeneous over the entire Florida Gulf or can conform to a metapopulation structure with a core population and multiple, genetically differentiated peripheral populations.

OYSTERS, SEWAGE AND DISEASE. Peter J. Biancani. Dauphin Island Sea Lab, Dauphin Island, AL.

We measured the effects of wastewater treatment plant (WTP) effluent on growth, survival, and concentrations of fecal coliform and male specific bacteriophage (MSB) in oysters. To definitively link biological effects and microbial concentrations to WTP effluent we measured nitrogen stable isotope ratios in oyster tissues and suspended particulate matter (SPM) in water at varying distances from Clifton C. Williams WTP outflow in Mobile Bay, Alabama. We then compared concentrations of fecal coliforms and MSB to N stable isotope ratios to determine whether these indicators were correlated with wastewater exposure and determine the relative effectives of each indicator. Preliminary investigations showed that nutrient levels in the water were higher closer to the WTP outflow, and WTP effluent had a low ∂15N value (–3.78‰). Accordingly, ∂15N values in SPM and oyster tissue increased with distance from the outflow. MSB concentrations were highest at the site closest to the outflow and were significantly correlated with ∂15N values, while fecal coliform concentrations were not. These results suggest MSB is a better indicator of wastewater exposure than fecal coliform.

POPULATION STRUCTURE AND DEMISE OF BAY SCALLOPS (*ARGOPECTEN IRRADIANS*) IN NEW JERSEY. **Paul A. X. Bologna.** Montclair State University, Department of Biology and Molecular Biology, Montclair, NJ 07043 USA.

Bay scallops were once plentiful and commercially harvested in New Jersey. However, since the mid-1970's, the population has seen dramatic declines below fishable levels. Some of the potential mechanisms impacting population size include the loss of seagrass habitat and recurrent brown-tide blooms in the coastal bays. While loss of habitat is certainly an important factor in the population decline, it was the persistent and recurrent brown-tides in the early 2000's which caused the local extirpation of bay scallops from New Jersey. In fact, surveys conducted during this time frame yielded only three adults and no spat from Barnegat Bay. By 2002 no live scallops were observed in the bay. In early 2004, after two consecutive non-brown-tide years, scallops were once again seen in the bay. The genetic analyses of these scallops indicated that they were spawned from New York source populations. This was a dramatic shift, because the early allozyme work indicated that New Jersey scallops were similar to those of the southern sub-species. As such, we had a sub-species shift in the New Jersey population. This genetic evidence was also seen in reproductive conditioning and spawning with earlier sets in the current population, compared to the southern sub-species.

NOVEL METHODOLOGY FOR GENERATING TRIPLOID GREEN SEA URCHINS—APPLICATIONS FOR OPEN-OCEAN AQUACULTURE. **S. Anne Böttger, Celeste C. Eno,** and **Charles W. Walker.** The University of New Hampshire, Department of Zoology, Durham, NH 03824.

Sea urchin fisheries have been valuable economically, leading to drastic overfishing of this resource. Aquaculture of sea urchins in land-based facilities can help restore populations and preserve this ecologically important herbivore. Triploidy, a successful aquaculture technique for fish and bivalves, has so far not been successfully developed for sea urchins. In this study we present the production of the first triploid green sea urchins, *Strongylocentrotus droebachiensis*. We denuded eggs (removing the vitelline membrane) using three methods. Chemical removal was most successful, however, none of the eggs developed after fertilization. Mechanical removal of the vitelline membrane was not particularly successful and resulted in the largest amounts of damaged eggs. Acidic denuding had a success rate of 73.54% ± 6.15 with little damage. Denuded eggs were fused and fertilized successfully and produced blastulae that were significantly larger compared to diploid blastulae. Chromosome counts determined that diploid sea urchins had 42 chromosomes while triploids displayed the presence of 63 chromosomes, verifying the production of triploids. Using these unconventional techniques it is therefore possible to produce triploid sea urchin embryos that should grow faster and develop into adults that are highly marketable. (Supported by USDA to CWW).

TEMPORAL AND DISTRIBUTIONAL VARIATION IN THE RECRUITMENT OF BAY SCALLOP SPAT USING SPAT BAGS IN NANTUCKET HARBOR. **Peter B. Boyce, Robert S. Kennedy, Meghan J. Massaua,** and **W. Forrest Kennedy.** Maria Mitchell Association, 4 Vestal Street, Nantucket, MA 02554.

During the last 4 years standard size spat bags have been deployed in Nantucket Harbor at various dates during the spawning season to sample the spawning and recruitment of the population of Bay Scallops (*Argopecten irradians irradians*). During the summers of 2006 and 2007 spat bags were set out at two week intervals at six locations within Nantucket Harbor. In earlier years, fewer locations and fewer time samples were made. After two months the bags were collected and the seed scallops within them were counted and measured. Both the numbers and average sizes of recruited seed scallops varied throughout each season. The water temperature in the harbor has been recorded hourly for the past two years, and weekly for the seven years before that. Within each season, the number of seed scallops showed a well-defined peak. The timing of this peak varied by more than a month from year to year, but the shift in the peak is not explained by variations in the water temperature. The size of the following year's harvest shows no correlation with the peak number of spat recruited in the spat bags.

EFFECTS OF TOXIC AND NON-TOXIC BROWN TIDE ON THE BIOCHEMICAL COMPOSITION AND METAMORPHIC SUCCESS OF *MERCENARIA MERCENARIA* LARVAE. **V. Monica Bricelj[1], Heather Robbins[2], Scott Macquarrie[1],** and **Fabrice Pernet[3].** [1]National Research Council, Institute for Marine Biosciences, Halifax, NS B3H 3Z1, Canada; [2]Dalhousie University, Halifax, NSB3H 4H6, Canada; [3]Laboratoire Environnement-Ressources du Languedoc-Roussillon, IFREMER, 34203 Sète, France.

Decadal changes in the toxicity of cultured *Aureococcus anophagefferens* (brown tide, BT) strains are documented based on a bioassay that measures grazing inhibition in juvenile mussels. We further investigate the effects of toxic and non-toxic strains of this alga on growth, biochemical composition (especially of lipids) and survival of clam larvae exposed to *A. anophagefferens*: a) throughout planktonic development, b) only during metamorphosis following rearing on a control diet, and c) over both development phases. Exposure to non-toxic BT supported growth comparable or only 32% lower than that of control larvae fed *Isochrysis galbana* (clone T-iso), but led to metamorphic failure. Toxic and non-toxic *A. anophagefferens* strains have a comparable biochemical composition, characterized by low triacylglycerol (TAG) levels as % of organics relative to *I. galbana*, resulting in highly reduced TAG levels in larvae fed both BT strains. Lipid class dynamics differed markedly, however, between larvae fed toxic and non-toxic BT strains. A more complex synergism of poor nutritional value and toxicity may need to be considered in future studies on BT effects on larval recruitment. Alternatively, characterization

of a non-toxic strain based on the mussel bioassay may not detect more subtle toxic effects operating on vulnerable early post-settlement stages.

CHARACTERIZATION OF OYSTER HERPES-LIKE VIRUS IN OYSTERS FROM DIFFERENT GEOGRAPHICAL REGIONS. **Gwynne D. Brown[1], Colleen A. Burge[2], Carolyn S. Friedman[2], Jean François Pepin[3], Tristan Renault[3],** and **Kimberly S. Reece[4].** [1]Virginia Institute of Marine Science, College of William and Mary, Environmental and Aquatic Animal Health, Gloucester Point, VA 23062 USA; [2]University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA 98195, USA; [3]IFREMER, La Tremblade, France; [4]Institute of Marine Science, College of William and Mary, Environmental and Aquatic Animal Health, Gloucester Point, VA 23062 USA.

Since 1972, there have been numerous reports of herpes-like viruses in marine bivalves around the world. These viruses are a serious pathogen of several oyster, scallop and clam species, causing severe economic losses, particularly in hatcheries where the viruses can cause massive mortalities in larvae and spat. Detection of oyster herpes-like virus (OsHV) can be difficult in asymptomatic adult oysters with latent infections. This problem is exacerbated by the presence of genetic variants among viral genomes. PCR primer sets utilized for detection of French and California isolates do not consistently amplify all Asian isolates. To determine the degree of genetic variation among OsHV strains from different geographical regions, DNA of infected oysters from California, France, China and Japan was examined. PCR was attempted for several regions of the genome using different primer sets. PCR primers designed for this study to target one area of the genome, open reading frame (ORF) 117, consistently amplified OsHV DNA from all samples tested. The sequences from positive amplifications of ORF117 and of the area previously referred to as the "A" region were compared and multiple polymorphic sites were discovered. In addition, some of the polymorphisms identified appear to be unique to each geographical region.

USING QUANTITATIVE POLYMERASE CHAIN REACTION (Q-PCR) TO DETECT AND QUANTIFY THE OYSTER HERPESVIRUS (OSHV). **Colleen A. Burge[1], Jean-François Pepin[2], Nicole Faury[3], Tristan Renault[3],** and **Carolyn S. Friedman[1].** [1]University of Washington, School of Aquatic and Fishery Sciences, Box 355020, Seattle, WA 98195, USA; [2]IFREMER, Laboratoire de Génétique et Pathologie, 17390 La Tremblade, FRANCE; [3]IFREMER, Laboratoire de Génétique et Pathologie, 17390 La Tremblade, FRANCE.

The Ostreid herpesvirus (OsHV-1) and similar oyster herpesviruses (OsHV) have been associated with mortalities in larval and/or seed bivalves in France, New Zealand, and California, USA, and have been identified in oysters from Japan, China, and Korea. Polymerase Chain Reaction (PCR) followed by sequencing has helped identify OsHV, especially in seed or adult oysters where descriptions of Cowdry Type A inclusions are rare and low level or latent infections exist. PCR provides a qualitative assessment of prevalence but can not quantify the virus. Quantitative PCR (Q-PCR), a more rapid and sensitive method, has been developed to quantify OsHV. OsHV-specific Q-PCR tests have been designed and optimized to quantify OsHV using several regions of the OsHV-1 genome including: A, B, C, and GP regions, and the DNA polymerase gene. An assessment of these Q-PCR assays has been made by comparing sensitivity in side-by-side comparisons using DNA from infected oysters from multiple origins (France, China, Japan, and California) where infection status/viral DNA quantity varied. Sensitivity varied among assays, and we are currently sequencing PCR products from all Q-PCR assays to determine which assays are more conserved and confident for diagnosis of samples from all geographic regions.

POPULATION STRUCTURE, DENSITY AND BIOMASS OF THE EASTERN OYSTER ON ARTIFICIAL OYSTER REEFS IN THE RAPPAHANNOCK RIVER, CHESAPEAKE. **Russell P. Burke** and **Romuald N. Lipcius.** Virginia Institute of Marine Science, The College of William and Mary, Gloucester Point, Virginia, USA.

Restored Eastern oyster (*Crassostrea virginica*) reefs have generally experienced marginal success and required reseeding and shelling to sustain populations in Chesapeake Bay. Many restored reefs vary significantly from natural reefs in having: limited vertical complexity, low reef stability, reduced substrate area for larval settlement, and diminished reef community structure. In 2005 and 2007, we quantified population structure, density and biomass of oysters and mussels on a novel artificial concrete modular reef deployed subtidally in the Rappahannock River, Chesapeake Bay. The modular reef was neither seeded artificially nor harvested. The reef was colonized heavily by native oyster and mussel larvae that recruited successfully and survived in a thriving oyster reef community since reef deployment in 2000. Oyster and mussel biomass and density values were among the highest recorded for natural and restored oyster reefs. Additionally, a large array of artificial concrete reefs, adjacent to the modular reef, were sampled in 2006. We estimate that within a subtidal footprint of less than 1 acre, these reefs contain >2 million oysters and >20 million mussels. Thus, we posit that restoration efforts with native oyster should utilize artificial reefs with the vertical structure and stability required to buffer environmental stress and predation pressure.

FIELD AND LABORATORY STUDIES TO UNDERSTAND DISEASE RESISTANCE IN DELAWARE BAY OYSTERS AND RESPONSE TO CLIMATE CHANGE. **David Bushek, Susan Ford, Ximing Guo, Iris Burt, Brenda Landau, Coren Milbury, Emily Scarpa,** and **Liusuo Zhang.** Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08345 USA.

To understand how host genetics and population dynamics, and environment interact with disease organisms to structure host populations, and how climate change may affect these processes in a marine species, we are studying the eastern oyster (*Crassostrea virginica*) in Delaware Bay, and its two lethal parasites *Haplosporidium nelsoni* (cause of MSX disease) and *Perkinsus marinus* (cause of dermo disease). Genetic resistance to both diseases has been demonstrated by selective breeding and natural selection has resulted in resistance to MSX in most of the wild population. Field and laboratory studies are grouped into four tasks designed to investigate the role of environmentally-modulated selection and transmission processes in producing genetic changes in the host population. We are particularly interested in the role of potential disease refugia in maintaining susceptible populations. Task 1 has begun to identify and map major resistance genes and quantitative trait loci (QTLs) in reference families. Task 2 will identify phenotypic and genotypic differences in oysters from putative refugia and non-refugia sites. Task 3 is determining mechanisms that allow refugia to exist. Task 4 will estimate temporal and spatial differences in the number of parents contributing to spat setting in different regions of the Bay. NSF EID Award 0622672.

SOFTSHELL CLAM CULTURE: GROW-OUT FROM PLANT TO HARVEST. **Joseph K. Buttner, Scott Weston,** and **Mark Fregeau.** Salem State College, Northeastern Massachusetts Aquaculture Center, Salem, MA 01970 USA.

Softshell clams (*Mya arenaria*) have long been a popular and commercially important bivalve in coastal waters of Massachusetts and New England, and now are the basis of a modest, but growing aquaculture industry. Typically, clams are stocked in late spring through summer at ≥10 mm shell length (SL). Clams are seeded at 25–50 clams/ft^2, preferably in a silty/sand or sandy/silt substrate. Before clams are stocked, the site is raked rigorously to dislodge and remove predators, mainly green crabs (*Carcinus maenus*). Seeded clams are covered with 3/8'' plastic netting to exclude predators. As an illustration, most clams stocked in mid May to late June 2006 at the Bathing Beach, Hingham, MA attained sexual maturity by late May 2007 (n = 1,026; avg = 37.2 mm SL; SD = 5.5 mm SL). By late fall 2007, many clams reached market size (>50.8 mm SL) at the age of 1 year$^+$ (n = 961; avg = 50.1 mm SL; SD = 7.0 mm SL). Survival and growth realized by clams at other sites in Boston Harbor at an age of 1 year$^+$ (Quincy and Weymouth, MA) varied with sediment type, beach kinetics and stock size being important influencing factors.

STATUS OF THE KUMAMOTO OYSTER IN ITS NATIVE HABITAT. **Mark Camara[1], Jonathan P. Davis[2], Christopher J. Langdon[3], Masashi Sekino[4], Sanford Evans[3], Gang Li[5],** and **Dennis Hedgecock[5].** [1]USDA-ARS, Hatfield Marine Science Center, 2030 SE Marine Science Dr. Newport, OR 97365 USA; [2]Taylor Resources, Inc., 701 Broad Spit Road, Quilcene, WA 98376 USA; [3]Oregon State University, Hatfield Marine Science Center, 2030 SE Marine Science Dr. Newport, OR 97365 USA; [4]Tohoku National Fisheries Research Institute, Fisheries Research Agency, 3-27-5 Shin-hama, Shiogama, Miyagi 985-0001, Japan; [5]Department of Biological Sciences, University of Southern California, 3616 Trousdale Pkwy, Los Angeles, California 90089-0371.

The status of the Kumamoto oyster *Crassostrea sikamea* in its native Japan is uncertain because of a lack of information and a suggestion that *C. sikamea* and *C. gigas* hybridize in the northern Ariake Sea. We collected wild oysters from three sites in Saga Prefecture located in the northern portion of the Ariake Sea, Kyushu, Japan, in September 2006 and used molecular methods to assign 628 sampled oysters to one of three species found in this region. *C. sikamea* proved to be the dominant organism on artificial hard substrates, comprising 91% of the oysters sampled and typed. *C. ariakensis* was present (8% of typed oysters), and *C. gigas* was rare (1%) at these sites. We found no evidence of hybridization between any of the species and were unable to repeat a previous study which suggested hybridization between *C. sikamea* and *C. gigas*. We conducted gamete compatibility tests among all combinations of Japanese and US *C. sikamea* and *C. gigas* broodstocks and found strong one-way gamete incompatibility between species of Japanese stocks, supporting the molecular diagnosis of *C. sikamea*. However, this one-way incompatibility was less evident in US stocks, indicating lower barriers to potential hybridization in commercially cultured stocks.

POPULATION WITHOUT 'DYNAMIC'—THE CASE OF COMMERCIALLY HARVESTED MUD COCKLES, *KATELYSIA* SPP., FROM SOUTH AUSTRALIA. **Agnes Cantin[1], Anthony Fowler[2],** and **Sabine Dittmann[1].** [1]Flinders University, School of Biological Sciences, GPO Box 2100, Adelaide SA 5001, Australia; [2]South Australian Research and Development Institute–Aquatic Sciences, 2 Hamra Avenue, West Beach SA 5024, Australia.

Mud cockles of the genus *Katelysia* (Veneridae) are harvested along the coast of South Australia, with a commercial and recreational fishery value of approximately AU$1,225,000 (2004/

05). Fisheries effort has increased in recent years, leading to questions of the sustainability of the fishery. A 12-month field study of mud cockles was carried out at the primary commercial fishery site near Port Adelaide. *K. scalarina* and *K. peronii* co-exist and are both subject to equal harvesting pressures. Distribution pattern, abundance, size-structure, gonad development and post-larval occurrence were recorded from three tidal levels. *K. peronii* was more abundant at all levels compared to *K. scalarina*, with abundances of both species decreasing over time. Size-frequency distributions were unchanged during the study period and no recruitment events were recorded. Condition index did not vary between months. Macroscopic staging of the gonads revealed that *K. scalarina* had more developed gonads during the winter and *K. peronii* during the summer months. While spawning must have occurred during these times, no juveniles of either species were found in the study area. Management of mud cockle harvesting has to consider this peculiar population dynamic.

IDENTIFICATION OF THE *PERKINSUS* SPP. OCCURRING IN THE SPANISH COAST AND EVALUATION OF THEIR INTRASPECIFIC VARIABILITY. **Asunción Cao[1], Elvira Abollo[1], Belén G. Pardo[2], Paulino Martínez[2],** and **Antonio Villalba[1].** [1]Centro de Investigacións Mariñas, Xunta de Galicia, Vilanova de Arousa, 36600, Spain; [2]Universidad de Santiago de Compostela, Facultad de Veterinaria, Departamento de Genética, Lugo, 27002, Spain.

Two species of the genus *Perkinsus* (*P. olseni* and *P. mediterraneus*) have been identified in European waters thus far, affecting various bivalve mollusc species. A project is being developed to identify the *Perkinsus* species occurring in different places of the Spanish coast where mollusc farming is an important activity and to evaluate *Perkinsus* intraspecific variability with virulence implications. By using PCR-RFLP, *P. olseni* has been detected in clams *Ruditapes decussatus* and *R. philippinarum* from various bays of Galicia (NW Spain), Andalucía (S Spain), and Delta de l'Ebre (Catalonia, NW Spain), and in clams *Venus verrucosa* from Menorca (Balearic Islands, Mediterranean Sea). *P. mediterraneus* has been detected in *V. verrucosa* (some times in mixed infection with *P. olseni*) and oysters *Ostrea edulis* from Menorca. In addition, *Perkinsus* cells were isolated from various mollusc species collected from different areas and were used to initiate *in vitro* cultures. Then clonal *in vitro* cultures have been established with replication for individual hosts, host species, and locations, for comparisons. Microsatellite markers are being used to analyse the genetic structure of *Perkinsus* populations and bidimensional electrophoresis is used for qualitative and quantitative comparisons of cellular and extra cellular proteins.

REMEDIATION OF EUTROPHICATION BY OYSTERS, *CRASSOSTREA VIRGINICA*. **Ruth H. Carmichael[1], William Walton[2],** and **Heidi Clark[3].** [1]Dauphin Island Sea Lab, Dauphin Island, AL 36528; [2]Cape Cod Cooperative Extension, WHOI Sea Grant, Barnstable, MA 02630; [3]Woods Hole Group, East Falmouth, MA 02536.

We tested the capacity of oysters to remediate eutrophication by transplanting juvenile oysters into 5 estuaries receiving different N loads.From our empirical data, we estimated the amount of N in oyster tissues at harvest size and compared that number to: 1) N loaded to each estuary from land and 2) N in suspended particles in each estuary. ^{13}C in oysters reflected phytoplankton regardless of ^{13}C values in bulk seston and sediment, indicating oysters primarily assimilated phytoplankton N. Based on estuary-specific growth rates and % N in oyster tissues, we estimated oysters have 0.2–0.4 g N in their tissues at harvest. The number of oysters needed to assimilate all land-derived or phytoplankton N ranged from 1.5×10^7 to 6.7×10^8 requiring more space for growth than available bottom area in each estuary. Although oysters alone may not have the capacity for total N remediation, our data suggest they may be used in combination with other N removal measures as part of integrated eutrophication management plans.

FACTORS CONTRIBUTING TO THE PERSISTENCE OF *CRASSOSTREA VIRGINICA* POPULATIONS IN DISEASE-INTENSE VIRGINIA WATERS. **Ryan B. Carnegie** and **Eugene M. Burreson.** VA Institute of Marine Science.

Diseases caused by *Haplosporidium nelsoni* and *Perkinsus marinus* have contributed to the recent decline of Crassostrea virginica in Chesapeake Bay. Yet *C. virginica* persists despite disease, reaching impressive abundances where recruitment is favorable. While reproduction by abundant small, pre-disease oysters may support populations in areas of high, consistent recruitment, this hardly explains the persistence of oysters where disease is annually intense but where strong recruitment is infrequent. We have begun to integrate study of oyster reproduction with that of oyster pathology to gauge the capacity of *C. virginica* to coexist with *H. nelsoni* and *P. marinus*. Several factors emerge that would favor oyster populations: decline of MSX disease as a major cause of mortality, leaving early- to mid-summer free of major disease impacts; substantial oyster reproductive activity in mid-summer, prior to seasonal dermo disease epizootics; ability of much of the population to remain in good health and condition despite being infected with *P. marinus*; and capacity for some oysters to survive to large size and high fecundity despite multiple disease challenges, favoring evolution of disease resistance. Natural *C. virginica* populations have a capacity for growth, despite disease, if substrate may be managed more effectively and the loss of reef arrested.

A BAY SCALLOP'S BRAVE NEW WORLD: CAN THE INTRODUCED CODIUM FRAGILE ACT AS AN EELGRASS SURROGATE? John Carroll[1], Bradley J. Peterson[1], Chris Smith[2], Dennis Bonal[3], Andrew Weinstock[3], and **Stephen T. Tettelbach[3].** [1]Stony Brook University, Marine Science Research Center, School of Marine and Atmospheric Sciences, Stony Brook, NY 11794; [2]Marine Program, Cornell Cooperative Extension of Suffolk County, Riverhead, NY 11901; [3]CW Post of Long Island University, Department of Biology, Brookville, NY 11584.

Bay scallops, *Argopecten irradians*, once supported a vibrant fishery on Long Island, but were pushed to the brink of local extinction after a series of brown tide blooms in the 1980's. Restoration efforts, which commenced at the time of the fishery collapse, were somewhat successful but since 1995 scallop populations have remained well below historic levels. Despite many reasons for this lack of recovery, loss and alteration of habitat is often considered the major player. The potential role of the existing eelgrass (*Zostera marina*), the preferred bay scallop habitat, and macroalgae as suitable bay scallop habitat was investigated at 4 time points over 2 years. Tagged juvenile bay scallops were free planted to the bottom and tethered in 6 different habitats for a period of one week and percent recovery was calculated. Recovery numbers were highest in eelgrass, however, dense stands of *Codium fragile* exhibited statistically identical recovery to eelgrass. Eelgrass and codium both performed significantly better than replicate releases on bare sediment and dense drift macroalgae. These results can help managers to plan more efficient restoration efforts by locating potential habitats where scallop survival would be highest, even in the absence of eelgrass.

GROWTH AND SURVIVAL OF THE EASTERN OYSTER *CRASSOSTREA VIRGINICA* IN JAMAICA BAY, NEW YORK. Margaret A. Carroll[1], Gary Sarinsky[2], Edward J. Catapane[1], and **Ebere Nduka[1].** [1]Medgar Evers College, Biology, Brooklyn, NY, 11225, USA; [2]Kingborough Community College, Biological Sciences, Brooklyn, NY, 11235, USA.

Jamaica Bay, NY a major inlet opening to the Atlantic Ocean, was abundant with oysters until early 1900's. Over-harvesting, pressure from predators, parasitic invasion and declining water quality are cited as causes for the decline. Despite actions to arrest and reverse the pollution, oysters are not reestablished. We studied factors relating to *Crassostrea virginica* rehabitation in Jamaica Bay to determine if water quality and environmental conditions are suitable for their survival. Oyster seed placed in Jamaica Bay grew well when housed in protective containers and growth was better when the seed were positioned 1 foot above the sediment as compared to 1 foot below the surface. the surface. Water temperature, pH, turbidity, salinity, conductivity, chlorophyll-a and dissolved O_2 were measured. To study growth and survival in a more natural condition, oyster seed and adults were placed just off the bottom in unprotected containers and photographed. After 1 year they grew and survived well with no serious signs of predation by crabs or starfish. After 3 years new oyster seed were found in the protected floats indicating that Jamaica Bay water quality is suitable for oyster survival and reproduction under the various conditions of our experiments.

BIOFOULING MANAGEMENT IN OYSTER CULTURE: IMPACTS ON PRODUCTION AND BIODEPOSITION RATES. Claire Carver[1], André Mallet[1], and **Matthew Hardy[2].** [1]Mallet Research Services, 4 Columbo Dr., Dartmouth, Nova Scotia, B2X 3H3, Canada; [2]Fisheries and Oceans Canada, Habitat Division, P.O. Box 5030, Moncton, New Brunswick, E1C 9B6, Canada.

Sustainable culture of the Eastern oyster (*Crassostrea virginica*) in New Brunswick, Canada, depends on optimizing production strategies for the short growing season while minimizing environmental impacts. One strategy to control biofouling levels on the floating bags used for oyster culture is to periodically turn them thereby exposing the submerged portion to air drying. The impact of different bag turning frequencies on fouling levels, oyster production, biodeposition rates and the settlement of nuisance species was assessed at two sites in northern New Brunswick. Over the 4-mo study period (June–October 2006), the fouling biomass increased exponentially to a maximum of 3 kg wet wt on bags which were never turned. Maintenance activity aimed at reducing fouling levels did not, however, enhance oyster production; growth and survival rates were similar in bags turned bi-weekly, monthly, once in mid-August or never. Biodeposition rates were also similar among handling treatments regardless of the accumulated fouling community and did not significantly exceed background levels in adjacent reference areas. Although these results suggested that the contribution of the fouling community to the overall biodeposition signal was relatively small, bag turning activity was associated with a short-term spike in biodeposition levels.

LEVELS OF HSP70 STRESS PROTEINS IN EASTERN OYSTERS CULTURED USING AN ADJUSTABLE LONG LINE SYSTEM EXPOSED TO AIR AND INFLUENCE ON OYSTER SHELF LIFE. Sandra M. Casas[1], Yanli Li[1], Fu-lin E. Chu[2], and **Jerome F. La Peyre[1].** [1]Louisiana State University Agricultural Center, Department of Veterinary Science, Baton Rouge, LA 70803, U.S.A.; [2]Virginia Institute of Marine Science, School of Marine Science, College of William and Mary, Gloucester Point, VA 23062, U.S.A.

A major problem of shipping live Gulf coast oysters in summer is their reduced refrigerated shelf-life. Conditioning to air exposure in oysters cultured using an adjustable long line system (ALS) or induction of stress proteins prior to harvesting may prolong valve closure in shipped oysters. Induction in stress proteins in various organisms has been shown to increase their survival when exposed to a variety of stress. The levels of hsp70 proteins were therefore determined during grow-out in oysters exposed daily or weekly to air and compared to control oysters held submerged. Hsp70 total protein concentration was measured

by an ELISA and the contribution of each isoform (hsp69, hsp72) was determined by western blot. No difference in stress protein levels were detected in the three groups of oysters. Hsp70 concentration was highest in summer compared to late spring and early fall with hsp69 being detectable by western blot in summer and early fall. Oysters heat-shocked at 40°C for 1 h had significantly higher hsp70 concentration, and their mortality was significantly decreased when held in a cold room for 21 days compared to control oysters. Conditions that can increase stress protein concentrations in oysters deployed in ALS need to be determined next.

EFFECTS OF GROWTH FACTORS AND HORMONES ON THE OYSTER PROTISTAN PARASITE *PERKINSUS MARINUS* AND IMPROVED METHODOLOGY FOR ITS CLONING IN FBS-FREE CULTURE MEDIUM. Sandra M. Casas and **Jerome F. La Peyre.** Louisiana State University Agricultural Center, Department of Veterinary Science, Baton Rouge, LA 70803, U.S.A.

Clonal cultures are essential for the genotypic and phenotypic characterization of *Perkinsus marinus*. While *P. marinus* has been cloned by dilution using culture-spent media and by micromanipulation using feeder layers, there is no data on cloning efficiency, and the time reported between seeding and proliferation in FBS-supplemented culture media varied greatly. Moreover, proliferation rates of *P. marinus* cloned in FBS-free culture medium JL-ODRP-2A are very low and need to be increased to speed up cloning in this essential medium. The effects of growth factors and hormones on the metabolic activity of *P. marinus* were therefore tested and the concentration of the most effective factor (i.e., ECGS) was optimized for *P. marinus* cultured at low densities. Optimal dilution of the culture medium with saline was also found to increase the viability of *P. marinus* at low densities. Finally, the results of dilution cloning using *P. marinus* stimulated with culture-spent medium, a feeder layer and ECGS alone or in combinations were compared. Using a combination of all three, the cloning efficiency was increased from 57.2% to 100% and the number of cells was increased by 52-folds 21 days after seeding, compared to single parasites seeded in culture medium only.

CONTROL OF THE LATERAL CILIATED GILL EPITHELIUM OF *CRASSOSTREA VIRGINICA* (BIVALVIA) AND THE NEUROTOXIC EFFECTS OF MANGANESE. Edward J. Catapane, Margaret A. Carroll, Kesha Martin, and **Turkesha Huggins.** Medgar Evers College, Biology, Brooklyn, NY, 11225, USA.

Lateral gill cilia of *Mytilus edulis* are controlled by a serotonergic-dopaminergic innervation from their ganglia. *Crassostrea virginica* and other bivalves have been studied to lesser degrees. Lateral cilia of most respond to serotonin and dopamine applied directly to gill, indicating possible neuro or endocrine mechanisms, but little has been done with respect to ganglionic control. We examined innervation of lateral gill cilia of *C. virginica*. Ciliary beating rates were measured by stroboscopic microscopy of preparations with the ipsilateral visceral or cerebral ganglion attached. Superfusion of gill, visceral or cerebral ganglia with serotonin increased ciliary beating rates and was antagonized by methysergide. Superfusion with dopamine decreased beating rates and was antagonized by ergonovine. Manganese causes Manganism, a Parkinson-like disease. Manganese is suspected to damage dopaminergic systems involved in control of body movements. Treating oysters 3 days with manganese (0.05–1.0 mM) resulted in dose dependant impairments of their dopaminergic, but not their serotonergic systems, in agreement with suspected mechanism of action of manganese toxicity in humans. Our work demonstrates a reciprocal serotonergic-dopaminergic innervation of lateral gill cilia, originating in the cerebral ganglion, similar to *M. edulis*.

TISSUE SPECIFIC CHARACTERIZATION OF GENE EXPRESSION USING RNA AMPLIFICATION METHODS IN *CRASSOSTREA GIGAS*. Maxine Chaney and **Andrew Y. Gracey.** University of Southern California, Marine Environmental Biology, Los Angeles, CA, 90089.

Physiological investigations of the Pacific oyster, *Crassostrea gigas*, have become increasingly important to identify individual susceptibility and resistance to summer mortality. Advances in molecular biology now allow the detection of links between gene expression and fitness variations. Fine scale differences in expression of gene families may be the key to uncovering physiological sensitivity to summer field conditions resulting in mortality. Microarray-based gene expression analysis is capable of measuring whole transcriptomes; however, it typically requires 20–200 ug of total RNA, which limits the type of tissue that can be used or requires pooling animals. I have optimized an RNA amplification method for *C. gigas* to proportionally increase mRNA for gene expression analysis, allowing the detection of low copy number transcripts and improved resolution between tissue specific signals. This method allows direct comparison of individual genotypic response to an identified fitness phenotype without the noise contributed from pooled treatments. To test this, I have compared tissue specific gene expression, especially that of hemolymph to gauge its cryptic role in tissue response.

DEVELOPMENT AND APPLICATION OF A NEW AMERICAN LOBSTER STOCK ASSESSMENT MODEL. Yong Chen[1], Carl Wilson[2], Michael Errigo[1], and **Minoru Kanaiwa[1].** [1]School of Marine Sciences, University of Maine, Orono, ME 04469; [2]Maine Department of Marine Resources, West Boothbay Harbor, ME.

We developed a seasonal, sex-specific, and size-structured stock assessment model for the American lobster *Homarus americanus*. The model was evaluated for its ability in quantifying lobster population dynamics under different conditions. The evaluation

study suggests that the proposed model can capture the dynamics of recruitment and stock biomass. Biased errors in the estimation of lobster growth could result in large errors in assessment. We applied the proposed model to assess Gulf of Maine lobster stock dynamics for 1981 to 2003. The assessment suggests that the female legal biomass tends to be higher than that of males, perhaps resulting from conservation measures taken in the Gulf of Maine lobster fishery. Despite heavy fishing, lobster legal biomass in the Gulf of Maine continued increasing since the 1980s, as a result of large increases in recruitment. However, stock recruitment, defined as the number of lobsters ranging from 53 to 68 mm carapace length, showed a decreasing trend in 2001. This assessment suggests that we need to pay close attention to the trend of recruitment in the next few years. A continuing decline of recruitment could result in decreases in legal stock biomass, leading to decreases in landings in the lobster fishery.

CASE STUDIES OF FIELD-DEPLOYABLE ENVIRONMENTAL AND BIOLOGICAL MONITORING INSTRUMENTATION FOR SHELLFISH FARMS. **Daniel Cheney** and **Andrew Suhrbier.** Pacific Shellfish Institute, Olympia, WA 98501 USA.

Technological innovation for shellfish aquaculture can take many forms. It has the potential of markedly increasing US shellfish production, expanding export opportunities, and improving our understanding of the complex relationships of the natural and human environment in these production systems. It also has important implications in key regulatory/policy areas. Improved water quality monitoring methods and other field-deployable tools are available for shellfish growers to document aspects of production management, disease control, ecological sustainability, and culture-related conditions. We will review specific examples including: 1) water quality and water flow measurement devices designed for continuous operation in intertidal environments; 2) submersible long-term time-lapse and real-time video recording equipment; 3) field deployable submersible instruments for multiple measurement of shellfish shell movements; 4) and advanced instruments to monitor particles in the water, including algae and organic debris, for both size and concentration. Recent case studies will be discussed where these instruments were deployed and tested on US west coast shellfish farms to provide reliable, stable and cost effective operation over time.

WHERE HAVE ALL THE SCALLOPS GONE? TRENDS IN RHODE ISLAND'S BAY SCALLOP POPULATIONS. **Marnita M. Chintala[1], Karin A. Tammi[2],** and **Boze Hancock[3].** [1]U.S. Environmental Protection Agency, Atlantic Ecology Division, Narragansett, RI 02882, USA; [2]Roger Williams University, Bristol, RI 02809 USA; [3]The Nature Conservancy, Narragansett, RI 02882 USA.

Rhode Island bay scallop (*Argopecten irradians*) populations have changed drastically over the past 100 years. In the early 1900s Narragansett Bay and its nearby coastal ponds supported prolific bay scallop populations; however, by the late 1950s, Rhode Island's harvests were at or near zero, and by the mid 1980s the state's scallop fishery had ceased. Many reasons have been given for this decline, including declining water quality (low oxygen and elevated nutrients), habitat degradation (loss of eelgrass specifically), predation, and brown tides. Since the 1970s, scallop restoration in Rhode Island has gained limited success; however, restoration projects conducted during the last 10 years have resulted in small populations of scallops. With the exception of some scallops found at the mouth of the Sakonnet River, these populations are restricted to the coastal salt ponds. The areas where scallops are found today may or may not have eelgrass, but they often have sandier or coarser sediment and higher salinity, and are in areas where larval retention could play a key role in maintaining populations. Results of spat collection from 2003–2006 indicate that the timing of scallop spawning and settlement in Rhode Island is concomitant with other New England locations.

MOLECULAR ANALYSIS OF THE BACTERIAL COMMUNITY IN HEMOLYMPH OF THE AMERICAN LOBSTER, *HOMARUS AMERICANUS*. **Andrei Y. Chistoserdov[1], Robert A. Quinn[1], Sal Laxmi Gubbala[1], Roxanna Smolowitz[2],** and **Andrea Hsu[2].** [1]University of Louisiana at Lafayette, Department of Biology, Lafayette, LA 70504, USA; [2]Marine Biological Laboratory, Woods Hole, MA 02543, USA.

Bacteria have been shown to be important agents in etiology of several forms of shell disease in the American lobster. To ascertain a possibility of an involvement of internal infection in the development of the shell diseases, we analyzed the composition of bacteria present in hemolymph of lobsters collected from several locations using denaturing gradient gel electrophoresis of PCR amplified portions of bacterial 16S rRNA genes. Hemolymph of both healthy lobsters and lobsters with various forms of shell disease were shown to harbor complex bacterial communities in their hemolymph. The community composition turned out to be similar in lobsters collected at various locations. Bacteria in the hemolymph can be found to be divided into three groups: 1) apparent symbiotic bacteria (such as a flavobacterial symbiont, also associated with other Arthropods), 2) various bacteria that may be associated with bacteremia (*Photobacterium profundum, Curvibacter gracilis, Vibrio lentus*, *Ralstonia pickettii*), and 3) some bacteria only identified at higher taxonomic levels (*Roseobacter* sp., *Dechloromonas* sp. and other α and β-proteobacteria). Preliminary data indicate that there is no connection between the bacterial community composition and the presence of shell disease. However, further analysis is required to confirm this notion.

PLOIDY VALIDATION OF *CRASSOSTREA ARIAKENSIS* BY QUANTITATIVE POLYMERASE CHAIN REACTION WITH NUCLEAR AND MITOCHONDRIAL MARKERS. **Arpita Choudhury[1], Ronald Lundstrom[1],** and **Geoff Scott[2].** [1]NOAA/NOS, CCEHBR, Charleston, SC, 29412, US; [2]NOAA/NOS, CCEHBR, Charleston, SC, 29412, US.

The introduction of *Crassostrea ariakensis* into the Chesapeake Bay, a response to declining *Crassostrea virginica* populations, focuses on triploid individuals to reduce the chance of expansion. Ploidy validation is of great importance for this endeavor since chromosomal instability can be exhibited in triploids. We created a molecular method to determine ploidy of *Crassostrea ariakensis* using quantitative polymerase chain reaction (QPCR) and fluorescent probes for nuclear and mitochondrial (internal control) loci. Ploidy was detected by comparing C_t values (the point when enough DNA has amplified to generate a fluorescent signal above threshold) of diploid and triploid individuals at multiple loci [nuclear (actin and tubulin) and mitochondrial (16s and cytochrome b)]. Triploid and diploid individuals exhibited a C_t value difference of one at nuclear markers and a C_t value difference of four with mitochondrial markers. Diploid individuals generated lower C_t values with nuclear markers whereas triploids generated lower C_t values with mitochondrial markers. With an extra chromosome set triploid individuals should theoretically have lower C_t values. The reason for this anomaly is not yet known. Results were validated by flow cytometry of the same individuals. This method has the potential of improved ploidy validation and could allow for validation in the field.

VERIFICATION OF ANNUAL GROWTH INCREMENTS ON THE SHELLS OF ATLANTIC SEA SCALLOPS (*PLACOPECTEN MAGELLANICUS*) BY STABLE ISOTOPES AND BY TRACKING COHORTS IN FISHERY CLOSURE AREAS. **Antonie S. Chute[1], Deborah R. Hart[1],** and **Samuel C. Wainright[2].** [1]Northeast Fisheries Science Center, Woods Hole MA 02543; [2]U.S. Coast Guard Academy, New London CT 06320.

Sea scallop growth can potentially be rapidly and inexpensively estimated using visible rings on the shell, but concerns have been raised as to whether these rings are annual. We tracked the growth of large cohorts of sea scallops (*Placopecten magellanicus*) at four sites in marine protected areas (MPAs), and compared the observed growth to that inferred from rings formed on shells of sea scallops collected at the same sites. Additionally, we aged a number of shells using stable oxygen isotope techniques, and compared these results to those from the visible growth rings. Both methods indicate that growth rings are generally annual, though the first one or more growth rings are often difficult to identify visually. The stable isotope analysis indicates that growth rings of sea scallops on Georges Bank and in the Mid-Atlantic Bight are laid down near the temperature maximum. Our work shows that growth can be reliably inferred from sea scallop shell rings.

APPLYING A TELEPHONE/INTERCEPT METHODOLOGY TO MEASURE THE RECREATIONAL BLUE CRAB FISHERY IN NEW JERSEY. **Nicole Comanducci** and **Heather Driscoll.** Macro International, Inc., 126 College Street, Burlington, Vermont, 05401.

In 2005, Macro International began surveying crabbers to develop catch and effort estimates for the recreational blue crab fishery in New Jersey. The data collection included telephone interviews and on-site intercept interviews, or creel surveys. Beginning in 2005, with no precedence in place, Macro worked with the New Jersey Department of Environmental Protection to develop the methodology, develop a site register, and train interviewers to collect biological data. The program ran for three years in three geographic areas covering coastal New Jersey. This presentation discusses our experiences with the foundational development of the data collection program and the practical issues of managing the telephone and intercept surveys. We will discuss the development of the sampling frames for both modes of data collection, the data collection instruments, training interviewers and monitoring collection activities.

A BIO-ECONOMIC FEASIBILITY MODEL FOR REMOTE SETTING IN VIRGINIA. **Michael S. Congrove[1], Standish K. Allen Jr.[1], and Jim Wesson[2].** [1]Virginia Institute of Marine Science, Gloucester Point, VA 23062; [2]Virginia Marine Resources Commission, Newport News, VA 23067.

During its peak, Virginia's historical oyster harvest was dominated by oysters grown on privately leased bottom using extensive aquaculture methods. Today extensive grow-out is virtually nonexistent due to a lack of seed, disease and more recently, intense cownose ray predation. The development of disease resistance and increased growth rates in selectively bred stocks has stimulated caged, intensive aquaculture in Virginia, but this mode of production is best suited for oysters destined for the half-shell market. The greatest current need for Virginia industry is a locally grown oyster for the shucking market.

To address this need Virginia producers have been experimenting with remote setting techniques to produce "spat-on-shell" oyster seed for extensive grow-out. To assess economic feasibility of this mode of production in Virginia a bio-economic model was constructed. Setting rate, survival, and growth, as well as labor and capital costs were tracked at ten Virginia setting sites to tune the model. A sensitivity analysis of this model suggests that setting rate is the most sensitive parameter while setting labor is one of the least. Upon completion, this model will be made available to industry in the form of an interactive budget.

THE INTERNATIONAL ABALONE INDUSTRY – HISTORICAL PERSPECTIVES AND FUTURE PROSPECTS. **Peter A. Cook.** University of Western Australia, Albany, WA 6332, Australia.

Perhaps the best known historical example of abalone fishing is the Ama divers of Japan, who have dived for abalone, without the use of artificial diving apparatus, since many hundreds of years ago. More recently, abalone fisheries, in many parts of the world, have shown similar trends, with landings rapidly increasing, and then falling as populations were over-fished. A rapid increase in the illegal exploitation of abalone has contributed to population crashes and, sometimes, to the complete de-commercialization of abalone fishing industries. Concurrently, however, has been a rapid increase in abalone farming and, to some extent, the current relationship between supply and demand is not too much different to that which existed in the 1970's. Research emphasis has changed from fisheries to aquaculture-dominated topics and, within the latter, evidence will be presented to show the way in which this has changed from an emphasis on farming systems and abalone nutrition, to genetic improvement and disease control. The relationship between supply and demand is unlikely to inhibit expansion of abalone farming in the near future, but that research leading to the successful management of diseases will become increasingly important in ensuring the future expansion of the abalone farming industry.

GENETICALLY EVALUATING THE SUCCESS OF *CRASSOSTREA VIRGINICA* HATCHERY-SELECTED LINES USED FOR OYSTER RESTORATION. **Jan F. Cordes[1], Jens Carlsson[2], Sharon J. Furiness[1], Standish K. Allen Jr.[3],** and **Kimberly S. Reece[1].** [1]Dept. of Environmental and Aquatic Animal Health, Virginia Institute of Marine Science, Gloucester Point, VA 23062 USA; [2]Duke University Marine Laboratory, Nicholas School of the Environment and Earth Sciences, Duke University, Beaufort, NC 28516 USA; [3]Aquaculture Genetics and Breeding Technology Center, Virginia Institute of Marine Science, Gloucester Point, VA 23062 USA.

Oyster restoration strategies for Chesapeake Bay have included imposing limits on commercial and recreational harvest, reef restoration, oyster translocation, and supplementation of existing wild populations through deployment of hatchery-reared spat, both cultchless and as spat-on-shell. It has been hypothesized that crossing wild oysters with hatchery strains selected for disease resistance and growth might allow selective advantages to be retained while avoiding inbreeding, which is common in domesticated stocks. We tested the utility of microsatellite markers for: 1) discriminating among four lines of hatchery oysters, 2) determining the genetic composition of progeny resulting from crosses among the lines, and 3) tracking the fate of deployed hatchery oysters and their progeny in the wild. Structure analyses based on eight microsatellites were able to discriminate among all hatchery lines, and retrospectively reconstruct the mechanics of various crosses among two or more lines. Analyses also discriminated among the hatchery lines, crossed lines, and wild populations, suggesting the usefulness of microsatellites for tracking hatchery oyster deployments. Results highlighted the difficulty of managing multiple lines and cross-breeding programs in large-scale oyster aquaculture, and pointed to the importance of molecular genetic tools for monitoring restoration efforts involving hatchery-based production of stocks for supplementation of wild populations.

EFFECTIVENESS OF BYCATCH REDUCTION DEVICES IN ROLLER FRAME TRAWLS IN THE FLORIDA SHRIMP FISHERY. **Charles R. Crawford[1], Anne L McMillen-Jackson[2], Phillip Steele[3],** and **Theresa M. Bert[2].** [1]Florida Fish & Wildlife Conservation Commission, Fish & Wildlife Research Institute; [2]FWC, Fish & Wildlife Research Institute, St. Petersburg, FL 33701 USA; [3]NOAA, St. Petersburg, FL, 33702 USA.

The roller frame trawl is a gear type unique to Florida that is used in seagrass beds to harvest both food shrimp and shrimp used for bait. Finfish and invertebrate bycatch can comprise a considerable portion of the total catch. We tested the effectiveness of two bycatch reduction devices (BRDs)—the Florida finfish excluder (FFE) and extended mesh funnel (EMF)—to reduce bycatch in roller frame trawls. Tests were conducted at two Florida locations: the nearshore waters off of Tarpon Springs and in Biscayne Bay. We sampled from 35-ft trawler boats equipped with two 3.7-m × 0.8-m roller frame trawls; a BRD-equipped net was deployed off one side of the boat, and a control net with no BRD was deployed off the other side of the boat. The effectiveness of the BRD configurations to retain shrimp while excluding bycatch varied considerably. The FFE retained shrimp, but did not significantly exclude finfish bycatch overall, although some significant species-specific exclusions were observed. The EMF performed well in Tarpon Springs with significant—albeit low—reductions in bycatch and shrimp loss. However, in Biscayne Bay, the EMF showed not only significant exclusion of bycatch, but also significant shrimp loss.

SCALLOPS AND URCHINS: POTENTIAL CULTURE PARTNERS? **Hilary Croston[1], Hank Stence[2], Mick Devin[2], Robert Peacock[2],** and **Alan Verde[1].** [1]Maine Maritime Academy; [2]RJ Peacock Canning Company.

The potential to culture *Placopecten magellanicus* and *Strongylocentrotus droebachiensis* together was investigated in a laboratory and field setting. In the laboratory, density and size of urchins dwelling within cages were manipulated to determine potential impacts on sea scallop growth. After 5 months, there was no significant difference ($P > 0.05$) on scallop growth regardless of urchin treatment. In the field, we investigated the effects of depth

and presence of urchins on the development of biofouling on bivalve enclosures. Bags containing large, small or no (control) urchins were deployed at one of two depths in mid-July and remained submerged for six months. Weight increase due to biofouling ranged from 3.11 kg (small urchins/deeper depth) to 6.01 kg (control/swallow depth). At both depths, bags with urchins had significantly less ($P > 0.001$) biofouling than bags without urchins. Bags maintained at 3 m had significantly less ($P > 0.001$) biofouling than the bags at 0.3 m. Urchin size had no effect on the amount of biofouling on the bags. The neutral impact on scallop growth indicates that urchins can reside with scallops in bivalve enclosures. The field study demonstrates the potential of urchins to control biofouling on such enclosures.

OYSTERS, INFLOWS AND THE *PERKINSUS* FACTOR IN AN UPPER TEXAS COAST ESTUARY. Jan Culbertson. Texas A&M University, Wildlife and Fisheries Sciences, College Station, TX 77843.

An integrative oyster population dynamics model was developed to demonstrate the complex relationship between biotic and abiotic factors that influence oyster health in an upper Texas coast estuary. Three natural oyster reefs spatially separated along a salinity gradient were targeted to predict oyster population responses to the pathogen Dermo (*Perkinsus marinus*). Multiple regression analyses were used to determine significance of temporal and spatial factors in the model. Climatic events in addition to reservoirs of Dermo infection within each oyster population appear to influence oyster recovery but do not preclude the potential relationship between reduced freshwater inflows and Dermo infection in oyster populations.

TOWARDS AN UNDERSTANDING OF PHEROMONE COMMUNICATION IN MOLLUSCS. Scott Cummins[1], Bernie Degnan[1], and **Gregg Nagle[2].** [1]The University of Queensland, Brisbane, Australia; [2]University of Texas Medical Branch, Galveston, Texas.

Life in the animal kingdom is about finding a mate, and in areas of marine environments where vision is limited, animals may rely solely on olfactory signals. Solitary creatures might never find each other were it not for these powerful molecules known as attraction pheromones—chemical stimuli that are released by one animal that prompt behaviour in another. Researchers have discovered thousands of attraction pheromones, but most of these have come from insects, whereas the marine environment has been largely neglected. In recent years, however, there has been important progress in our understanding of marine pheromones, particularly in the sea slug *Aplysia*. Our research is aimed at decoding its pheromone-induced behavioural system, as a means toward understanding molluscan communication. This multidisciplinary research has demonstrated that *Aplysia* attraction and resultant breeding aggregations is the result of water-borne pheromones that are released during the process of egg laying. This requires a cocktail of protein pheromones, which we have aptly named "attractin", "enticin", "temptin" and "seductin" due to their attraction-induced affects. Pheromone detection may rely on putative chemosensory receptors present on rhinophore sensory epithelia.

QPX DISEASE PROGRESS IN CULTURED AND WILD TYPE HARD CLAMS IN NEW YORK WATERS. Soren F. Dahl and **Dr. Bassem Allam.** Stony Brook University, School of Marine and Atmospheric Sciences, Stony Brook, New York, 11794-5000.

A field assay was conducted to compare the performance of different hard clam, *Mercenaria mercenaria*, seed strains in local clam growing waters of New York State (NYS). Experimental strains included a *notata* seed obtained from a Florida broodstock, and two NYS seed types obtained from local hatcheries including a cultured *notata* strain and a first generation "wild type" strain. QPX was acquired by the Florida seed in less than two months of a July deployment of grow-out cages. Prior field studies comparing susceptibility of northern and southern seed strains observed QPX acquisition after clams had over-wintered in the field, raising the question that higher susceptibility observed in southern seed clams could be a result of poor adaptation to winter water temperatures. Our results show that the southern strain acquired QPX after the clams had only been exposed to the warmest period of water temperatures for this field site (22.3°C ave.), thus excluding poor acclimation to winter temperatures as an aggravating factor. Results also showed that the NYS "wild type" was more resistant to the infection than the NYS cultured *notata* strain suggesting that aquaculture practices (e.g. selection of fast-growing stocks) may exacerbate QPX disease problems.

DESCRIPTION OF A NEW PATHOLOGY AFFECTING THE ADDUCTOR MUSCLE OF MANILA CLAM (*RUDITAPES PHILIPPINARUM*) IN ARCACHON BAY (SW FRANCE). Cécile Dang[1], Xavier De Montaudouin[1], Patrice Gonzalez[1], Nathalie Mesmer-Dudons[1], and **Nathalie Caill-Milly[2].** [1]Université Bordeaux 1 - CNRS - EPOC - UMR 5805 - Station Marine d'Arcachon - 2 rue du Pr Jolyet - 33120 Arcachon – France; [2]Laboratoire Ressources Halieutiques Aquitaine - IFREMER - 1 allée du Parc Montaury - 64600 Anglet - France.

Ruditapes philippinarum was introduced in 1972 in Arcachon bay (France) which currently ranks at the first French place in term of stock and annual production. Few years ago, a new pathology called brown muscle disease (BMD) emerged specifically in clam populations. This disease induces a brown calcification of the adductor muscle and affects differently both muscular tissues. Two indices were created to quantify symptoms (MPI and FDI) and a monitoring was undertaken for two years in four locations. The mean prevalence was under 12% without seasonal variation in three sites against 30% with a winter peak in one site. The latter site was accurately surveyed and revealed that clams at the surface of the sediment were three folds more infected than buried clams. In order to detect a causal agent and to examine the muscular damages, histological

sections were realized. Observations revealed an important inflammatory response with invasion of hemocytes and a heavy necrosis of muscular fibers. Alternatively, molecular analyses were achieved to search pathogen agents. In both cases (histological and molecular assays), bacteria, protozoans and fungi were discarded. Finally, small virus-like particles were perceived and are highly suspected as the etiological agent of BMD.

TEMPERATURE CONTROLS CLUTCH PRODUCTION IN THE BLUE CRAB *CALLINECTES SAPIDUS*. **M. Zachary Darnell** and **Dan Rittschof.** Duke University Marine Laboratory, Beaufort, NC 28516.

Blue crabs, *Callinectes sapidus* Rathbun, are a valuable commercial species along the Atlantic and Gulf Coasts. Effective management of the blue crab fishery requires that managers are provided with a thorough understanding of blue crab reproductive and spawning biology. To examine lifetime clutch production, mating pairs were collected near Beaufort, North Carolina. After mating was complete, females were measured and held sub-tidally in partially-buried minnow traps. Crabs were fed daily when water temperatures were above 58°C and were checked weekly for presence and condition of eggs. Daily mean water temperatures were calculated and found to be a significant predictor of size at maturity, as carapace width was negatively correlated with water temperature on the day of molting. Both time to first clutch (degree-days) and time between clutches were positively correlated with carapace width. Of the crabs that survived to spawn, 82.2% produced at least 2 clutches and 40% produced at least 5 clutches in their lifetime. Crabs regularly produced several clutches of eggs before overwintering and resuming clutch production in the spring. These data, combined with recent data showing that most size classes have similar reproductive potential, suggest that a reassessment of traditional management assumptions may be necessary.

MANGANESE DISRUPTION OF MITOCHONDRIAL RESPIRATION IN THE BIVALVE *CRASSOSTREA VIRGINICA* AND ITS PROTECTION BY P-AMINOSALICYLIC ACID. **Kiyya Davis[1], Claudette Saddler[2], Margaret A. Carroll[1],** and **Edward J. Catapane[1].** [1]Medgar Evers College, Biology, Brooklyn, NY, USA; [2]Kingsborough Community College, Biology, Brooklyn, NY, USA.

Manganese is an essential metal that at excessive levels in the brain produces extrapyramidal symptoms called Manganism which is similar to Parkinsons Disease. The mechanism of action of manganese is not completely understood but is thought to be due to factors including decreased brain dopamine levels, altered dopamine receptor activity and/or oxidative stress in mitochondria. p-Aminosalicylic acid (PAS) is a drug which recently is being shown to alleviate symptoms of Manganism. We studied the effects of manganese and PAS on mitochondrial respiration in gill of the bivalve mollusc, *Crassostrea viginica*. *C. viginica* gill is a tissue which is innervated by dopaminergic neurons. Mitochondrial respiration was measured using a YSI Micro-Biological Oxygen Monitor with a micro-batch chamber. Additions of manganese (0.1 – 10 mM) caused dose dependent decreases in mitochondrial O_2 consumption. Adding PAS (0.1 – 1 mM) prior to manganese additions protected the mitochondria. The study demonstrates that manganese does adversely affect mitochondrial respiration and that the protective actions of PAS may in part be due to its ability to shield mitochondria from manganese induced oxidative stress.

PRELIMINARY INVESTIGATION OF MARINE BIOTOXINS IN SCALLOP TISSUES ALONG THE U.S. NORTHEAST CONTINENTAL SHELF. **Geoffrey Day[1], Richard Taylor[2], Donald M. Anderson[3], Frances Van Dolah[4], J. Michael Hickey[5],** and **David Whitaker[5].** [1]Seafood Research Associates, Arnie's Fisheries, Inc., New Bedford, MA 02740; [2]www.seascallop.com, Arnie's Fisheries, Inc., New Bedford, MA 02740; [3]Woods Hole Oceanographic Institution, Woods Hole, MA 02543; [4]Center for Coastal Environmental Health and Biomolecular Research, NOS, Charleston, SC; [5]Massachusetts Division of Marine Fisheries, New Bedford, MA 02740.

The Atlantic sea scallop (*Placopecten magellanicus*) fishery currently does not retain scallop roe, in great part due to the potential uptake of marine biotoxins. Worldwide safe harvest of roe-on scallops is controlled by public health officials through tissue screening, water testing and closures, however these policies had not been instituted in US federal waters. From July 2004 through September 2007 commercial scallop vessel captains collected over 12,000 animals from over 1,100 sample locations across the US range of the species, from the waters off Virginia to the International Court of Justice line on Georges Bank. Testing of the sample groups was accomplished using two newly developed methods, Jellett Rapid Test and Receptor Binding Assay, with a portion crosschecked with both High Performance Liquid Chromatography (HPLC) and the ISSC approved Mouse BioAssay methods. In all years, roe-on scallops were well below federal action levels in the Mid-Atlantic, with highest levels localized to a 1 degree block in the Great South Channel. The intense red tide of 2005 produced only a small number of toxic scallop roe but sharply increased toxicity in other viscera parts. Results from samples collected in 2007 indicate a more widespread area of toxicity in the Georges Bank region.

TRANSLOCATION TO RESTORE ABALONE STOCKS: HOW DO ABALONE RESPOND TO HABITAT CHANGE? **Robert Day, Cameron Dixon, Luke McAvaney,** and **Emma Hickingbotham.** Zoology Department, University of Melbourne, Parkville 3010, Australia.

Translocation may be much more effective than seeding larvae or juveniles to restore stocks. We moved stunted adults from two source areas to two areas where there are more food algae and *Haliotis laevigata* reach larger lengths. Controls were transplanted into each source area and resident abalone tagged at each destination area. After both 6 and 18 months, smaller transplants increased growth, but not size-specific gonad size, relative to source controls. Larger transplants increased both, and those close to the source population asymptotic length did not grow, although residents of the same size at the same site grew substantially. Gonad mass of transplants was greater than residents of the same length. We suggest a tradeoff between future growth and reproductive output may be set by site conditions before abalone become fully mature. Thus stunted abalone transplanted into depleted areas where food is plentiful would direct most resources towards reproduction; and would stay stunted, so that a suitable size limit would preserve them as broodstock. Further, they would boost recruitment of new juveniles soon after transplantation, as opposed to delayed production of new recruits by seeded juveniles. Transplants may also maintain suitable habitat for larval settlement.

SAPKS AND HYPEROSMOTIC VOLUME REGULATION IN BIVALVES. **Lewis E. Deaton.** University of Louisiana at Lafayette, Biology Department, Lafayette, LA 70504 USA.

Cellular volume regulation in bivalves involves changes in the size of the cytoplasmic pool of organic osmolytes. Exposure of bivalve tissues to hyperosmotic seawater (SW) results in a rapid increase in the cytoplasmic concentration of alanine. Several studies have shown that a few members of the large family of mitogen-activated protein kinases are stimulated by cellular stressors, including hyperosmotic media. The proteins that make up these signaling pathways are called stress-activated protein kinases (SAPKs). Ventricles isolated from the mussel *Geukensia demissa* acclimated to 250 mOsm SW were incubated in either 250 mOsm or 1,000 mOsm SW for 4 hr. Ventricles incubated in 1,000 mOsm SW contained 75 umol/g alanine. The alanine content of ventricles incubated in 1,000 mOsm SW containing the SAPK inhibitor cyclosporin (10 ug/ml) was 21 umol/g. The alanine content of ventricles incubated in 250 mOsm SW was 7 umol/g dry wt. Ventricles incubated in 250 mOsm SW containing the SAPK activators anisomycin (10 ug/ml) or ceramide (10 uM) contained 31 and 18 umol/g alanine, respectively. These results suggest that SAPK cellular signaling pathways may play a role in the accumulation of alanine that is responsible, in part, for hyperosmotic cellular volume regulation in bivalves.

A SYSTEM APPROACH TO THE DEMAND FOR OYSTERS IN THE UNITED STATES: THE IMPACTS OF WARNING LABELS. **Cheikhna Dedah[1], Walter Keithly[2],** and **Richard Kazmierczak[2].** [1]Louisiana State University, Dept. of Agricultural Economics, Baton Rouge, Lousiana, 70803, USA; [2]Louisiana State University, Dept. of Agricultural Economics, Baton Rouge, Louisiana, 70803, USA.

California initiated a program in March 1991 that required anyone selling raw oysters to notify potential consumers that the "consumption of raw oysters can cause serious illness and death among people with liver disease, chronic illness, or weakened immune systems." This mandatory warning label, followed shortly thereafter by a similar warning in other states, received extensive media coverage. The primary objective of this study was to consider the impact of mandatory warning labels within the context of a complete demand system. Given that previous research reported that the consumers have some difficulties differentiating among product sources in warning label context, the introduction of the warning label on the Gulf product might have negative or positive impact on the demand of oysters in other regions. A secondary objective of this study is to estimate the cross quantity substitution effects that changes in oyster production in one region have on the prices of oyster produced in other regions. In order to achieve these objectives, the demand of Gulf, Pacific, Chesapeake, and imported oysters for the period 1985–2006 is estimated using an inverse almost ideal demand system (IAIDS). The IAIDS model is adjusted to account for seasonality, and time trend effects.

DEVELOPMENT AND VALIDATION OF A QUANTITATIVE REAL TIME PCR ASSAY FOR THE DETECTION AND QUANTIFICATION OF *PERKINSUS MARINUS* IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. **J. Defaveri[1], S. Roberts[2],** and **R. Smolowitz[3].** [1]Marine Biological Laboratory, Woods Hole, MA, 02543, USA; [2]University of Washington, School of Aquatic and Fishery Science, Seattle, WA, 98195, USA; [3]New England Aquarium, Boston, MA, USA.

Perkinus marinus causes a devastating disease, known as Dermo, in the Eastern oyster *Crassostrea virginica*. Routine detection of the disease is traditionally accomplished by histological evaluation of oyster tissue sections, or by the use of the Ray/Makin assay, using Fluid Thioglycollate Media (RFTM). A real-time quantitative PCR assay was developed as a diagnostic tool to detect and quantify *P. marinus*, to complement and serve as an alternate to the RFTM method. Using a dual-labeled probe approach, a sensitive assay was designed to accurately detect a range of one to several thousand *P. marinus* organisms present in oyster tissues. Cultured *P. marinus* cells were quantified prior to DNA extraction, generating a standard curve and allowing cell counts to be derived from PCR cycle threshold values. Direct comparison of the RFTM and real-time

PCR methods was accomplished by using tissue samples from the same oyster for both tests. Plotting cycle threshold values against the known Makin index value generated a standard curve with a coefficient of regression of 0.9. Our results indicate that correlations could be made between this molecular based approach and traditional methods for simplified interpretation.

CHARACTERIZING GENE EXPRESSION PATTERNS IN THREE STRAINS OF NORTHERN QUAHOGS *MERCENARIA MERCENARIA* IN RESPONSE TO INFECTION BY QPX. J. Defaveri[1], S. Roberts[2], R. Smolowitz[3], D. Murphy[4], and **W. Walton[4].** [1]Marine Biological Laboratory, Woods Hole, MA, USA; [2]University of Washington, School of Aquatic and Fishery Science, Seattle, WA, USA; [3]New England Aquarium, Boston, MA, USA; [4]Cape Cod Cooperative Extension, Barnstable, MA, USA.

Quahog Parasite Unknown (QPX) has persistently infected Northern quahogs (hard clam, *Mercenaria mercenaria*) along the Eastern coast of the United States for the past 15 years. Significant disease and mortality due to QPX infection has had a devastating impact on the aquaculture industry. Significant disease has generally been confined to the Northeastern coast, with lesser morbidity and mortality occurring in the mid-Atlantic coastal areas. Recent studies have suggested that clams' resistance to QPX varies with geographic origin of the brood stock. Gene expression patterns were used to investigate the association between disease resistance, season/temperature and geographic origin of the Northern quahog. Naïve seed clams were obtained from hard clam nurseries in Florida, New Jersey and Massachusetts, representing three geographically distinct strains. All clams were planted in Massachusetts in 2005 and monitored during the spring, summer and fall of 2006 and 2007. Total RNA was extracted from the hemocytes of both infected and non-infected clams from each strain. Using differential display and quantitative real time PCR analysis, gene expression patterns were characterized across strains. Results provide important information on the immune response of *M. mercenaria*, and how this varies across strains.

THE EFFECTS OF JUVENILE DIET ON GONADAL GROWTH (OR ROE PRODUCTION) OF THE GREEN SEA URCHIN, *STRONGYLOCENTROTUS DROEBACHIENSIS*. Michael Devin[1], Stefanie A. Böttger[2], Henry D. Stence[1], Charles W. Walker[2], and **Robert J. Peacock[1].** [1]Peacock Canning Company, Lubec, ME 04652; [2]Department of Zoology, Rudman Hall, University of New Hampshire, Durham, NH 03824.

Sea urchin fisheries have resulted in overharvesting of natural populations. Aquaculture may prove to restore populations and produce a commercially valuable product. Although many areas of sea urchin culture have been investigated, optimization of juvenile diets has not. We maintained juvenile (2–20-mm diameter) *Strongylocentrotus droebachiensis*, on seven diets for 30 months, followed by feeding formulated sea urchin diet for three months. Animals fed *Laminaria* and *Laminaria*/mussel displayed maximum wet weight increases. Gonad indices were largest in females initially fed *Palmaria*, mixed and artificial diets, while males fed *Laminaria*/mussel yielded the largest gonads indicating that high plant protein diets are more effective for roe production in females, while males respond more favorable to high animal and low plant protein diets. Cellular composition of the gonads changed in males fed *Palmaria*/mussel and *Laminaria*/mussel where spermatogonial columns increased. Amounts of oogonia and oocytes as well as oocyte diameters decreased in females when fed *Laminaria* only. These results indicate that males require animal protein for higher gonial cell production, while females require dietary protein higher than 10% during juvenile growth to have comparable reproductive development as adults. Our results indicate that juvenile diet affects quantity and quality of gonad production in adult urchins.

MUSSEL AQUACULTURE IN SCOTLAND: MANAGING MIXED SPECIES *MYTILUS* CULTIVATION. P. Joana Dias[1], M. Bland[1], A. M. Shanks[1], A. Beaumont[2], S. Piertney[3], I. Davies[1], and **M. Snow[1].** [1]FRS Marine Laboratory, AB11 9DB Aberdeen, Scotland, UK; [2]School of Ocean Sciences, University of Wales, Bangor, Menai Bridge, Gwynedd LL59 5AB, UK; [3]School of Biological Sciences, University of Aberdeen, AB24 2TZ, Scotland.

Shellfish farming is an important and growing industry in Scotland, and until recently was thought to be based exclusively on *Mytilus edulis*, the endemic species. However, a uniquely complicated area of hybridization has recently been reported where *M. edulis*, *Mytilus trossulus*, *Mytilus galloprovincialis* and their hybrids were found to be present in cultivation in one sea loch. The present study focuses on the distribution of *Mytilus* species on ropes at ten cultivation sites in that area, where the prevalence of *M. trossulus* (37%) on farms exceeds that of *M. edulis* (31%). No differences in species distribution with year of settlement, site location or salinity were found. However, *M. edulis* was more frequent at 8 m depth on ropes, whereas *M. trossulus* was more common nearer the surface. These differences might be exploitable in management strategies in order to decrease the numbers of *M. trossulus* at shellfish farms in favour of the most desirable species (*M. edulis*). Based on these observations, and taking account of Canadian experience of mixed species cultivation management, strategies such as optimization of spat collection, spat grading and seed transfer are considered.

EVALUATING NORTHERN QUAHOG (*MERCENARIA MERCENARIA*) RESTORATION: ARE TRANSPLANTED CLAMS SPAWNING AND RECONDITIONING? Michael H. Doall[1], Dianna K. Padilla[1], Carl Lobue[2], Chris Clapp[2], and **Anna R. Webb[1].** [1]Stony Brook University; [2]The Nature Conservancy.

Spawner sanctuaries, or harvest-free areas planted with high densities of adult clams, is a strategy employed to restore self-sustaining populations of *Mercenaria mercenaria* to Great South Bay (GSB), NY. To evaluate and guide this strategy, we have monitored the condition and spawning of clams transplanted from Long Island Sound since April 2004. Transplanted clams were in relatively high condition and gonad ripeness at time of transplant, spawned the first spring/summer after transplant, and reconditioned and spawned to varying degrees in subsequent years. All populations showed similar annual patterns of condition index and gonad ripeness: both peaked in mid- to late spring, dropped steeply through summer, and were lowest in autumn. Condition sometimes began to increase during autumn, changed little during winter, and continued to rise in spring to its peak. When reconditioning was greatest during autumn, spring peak condition was highest. Transplanted clams rarely reconditioned to their initial transplant levels, and were in significantly lower condition than clams in the source populations, as well as native GSB clams in 2006–2007. These data suggest that local adaptation may be especially important when considering transplantation, and at present GSB is not as good an environment for hard clams as the source localities.

VISUAL AND TASTEFUL EVALUATION OF OYSTER QUALITY. Arne Duinker[1], Stein Mortensen[2], Simon Nesse økland[3], and **Eivind Bergtun[4].** [1]National Institute of Nutrition and Seafood Research, P.O. Box 2029 Nordnes, 5817 Bergen, Norway; [2]Institute of Marine Research, P.O. Box 1870 Nordnes, 5817 Bergen, Norway; [3]Vest i havet AS, Bømlo, Norway; [4]Bømlo Skjell AS, Bømlo, Norway.

A study of seasonal variations in quality measures was conducted with farmed European flat oysters, *Ostrea edulis*. Three sites were followed with sampling every 1–3 months between September 2006 and June 2007. Each oyster was given a score on a five point scale for "visual fatness" according to the degree the creamy white storage and gonadal tissue was covering the digestive gland, and similarly scores on sweetness and mineral taste.

There was a marked increase from September to late November for visual fatness, mineral taste and sweetness, and the period around December had in general the most tasteful oysters. The variation in visual fatness, mineral taste and sweetness exceeded the variations in condition indices, and our impression is that physiological processes are affecting the taste and visual impression that cannot be seen if only evaluating condition indices. The visual fatness category five was notably stable in sweetness throughout the study compared to the other categories where seasonal differences were seen as described above. There was a correlation between visual fatness and sweetness. Based on this, together with the practical usage, we suggest that a three or five point scale of visual fatness is a good tool for evaluating oyster palatability.

OYSTER CULTURE IN WILLAPA BAY WASHINGTON: A CASE STUDY AND FRAMEWORK FOR EXAMINING RESILIENCE OF COASTAL ESTUARIES TO DISTURBANCE. Brett R. Dumbauld[1] and **Jennifer Ruesink[2].** [1]USDA-ARS, Newport, Oregon, 97365, USA; [2]University of Washington, Dept. of Biology, Seattle, Washington, 98195, USA.

Oyster aquaculture can be characterized as a disturbance to coastal estuarine systems. We summarize our current knowledge of the ecological effects of this disturbance in Willapa Bay, Washington, the largest single estuarine source of farmed oysters in the United States, and place this in context with other such human induced and natural disturbances. Adopting " resilience thinking", a conceptual view of the world at whose heart is the simple notion that "things change", we then develop a framework for examining ecological effects of aquaculture in any estuary. We acknowledge the limits of predictability and that traditional resource management has tended to place humans outside of these socio-ecological systems and suggest solutions, or at least pathways forward utilizing adaptive management.

ARAGONITE-FIBER CALCIFICATION OF THE HINGE LIGAMENT MECHANICAL ANTAGONIST TO VALVE ADDUCTION IN OYSTERS. Christopher F. Dungan. Maryland Department of Natural Resources, Cooperative Oxford Laboratory, 904 S. Morris St., Oxford, MD 21654 USA.

Hinge ligaments of bivalve molluscs serve as mechanical antagonists to valve adduction by adductor muscles, and in mechanical alignment and connection of the valves. All of these support critical contributions of pelecypod valves to essential feeding, reproductive, and defensive functions. Hinge ligament mechanical functions are partitioned between two structural subunits. The central resilium is compressed during muscular valve adduction, and actively parts the valves again when muscular adduction is relaxed. Paired tensilia align and bind the valves together, adjacent to both sides of the central resilium. These different mechanical subunit functions are reflected in their diverse structural and biochemical compositions, and in the cytological and histological characteristics of specialized subligamental ridge mantle epithelia that secrete and maintain them. In particular, the central resilium of oysters is plentifully invested with long, articulated aragonite fibers of 65–70 nm diameters, which are oriented parallel to the resilium axis that is deformed during compressions from valve adduction. These longitudinally articulated aragonite fibers may serve to enhance compression strength of the resilium, and its ability to store compression energy for use in

re-opening oyster vales when active adductor muscle-compression is relaxed. Diagrammatic, histological, and electron microscopic evidences and observations are presented.

EFFECTS OF HEAVY METALS AND PESTICIDES ON HEALTH AND PHYSIOLOGY OF OYSTERS (*CRASSOSTREA VIRGINICA*) IN HENDRY CREEK, ESTERO BAY, FLORIDA. Erin C. Dykes[1], Aswani Volety[1], Jennifer Nelson[2], and **James T. Winstead[3].** [1]Florida Gulf Coast University, 10501 FGCU Blvd. South, Fort Myers, FL 33965; [2]Florida Department of Environmental Protection, South District, 2295 Victoria Ave. Suite 364, Fort Myers, FL 33901; [3]Winstead Diagnostics, 3052 Rosa Del Villa, Gulf Breeze, FL 32563.

Although historical records indicate that oyster reefs were once a significant feature of Gulf of Mexico estuaries, alterations in freshwater inflow resulting from watershed development and water management practices have impacted salinity, water quality, and led to declines in oyster populations within southwest Florida estuaries including Hendry Creek, Estero Bay. This study examined the relationship between contaminants and water quality on the responses of American oyster, *Crassostrea virginica* in Hendry Creek within Estero Bay Estuary. Levels of heavy metals, pesticides, and PCBs in the water column and oyster tissues plus water quality parameters measured during the study were correlated with condition index, disease prevalence of *Perkinsus marinus*, reproductive state of adult oysters, growth and survival of caged juvenile oysters, and spat settlement.

Results indicate that oyster condition index, spat recruitment, prevalence and infection intensity of *P. marinus* showed a seasonal trend which increased downstream. Heavy metals and pesticide concentrations varied between sampling locations and months. Average metal concentrations were below national averages. Oyster responses varied more with seasonality (salinity), rather than due to contaminant levels. These results will help establish water quality targets for restoration and to better understand the cumulative impacts of land use management practices.

DEVELOPMENTAL AND HEAT SHOCK INDUCED EXPRESSION OF HSP70 IN *ARTEMIA*. Brenna Ehmen, John Freeman, and **Anne Boettcher.** University of South Alabama.

Artemia spp. are a model system used to examine stress responses in invertebrates. Changes in the expression of markers for stress response in this organism, including small heat shock protein (HSP) p26, HSP 70, and HSP 90 have been examined. However, the combined effects of development and temperature stress on HSP70 expression have not been studied. In the current study, developmental and heat shock induced expression of HSP70 isoforms in cysts and the first three larval stages of *Artemia* were investigated. In our initial experiment, *Artemia* were cultured at 22°C or 28°C, and both developmental rate and HSP70 expression were examined. *Artemia* raised at 22°C developed at a slower and less uniform rate than those raised at 28°C. Three isoforms of HSP70 were expressed by the *Artemia*. The expression of these varied according to both developmental stage and culture temperature. The effects of heat shock at 38°C on the expression of HSP70 in cyst and Stage 1 larvae were then examined. Heat shock increased expression of the previously detected isoforms of HSP70 and induced expression of a fourth isoform. Investigations of the role of HSP70 in development may help us better understand how early life history stages respond to stress.

ABALONE GENETIC RESEARCH: AUSTRALIAN REVIEW AND PROSPECTS. Nick Elliott. CSIRO Food Futures Flagship, Hobart, Tasmania 7000, Australia.

Abalone or muttonfish have an important role in Australian culture. There are more than 15 purported *Haliotis* species in Australian waters, although two dominate; blacklip *H. rubra* and greenlip *H. laevigata*. Abalone currently ranks as Australia's third highest value fishery; annual wild harvest ca. 5,000 t and an emergent aquaculture industry. Genetic research on Australian abalone spans about 20 years, and mainly covers four species. Initially, allozyme work was undertaken to support fisheries management, and that has since been followed by several additional population studies applying alternative DNA technologies. In the past few years the focus has shifted more towards assisting the aquaculture industry and in understanding fundamental gene regulation. The former centres on selective breeding, and the latter on the very suitable 'lab mollusc'—the tropical *H. asinina*. Recent research also includes investigations into polyploidy, full sequencing of the mitochondrial genome and a broad-scale *H. rubra* genetic map. This paper will present a review of the genetic research on abalone in Australia. It will assess where we have got to in providing both scientific knowledge and a return to our industries and their managers, and importantly where Australian and international abalone genetic efforts could be heading.

RE-EMERGENCE OF VIBRIOSIS IN SHELLFISH HATCHERIES AND NURSERIES Ralph Elston[1], Claudia Häse[2], Hiro Hasegawa[2], Karen Humphrey[1], and **Ildiko Polyak[1].** [1]AquaTechnics, 455 West Bell Street, Sequim, WA 98382 USA; [2]Department of Biomedical Sciences, College of Veterinary Medicine, Oregon State University, Corvallis, OR, 97331 USA.

During 2006 and particularly 2007, we documented the re-emergence of vibriosis caused by *Vibrio tubiashii* in shellfish hatcheries on the west coast of North America and elsewhere. Lost larval and juvenile production included Pacific and Kumamoto oysters (*Crassostrea gigas* and *C. sikamea*) and geoduck clams (*Panope abrupta*) with a measured production decline of about 36% in one hatchery. These losses could severely limit production of edible shellfish in succeeding years. Occurrence of vibriosis was associated with intermittent upwelling and intrusion

of unusually elevated temperature of surface seawater. Our studies suggested that loss of natural populations of shellfish larvae was also associated with *V. tubiashii* blooms in the coastal environment in which the concentration of dominant shellfish pathogenic *Vibrio* reached 1.6×10^5 cfu/mL. The bacteria were identified as closely associated or identical with the described isolates of *V. tubiashii* and possessed genes coding for a protease and hemolysin described for this species. Many isolates showed activity of these peptides. Management and prevention require reduction of incoming concentrations of the bacteria and interrupting the cycle of bacterial amplification in the hatchery. Establishment of *V. tubiashii* in algal food cultures is one damaging occurrence due to the amplification of bacterial concentration.

HSP70 EXPRESSION IN TRIPLOID AND DIPLOID HARD CLAMS *MERCENARIA MERCENARIA NOTATA* EXPOSED TO HEAT SHOCKS. Eman El-wazzan[1], David Carroll[1], and **John Scarpa[2].** [1]Florida Institute of Technology, Department of Biological Sciences, Melbourne, FL 32901 USA; [2]Harbor Branch Oceanographic Institute at Florida Atlantic University, Center for Aquaculture & Habitat Restoration, Fort Pierce, FL 34946 USA.

Higher than average summer mortality has been reported by hard clam culturists in Florida. Heat shock protein 70 (hsp70) is involved in protecting some marine organisms against stressful environmental conditions, including thermal stress. Triploid clams, having three sets of chromosomes, may synthesize more hsp70 and exhibit greater thermo-tolerance than diploid clams. Hsp70 protein was measured by immunoblotting of tissue from diploid and triploid hard clams cultured under ambient (20–25°C) and heat shock (5–10°C above ambient) conditions. Two hsp70 isoforms were detected (70 and 75 KDa) in clam tissue. Hsp70 was constitutively expressed at ambient temperature. The relative hsp70 levels increased by ~1.7 fold in clams exposed to moderate heat shock (31°C for 24 hours) than in clams maintained at ambient temperature or exposed to short heat shock (1 hr at 31°C). This Hsp70 increase may be attributed to the synthesis of inducible isoforms of hsp70. Survival of clams exposed to severe prolonged heat shock (5–7 days at 35°C) was more influenced by genetic background; different families ($P = 0.042$) rather than by ploidy ($P = 0.184$). There was no significant difference in overall survival between triploids and diploids, although triploids had similar or slightly higher survival than diploids. This research was supported by FLSG R-LR-A-39.

THE EFFECTS OF MULTIPLE ENVIRONMENTAL STRESSORS ON HARD CLAM SURVIVAL AND PHYSIOLOGY. Vincent Encomio, Madeleine Goncalves, Holly Abeels, Andrew Griffith, and **Aswani K. Volety.** Coastal Watershed Institute—Florida Gulf Coast University Fort Myers, FL 33928 USA.

In Southwest Florida, hard clams (*Mercenaria mercenaria*) experience multiple stressors (freshets, high temperatures and red tide). Several lab experiments simulating these conditions were conducted. In the first experiment hard clams were exposed to salinities at 10, 20 and 30 ppt for 2 weeks. Clams were then heat shocked at 38°C for one hour, returned to ambient temperatures and monitored for survival for two weeks. There were significant differences in log-rank survival between treatments ($P < 0.05$). Survival was significantly lower at 10 ppt (ANOVA: $P < 0.05$). In a subsequent experiment, clams were exposed to *Karenia brevis* (1,000 cells/ml, 2 times per week) for 2 weeks and transferred to variable salinities (*K. brevis* → Δ salinity; 10, 20 and 30 ppt) for 2 weeks, simulating rainy season effects after red tide. Phagocytosis, RNA:DNA and Hsp70 expression were measured after 2 weeks in variable salinities to characterize sublethal effects of red tide and lowered salinity. Preliminary results show that phagocytotic index was higher in clams exposed to *K. brevis*, more significantly after heat shock (ANOVA: $P < 0.05$). A third converse experiment examining clams' responses to *K. brevis* after prior exposure to low salinity (Δ salinity → *K. brevis)* will simulate red tide following rainy season.

THE SWEET RELATIONSHIP BETWEEN MICROALGAE AND *CRASSOSTREA VIRGINICA*: IMPLICATION OF CARBOHYDRATE AND LECTIN INTERACTIONS IN PARTICLE SELECTION IN SUSPENSION FEEDING BIVALVES. Emmanuelle Pales Espinosa[1], Mickael Perrigault[1], Sandra E. Shumway[2], J. Evan Ward[2], Gary Wikfors[3], and **Bassem Allam[1].** [1]School of Marine and Atmospheric Sciences, State University of New York, Stony Brook, NY 11794; [2]Department of Marine Sciences, University of Connecticut, Groton, CT 06340; [3]NOAA Fisheries Northeast Fisheries Science Center Milford laboratory NMFS Milford, CT 06460.

Despite advances in the study of particle selection in suspension feeding bivalves (SFB), the mechanisms upon which bivalves rely to discriminate among particles have not been elucidated. In order to test the hypothesis that particle sorting in SFB could be based on a biochemical recognition mechanism, the mucus that covers the feeding organs of *Crassostrea virginica* was investigated and its effect on particle sorting was evaluated. Results showed that mucus was able to agglutinate several microalgae species and red blood cells, demonstrating the presence of lectins. Hemagglutination (HA) and HA inhibition assays, used to determine the carbohydrate specificity of the lectin activity, showed that mucus contains mannose-binding lectins. The presence of carbohydrates moieties,

potential ligands for lectins, on the surface of several microalgae species were detected using FITC-labeled lectins. In addition, the incubation of microalage with pallial mucus significantly reduced the binding of FITC-labeled lectins to their surface ligands suggesting that lectins present in mucus competitively blocked binding sites. Results of particle selection studies with *C. virginica* strongly suggest the involvement of lectin/carbohydrate interactions in the mechanisms of microalgae recognition. In conclusion, this work confirms the presence of lectins in mucus that covers the feeding organs of oysters and emphasizes their implication in particle sorting.

USING MICROSATELLITES TO DETERMINE IF TWO RIVERS IN THE DELAWARE BAY ARE SUPPORTING DISEASE REFUGIA FOR THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*). Thomas Evans[1], Coren Milbury[2], Ximing Guo[2], and **David Bushek[2].** [1]Juniata College, Department of Biology, Huntingdon, PA, 16652 USA; [2]Rutgers, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349 USA.

The fishery for the eastern oyster (*Crassostrea virginica*) in Delaware Bay (USA) has been heavily damaged by the pathogens, *Haplosporidium nelsoni* (MSX) and *Perkinsus marinus* (Dermo). Oysters in the bay have undergone and continue to experience heavy selection for resistance to MSX and Dermo. However, bay populations still struggle against both diseases even after many years of exposure (>50 years for MSX, and >15 years for Dermo). Reproduction by oysters in adjacent bodies of low salinity water (tributaries to the bay) may limit or retard the ability of bay populations to develop resistance. These low salinity populations usually remain unchallenged by disease, because neither MSX nor Dermo cause serious infections in low salinity areas. As a result larvae, produced from unexposed parent stock, may not acquire disease resistant traits. Microsatellite analysis can be used to determine population structure, recruitment origin, and potential disease refugia. The intent of this project was to identify population structure, using oysters collected from two Delaware Bay rivers (Leipsic and Cohansey), through the analysis of three microsatellite markers. Results reported here reveal potential population differentiation which may be useful in identifying disease refugia. This work was supported by an NSF REU supplement to award #0622642.

TOTAL BACTERIA AND VIBRIONACEAE IN *CRASSOSTREA VIRGINICA* IN DELAWARE. Johnna Fay and **Gulnihal Ozbay.** Delaware State University, Department of Natural Resources, Dover, DE, 19901, USA.

Historically, the Eastern oyster (*Crassostrea virginica*) has been a keystone species in Delaware Inland Bays, forming reefs that supply habitat to numerous species. The primary objective of this study was to evaluate the total bacteria and *Vibrionaceae* levels in *Crassostrea virginica* collected at three large oyster gardening sites within Delaware Inland Bays, and to determine the relationship between measured water quality and bacteria levels. Two gardening sites selected were located at Fenwick Island at the end of a man-made canal and in an open location within Little Assawoman Bay, and the third site was located in an open area in Indian River Bay. A simple colony overlay procedure for peptidases (COPP) was used to quantify *Vibrionaceae* in oyster tissue. Preliminary studies measuring the total bacteria and *Vibrionaceae* levels in oysters have shown an increase in total bacteria and *Vibrionaceae* levels over time during the summer months. Each study site also experienced relatively low levels of total nitrogen and total phosphorus for the summer months. Future research should focus on water quality and bacterial levels at more oyster gardening sites in Delaware Inland Bays. This information can be utilized by the oyster gardening program and be beneficial when harvesting oysters.

PRODUCTION OF QUAHOG, *MERCENARIA MECENARIA* AT THE WESTPORT MUNICIPAL SHELLFISH HATCHERY IN WESTPORT, MASSACHUSETTS, USA. Johnna Fay[1], Karin A. Tammi[2], Gary Sherman[3], and **Dr. Timothy Scott[2].** [1]Department of Agriculture and Natural Resources, Delaware State University, Dover, Delaware 1990; [2]Center for Economic and Environmental Development, Roger Williams University, One Old Ferry Road, Bristol, Rhode Island 02809-2921; [3]Westport Shellfish Department, Westport Town Hall, 816 Main Road, Westport, MA 02790.

During the summer of 2007, RWU shellfish researchers helped the Town of Westport Massachusetts produce quahog seed, *Merceanria merceanria* for planting in the Westport River Estuary. The Westport Municipal Shellfish Department's 200 ft^2 Shellfish Hatchery was established in 2002 to produce seed to help enhance shellfish stocks and to educate the public about the town's shellfish resources. The hatchery was built on the town's historical Lee's Wharf with funding and construction assistance from members of the Southeastern Shellfish Association. Last summer, the hatchery implemented batch culture growing algae from 125 ml to 1,000 ml stock cultures to 20 L glass carboys and 100 L culture tubes. Algal varieties cultured include: *Chaetoceros muelleri, Thalassiosira weisfloggii, Isochrysis galbana, Isochrysis sp.* and *Tetraselmis sp.* Native quahogs were individually spawned and the larvae were cultured in 500L tanks. Having no running fresh water for cleaning, the RWU students managed to set more than 500,000 quahogs onto down-welling screens which were later moved to land-based upwellers and planted on the public beds. Despite various limitations in the hatchery, the RWU students cultured algae, conditioned, spawned and produced an estimated 150,000, + 2 mm quahog seed during the summer of 2007.

MAXIMIZING BAY SCALLOP, *ARGOPECTEN IRRADIANS*, POPULATION REPRODUCTIVE CAPACITY: PILOT TESTS OF POTENTIAL RESTORATION OPTIONS IN NORTH CAROLINA. Stephen R. Fegley, David Gaskill, and **Charles H. Peterson.** Univ. of North Carolina Institute of Marine Sciences, Morehead City, NC 28557.

Since 2004 no harvest of bay scallops has occurred in North Carolina due to extremely low adult abundances. Additionally, intense late summer ray predation reduces spawning scallop densities below levels previously demonstrated necessary to support natural scallop population recovery. To enhance the existing low scallop population reproductive capability we need to collect and protect juvenile scallops until they are old enough to spawn. We placed replicate spat collectors, consisting of plastic mesh inside onion bags, in four locations known to support scallop populations historically and in a shore-side, relatively predator-free, salt pond that continuously received seawater. Through the fall we assessed site-specific settlement, survival, and growth of bay scallops in the collectors. Site-specific differences occurred but scallops recruited and survived in collectors at all sites. Some sites experienced spat collector attrition due to storms. We also observed high recruitment of juvenile scallops onto grass shoots outside of spat bags in the salt pond with subsequent high scallop survival and growth suggesting an alternative restoration option. Finally, we protected patches of unspawned, adult scallops by constructing PVC pole stockades to exclude rays. Stockades were effective in protecting scallops from rays but not from illegal human predation.

CYCLES OR SLIDES: DETECTION OF QPX IN THE QUAHOG *MERCENARIA MERCENARIA*. Chelsea Fitzsimons-Diaz[1], Jackie Defaveri[2], Dale Leavitt[3], and **Roxanna Smolowitz[4].** [1]Roger Williams University, Marine Biology Department, Bristol, RI 02809 & Marine Biological Laboratory, Woods Hole, MA 02543; [2]Marine Biological Laboratory, Woods Hole, MA 02543; [3]Roger Williams University, Marine Biology Department, Bristol, RI 02809; [4]New England Aquarium, Medical Center, Boston, MA 02110 & Marine Biological Laboratory, Woods Hole, MA 02543.

Real-time PCR (qPCR) allows for the direct observation of an increase in DNA as it is amplified, potentially leading to an improved method of pathogen detection in diseased animals. This study compared qPCR, as an efficient and accurate method of diagnosing Quahog Parasite Unknown (QPX) in hard clams (*Mercenaria mercenaria*), to the more traditional technique of histopathological observation. Subsamples of clam tissue from the same individuals were run on qPCR as well as being processed for traditional H&E stained histopathological sectioning. Tissues were collected from QPX-infected clams, harvested from aquaculture plots, three times during 2006 and were either processed for sectioning or stored at –20°C until analyzed by qPCR. qPCR subsamples were extracted for DNA using Qiagen's Stool Kit. DNA samples were run using Brilliant SYBR Green qPCR Master Mix (Strategene) with QPX primers amplifying a transcript of QPX DNA. Positive samples were quantified against a standard curve plotting Ct values against QPX organism concentrations. A comparison of the results from the qPCR method to results of the histological analysis suggests that qPCR may be used as a diagnostic tool for detection of QPX organism in hard clams. However, there are limitations to the amount of information one may conclude from this new technique.

CLIMATE CHANGE AND A TALE OF TWO PARASITES. Susan Ford. Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349 USA.

Dermo and MSX diseases have been major killers of eastern oysters for the past half century. The causative parasites, *Perkinsus marinus* and *Haplosporidium nelsoni*, respectively, both respond to seasonal temperature increase by proliferating in oysters. The northward spread of Dermo disease, once restricted to the southern US, is well documented and was coincident with a pronounced winter warming trend. *Perkinsus marinus* is now prevalent in oysters of the northeastern US. *Haplosporidium nelsoni* is also distributed along much of the US east coast, but "spread" from a midAtlantic focus in both northerly and southerly directions. Curiously, epizootics of MSX disease have occurred in northern sites, but not in southern sites. If *H. nelsoni* proliferates as temperatures increase, would that not favor the parasite's establishment in the south? The answer must lie in aspects of the two parasites that are not strictly tied to temperature. One important difference is that *P. marinus* is transmitted directly from oyster to oyster, whereas *H. nelsoni* probably has another host involved in its life cycle. Biotic or abiotic factors that block the life cycle, and hence the transmission, of *H. nelsoni* may be responsible for limiting outbreaks of MSX disease in the southern US.

COMPARATIVE ANALYSIS OF PUMPING ACTIVITIES AMONG THREE SPECIES OF BIVALVE MOLLUSC FED DIETS OF TWO DIFFERENT QUALITIES IN A DEPLETION RATE ASSAY. Dana M. Frank, J. Evan Ward, Sandra E. Shumway, and **Bridget A. Holohan.** Department of Marine Sciences, University of Connecticut, 1080 Shennecossett Rd., Groton, CT 06340 USA.

Many studies have examined the feeding activity of *Mytilus edulis* in response to varying concentrations and qualities of algal diet. Results from these studies are often used as evidence when discussing responses of any bivalve to similar conditions. It is our premise that not all bivalve species respond in the same way when presented with the same conditions. We measured exhalant current velocities and bulk flow over time, which are independent of food concentration. We performed depletion rate assays to assess and compare the pumping behaviors of three species of bivalve mollusc (blue mussel, *Mytilus edulis*, eastern oyster, *Crassostrea virginica*, bay scallop, *Argopecten irradians)* under conditions of varying

food quality and quantity. Animals were each exposed to one of two different diets; high quality = 100% *Tetraselmis chui*, low quality = 25% T. chui: 75% *Spartina sp*. Each animal was exposed to $5.0x10^4$ particles·ml^{-1} and sampled every 10 minutes for the duration of the depletion rate assay which concluded when the animal closed its shells for at least 2 sampling cycles. Three components were sampled concurrently. Exhalent velocity was measured using particle image velocimetry, cross-sectional area of the exhalant siphon was measured using video analysis and water samples were taken to assess clearance rate.

HERITABILITY FOR BODY WEIGHT OF THE NATIVE OYSTER (*CRASSOSTREA VIRGINICA*) IN THE FIRST SEASON OF GROWTH. A. S. Frank-Lawale and **S. K. Allen Jr.** Aquaculture Genetics and Breeding Technology Centre, Virginia Institute of Marine Science, Gloucester Point, VA 23062, USA.

In the absence of disease, body weight is emerging as the primary breeding objective in Virginia, particularly in low salinity areas where mortality from the diseases MSX and Dermo is low. Commercial operations aim to harvest their crop in 18 months thus, growth performance in the time period before the first winter is essential. It is therefore important to test if additive genetic variation exists for this phase of growth. 100 juvenile oysters from each of 67 full-sib families developed from a partial factorial cross of 23 sires and 34 dams was used in this trial. Families were reared separately throughout the larval culture and graded into two groups at 12 weeks post spawning using a 0.635 cm screen. Fifty5 animals within each grade were selected at random from all the families and individually weighed. Each group of 50 was put in a small plastic mesh bag and randomly placed in big oyster culture bags for growout. Oysters were grown for 5 months starting 1st of August 2007. Individual weights of all the surviving animals were taken in December 2007. Heritability estimates for body weight were around 0.31 indicating moderate additive genetic variance for increasing early body weight.

ABALONE HEALTH: A REVIEW OF DISEASES AND RESEARCH DIRECTIONS. Carolyn S. Friedman. School of Aquatic and Fishery Sciences, University of Washington, P.O. Box 355020, Seattle, WA 98195, USA.

Until the mid-1980s, few abalone diseases were reported (abalone perkinsiosis, larval vibriosis, shell boring pests, etc). Since the mid-1980s several severe bacterial (withering syndrome in California; vibriosis in European abalone) and viral diseases (herpes-like viral infections in Australasia) have emerged. Novel disease agents have also been documented at single locations where they caused catastrophic losses but were not observed in subsequent years including *Labyrinthuloides haliotidis* in western Canada and *Urosporidium* sp. in New Zealand. A previously unknown sabellid polychaete from South Africa has caused severe economic losses culturists where it is endemic or has been introduced. Determining the origin of these newly observed agents relies on knowledge of their presence, distribution, and seasonality. Unfortunately, such information is often lacking and continues to hamper disease research and management. Shellfish disease research is traditionally based on histopathology-electron microscopy combined with field and laboratory trials. Modern molecular methods such as PCR (conventional and quantitative), whole genome amplification and sequence analyses, gene expression, and plasmid manipulation now complement this research and enable researchers to better identify and characterize diseases and their agents. Use of multidisciplinary research combining traditional pathology methods with ecology, physiology and genetic/molecular methods has grown and facilitates more informed management decisions.

A BAC-BASED PHYSICAL MAP FOR THE PACIFIC OYSTER GENOME. Patrick M. Gaffney. University of Delaware.

As part of the Oyster Genome Consortium (OGC) effort to develop genomic resources for oysters, a BAC (Bacterial Artificial Chromosome) library was prepared from sperm from a single inbred Pacific oyster (*Crassostrea gigas*). A total of 64,403 clones were fingerprinted and assembled at the Genome Sciences Centre (Vancouver, BC) using the traditional agarose fingerprint method. 61,825 of the BAC clones (96%) were assembled into 3,374 contigs, with an average of 18 clones per contig. The resulting map and BAC library will be available to the oyster research community, and will serve as a valuable asset for gene discovery, characterization of quantitative trait loci (QTL) and other genes of interest, and provision of genetic markers well spaced across the oyster genome. Future directions include the integration of physical, cytogenetic and genetic linkage maps for *C. gigas*, as well as comparative genomic studies of the eastern oyster *C. virginica*.

LARVAL SHELL FORMATION: REQUIREMENT FOR SR MAY BE EXPLAINED BY AMORPHOUS CALCIUM CARBONATE AS A PRECURSOR PHASE FOR ARAGONITE. Scott M. Gallager[1], Amber D. York[1], Yvette Longonje[2], and **Sheri White[3].** [1]Woods Hole Oceanographic Institution, Biology Department, Woods Hole, MA 02543; [2]Howard University; [3]Woods Hole Oceanographic Institution, Applied Ocean Engineering, Woods Hole, MA 02543.

To form normal shells, Mollusc larvae are known to require elevated levels of Sr^{+2} (>6 ppm, ~80 μmol/Kg) in seawater for a very brief and specific temporal window during early shell formation (Gallager et al. 1989). Using micro-Raman spectroscopy on bivalve larvae (*Placopecten magellanicus* and *Mercenaria mercenaria*) during early shell formation we found that the very first calcium carbonate detected in the late trochophore stage was amorphous calcium carbonate (ACC). The ACC in these early stages was not birefringent under polarized light microscopy. Not until the organic layer was fully formed at least 20 h following fertilization was birefringence noted. At this time where ACC was

first detected, aragonite predominated. Once the larval shell consisted entirely of aragonite, about 24 h following fertilization, elevated levels of Sr^{+2} were no longer required for further normal shell formation. We hypothesize that ACC is first deposited onto the organic layer like toothpaste and is stabilized in this non-crystaline phase by the presence of Sr^{+2}. Once ACC completely covers the organic layer Sr^{+2} is removed from the area allowing the ACC to crystallize into aragonite. This process has important implications for the evolutionary and eco-physiological constraints placed on the Mollusca.

THE NORTHEAST BENTHO-PELAGIC OBSERVATORY (NEBO) TO SUPPORT SEA SCALLOP FISHERIES AND ECOSYSTEM APPROACHES TO MANAGEMENT. **Scott M. Gallager[1], Richard Taylor[2], Norman Vine[2], Amber D. York[1], Steve Lerner[3], Hauke Kit-Powell[4], Larry Mayer[5], Peter Auster[6], Dvora Hart[7], Michael Fogarty[7],** and **Lakshman Prashad[8].** [1]Woods Hole Oceanographic Institution, Biology Department, Woods Hole, MA 02543 USA; [2]Advanced Habitat Imaging Consortium; [3]Woods Hole Oceanographic Institution, Applied Ocean Engineering, Woods Hole, MA 02543 USA; [4]Woods Hole Oceanographic Institution, Marine Policy, Woods Hole, MA 02543 USA; [5]Center for Coastal Ocean Mapping, University of New Hampshire, Durham, NH 03824; [6]National Undersea Research Center and Department of Marine Sciences, University of Connecticut, Groton, CT 06340; [7]Northeast Fisheries Science Center, Woods Hole, MA 02543; [8]Los Alamos National Laboratory, Los Alamos, NM 87545

This project is designed to produce unique data products for fisheries and marine protected area managers and to foster development of ecosystem approaches to management (EAM). We are observing and quantifying key taxa, benthic community structure, species diversity, seafloor habitat characteristics, and coincident water column properties with repeated measurements in multiple, sentinel sites on time scales of weeks to years. At sentinel sites along the US Northeast coast that have both high fisheries and conservation value, we are quantifying how communities respond to system change (climate events, fishing activity, position of oceanographic features [fronts], etc). This requires fusion of disparate, synoptically acquired data sets, including high-resolution acoustic bathymetry and backscatter (on scales of meters to kilometers), stereo optical imagery (on scales of millimeters to meters), water column plankton distributions (microns to millimeters), and the development of image bioinformatic tools for classifying targets and substrates. Integrated data products are being developed using advanced visualization tools so key fishery target species and non-target community responses to regulatory practices can be observed and quantified at multiple, relevant space and time scales, in relation to variations in seafloor habitat and boundary layer conditions.

HATCHERY PRODUCTION OF THE BAY SCALLOP (*ARGOPECTEN IRRADIANS*) FOR RESTORATION & RESEARCH. **Ryan L. Gandy** and **Curtis D. Hemmel.** Bay Shellfish Co., P.O. Box 289, Terra Ceia, FL 34250.

The Bay Shellfish Co. (BSC) hatchery was established in 1996 to provide hard clam seed to the emerging aquaculture industry. In 2001, research and development efforts were undertaken to investigate various endemic bivalve species for their commercial potential, one of which was the bay scallop (*Argopecten irradians*). The BSC hatchery was given the opportunity, in 2004, to produce its first bay scallop seed for restoration purposes. This work continues yielded valuable information with regard to conditioning broodstock, spawning, larval rearing and post-set production. Though these data are beneficial for production, further investigation is necessary to achieve consistent year round culture. Continuing improvements to flow through designs, critical water quality assessment, animal health assessment, genetic diversity and reduced production costs are essential to further success. BSC's commitment to providing seed for bay scallop restoration is driven by a desire to assist in the recovery of Florida bay scallop populations and demonstrate the advantages of private/public partnerships.

STABLE ISOTOPIC COMPOSITION OF GEODUCK SHELLS (*PANOPEA ABRUPTA*) AND THE POPULATION INDEX STATIONS IN HOOD CANAL. **Yongwen Gao[1], Bob Sizemore[2],** and **Todd Palzer[3].** [1]Makah Fisheries Management, P.O. Box 115, Neah Bay, WA 98357, USA; [2]Washington Department of Fish and Wildlife, 600 Capitol Way N, Olympia, WA 98501-1091, USA; [3]Washington Department of Natural Resources, 1111 Washington St. SE, Olympia, WA 98504-7027, USA.

The use of stable oxygen and carbon isotope ratios of geoduck shells (*Panopea abrupta*) to examine the environmental conditions that the clam experienced is a new attempt. In this study, we analyzed geoduck shell and seawater samples collected from the northern (Vinland), central (Hamma-Hamma), and southern (Tahuya) Hood Canal of Puget Sound, Washington, and compared with the population index stations established by the Department of Fish and Wildlife. The isotopic results showed that $\delta^{18}O$ values of Hood Canal geoduck shells ranged from –1.34 to +0.95‰ VPDB, whereas the $\delta^{13}C$ values ranged from –2.19 to +0.35‰ VPDB. There were significant differences between the three sampling sites, and the pattern of isotopic variations was markedly different. The distinct $\delta^{18}O$ depletion of Hamma-Hamma samples indicated that significant amount of freshwater entered the central Hood Canal, establishing a salinity-related difference in $\delta^{18}O$ of seawater. The consistent decrease of $\delta^{13}C$ in Tahuya samples, in contrast, showed that changes of geoduck diet in the southern Hood Canal were larger than those in the northern sub-region. Overall, our study supports the establishment of

geoduck index stations and isotopic data can be used as evidence for environmental changes over a small geographic scale such as Hood Canal.

GROWTH AND FEEDING PHYSIOLOGY OF JUVENILE RED ABALONE, *HALIOTIS RUFESCENS*, REARED IN LABORATORY WITH FRESH KELP AND BALANCED DIETARY PROTEIN. **Zaul Garcia-Esquivel[1]** and **Horst Felbeck[2].** [1]Universidad Autónoma de Baja California, Instituto de Investigaciones Oceanológicas, Km 103 carretera Tijuana-Ensenada, Ensenada B.C., México; [2]Scripps Institution of Oceanography, UCSD, 9565 Gilman Dr. La Jolla, CA 92092-0202.

Juvenile *Haliotis rufescens* were reared in the laboratory in order to investigate the extent to which fresh kelp and formulated feed with 25% (25P) and 38% protein content (38P) affected their growth rate, gut residence time (GRT), food consumption (C), food conversion ratio (FCR) and digestibility. Abalone from 38P attained the highest growth rate (70.5 ± 4.2 μm d^{-1}, 98.3 ± 6.95 μg d^{-1}), followed by 25P (47.9 ± 2.79 μm d^{-1}; 67.4 ± 2.82 μg d^{-1}) and kelp (23.6 ± 3.36 μm d^{-1}; 28.2 ± 4.11 μg d^{-1}). No significant differences were observed in consumption rate among treatments (0.61 to 0.68% BW d^{-1}), yet kelp-fed abalone exhibited higher FCR (2.44), PER (4.42), and apparent digestibility of dry matter, protein and gross energy (69.5 to 73.2%) than 38P organisms (59.8 to 62.4%). They also showed longer GRT (23.1 ± 0.93 h). This study demonstrated that formulated diets with 25% and 38% protein inclusion can sustain higher growth rates of juvenile *H. rufescens* than fresh algae. These differences seem to be due to the amount of dietary protein. Kelp meal appears to improve the consumption and digestibility of balanced diets, and its inclusion in formulated diets is recommended.

COMPARISON OF INTERTIDAL OYSTER POPULATIONS BETWEEN A LIMESTONE BREAKWATER AND A NATURAL REEF IN COASTAL LOUISIANA. **Nicholas Gaspard[1], Earl Melancon[1],** and **Jean Landry[2].** [1]Nicholls State University, Department of Biological Sciences, Thibodaux, LA 70310, USA.; [2]The Nature Conservancy, Grand Isle Field Office, P.O. Box 675, Grand Isle, LA 70358, USA.

Limestone breakwaters have the potential to be an important substrate for oyster recruitment and reef building as well as for erosion control. We studied three intertidal habitats for a year; the windward and leeward sides of a breakwater and a natural reef. We focused on oyster and barnacle recruitment, survival and population structure between the habitats. Results indicate typical annual bimodal oyster recruitment events at all three sites. Oyster spat density and survival was greatest at the natural reef, followed by the leeward side of the breakwater and then the windward side. Oyster size frequency analyses suggest oyster population complexity in the order of natural reef-leeward breakwater-windward breakwater. Barnacle recruitment and density appears to follow the same recruitment and density trends as oysters. The oyster drill, *Stramonita haemastoma*, a principal predator of oysters, was at a breakwater density several orders of magnitude greater than the natural reef. In conclusion, the leeward side of the breakwater appears to be functioning as an oyster habitat more so than the windward side, but less than the natural reef. This study is part of a larger breakwater habitat study funded by the NOAA Community-based Restoration Program through the Louisiana Nature Conservancy and the University.

DISTRIBUTION OF QUAHOG PARASITE UNKNOWN IN THE COASTAL MARINE ENVIRONMENT. **R. J. Gast[1], D. M. Moran[1], C. Audemard[2], M. M. Lyons[3], J. Defavar i[4], K. R. Uhlinger[4], K. S. Reece[2], D. F. Leavitt[5],** and **R. Smolowitz[6].** [1]Woods Hole Oceanographic Institution, Woods Hole, MA 02543 USA; [2]Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, VA 23062 USA; [3]University of Connecticut, Avery Point, CT 06340 USA; [4]Marine Biological Laboratory, Woods Hole, MA 02543 USA; [5]Roger Williams University, Bristol, RI 02630 USA; [6]Marine Biological Laboratory, Woods Hole, MA 02543 USA.

The thraustochytrid protist Quahog Parasite Unknown (QPX) is a significant cause of hard clam, *Mercenaria mercenaria*, mortality along the Northeast coast of the United States. Here we report on the assessment of the environmental persistence of QPX in several sites in Virginia and Massachusetts. We were able to detect QPX using DGGE in almost all of our different sample types (water, sediment, algae, invertebrates, detritus), suggesting that the parasite was widely distributed in the environment. Using in situ hybridization we were also able to observe cells in or on macrophyte or detritus samples. More samples from Massachusetts were positive than from Virginia, reflecting the prevalence of QPX in clams in those regions, and there was a seasonal pattern to the types of samples positive from Massachusetts. The method has also been used to investigate the effectiveness of removing dead and dying clams from an infected area to reduce persistence of the parasite in the environment. Our data suggests that although it may be difficult to completely eradicate QPX from the environment, it may be possible to keep the incidence of disease under control through a rapid response of clam removal and subsequent good plot husbandry.

RESTORATION STRATEGIES FOR FLORIDA'S HARD CLAM, *MERCENARIA MERCENARIA*. **Stephen P Geiger, Sarah Stephenson,** and **William S. Arnold.** Florida Fish & Wildlife Conservation Commission—Fish & Wildlife Research Institute.

The hard clam fishery in Florida is erratic, characterized by booms and busts, and must compete with a growing aquaculture industry. Two peaks in wild harvest have exceeded one million

pounds per year (1984–1987; 1993–1995). In Brevard County, a special commercial clam license is required and funds raised from the license have been used for researching methods intended to revitalize the local fishery. Early methods focused on seeding and transplants. We have also investigated the use of hatchery-reared larvae to create widely distributed sets of clams. Initially, we released commercially-produced fertilized embryos and tracked their dispersal. Anecdotal reports from fishermen were encouraging. Monitoring of condition in wild stocks should allow the use of wild caught broodstock in larval release efforts without conditioning in a hatchery. These methods are intended to minimize cost and effort but are difficult to assess. Recently, we have begun to release pediveligers (ready-to-set larvae) into containment booms. Hopefully, the very high density, ~1,000,000 larvae per $75m^2$, will allow us to evaluate early survival rates. Preliminary estimates indicate settlement 50 times higher inside the enclosure than background levels outside the enclosures, offering a tool for settlement studies in minimally modified environments.

GEOGRAPHIC INFORMATION SYSTEMS (GIS) TRAINING FOR MUNICIPAL SHELLFISH COMMISSIONS: TOOLS FOR SHELLFISHERIES AND AQUACULTURE MANAGEMENT **Tessa Getchis[1,2], Michael Prisloe[2], Cary Chadwick[2], David Carey[3],** and **Kristin Frank[3].** [1]University of Connecticut, Sea Grant Extension Program; [2]University of Connecticut, Cooperative Extension System; [3]Connecticut Department of Agriculture, Bureau of Aquaculture.

Connecticut's shellfish commissions are responsible for managing recreational and commercial shellfisheries within their town waters. Each commission is required to develop a management plan that also includes a process for reviewing applications for aquaculture. As part of this process, commissions assess potential social and use conflicts, as well as effects on protected habitats and species resulting from aquaculture activity. Shellfish commissions use several types of information in the evaluation of aquaculture applications including distribution and abundance of local marine resources, mooring positions, shellfish classification areas, water quality data, and location of existing leases. While much of this information is available in Geographic Information System (GIS) data layers, the many managers have not obtained training in the utilization of Global Positioning Systems (GPS), GIS and geospatial data sets, and thus continue to rely on paper maps Recognizing the need for better shellfisheries management tools, extension specialists developed a GIS training course for municipal managers. The course provides commissions the necessary tools for collecting, inputting, and editing geospatial data used for managing shellfisheries in their respective towns. The course introduces local commissions to the basics of desktop GIS, and is constructed around Environmental Systems Research Institute's (ESRI) ArcGIS software.

THE HISTORY AND STATUS OF BAY SCALLOP, *ARGOPECTEN IRRADIANS IRRADIANS*, POPULATIONS IN CONNECTICUT AND NEW YORK. **Ronald Goldberg[1]** and **Stephen T. Tettelbach[2].** [1]National Oceanic and Atmospheric Administration, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Avenue, Milford, Connecticut 06460 USA; [2]Dept. of Biology, C.W. Post Campus of Long Island University, Brookville, NY 11548 USA.

Eastern Connecticut's estuaries supported bay scallop populations for much of the last century, but numbers have declined markedly in recent decades. In the 1990s, Milford Laboratory conducted experiments in the Niantic River to support the Waterford-East Lyme Shellfish Commission's enhancement efforts. Experiments revealed high survival of large seed, planted late in the fall. Hatchery seed were overwintered and stocked in spawner sanctuaries. Other projects included production of selectively-bred, distinctively marked scallops and establishment of net-pens to exclude predators. After years of low abundance, a small population was discovered in 2008, prompting a limited recreational harvest. Commercial bay scallop harvests in eastern Long Island, New York averaged ~300,000 lbs/year from 1960–1984, but 1985–1988 brown tides decimated bay scallop populations and fisheries. Subsequent reseeding efforts contributed to increases in scallop populations. In 1994, commercial landings reached 271,000 lbs, but severe brown tide in 1995 again decimated stocks. Since then, annual harvests have averaged <2% of historic levels, but resurgence of scallop populations has occurred in localized areas over the last 5 years. Reasons for the lack of a complete population recovery and contributions of ongoing, large scale restoration programs by Cornell Cooperative Extension of Suffolk County and Long Island University are discussed.

EFFECTS OF *KARENIA BREVIS* ON THE DEFENSE RESPONSES OF THE HARD CLAM *MERCENARIA MERCENARIA*, THE OYSTER *CRASSOSTREA VIRGINICA*, AND THE MUSSEL *PERNA VIRIDIS*. **Madeleine Gonçalves[1], Philippe Soudant[2], Vincent G. Encomio[1],** and **Aswani K. Volety[3].** [1]Coastal Watershed Institute, Florida Gulf Coast University, 10501 FGCU Blvd, Fort Myers, FL 33965. USA.; [2]LEMAR. IUEM. UBO, UMR 6539, Technopole Brest-Iroise, Place Nicolas Copernic, 29280 Plouzané, France; [3]Coastal Watershed Institute, Florida Gulf Coast University, 10501 FGCU Blvd, Fort Myers, FL 33965. USA.

Harmful algal blooms can occur and persist along the west coast of Florida. *Karenia brevis* has been shown to be the main algae responsible for those blooms, commonly called "red tides". Previous studies have demonstrated that *K. brevis* has a deleterious impact upon humans and marine species including shellfish. This study focused on the acute effect of *K.brevis* on three bivalve species in Southwest Florida: the hard clam *Mercenaria mercenaria*, the eastern oyster *Crassostrea virginica*, and the invasive green

mussel *Perna viridis*. For each species, defense responses (hemocytes mortality, phagocytosis and reactive oxygen species production) were examined after direct exposure to *K. brevis* (1,000 cells/mL + L1-Si medium; L1-Si medium alone; seawater control) using flow cytometry techniques. *K. brevis* hemolytic activity (using horse red blood cells) was at its peak 15-17 days after inoculation (60% lysis after 24 hours of incubation). Significant differences between controls and *K.brevis* exposed bivalves were observed. There was an increase in hemocyte mortality for all three species upon exposure to *K. brevis*. In addition, a decrease in the phagocytic capacity for *M. mercenaria*, and an increase in the reactive oxygen species production for *C. virginica* and *P. viridis* (ANOVA; $P < 0.05$) were observed.

DEATH BY DISSOLUTION: SEDIMENT CALCIUM CARBONATE SATURATION STATE AS A MORTALITY FACTOR FOR JUVENILE BIVALVES. Mark A. Green[1], George Waldbusser[2], Shannon Reilly[1], and **Karla Emerson[1].** [1]Saint Joseph's College of Maine, Standish, ME 04084; [2]UMCES-Chesapeake Biological Laboratory, Solomons, MD 20688.

We use a new experimental method to evaluate the effect of carbonate saturation state at the sediment water interface on survivorship of the juvenile clam (*Mercenaria mercenaria)* at 3 size classes (0.2, 0.4, 0.6 mm). Our experiments manipulated saturation state of sediment from beneath with CO_2 to yield $\Omega CaCO_{3aragonite}$ values of 0.4, 0.6, and 1.6, values frequently encountered in coastal mud deposits. We then evaluated mortality of juvenile bivalves deposited on the sediment surface as a function of time. Mortality was highest in the smaller size classes and at the lowest saturation states. Significant mortality of 0.2 mm *M. mercenaria* was found in both undersaturated treatments ($\Omega_{aragonite} = 0.4, 0.6$; $P < 0.05$). The 0.4 mm *M. mercenaria*, experienced significant mortality under the most undersaturated treatment ($\Omega_{aragonite} = 0.4$; $P < 0.05$), although for $\Omega_{aragonite} = 0.6$ treatment mortality was nearly significant (P-value of 0.07). Similarly, the 0.6 mm clams experienced significant mortality under the most undersaturated sediments ($\Omega_{aragonite} = 0.4$), although again the $\Omega_{aragonite} = 0.6$ treatment was nearly significant at $P = 0.06$. Results show that death by dissolution may be a very significant mortality factor and can no longer be ignored in studies of recruitment of carbonate-bearing fauna to coastal deposits.

RESTORATION OF A BYPASSED BIVALVE: OLYMPIA OYSTERS OF THE PACIFIC COAST. Kerry Griffin. National Marine Fisheries Service, Silver Spring, MD 20910.

The Olympia oyster (*Ostrea conchaphila* or *O. lurida*) is the only oyster species native to the US West Coast. Although population abundance has declined along most of the West Coast, they remain widely distributed, and have shown themselves to be resilient and restorable. In response to growing interest and practice of oyster restoration, a group made up of NGOs, academia, Native American Tribes, industry, and government agencies convened two workshops on the science, practice, and social aspects of native oyster restoration. The proceedings from these two workshops (in 2006 and 2007) tell a story of the science, practice, and social aspects of restoration; but more importantly, remind us of how much we don't know about this little bivalve. This species is an important component of estuarine ecosystem functioning, and is ripe for larger-scale restoration. But what is the right mix of science, political will and funding, to achieve this objective?

STEAMER CLAM (*MYA ARENARIA*) RESTORATION EFFORTS IN TWO COASTAL PONDS IN OAK BLUFFS, MASSACHUSETTS (MARTHA'S VINEYARD ISLAND). David W. Grunden, Danielle Ewart, and **Peter Estrella.** Town of Oak Bluffs Shellfish Department, Oak Bluffs, MA 02557.

This project began in 2001 when the Town of Oak Bluffs purchased an axial flow upweller. Three trial restoration sites were chosen. One site has continually remained open for harvest. The other two sites were alternated one being open every other year. All three sites were utilized primarily for recreational shellfishing. We are now seeding additional areas.The first year only 200K steamer seed was grown in the upweller and broadcast seeded at 12–15 mm. In subsequent years we have grown a minimum of 600K *Mya arenaria* annually. Additionally sand filled nursery rafts were constructed to achieve a larger sized clam before being seeded into public beds. The seed size range, when broadcasted after growing in the nursery rafts until the fall, has been 22.4–38.2 mm. The fishing effort has been monitored by the Shellfish Department and we have seen an increase in the steamer clam landings within the Town from 78 bushels in 2001 to 249.5 bushels in 2007.

EFFECTS OF *ALEXANDRIUM MINUTUM* EXPOSURE ON PHYSIOLOGICAL AND HAEMOCYTE PARAMETERS OF THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*. H. Haberkorn[1], C. Lambert[1], N. Le Goïc[1], A. Le Long[2], P. Lassus[2], and **P. Soudant[2].** [1]LEMAR, UMR 6539, IUEM-UBO, Technopole Brest-Iroise, Place Nicolas Copernic, 29280 Plouzane, France; [2]LEMAR, UMR 6539, IUEM-UBO, Technopole Brest-Iroise, Place Nicolas Copernic, 29280 Plouzane, France.

The effects of an artificial bloom of the toxin-producing dinoflagellate, *Alexandrium minutum*, upon physiological and haemocyte parameters of the Pacific oyster, *Crassostrea gigas*, were assessed. Diploid and triploid oysters were exposed for 4 days to a 10 ml·min^{-1} continuous flow of 5×10^3 cells ml^{-1} cultured *A. minutum* and compared to control diploid and triploid oysters fed T-*Isochrysis*. Experiments were repeated twice, in April and mid-May 2007, when diploid oysters were

immature and mature, respectively. In both experiments, triploid oysters accumulated more PST (approximately 2X) than diploid oysters. Coincidentally, a significant decrease in fatty alcohols in digestive glands of oysters exposed to *A. minutum* was observed. Significant differences, in terms of phenol-oxidase activity, number and morphology of haemocytes, and haemocyte reactive oxygen species (ROS) production, were observed between *A. minutum*-exposed and non-exposed oysters. Also, significant positive correlations between PST accumulation in digestive gland and several of the measured physiological and haemocyte parameters in *A. minutum*-exposed oysters were found. This suggests that some of the observed biological changes may result from PST intoxication in a dose-dependent manner. This study also incorporates results from histological observations and gene-expression analyses.

MODELING CIRCULATION AND TRANSPORT PATHWAYS FOR OYSTER LARVAE IN DELAWARE BAY. D.B. Haidvogel, J. Wilkin, and **D. Herceg.** Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ, 08901, USA.

As part of a collaborative project, supported by the National Science Foundation Ecology of Infectious Diseases (NSF EID) program, we have developed and validated a three-dimensional circulation model of the Delaware Bay. The model, based upon the Regional Ocean Modeling System (ROMS), is forced by observed tidal, riverine and atmospheric fluxes. Validation of tidal heights, and surface and bottom currents, for a target period in 1984 shows high quantitative agreement between the model fields and concurrent observations. Reconstruction of Lagrangian particle tracks has been used to begin to infer transport pathways of larvae of eastern oysters (*Crassostrea virginica*) and MSX and Dermo disease pathogens. Initial results of these drifter release experiments also agree qualitatively with known oyster larval distribution patterns and as such provide a starting point for development of understanding of genetic exchange in Delaware Bay oyster populations. In the next phase of this project, oyster larvae behavior will be added to the Lagrangian particle tracking analysis.

SCALLOP RESTORATION IN RHODE ISLAND: NORTH CAPE SCALLOP RESTORATION AND BEYOND. Boze Hancock[1], Bryan Deangelis[2], James Turek[2], John Catena[3], Najih Lazar[4], George Taber[5], and **Robert Hudson[6].** [1]The Nature Conservancy, Global Marine team, Narragansett, RI, 02882; [2]NOAA, Restoration Center, Narragansett, RI, 02882; [3]NOAA, Restoration Center, Gloucester, MA, 01930; [4]RI Dept. of Environmental Management, Division of Fish and Wildlife, Wakefield, RI, 02879; [5]Block Island Maritime Institute, Block Island, RI, 02807; [6]Save The Bay, Narragansett Bay, Providence, RI, 02905.

Bay scallop (*Argopecten irradians*) restoration in Rhode Island began in the 1980s with broadcast seeding and limited monitoring. In 2002 the *North Cape* Shellfish Restoration Program, a federal-state trustee oil spill mitigation partnership, increased the scale of direct seeding, including performance monitoring, but results were disappointing. Since 2004 caged spawner-sanctuaries have been successful at establishing self sustaining populations in Ninigret and Quonochontaug Ponds along the south coast of Rhode Island. Ten to twenty thousand broodstock were placed in cages annually for 2004 and 2005 in Ninigret and 2006 and 2007 in Quonochontaug Ponds. The relative abundance of larval settlement was monitored using spat bags, and mature scallop abundance using random transect dive surveys. The Ninigret settlement rose rapidly to 2005 resulting in approximately 190,000 scallops in 2006. Poor larval survival in 2006 reduced the population in 2007 but larval settlement again increased in 2007. Settlement results in Quonochontaug Pond have reflected broodstock abundance since 2006. The early success of scallop restoration in the South County salt ponds initiated analogous restoration projects by Save The Bay in Narragansett Bay and by the Block Island Maritime Institute in Great Salt Pond, Block Island. Preliminary results from these projects will be presented.

THE BAMBOO WORM INVASION OF SAMISH BAY: ECOLOGY AND CONTROL OF *CLYMENELLA TORQUATA* IN A NORTHEASTERN PACIFIC ESTUARY. Lillian P. Hancock, P. Sean Mcdonald, Freya E. Goetz, and **Paul Dinnel.** Western Washington University, Shannon Point Marine Lab, Anacortes, WA, 98221, USA.

The bamboo worm, *Clymenella torquata*, is a tube-building polychaete native to the northwestern Atlantic. Invasive *C. torquata* in the northeastern Pacific have negatively impacted oyster culture operations. In Samish Bay, Washington, bioturbating worms destabilize sediments, thereby indirectly increasing mortality of oysters that subside into unconsolidated mud. The present study investigated: 1) the ecology of invasive *C. torquata* along beaches adjacent to abandoned culture grounds to determine factors affecting worm distribution, and 2) potential control measures on tidelands. Survey results corroborate previous observations that a significant negative relationship exists between *C. torquata* and sediment compaction/firmness; worms also alter grain composition of the substrata. The efficacy of five potential physical control methods (shell application, rototilling, hydraulic pumping, covering, and compression) in reducing worm biomass and tube mass and increasing sediment firmness were tested in a field experiment. Although worm and tube biomass did not significantly decrease within one month of treatment, sediment firmness significantly increased. In order to determine how physical disturbance could be used to control the worm, we also assessed burrowing speed, tube-building rates, and regeneration abilities in the laboratory. Experiments suggest that physical control measures could be used to reduce the impact of *C. torquata* on oyster culture operations.

ANALYSIS OF SEA SCALLOP (*PLACOPECTEN MAGELLANICUS*) GROWTH FROM SHELL INCREMENT DATA USING LINEAR MIXED-EFFECTS MODELS. Deborah R. Hart and **Antonie S. Chute.** Northeast Fisheries Science Center, Woods Hole MA 02543 USA.

Many invertebrates are difficult to reliably age, so that growth needs to be inferred from growth increment data. Traditional methods that infer growth parameters from this type of data can be biased if, as is usually the case, growth varies among individuals in the population. We present a novel, linear mixed-effects method for estimating von Bertalanffy growth parameters from growth increment data which is approximately unbiased in the presence of individual growth variability. Our method was applied to growth increments from over 6,500 sea scallop (*Placopecten magellanicus*) shells collected between 2001 and 2007 from the principal US sea scallop fishing grounds on Georges Bank and in the mid-Atlantic Bight. Sea scallops grow faster and attain larger sizes at both shallower depths and in areas closed to fishing. Scallop density had little or no effect on growth.

IDENTIFICATION OF BIVALVE LARVAE BY FLUORESCENCE *IN SITU* HYBRIDIZATION. Susan A. Heaney, Aaron P. Maloy, and **John W. Slater.** Centre of Applied Marine Biotechnology (CAMBio), Letterkenny Institute of Technology, Letterkenny, Ireland.

A reliable method for the rapid and accurate identification of bivalve larvae would prove invaluable for both ecological studies and commercial interests. Morphological identification of bivalve larvae is notoriously difficult. Although immunological and molecular techniques have been reported, each has unique advantages and disadvantages. The aim of this project is to develop a more robust method of identification based on fluorescence in situ hybridization (FISH). Results demonstrated that the initial fixation step resulted in a significant increase in autofluorescence. We have shown that post-fixation treatment with Chemicon® reduces autofluorescence to an acceptable level, although fresh, unfixed larvae still exhibit the lowest levels observed. We are currently optimizing hybridization and washing protocols with the intention of developing a multiplex method for the detection of commercially valuable species in Irish waters.

ECOSYSTEM SERVICES PROVIDED BY OYSTER REEFS: AN EXPERIMENTAL ASSESSMENT. Kenneth L. Heck Jr.[1], Just Cebrian[1], Sean Powers[1], Kelly Majors[2], Dorothy Byron[1], Rochelle Plutchak[2], and **Nate Geraldi[3].** [1]Dauphin Island Sea Lab, 101 Bienville Blvd., Dauphin Island, AL 36528; [2]University of South Alabama, Mobile, AL; [3]University of North Carolina, Chapel Hill, NC.

We experimentally assessed the ecosystem benefits of oyster reef restoration in marsh creeks in Mobile Bay, AL. The project used a Before-After-Control-Restoration (BACR) design in which 3 pairs of marsh creeks were monitored for 8 months prior to adding oysters. Oyster additions, which produced densities higher than ever reported in the study area, took place in one randomly selected creek of each of the creek pairs. Sampling was conducted for sixteen months after oyster additions. While there were small-scale increases in water clarity, there were no observable changes in nutrient dynamics, water-column primary production, benthic primary and secondary production, or abundance of young of the year finfish, crabs or shrimp between experimental and control creeks. The absence of effects may be due to a combination of large inputs of POM from surrounding marshes, limited mixing, resuspension of benthic algae, and an unusually large number of tropical storms. Regardless of cause, we did not find the expected changes in water clarity and biological activity, and we urge caution in promoting the effects of reef restoration in marsh creeks. We conclude with a plan for follow-up studies to evaluate the alternative explanations for why we did not observe large effects of reef restoration.

INSIGHTS INTO OYSTER POPULATION GENETICS FROM AN INDIVIDUAL BASED MODEL. Dennis Hedgecock[1], John M. Klink[2], Eric N. Powell[3], Louis Plough[1], and **Eileen Hofmann[2].** [1]University of Southern California, Department of Biological Sciences, Los Angeles, CA 90089-0371, USA; [2]Old Dominion University, Center for Coastal Physical Oceanography, Norfolk, VA 23529, USA; [3]Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349, USA.

A population genetics sub-model of a traditional individual-based model has been developed for the Pacific oyster *Crassostrea gigas*, enabling research into how variability in larval survival, growth, and recruitment influence long-term population dynamics. Model oysters have 10 chromosome pairs, with multiple genes per chromosome, multiple alleles per locus, and recombination. Adults produce larvae with specific genotypes, following meiosis and Mendelian inheritance, and with prescribed relative fitness. The fraction of parents reproducing can be varied to simulate sweepstakes reproductive success (SRS), leading to reductions in the N_e/N ratio and increases in random genetic drift. Effective population sizes (variance, N_{ev}, and inbreeding, N_{ei}) are calculated each generation from stored demographic data. N_{ev} values in simulations match estimates based on temporal changes in allelic frequencies, which are also stored. Mutation rate is a function of the number of cell divisions leading to gamete production, allowing for fecundity-driven mutation pressure and the possibility of clustered new mutations. This genetics model has been used to investigate: 1) changes in genetic composition as a function of the effective number of parents (random genetic drift from SRS) and 2) maintenance of recessive highly detrimental mutations and the effect of mutational load on larval survival and recruitment.

EFFECT OF TEMPERATURE ON HEMOCYTE RESPONSES OF NORTHERN QUAHOGS (= HARD CLAMS, *MERCENARIA MERCENARIA*) FROM DIFFERENT POPULATIONS. **Hélène Hégaret[1], Roxanna M. Smolowitz[2], Gary H. Wikfors[3], Jacquelin Defaver i[2], William Walton[4], Diane Murphy[4],** and **Sandra E. Shumway[1].** [1]University of Connecticut, Department of Marine Sciences, 1080 Shennecossett Road, Groton, CT 06340; [2]Marine Biological Laboratory, MRC 213, 7 MBL Street, Woods Hole, MA 02543; [3]Northeast Fisheries Science Center, NMFS, NOAA, 212 Rogers Avenue, Milford, CT 06460; [4]Cape Cod Cooperative Extension, Barnstable, MA 02630.

Temperature triggers, and geographic population differences, have been hypothesized for progression of QPX (Quahog Parasite Unknown) in northern quahogs (*Mercenaria mercenaria*). To test these hypotheses, quahogs from three different locations (Florida; New Jersey, Massachusetts) were deployed in 2005 in Barnstable, MA, at two sites with different QPX levels in indigenous clams. Planted clams were sampled in spring, summer, and fall—seasons representing temperature thresholds in progression of the disease—for 2 years. At each sampling, clams were analyzed for prevalence and intensity of QPX, as well as for hemocyte characteristics (concentration and morphology of circulating hemocytes) and immune functions. QPX and hemocyte variables were contrasted for clams from the three origins, two planting sites, and three seasons; relationships between prevalence and intensity of QPX and clam hemocyte responses also were explored. Results indicate that clams from the three populations reacted differently, according to season and site. The most-pronounced difference was that clams from Florida consistently were more-heavily infected, which led to differences in clam hemocyte responses according to site and season. These results underscore the importance of clam origin and local temperature regimes in QPX progression, and also document changes in circulating hemocytes associated with seasonal QPX-infection patterns.

NEW PERSPECTIVES ON THE DISPERSAL AND EVOLUTION OF *BONAMIA* SPECIES, HAPLOSPORIDIAN PARASITES OF OYSTERS. **Kristina M. Hill[1], Delonna M. White[1], Nancy A. Stokes[1], Ryan B. Carnegie[1], Nejla Aloui-bejaoui[2], Steven C. Webb[3], P. Mike Hine[4], Marina A. Kroeck[5], Refka Ghars alli[2], Rita K. Crockett[1], Teresa D. Lewis[6], Kimberly S. Reece[1],** and **Eugene M. Burreson[1].** [1]Virginia Institute of Marine Science, College of William and Mary, Environmental and Aquatic Animal Health, P.O. Box 1346, Gloucester Point, VA 23062, USA; [2]Institut National Agronomique de Tunisie, Unité de Biologie, écologie et parasitologie des organismes marins. 43, Avenue Charles Nicolle—1082 Tunis, Tunisia; [3]Cawthron Institute, 98 Halifax Street East, Private Bag 2, Nelson, New Zealand; [4]Fouras, France; [5]Insituto de Biología Marina y Pesquera, Almirante Storni, Laboratorio de Histopatologia de Moluscos, Güemes 1030, San Antonio Oeste 8520 (Rio Negro), Argentina; [6]The Hawai'i Institute of Marine Biology, School of Ocean and Earth Science and Technology, University of Hawai'I at Manoa, P.O. Box 1346, Kane'ohe, HI 96744, USA.

Protistan oyster parasites in the genus *Bonamia* (phylum Haplosporidia) are increasingly being observed in new hosts and locations. Subsequent phylogenetic and histological analyses are altering our view of the biology, evolution, and dispersal of this group. We hope to further elucidate the phylogenetics and phylogeography of this genus through sampling of additional potential oyster hosts, especially the little-studied non-commercial species. Toward this end, *Ostrea stentina* from Tunisia, *Ostrea aupouria* from New Zealand, and *Ostrea sandvicensis* from Hawaii were collected and screened for *Bonamia* spp. using genus-specific PCR assays and histological examination. Phylogenetic analyses of observed parasites based on SSU and ITS rRNA gene sequences suggest that the *Bonamia* spp. found in *O. stentina* and *O. auporia* are closely related to southern hemispheric *Bonamia roughleyi* and *Bonamia exitiosa*. The *Bonamia* sp. found in *O. sandvicensis*, however, is novel and basal to the rest of the *Bonamia* clade. Surprisingly, this species presents uninucleate microcells within hemocytes and lacks sporogonic forms–an unexpected result given its position basal to *Bonamia perspora*. We plan to develop new loci (actin and CO1) to enhance our phylogenetic analysis, and to continue our search for new hosts, with a new emphasis on tropical ostreid, saccostreid, and lophine oyster species.

FIELD AND MODELING STUDIES IN SUPPORT OF UNDERSTANDING DISEASE RESISTANCE IN ESTUARINE POPULATIONS AND RESPONSES TO CLIMATE CHANGE. **Eileen E. Hofmann[1], David Bushek[2], Susan E. Ford[2], Ximing Guo[2], Eric Powell[2], Dale B. Haidvogel[3], John Wilkin[3], Dennis Hedgecock[4],** and **John M. Klinck[1].** [1]Center for Coastal Physical Oceanography, Old Dominion University, Norfolk, VA 23529; [2]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ 08349; [3]IMCS, Rutgers University, New Brunswick, NJ 08910; [4]Department of Biological Sciences, University of Southern California, Los Angeles, CA 90089.

The NSF Ecology of Infectious Diseases initiative recently funded an investigation of host-parasite relationships in molluscan populations impacted by protozoan diseases and how these might be affected by climate change. The project targets eastern oyster (*Crassostrea virginica*) populations in Delaware Bay, which suffer from two lethal diseases, MSX and Dermo. The focus is on understanding the (1) role of disease refugia, (2) effect of variability in the number of parents (disease-resistant or not) that successfully reproduce each year, (3) role of environmentally-modulated selection and transmission processes in producing genetic changes in the host population, and (4) response of the oyster-parasite interaction to climate change and consequent effects on overall host population genetic structure. This poster provides a project overview, describes ongoing laboratory and field designed to underpin models that include explicit genetic structure, disease processes, and oyster

population dynamics, and shows results from Lagrangian particle tracking simulations obtained from a circulation model developed for Delaware Bay as part of this project. The particle tracking simulations allow quantification of the effects of parasite and larval transport on genetic exchanges in different regions of Delaware Bay, which have important implications for understanding disease resistance and host population genetic structure.

TREASURES IN ARCHIVED HISTOPATHOLOGY COLLECTIONS: PRESERVING THE PAST FOR FUTURE UNDERSTANDING. Doranne Borsay Horowitz[1], Esther C. Peters[2], Inke Sunila[3], and **Dvm Dacvp Jeffrey C. Wolf[4].** [1]Atlantic Ecology Division, US Environmental Protection Agency, 27 Tarzwell Drive, Narragansett, RI 02882; [2]Tetra Tech, Inc., 10306 Eaton Place, Suite 340, Fairfax, VA 22030; [3]State of Connecticut, Department of Agriculture, Bureau of Aquaculture, P.O. Box 97, Milford, CT 06460; [4]Experimental Pathology Laboratories, 45600 Terminal Drive, Sterling, Virginia 20166.

Extensive collections of histopathology materials from studies of marine and freshwater mollusks, crustaceans, echinoderms, and other organisms are archived in the Registry of Tumors in Lower Animals (RTLA), the US Environmental Protection Agency, NOAA's National Marine Fisheries Service, and other agency or academic institutions. These collections are valuable resources for scientists seeking to understand health/disease in diverse species, train new invertebrate pathologists, predict risks from biotic/abiotic stressors (e.g., toxicant impacts on organisms in multiple locations), determine disease status through DNA extraction and analysis, supply data for historical reconstructions (e.g., when a virus first affected a host species), examine trends in parasite distribution and prevalence, and improve interpretation of host/parasite population fluctuations for modeling ecosystems. However, they are in danger. For example, RTLA's collection (www.pathology-registry.org) now at Experimental Pathology Laboratories, Sterling, VA, formerly National Cancer Institute funded, lacks current funding for maintenance or processing of additional case submittals. To ensure future availabilities of these irreplaceable resources, online databases with cross-linking records of materials for search and retrieval—as is being developed for the EPA's Atlantic Ecology Division's collections— can provide access, but these collections need cross-agency support to improve their database capabilities, maintain histoslides, and provide hands-on examination and study.

FEASIBILITY OF HARD CLAM AQUACULTURE IN GRAND BAY, ALABAMA. Jonathan Jackson, Dr. Ladon Swann, and **Scott Rikard.** Auburn University.

The hard clam, *Mercenaria mercenaria*, is a profitable aquaculture species along the Eastern seaboard and the west coast of Florida. The culture of *M. mercenaria* in the North Central Gulf of Mexico has not been thoroughly investigated. The feasibility of clam culture was analyzed using two grow-out systems in the coastal waters of Grand Bay, Alabama. Clams were stocked into replicate mesh bags at four stocking densities (188/m^2, 375/m^2, 750/m^2, and 938/m^2) in a belt system placed on bottom and in bags suspended from a long-line system. The mesh bags placed on bottom allow clams to burrow into the sediment, while clams placed in the long-line system were suspended mid-water column. After five months clams in the belt system showed a 25.0% increase in size with 42.6% survival compared to only a 14.6 % increase in size for clams in the long-line system with a 24.3% survival. The growth and survival in both systems was meager when compared to published data for clams along the east coast of Georgia, Florida and South Carolina. The poor performance may be related to biofouling by tunicates and polycheates on the belt bag system and siphon nipping by fish and crabs in the long-line system.

A REVIEW OF CURRENT RESEARCH ON FARMING OF THAI ABALONE, *HALIOTIS ASININA*, LINNAEUS 1758. Padermsak Jarayabhand, Aquatic Resources Research Institute, Chulalongkorn University, Bangkok 10330, Thailand.

Two species of tropical abalone are being commercially farmed in Thailand. These species are generally known as cocktail size abalone which classified as lower value species when compared to the larger temperate species. However, in many cases their demands are still higher than their supplies. At any rate, it should be pointed out that the first species is an introduced one named, *Haliotis diversicolor supertexta*. This species is also known as tokobushi or Taiwanese abalone. The second is a species native to Thai waters, *Haliotis asinina*. This species is also currently known among Thais as Thai abalone. Due to many advantage points in this Thai species, a large number of research projects have been carried out with an aim to come up with an appropriate farming technique in this species as well as ways to further improve its production efficiency. In this report, current knowledge on various aspects of aquaculture in this species i.e. broodstock conditioning, spawning induction, seed production, grow out technique, nutrition, disease, genetics and biotechnology will be presented. In addition, further investigations for each aspect are also suggested.

VISUALIZATION OF SHELL MATRIX PROTEINS IN HEMOCYTES AND TISSUES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. Mary Beth Johnstone. Clemson University, Clemson, SC 29634.

The tissues of the oyster were examined for the presence of shell matrix proteins (SMPs) using a combination of Western, proteomic, and epi-fluorescent microscopy techniques. SMP, including 48 and 55 kDa phosphoproteins, was detected in the epithelial cells of mantle, gill, heart, and adductor muscle and linings of arteries and veins. The 48 kDa SMP circulates continuously within the

hemolymph, and is present in the immune system hemocytes. It appears to be secreted from hemocytes on induction of shell repair. We suggest that the 48 and 55 kDa proteins are multifunctional and bridge the process of soft tissue repair and shell formation by mediating cellular activities during immune response as well as interacting with the mineral phase during deposition.

HOW LONG CAN AN OYSTER HOLD ITS BREATH? USING BIOLOGICAL AND PHYSICAL DATA TO ESTIMATE REEF RESTORATION REQUIREMENTS IN AREAS OF LOW OXYGEN CONCENTRATION. **Matthew W. Johnson[1], Sean P. Powers[2], Joseph Senne[2],** and **Keyong Park[2].** [1]Dauphin Island Sea Lab, Dauphin Island, AL, 36528, USA; [2]University of South Alabama, Dauphin Island Sea Lab, Dauphin Island, AL, 36528, USA.

Oyster production is one of the largest fisheries in Mobile Bay, but in the recent past there has been a loss in total reef area and a decline in oyster harvest. One of the primary reasons for this loss is the increase in hypoxic events. Efforts are underway to restore some of the relic reefs that are located in western Mobile Bay to help increase oyster stocks; however, this area can be prone to low oxygen conditions during the mid to late summer months. During the summer of 2007, we deployed replicated oyster panels at three different depths (bottom, 1 m, surface) to determine if a 1 m reef height would be substantial enough to allow for restoration of reefs and maintain a thriving oyster population. Panels were also deployed at locations north and south of the reef. Additionally, we conducted regular CTD transects in the reef area and established several permanent monitoring sites near the site, north of the site and south of the site to measure dissolved oxygen at regular intervals. Preliminary results suggest that low oxygen events are common in this area and that a reef in excess of 1 m in height may be required for sustainable oyster populations.

MARYLAND'S OYSTER SHELL PROGRAM ENDS AFTER 47 YEARS (1960-2006): IMPACT ON INDUSTRY AND RESTORATION. **Christopher Judy.** Maryland Department of Natural Resources, Shellfish Program, Annapolis, MD USA.

Since 1960, Maryland has conducted a large-scale shell planting program. The program ended in 2006 and with it the largest oyster habitat initiative on the US East Coast; an average of 4 million bushels were planted per year to enhance spat set. Resulting oysters yielded a harvest, produced seed oysters, and provided ecological benefits. The program produced up to 80% of the annual harvest. Market oysters worth $25 per bushel required an investment of $8–$13 to produce. Shells were also used in sanctuary projects off limits to harvest. Oyster projects by the State, the Corps of Engineers, and many Chesapeake oyster groups depended on the program for shell habitat. For the past two decades, diseases have impacted the program and eroded its effectivenesss—both for industry and sanctuaries—and greatly diminished results. Data will be presented on the scale of the program, the total costs and unit costs for shell, the cost to produce market oysters, the impacts of disease, and the impact of the loss of the program on oyster restoration and the industry. Perspectives on future directions will be presented. What alternatives exist to the historic shell program? Where do we go from here regarding industry and sanctuaries?

GENETIC DIFFERENTIATION OF THE ASIAN OYSTER (*CRASSOSTREA ARIAKENSIS*) BETWEEN SEOMJIN RIVER, KAWHA RIVER AND KANGWHA-DO POPULATIONS. **Hyungtaek Jung[1], Ilseon Baek[2],** and **Woo-jin Kim[3].** [1]Graduate College of Marine and Earth Studies, University of Delaware, DE 19958, USA; [2]College of Fisheries and Ocean Science, Chonnam National University, Yeosu 550-749, South Korea; [3]Biotechnology Research Institute, National Fisheries Research and Development Institute, Busan 619-705, South Korea.

Despite the huge interest in the non-native oyster, *Crassostrea ariakensis*, few studies have been carried out for Korean populations within its native range. In order to evaluate the genetic structure of Korean populations, we examined DNA sequence variation using newly developed mitochondrial markers from three locations in Korea (Seomjin River, Kawha River and Kangwha-Do). No significant genetic differentiation was detected between samples, although comparisons may have been influenced by small sample sizes (n = 20). Since the recent confusion of nomenclature and origin in this species, we propose that Korea has its own native *C. ariakensis* population (for there is no history of Korean *C. ariakensis* introductions from China or Japan) as Chinese researchers believe they have their own native species. A more extensive examination of the geographic ranges of East Asia *C. ariakensis* may help resolve questions regarding population structure of the species. The mitochondrial markers developed here would be useful for population structure in this species. Considering the availability of sequence data for a variety of nuclear genes in *Crassostrea*, the development of additional marker loci may be more productive to understand a mosaic of remnant wild populations and widely distributed culture stocks.

INFERRING KOREAN OYSTER PHYLOGENIES, INCLUDING THE EAST ASIAN OYSTER (*CRASSOSTREA ARIAKENSIS*) AND ITS POPULATION STRUCTURE INFER. **Hyungtaek Jung[1], Seongil Eyun[2],** and **Woo-Jin Kim[3].** [1]Graduate College of Marine and Earth Studies, University of Delaware, DE 19958, USA; [2]School of Biological Sciences, University of Nebraska-Lincoln, USA; [3]Biotechnology Research Institute, National Fisheries Research and Development Institute, Busan 619-705, South Korea.

In order to determine phylogenetic relationships among the Korean oysters and an East Asia species (*Crassostrea ariakensis*) using a concatenated sequence tree and a single consensus tree, we

sequenced mitochondrial gene and nuclear DNA Type I markers. The sequence data provides for a more robust population structure and for the detection of interspecific hybrids. Among loci, discordance in tree structures was observed, reflecting the stochastic nature of the genealogical process and possible natural selection. The first attempt of concatenation of the gene sequences (using ML, MP and NJ algorithms) and Mr. Bayesian approaches for the phylogenies of Korean oysters (*C. ariakensis*, *C. gigas*, *C. nippona*, and *Ostrea denselamellosa*) gave a better resolution than did any of the individual analyses. In order to evaluate *C. ariakensis* population structure, we also examined DNA sequence variation in two mitochondrial gene regions from six locations (two Chinese populations, one Japanese population and three Korean populations). Despite small sample sizes, mitochondrial gene data indicated the existence of two genetically distinct stocks: a northern and a southern haplotype. Therefore, molecular markers and phylogenetic assumptions developed here will provide for more extensive analyses of systematic relationships in *Crassostrea* species as well as for the analysis of population structure in *C. ariakensis*.

AGGREGATES FACILITATE THE UPTAKE OF BACTERIA AND NANO-PARTICLES BY SUSPENSION-FEEDING MOLLUSCS. **Dustin J. Kach** and **J. Evan Ward.** Department of Marine Sciences, University of Connecticut, Groton, CT 06340.

Many suspension-feeding molluscs capture individual particles less than 1 μm with a retention efficiency of less than 20%, leading to the assumption that such particle are not ingested in large numbers. Bacteria and other sub-micrometer particles, however, are often concentrated within marine aggregates (e.g., marine snow) which are abundant in coastal environments where large populations of molluscs thrive. If molluscs capture and process aggregates, which range in size from a few micrometers to more than a millimeter, they may be able to ingest sub-micrometer particles as well. We fed clams (*Mercenaria mercenaria*), mussels (*Mytilus edulis*), bay scallops (*Argopecten irradians*), and eastern oysters (*Crassostrea virginica)* fluorescently labeled 1-μm bacteria or polystyrene beads that were (1) dispersed in seawater, or (2) embedded within aggregates generated in the laboratory. Our results indicate that aggregates significantly enhance the uptake of 1-μm and 0.1-μm particles. Compared to mussels and clams, scallops and oysters ingested fewer aggregates, and slipper snails ingested more dispersed bacteria and beads. These interspecific differences may be a consequence of variations in gill structure and mechanisms of particle processing. Our data suggest that aggregates allow some suspension feeders to often uptake embedded bacteria and nano-particles with potentially positive (food) or negative (disease, toxins) consequences.

SURVIVAL AND PHYSIOLOGICAL RESPONSES OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* TO THERMAL STRESS AND AIR EXPOSURE. **Do-Hyung Kang[1], Fu-lin E. Chu[2], Eric D. Lund[2], Jennifer A. Podbesek[3],** and **Kwang-Sik Choi[4].** [1]Marine Ecosystem & Conservation Division, Korea Ocean Research & Development Institute (KORDI), Ansan P.O.Box 29, Seoul 426-744, Republic of Korea; [2]Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, Virginia, 23062, U.S.A.; [3]Virginia State Healthy Department, Virginia; [4]School of Applied Marine Science, College of Ocean Science, Cheju National University, 1 Ara 1-Dong Jeju 690-756, Republic of Korea.

Environmental condition is a significant determinant of oyster survival and progression of disease caused by *Perkinsus marinus* (Dermo). We examined the effects of sublethal heat shock (40°C for 1 hr) and air exposure (intertidal cultivation) on Dermo progression, survival and physiological condition of oysters. Oysters (n = 180) were acclimated to experimental conditions for one week, and then their condition, survival and the progression of Dermo infection were assessed under different treatment conditions. There were four treatment groups (3 replicates tank/group; n = 15 oysters/replicate): sublethal heat shock with aerial exposure (+HS+AE) or no aerial exposure (+HS–AE) and no heat shock with aerial exposure (–HS+AE) or no aerial exposure (–HS–AE). There was no significant difference in survivorship among treatments overtime. Highest survival, however, was recorded in the +HS+AE treatment compared to other treatment groups at the end. Air exposure significantly reduced the oyster condition index (CI). Dermo intensities in the aerial exposure treatments (+HS+AE and –HS+AE) did not change significantly from the initial and significant lower than those in the non aerial exposure oysters (+HS–AE and –HS–AE). Our results suggest that intertidal cultivation combined with sublethal heat treatment may have the potential to reduce disease pressure and enhance survival.

STRATEGIES FOR THE MANAGEMENT OF A BAY SCALLOP FISHERY, LESSONS FROM AQUACULTURE. **Richard C. Karney** and **Amandine Surier.** Martha's Vineyard Shellfish Group, Inc., Oak Bluffs, MA 02557, USA.

As in other commercial shellfisheries, recruitment in bay scallop populations is sporadic. Unlike other shellfish species, the bay scallop's short life span introduces greater instability in its populations and greater challenges to its management. Management requires an understanding of the factors controlling recruitment, the identification of which of those factors can be controlled, and finally, a prioritization of the controllable factors so as to achieve the greatest impact with available resources. Shellfish aquaculture operations are microcosms of natural shellfisheries. They provide both controlled environments to better understand the factors influencing recruitment and technologies applicable to a

shellfish management program. The application of knowledge gained from aquaculture to the management of the bay scallop fishery on Martha's Vineyard is discussed.

INITIAL INVESTIGATIONS INTO THE POTENTIAL FOR MUSSEL CULTURE IN THE OFFSHORE WATERS OF MARTHA'S VINEYARD. Richard C. Karney, Tom Osmers, and **Amandine Surier.** Martha's Vineyard Shellfish Group, Inc., Oak Bluffs, MA 02557, USA.

In the wake of diminished wild fish stocks, a mussel aquaculture industry in the off-shore waters of Martha's Vineyard promises to provide alternative employment for Vineyard fishers. This project represents the first steps to adopt the off-shore submerged longline culture technology developed by Richard Langan of UNH in Vineyard waters. In addition to deep water siting, Langan identified several unknowns critical to the success of using his methods to grow mussels off Martha's Vineyard, including identification of seed collection sites, temperature at growout sites, and the presence of pea crabs. In this study, Island fishermen assisted in field investigations at potential grow-out sites to answer these preliminary key questions. Socks of seed mussels and continuous temperature recorders were deployed on moored lines at the five offshore sites in July and August 2006. Data was retrieved from three of the five sites. Mussels remained attached to the lines despite the fact that seawater temperatures exceeded 65 F, a temperature above which they were expected to drop from the lines. Based on measurements taken in November 2007 and January 2008, the mussels grew at an average rate of 4.8 mm/month. Only one pea crab, thought to have been introduced with the seed, has been found in over 350 mussels examined.

SPECULATIVE VALUE ASSOCIATED WITH LOUISIANA OYSTER LEASES AND POTENTIAL IMPACTS ON COASTAL RESTORATION ACTIVITIES. Walter Keithly[1], Richard Kazmierczak[1], and **James Wilkins[2].** [1]Louisiana State University, Dept. of Agricultural Economics, Baton Rouge, Louisiana, 70803, USA; [2]Louisiana State University, Office of Sea Grant Development, Baton Rouge, Louisiana, 70803, USA.

At its core, our analysis indicates that the speculative value of leases is likely equal to or exceeds lease value based on income generated from oyster production and harvesting activities. Gross income to lease holders from oil and gas activities was estimated to be from $10.1 million to $14.79 million per year under current conditions. Given current leased acreage of approximately 392,000 acres and rental fees of $2.00 per acre, this translates into approximate net revenues derived from oil-and-gas activities in the range of about $24 per acre to $36 per acre. Over the same time period, net revenues to fixed costs for oyster production and harvesting were estimated to equal approximately $31 per acre. Furthermore, this compensation-based revenue stream appears to flow to leases irrespective of their ability to produce marketable oysters, suggesting that one reason leases exists in non-producing areas is to provide lessees with an opportunity to receive compensation payments. As will be discussed, the high speculative value of these leases has likely exacerbated conflicts between the oyster industry and state managers charged with coastal restoration activities.

AN ECONOMIC ANALYSIS OF GULF OF MEXICO OYSTER PROCESING ACTIVITIES Walter Keithly[1] and **William "Corky" Perret[2].** [1]Louisiana State University, Dept. of Agricultural Economics, Baton Rouge, Louisiana, 70803, USA; [2]Dept. of Marine Resources, Biloxi, Mississippi, 39530, USA

Based on National Marine Fisheries Service end-of-the-year annual processor survey, this paper reviews Gulf of Mexico oyster processing activities during the 1980–2006 period. This review covers several areas including: (a) changes in the number of processing facilities, (b) changes in productivity per firm, and (c) changes in distribution of processing activities among firms (i.e., an analysis of changes in concentration. In addition, the paper examines the relationship between harvesting activities and processing activities and changes in the markup between the price of the harvested product and the price of the processed product. Finally, the paper briefly examines movement of raw Gulf of Mexico to the Chesapeake for processing and the implications of this activity.

DIPLOID *CRASSOSTREA VIRGINICA* AND *CRASSOSTREA ARIAKENSIS* STUDIES IN MESOCOSMS SIMULATING CHESAPEAKE BAY AND FLORIDA ESTUARIES. Christopher J. Kelly[1], Roger I.E. Newell[1], John Scarpa[2], Susan E. Laramore[2], and **Ryan B. Carnegie[3].** [1]Horn Point Laboratory, University of Maryland Center for Environmental Science, Cambridge, MD 21613; [2]Harbor Branch Oceanographic Institute at Florida Atlantic University, Ft. Pierce, FL 34946; [3]Virginia Institute of Marine Science, Gloucester Point, VA 23062.

It has been proposed that the Suminoe oyster, *Crassostrea ariakensis*, be introduced into Chesapeake Bay to supplement declining populations of the eastern oyster, *C. virginica*. We compared growth and survival of diploid oysters of both species in quarantine mesocosms supplied with flowing water (annual ranges of 1 to 28°C and salinity 7 to 15). Shell growth in *C. virginica* occurred in the late spring through late summer with negligible growth during other seasons. Growth of *C. ariakensis* was significantly faster than *C. virginica* in late spring and summer, with continued growth in fall and early spring. Similarly, we compared these oysters in mesocosms located in Florida (salinity 27 to 37; temperature 16 to 30°C). In contrast, *C. virginica* grew significantly faster compared to *C. ariakensis* during the first three months of the study (October to December 2006); and generally had a faster, but not significantly different, growth rate during the remaining 7 months of the study. *Crassostrea ariakensis* suffered total mortality by the end of the experiment. Our results suggest that while *C. ariakensis* may be well suited to mesohaline Chesapeake Bay, their distribution elsewhere may be limited. Funding for this project is provided by Maryland DNR and NOAA.

STATUS OF THE BAY SCALLOP *ARGOPECTEN IRRADIANS IRRADIANS* ON NANTUCKET ISLAND, MASSACHUSETTS—PAST, PRESENT AND FUTURE. **Robert S. Kennedy[1], Jeffrey M. Mercer[2], Peter B. Boyce[3], Valerie A. Hall[4],** and **W. Forrest Kennedy[5].** [1]Maria Mitchell Association, 4 Vestal Street, Nantucket, MA 02554, USA; [2]Nantucket Marine and Coastal Resources Department, 34 Washington Street, Nantucket, MA 02554, USA; [3]Maria Mitchell Association, 4 Vestal Street, Nantucket, MA 02554, USA; [4]Maria Mitchell Association, 4 Vestal Street, Nantucket, MA 02554, USA; and School for Marine Science and Technology, University of Massachusetts Dartmouth, 706 South Rodney French Boulevard, New Bedford, MA 02744, USA; [5]Maria Mitchell Association, 4 Vestal Street, Nantucket, MA 02554, USA; and New England Aquarium, Central Wharf, Boston, MA 02110, USA.

Nantucket Island, Massachusetts has a rich history of bay scallop fisheries that includes both commercial and family scalloping seasons. Over the past several decades commercial landings have ranged from a high of 117,000 bushels in 1980 to a low of 3,800 bushels in the season ending in 2007. Fortunately, the 2007/8 scalloping season reached 15,000 bushels during the first half of the season. The Nantucket population is the last remaining, commercially viable, virtually unmanaged, wild population of bay scallops in Eastern North America, and as such, has been named a "National Treasure" by scallop researcher Dr. Bill Arnold and many others. Here we present a summary of the history of the bay scallop and scalloping on Nantucket, outline past and present scallop research, discuss current management practices, status of eelgrass beds and water circulation in Nantucket Harbor, and review possible reasons for lower commercial landings in 2005 and 2006. In addition, we present what research and management practices are planned for the future and what the Nantucket community is doing to maintain the health of its harbors and surrounding waters.

EVOLUTION OF LIPIDS RESERVES DURING *CRASSOSTREA GIGAS* LARVAL DEVELOPMENT: A QUANTITATIVE STAINING STUDY. **Rym Ben Kheder[1], Anne Henocq[1],** and **Rene Robert[1].** [1]Ifremer, PFOM/LPI/UMR PE2M, Station Expérimentale d'Argenton, 11 Presqu'île du Vivier, 29840 Landunvez, France.

Despite an indisputable know-how in mollusc hatchery some biological aspects remain feebly known and beyond them indices of larval development and metamorphosis are still lacking. A new physiological index (lipid area/total larval surface) based on a staining lipid method with Nile red, epifluorescence observations and image analysis treatment is described here. This index was concomitantly used to study the influence of temperature and food on *Crassostrea gigas* larval lipid storage and larval performances. At high temperature (32°C) larvae actively catabolysed lipid reserves to cover metabolic demand while in contrast larvae reared at low temperature (17°C) stored lipid. On the other hand, higher was the feeding rations upper was larval lipid storage throughout larval life. Indeed larvae fed half ration (25–100cells μl^{-1}) exhibited weak lipid ratio (11%) compared to the standard and double ration treatments (28–30%). Lastly larvae fed *Pavlova lutheri* (P) or *Isochrysis aff. galbana* (T) or this combined diet (PT) showed deficient lipid reserves (<5%) as well as weak development performances. In contrast an active lipid storage characterised larvae fed *Chaetoceros calcitrans* f. *pumilum* diet assemblages. This simple method is accordingly highly promising to study molluscs larval lipid evolution.

TRANSPORT OF OYSTER LARVAE IN RESPONSE TO TIDE, RIVER AND WIND CONDITIONS IN MOBILE BAY AND THE ADJACENT EASTERN MISSISSIPPI SOUND. **Choong-Ki Kim, Kyeong Park,** and **Sean P. Powers.** University of South Alabama, Department of Marine Sciences, Dauphin Island Sea Lab, 101 Bienville Blvd., Dauphin Island, AL 36528.

As a part of a comprehensive oyster restoration program for coastal Alabama, a three-dimensional larval transport model has been developed to study the larval transport of eastern oyster (*Crassostrea virginica*) in Mobile Bay and the adjacent Eastern Mississippi Sound, AL. The simulated larval distribution showed a good agreement with the larval recruitment patterns observed in 2006. The characteristics of larval transport in response to the variations in tide, wind and river discharge were investigated by scenario simulations. Variations in spawning time in relation to tidal phase results in little changes in larval distribution, while variations in river discharge and winds play a significant role in the larval transport and retention inside the Bay and the Sound. Limited larval transport occurs between the west and east side of Mobile Bay regardless of tide, river and wind conditions. The scenario simulations show that large spawning stocks in Cedar Point result in high larval supply into the west side of Mobile Bay and the Eastern Mississippi Sound, suggesting that the differences in larval supply may be responsible for the west-east gradient in larval recruitment of oysters that have been consistently observed in Mobile Bay over the past 40 years.

GENETIC DIVERSITY AND POPULATION GENETIC STRUCTURE OF PACIFIC OYSTER (*CRASSOSTREA GIGAS*) FROM KOREA USING MICROSATELLITE MARKER. **Woo-Jin Kim[1], Ki-Yeol Park[2], Bo-The Nam[1], Hee Jeong Kong[1], Young-Ok Kim[1], Eun-Mi Park[1],** and **Tae-Ik Kim[3].** [1]Biotechnology Research Institute, National Fisheries Research and Development Institute, Busan 619-705, South Korea; [2]Shellfish Research Center, National Fisheries Research and Development Institute, Namhae 668-821, South Korea; [3]General Service Team, National Fisheries Research and Development Institute, Busan 619-705, South Korea.

We examined genetic variability and population genetic structure by means of microsatellite analysis in one hatchery strain and nine wild populations of Pacific oyster (*Crassostrea*

gigas) from Korea. All of the 6 microsatellite loci examined in this study showed marked polymorphism. Compared with the wild populations, the hatchery strain showed marked reductions in all indicative of genetic diversity such as number of alleles per locus, number of low-frequency alleles, number of unique alleles and expected heterozygosity. These indicated that bottleneck effects in hatchery strain examined occurred. All wild populations were highly variable (number of alleles per locus, 24.5-28.8; average of expected heterozygosity, 0.91–0.95). A significant population differentiation was found between Muan and Goseong and between Gwangyang and Geseong based on fixation index (F_{ST}) and genetic distance (D_S). These distinct groups may not be associated with geographic characteristics. The results suggest that most of the *C. gigas* populations in Korea may intermix because of transplanting from one location to another for higher production.

EFFECTS OF CLIMATE CHANGE ON INTERANNUAL VARIATIONS IN PARASITES, PATHOLOGIES, AND PHYSIOLOGICAL ATTRIBUTES OF BIVALVES FROM THE U.S. EAST, GULF, AND WEST COASTS. Yungkul Kim and **Eric N. Powell.** Haskin Shellfish Research Laboratory, Rutgers University, Port Norris NJ 08349-3167, USA.

Using data from NOAA's National Status and Trends "Mussel Watch" Program, we analyzed weighted prevalence of various parasites and pathologies from 1995 to 2006 along with a set of physiological variables to determine the degree of concordancy in their interannual variations over 500-km stretches of coastline. The variables examined in both mytilid mussels and oysters fell into three groups based on the temporal patterns observed. Overall, principal pathologies and diseases, bivalve physiological indicators, and the common gregarine parasites tended to show concordant behavior, suggesting that large-scale climatic processes (e.g., ENSO, NAO) are important determinants of their interannual variation. Overall, multicellular parasites, prokaryotes, and ciliates rarely showed concordant behavior, indicating that parasite body burden was controlled by local (within-bay) forcing factors. Both bivalve groups, mussels and oysters, contained variables that expressed concordant behavior not only over long stretches of coastline, but on multiple coasts, and variables that expressed concordant behavior for more limited coastline stretches. The degree and pattern of concordancy are fingerprints for the relative influence of local versus climatic forcing as determinants of population dynamics in these bivalve populations and the populations of their parasites.

FROM THE HEADWATERS TO THE COAST: A WATERSHED-BASED PERSPECTIVE ON BIVALVE SHELLFISH RESTORATION. Danielle Kreeger[1] and **David Bushek[2].** [1]Partnership for the Delaware Estuary, Wilmington, DE 19801 USA; [2]Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349 USA.

Bivalve shellfish are valued for their biodiversity, utility as bioindicators, commercial value, and ecoservices. Debate rages about the magnitude of ecoservices such as biofiltration and fish habitat, but other benefits have largely been ignored; e.g., "living shorelines" that stabilize marsh erosion and ecoservices from freshwater bivalves. To gain a watershed perspective on bivalves as "ecosystem engineers," population-level water processing was contrasted among three key bivalves in the Delaware Estuary by integrating summer physiological data with abundance estimates. Total potential water processing by oysters (~10 billion L/h) and a freshwater mussel (~10 billion L/h) was dwarfed by an estuarine mussel (~60 billion L/h). Nevertheless, this first attempt at a watershed comparison indicates bivalves from fresh to marine waters can furnish valuable ecoservices. Not all restoration investments, however, will provide the same type or value in return. A systems approach should be used that considers other important factors such as the possibility that freshwater mussels might intercept pollutants before reaching the estuary, or that some species are more disease sensitive than others. A natural capital assessment of stacked ecoservices, values and tradeoffs associated with restoring different bivalves throughout a watershed is warranted to ensure that limited restoration dollars are invested most wisely.

DEVELOPMENT AND COMMERCIALIZATION OF TECHNOLOGY FOR OPEN OCEAN MUSSEL FARMING. Richard Langan. University of New Hampshire, Atlantic Marine Aquaculture Center, Durham, NH, 03824, USA.

With consumer demand on the rise and market value steadily increasing, mussels have become an increasingly attractive species for farmed production. While practices for mussel farming in protected nearshore waters are well established, degraded water quality, user conflicts, and resistance by shorefront property owners have limited opportunities for growth in the US. Beginning in 1999 with funding from NOAA for the Open Ocean Aquaculture Project, researchers at the University of New Hampshire embarked upon the development of technology for offshore mussel farming at an experimental site off the New Hampshire coast. The project was able to demonstrate that offshore farming using submerged longlines is not only feasible, but that the production cycle was comparable to if not better than estuarine sites in New England, and that the product quality was excellent. An economic analysis concluded that offshore farming could be profitable at multiple scales. With all aspects of offshore mussel farming looking favorable for commercialization, project personnel engaged in technology transfer activities that have resulted in the establishment of a

commercial farm off the New Hampshire coast, followed by farms in Maine and Santa Barbara, CA, demonstrating the potential for broader regional and national application of the technology.

SELECTION FOR DESIRABLE TRAITS IN THE PACIFIC OYSTER *CRASSOSTREA GIGAS*. **Chris Langdon, Alan Barton,** and **Ford Evans.** Coastal Oregon Marine Experiment Station, Department of Fisheries and Wildlife, Oregon State University, Newport, OR 97365, USA.

The Molluscan Broodstock Program (MBP) was established in 1995 as a selective breeding program to improve broodstock for commercial production of Pacific oysters on the West Coast, US. After two generations of family-based selection, average survival, final individual weight and yield were 16%, 9% and 33% greater than those of oysters from unselected broodstock, respectively; whereas, average survival, final individual weight and yield of the top (10%) families from each cohort were 56%, 26% and 83% greater than those of oysters from unselected broodstock, respectively. Survival and final weights of oysters were inversely correlated in some field-trials, complicating selection for both traits simultaneously. However, selection for family yield (a product of both survival and growth) avoids the inadvertent selection of high surviving families with poor growth rates. Another trait of marketing interest is shell color. Shell color was heritable ($h2 = 0.59$), was not greatly affected by culture environment (4–10% of total variation) or genotype-environment interactions (<6% of total variation) and was not correlated with either survival or growth. Market analyses need to be undertaken to determine the most desirable shell characteristics (color, shape etc) for consumers so that breeding programs can be implemented to improve these traits.

DETERMINATION OF THE OPTIMUM HARVESTING TIME OF UNIALGAL FOOD STOCKS IN SHELLFISH AQUACULTURE. **Alexandra Lawlo, Karin A. Tammi, Kari Pohl, Jessie Alden,** and **Dr. Timothy Scott.** Center for Economic and Environmental Development, Roger Williams University, One Old Ferry Road, Bristol, Rhode Island 02809-2921, USA.

Algal production can account for almost 50% of the cost for rearing shellfish seed in a hatchery. Roger Williams University's shellfish hatchery maintains a variety of flagellate and diatom unicellular marine microalgal strains that are used as food for the shellfish. To feed the shellfish, the hatchery cultures *Chaetocerous muelleri, Isochrysis* sp. (TISO), *Pavlova pinguis*, and *Tetraselmis* PLY 429. Beginning in January 2007, we monitored these strains for two months to determine the specific growth rate of each strain and to document our algal production. Batch cultures were transferred through volumes beginning at 125 ml up to 240 L. Estimated growth rates for each strain were calculated for two months based on direct haemocytometer counts. The results of this study indicated that logarithmic growth was achieved in the 240 L Kalwall® tubes, approximately 5 to 12 days after inoculation from a 20 L batch culture. *Isochriysis* and *Pavlova* achieved maximum cell densities between 7 and 12 days, respectively, followed by *Chaetocerous* and *Tetraselmis* strains, 5 and 9 days, respectively. This investigation determined the best time to harvest the algae, thus optimizing algal production for the shellfish hatchery.

CAN WE UPGRADE THE FLUPSY FOR IMPROVED PERFORMANCE WITH REDUCED OPERATING COSTS?. **Dale Leavitt[1], Daniel Abbate[2], Jean-Paul Brice[2], Michael Debellis[2], Soukdao Phosthisane[2], Colin White[2], Charles Thomas[2],** and **Linda Riley[2].** [1]Roger Williams University, Marine Biology Department, Bristol, RI 02809; [2]Roger Williams University, School of Engineering, Bristol, RI 02809.

The traditional Floating Upweller System (FLUPSY) used in the northeast is a raft frame with silos and discharge trough suspended in the water column below the frame. The system is powered by a simple submerged axial flow pump operating off a 110 VAC power source. With these systems normally restricted for use off docks or in marinas with shore power accessible, there are limitations to the versatility of their use. Following characterization of the flow dynamics and energy use of the traditional FLUPSY, a scale model was constructed to allow for testing of proposed improvements to the pump and water flow characteristics. A variety of pump and power configurations were tested using mathematical flow models and the constructed scale model to attempt to optimize power use. The ultimate goal is to increase the efficiency of power consumption to allow for removing the FLUPSY from the conventional power grid and to investigate alternative power sources for providing the water flow characteristics required for shellfish growth. A proposed design modification will be presented for retrofitting existing FLUPSYs to improve their performance.

A BRIEF HISTORY OF BAY SCALLOP RESTORATION IN FLORIDA: PEOPLE, PLACES AND STRATEGIES. **Jay Leverone[1], William Arnold[2], Norman Blake[3], Stephen Geiger[2], Curt Hemmel[4],** and **Peter Clark[5].** [1]Mote Marine Laboratory, Center for Coastal Ecology, 1600 Ken Thompson Pkwy, Sarasota, FL, 34236, USA; [2]Fish and Wildlife Research Institute, 100 Eighth Avenue SE, St. Petersburg, FL, 33701, USA; [3]University of South Florida, 140 Seventh Avenue S, St. Petersburg, FL, 33701, USA; [4]Bay Shellfish Company, P.O. Box 289, Terra Ciea, FL, 34250, USA; [5]Tampa Bay Watch, 3000 Pinellas Bayway S, Tierra Verde, FL, 33715, USA.

Florida bay scallop restoration has had an interesting thirty-year history, progressing from a few simple, isolated projects to a more formally organized restoration program. This history has seen improvements in hatchery production and major shifts in restoration strategy. Today, scallop restoration in Florida involves multi-institutional cooperation with the goal of restoring critical links in the gulf coast metapopulation. Early efforts (1980–1995) involved transplanting scallops from healthy populations to spawner sanctuaries in Tampa Bay, where scallops had essentially been extirpated. A dedicated scallop hatchery was built, thereby reducing pressure on vulnerable donor populations. Hatchery-

produced scallops were deployed in cages (or free-released) from Crystal River to Sarasota Bay. Several projects involved the participation of waterfront residents, who suspended scallops in cages beneath their docks. A major shift in restoration strategy occurred in 2003 when the program expanded southward into Pine Island Sound. Hatchery-produced pediveliger larvae were released into field enclosures which enabled an assessment of settlement success. This strategy resulted in a dramatic recovery of this local population. Currently, this larval release technique is being used in Pine Island Sound, Tampa Bay and St. Andrews Bay.

A REAL-TIME PCR ASSAY FOR DETECTION AND QUANTIFICATION OF THE BLUE CRAB PARASITIC DINOFLAGELLATE *HEMATODINIUM* SP. IN ENVIRONMENTAL SAMPLES. **Caiwen Li, Kimberly S. Reece, Katrina Pagenkopp,** and **Jeffrey D. Shields.** Department of Environmental and Aquatic Animal Health, Virginia Institute of Marine Science, The College of William & Mary, Gloucester Point, Virginia 23062 USA.

Hematodinium is a parasitic dinoflagellate that is highly pathogenic to juvenile and female crustaceans. The periodic outbreaks of *Hematodinium* disease have significantly impacted stocks of various major commercial crustaceans around the world, including the American Blue crab *Callinectes sapidus* along the Atlantic Coast of the USA. The life cycle of the parasite in the Blue crab is poorly understood, and it is not clear how the free-living stage in the environment may contribute to waterborne transmission of the disease. Using a previously designed specific primer set targeting the multi-copy internal transcribed spacer region 1 (ITS1) of the ribosomal RNA (rRNA) gene complex, we developed a sensitive real-time PCR assay for detection and quantification of the parasite in the water column. The assay has a limit of detection equivalent to 0.5 parasite cells/100 ml of environmental water sample. This assay offers an efficient approach to monitoring the free-living stage of *Hematodinium sp.* in environment samples and will contribute to our future studies on the transmission dynamics of the parasite.

QUAHOG PARASITE UNKNOWN (QPX) DYNAMICS IN WILD HARD CLAMS FROM RARITAN BAY, NEW YORK. **Qianqian Liu[1], Jackie L. Collier[1], Sujata Pawagi[1], Debra Barnes[2],** and **Bassem Allam[1].** [1]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY,11794,USA; [2]New York State Department of Environmental Conservation, East Setauket, NY, 11733,USA.

Quahog Parasite Unknown (QPX) is a fatal pathogen of the hard clam *Mercenaria mercenaria* along the Northeastern coasts of the United States. Since the summer of 2002, when the first reported QPX outbreak in New York emerged in Raritan Bay, QPX prevalence in this clam population has been extensively surveyed using histopathology techniques. In this study, a quantitative Real-Time PCR (QPCR) assay specific for QPX was developed and applied to specifically detect and quantify QPX abundance in clams and in environmental samples. From April to September in 2006, QPX prevalence in clams from two sites in Raritan Bay was examined by both histology and QPCR. Although QPCR detected a substantially greater prevalence of QPX disease than histology, the temporal patterns revealed by these two methods were similar: the prevalence increased from spring to summer, peaked in August, and declined in fall. The disease intensity data from the QPCR assay also followed the same trend. These results underline the seasonality of QPX disease and strongly suggest the impact of environmental factors on disease development. In addition, QPX was detected by Q-PCR in sediments during May and September, suggesting that sediment represents a natural reservoir for the parasite.

SURVIVAL RATES OF NORTHERN QUAHOG (*MERCENARIA MERCENARIA*) TRANSPLANTED INTO GREAT SOUTH BAY, NY. **Carl LoBue[1], Chris Clapp[1],** and **Mike Doall[2].** [1]The Nature Conservancy, Long Island Chapter, Cold Spring Harbor, NY, 11724, USA; [2]Stony Brook University, Department of Ecology and Evolution, Stony Brook, NY, 11790.

Since 2004 The Nature Conservancy (TNC) has been working to restore self-sustaining populations of Mercenaria mercenaria to Great South Bay (GSB), NY. To help rebuild spawning potential, TNC has established a network of spawner sanctuaries where adult clams are stocked on natural bottom at densities ranging from 7–20 clams/m^2. To date approximately 3 million clams have been stocked at over 40 locations. To assess the longevity of these spawner sanctuaries as restoration tools, post-stocking survival rates were estimated using diver surveys at various time intervals after stocking. Handling stress contributed to initial mortality after stocking. However, predation by whelk was the major factor effecting survival over a longer period. Dive surveys showed that whelk were significantly more abundant on sanctuary sites than on areas immediately adjacent to them suggesting that whelk are attracted to the sanctuaries. Predation induced mortality was higher on transplant populations of smaller clams (mean = 61.85 ± 8.5 mm shell length) compared to adjacent populations of larger clams (mean = 87.25 ± 8.0 mm shell length). There was also high variability in survival rates among locations within the bay. Our data indicate that the size of clams and the location of within the bay are critical determinants of sanctuary longevity.

ACTIN GENES IN BONAMIA OSTREAE : CHARACTERIZATION AND APPLICATION TO PHYLOGENY AND DIAGNOSTICS. **I. Lopez-Lores[1], M. Robert[1], V. N. Suarez-Santiago[2], D. Longet[3], D. Saulnier[1], B. Chollet[1],** and **I. Arzul[1].** [1]IFREMER Laboratory of Genetics and Pathologue, La Tremblade, France; [2]Department of Botany, Faculty of Sciences, University of Granada, Spain; [3]Department of Zoology and Animal Biology, University of Geneva, Switzerland.

Bonamia ostreae is a protozoan parasite that infects the European flat oyster *Ostrea edulis* causing systemic infections and resulting in massive mortalities. Previously, isolation of the gene

coding the SSU rRNA allowed us to perform a phylogenetic analysis which placed *Bonamia* within the Haplosporidia. Moreover, genes coding proteins like actin genes have a different evolutionary rate compared to those governing ribosomal genes and in this respect, may contribute to a wider knowledge of relationships within the haplosporidian species. In this work *B. ostreae* actin genes were characterized and their sequences were used for phylogenetic analyses and for the development of a quantitative PCR assay. Characterization of the sequences allowed us to identify two sequence types encoding two proteins and suggested that two paralogous actin genes are present in the parasite genome. Actin phylogeny based on nucleotide sequences supported previous studies based on SSU rDNA sequences and placed *B. ostreae* in a clade with *Minchinia tapetis*, *Minchinia teredenis* and *Haplosporidium costale* as its closest relatives. Also, primers were designed on the actin gene sequences in order to develop a real time PCR aiming at quantifying parasite burden in oysters.

IMPACT OF OYSTER CULTURE ON INTERTIDAL MACROBENTHIC INFAUNA. Lin Lu and **Jon Grant.** Dalhousie University, Department of Oceanography, Halifax, Nova Scotia, B3H 4J1, Canada.

Macrobenthic infauna was investigated bimonthly from June to October at an intertidal site with oyster culture in St-Simon Bay, New Brunswick, Canada. Sediment organic content was significantly higher inside the oyster farm than outside the farm. Abundance and species number of macrobenthos were significantly lower inside the farm than outside the farm, and generally increased over the study period. Multivariate analyses show significant differences in community structure between the inside-farm and outside-farm communities, between mid-tidal and low-tidal zones, and between the sampling months. The results suggest a significantly negative impact of biodeposition from oyster culture on intertidal macrobenthic community. The study also demonstrates that tidal zones play an important role in determining the community structure of intertidal macrobenthic infauna.

THERMAL TOLERANCE OF DERMO TOLERANT/RESISTANT OYSTERS: A COMPARISON OF GOOD AND MODERATE/POOR PERFORMING FAMILIES. Eric D. Lund, Fulin E. Chu, Paul Littreal, and **Kate Ruck.** Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, VA 23062.

The thermal tolerance of good and moderate/poor performing families of *Crassostrea virginica* was compared. They were heat shocked for 1 hr at 41, 42, 43, or 44°C and their mortalities were monitored up to 10 days. Surviving oysters were assayed for condition index and *Perkinsus marinus* infection intensity. Survivorship in the poor/moderate group was greater than 87% at all heat shock temperatures except at 41°C, which had a survivorship of 68 ± 10%. Survival of the good groups ranged from 92–100% at all tested temperatures. *P. marinus* infection intensities were significantly ($P < 0.001$) higher in the poor/moderate group than in the good performance group, but did not vary significantly with heat shock temperatures. Condition index of the good performing group was significantly ($P < 0.001$) higher than that of the poor/moderate group with no significant effect of heat shock temperature. Higher survival at different heat shock temperatures compared to our previous results (33–87% at 43–44°C, 100% mortality at 45°C) is believed due to the experimental oysters having been maintained in warm ambient water (24–28°C). Previously tested oysters were maintained at 20–21°C. Results suggest that LT 50 in *C. virginica* may vary significantly with seasonal acclimation temperature (sponsored by Sea Grant Development Fund).

THE ULTIMATE BENTHOS: A SAGA OF HYDROTHERMAL VENT FAUNA. Richard A. Lutz. Rutgers University, Department of Marine and Coastal Sciences, New Brunswick, NJ. 08901.

In 1977 a group of geologists and geochemists set sail with the deep-diving submersible Alvin on the R/V Lulu without a single biologist on-board to a site 200 miles off the Galapagos Islands. They were to make one of the most important biological oceanographic discoveries of the century, if not of all time. They descended a mile and a half to the crest of an undersea volcanic ridge and discovered an ecosystem that was based, not on photosynthesis, as virtually every other ecosystem we knew on earth at the time, but rather one based on chemosynthesis. Bacteria, serving as the lower link of a bizarre food chain were deriving their energy from geothermal processes deep within the earth. Every organism they encountered was unknown to science in 1977. Since that first journey to a deep-sea hydrothermal vent, over 500 new species have been described from countless similar vent environments throughout the world's oceans. In 1991 a volcanic eruption on the crest of the East Pacific Rise afforded a rare opportunity to follow biological succession from the "birth" of a hydrothermal system, radically altering our views of the rates at which biological processes occur in these unique deep-sea ecosystems.

COMPOSITION AND SEASONALITY OF EPIFAUNAL COMMUNITIES AND INVASIVE TUNICATES IN THE BLUE MUSSEL AQUACULTURE OF EASTERN PRINCE EDWARD ISLAND Vanessa Lutz[1], Aaron Ramsay[2], Jeff Davidson[2], and **Pedro Quijon[1].** [1]Department of Biology; [2]Atlantic Veterinary College, University of Prince Edward Island, 550 University Avenue, Charlottetown, PE, C1A 4P3, Canada

Suspended mussel socks and lines introduce a three-dimensional habitat into the water column that is colonized by a variety of fouling and epifaunal invertebrates. In recent years, four species of invasive tunicates have become prominent components of these communities, interacting with mussels and other epifauna in a way that is still far from well known. While some epifaunal organisms may interfere, prey on, or compete with the growing

mussels, others may become beneficial due to their potential interactions with one or more species of invasive tunicates. This study documents the seasonality effects on the most prominent groups of epifauna, including native and invasive tunicate species, on aquaculture lines located in an eastern Prince Edward Island estuarine system. Specifically, we evaluate the dynamics of these organisms in relation to four variables relevant to the mussel aquaculture industry: season of mussel line deployment, mussel stocking density, mussel line (location), and timing along the mussel growing season. Although tunicates and epifaunal assemblages changed broadly with most of these variables, the main driver of species composition and abundance in this area appear to be the timing along the growing season. We discuss these results in relation to timing of tunicate colonization and potential mitigation measures.

DOES TIDAL STAGE AFFECT THE DISTRIBUTION OF SHELLFISH PATHOGENS? M. Maille Lyons[1], J. Evan Ward[1], Bridget Holohan[1], Jacqueline Defavari[2], Roxanna Smolowitz[3], and **Steven Roberts[4].** [1]University of Connecticut, Department of Marine Sciences, Groton, CT USA 06340; [2]Marine Biological Laboratory, Woods Hole, MA USA; [3]New England Aquarium, Director of Animal Health, Boston, MA USA; [4]University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA, USA.

This study focuses on the physical characteristics of marine aggregates and the distribution of QPX-positive samples with respect to tidal stage. Data from one of oursampling periods will be presented. The highest concentration of aggregates was recorded on the incoming tide whereas the lowest concentration of aggregates was recorded on the outgoing tide. Data for the size distribution of aggregates were highly skewed, but most aggregates (>75% of observations) were less than 500 μm for all tidal stages. The QPX organism was detected in samples collected on all tidal stages except high tide, but the highest percentage of positive samples was detected in samples collected immediately preceding low tide. Our results demonstrate the need to evaluate the effects of tidal stage (and therefore inter-tidal planting location of cultured bivalves) on the distribution of shellfish diseases.

AN EPIZOOTIOLOGICAL APPROACH TO THE STUDY OF BIVALVE DISEASES. M. Maille Lyons[1], Roxanna Smolowitz[2], Marta Gomez-Chiarri[3], J. Evan Ward[4], and **Rebecca J. Gast[5].** [1]University of Connecticut, Department of Marine Sciences, Groton, CT USA 06340; [2]New England Aquarium, Director of Animal Health, Boston, MA, USA; [3]University of Rhode Island, Department of Fisheries, Animal and Veterinary Sciences, Kingston, RI, USA; [4]University of Connecticut, Department of Marine Sciences, Groton, CT USA; [5]Wood Hole Oceanographic Institution, Woods Hole, MA.

The economically important marine bivalve mollusc, *Mercenaria mercenaria*, (commonly called a northern quahog or hard clam), has endured considerable mortalities due to the thraustochytrid pathogen called Quahog Parasite X (QPX). Data on the percent prevalence of QPX infections were compiled from published reports in order to describe the epizootiology of QPX disease. Advantages and disadvantages of an epizootiological approach to studying bivalve diseases will be presented in the context of our results for QPX. For example, the highest prevalences of QPX infections occurred in clams from samples with an intermediate size range (shell lengths 20–55 mm), suggesting that clams of this size should be used in experiments regarding transmission of QPX. Overall, our summary of information on QPX disease highlights the need for the collection of a specific type of information regarding factors believed to be associated with the presence and severity of diseases in bivalve molluscs.

MASSACHUSETTS BAY SCALLOP PRODUCTION: AN OVERVIEW. Sandra Macfarlane. Coastal Resource Specialists, P.O. Box 1164, Orleans, MA 02653, USA.

Massachusetts, one of the top producers of bay scallops until the mid-1980s, experienced steep declines in harvests throughout the state, though Nantucket and Martha's Vineyard were affected the least and continued to produce reduced harvests. Theories emerged but no definitive cause was ever found. As a first step in developing a restoration program, we surveyed municipal shellfish officers to obtain anecdotal observations on the health of the estuaries that had produced bay scallops in the past and might be able to bounce back given a helping hand. Restoration projects will be presented separately. The Massachusetts Estuary Program has great potential for the future. Adhering to state mandated calculations for Total Daily Maximum Loads (TMDLs) of nitrogen, individual communities and regions are currently planning wastewater management programs to decrease the amount of nitrogen flowing into the estuaries. In Cape Cod's Pleasant Bay, restoring eelgrass cover to historic abundance mapped in the 1950s will determine whether reduced nitrogen concentration through implemented wastewater management plans is achieved. Natural barrier beach dynamics also figure prominently in the bay. The effect of inlet formations for bay-wide dynamics and scallop habitat will be highlighted.

EMBRACING SHELLFISH AQUACULTURE BEST MANAGEMENT PRACTICES ON THE EAST COAST. Sandra Macfarlane[1], Gef Flimlin[2], Edwin Rhodes[3], and **Kathy Rhodes[3].** [1]Coastal Resource Specialists, P.O. Box 1164, Orleans, MA 02653, USA; [2]Rutgers Cooperative Extension of Ocean County, 1623 Whitesville Road, Toms River, NJ 08755, USA; [3]East Coast Shellfish Growers Association, 49 Reed Street, Milford, CT 06460, USA.

Developing shellfish aquaculture Best Management Practices (BMPs), a priority need identified throughout the region, is a project of the East Coast Shellfish Growers Association. At workshops scheduled in the winter of 2008, growers, regulators, environmental groups and other stakeholders came together to discuss issues under

broad categories and suggest approaches to address the issues. This bottom-up process avoided any specific agendas or direction by outside organizations or user groups. An introductory presentation provided information on the project purpose, culture types being practiced, and workshop format. Participants then separated into small breakout groups where communication and interaction among all stakeholders was fostered. We anticipate, through response analysis, that some issues will transcend geographic variability and others will be either geographically or species specific. The final product will incorporate existing BMPs where they exist to the greatest extent possible, will include a generic Code of Practice—a pledge for growers that they will act responsibly, and may lead to some kind of industry certification program. A second set of workshops will be held in 2009 to review the draft document and suggest changes prior to publication of the final document, anticipated for the summer of 2009.

PREVALENCE OF PARASITES IN BLUE CRABS (*CALLINECTES SAPIDUS*). Angie Machniak, Anne McMillien Jackson, and **Jan Landsburg.** Florida Wildlife Research Institute Florida Wildlife Commission Crustacean Fisheries St. Petersburg FL 33701.

The blue crab (*Callinectes sapidus*) is a keystone species in estuaries throughout the eastern US, and of high economic value in the Tampa Bay area: 869,430 pounds of blue crabs valued at $800,000 dockside were landed here during 2006. We conducted a year-long assessment of blue crab health in Tampa Bay to determine the identity and prevalence of parasites with regard to seasonality and environmental conditions. A range of parasite conditions were documented, including *Hematodinium* and microsporidia in the hemolymph. The overall prevalence of *Hematodinium* sp. in the hemolymph of blue crabs from Tampa Bay was 17.3%, with the highest prevalence noted in April. The prevalence of infection ranged 12.4–21.0% during the cold season (bottom water temperature <24°C) and 4.6–26.5% during the warm season (temperature >24°C). The overall prevalence of microsporidia was 3.8%. Microsporidian infections in the hemolymph were only found from late summer to fall, with the greatest intensity occurring in September. The prevalence of infection ranged 0.0–2.3% during the cold season and 5.3–12.1% during the warm season. Overall the presence of both parasites is low in the population (less than 4%). We hope to expand our assessment of crab health.

HISTORY OF THE BAY SCALLOP (*ARGOPECTEN IRRADIANS* SPP.) FISHERY, MASSACHUSETTS THROUGH FLORIDA. Clyde L. Mackenzie Jr. [1]James J. Howard Marine Sciences Laboratory, Northeast Fisheries Science Center, 74 Magruder Road, Highlands, NJ 07732.

Bay scallops (*Argopecten irradians* spp.) were harvested on a small scale by Native Americans. Along the Atlantic Coast, a commercial fishery for bay scallops began in the 1870's, when the A-frame dredge became available, railroads were constructed that could transport them to markets, and consumers began to eat them. Rowboats, catboats and sloops were the first harvesting boats. In the 1910's and 1920's, the sails in catboats were replaced with engines. In the 1940's, outboard motors became available to propel rowboats. This enabled many part-timers to harvest scallops. As the scallops have been a highly-priced commodity, the fishery brought a substantial quantity of money into local economies. In the 1960's, fiberglass boats, 6–7 m long and propelled by outboard motors, replaced the rowboats and catboats for scalloping. Massachusetts led in bay scallop landings, 190,000 bushels/year, in the early 1980's, while New York and North Carolina each landed about 45,000 bushels/year. Since 1985, bay scallop landings have fallen sharply due to noxious brown tides." The North Carolina landings have fallen since a "red tide" in 1987–88 and predacious cownose rays, *Rhinoptera bonsais*, became abundant. The scallop fishery remains consistently viable only on Martha's Vineyard and Nantucket.

THE DECLINE IN LANDINGS OF NORTHERN QUAHOGS (*MERCENARIA MERCENARIA*) IN GREAT SOUTH BAY, NEW YORK, AND RECENT INCREASE IN THEIR LANDINGS. Clyde L. Mackenzie Jr. James J. Howard Marine Sciences Laboratory, Northeast Fisheries Science Center, 74 Magruder Road, Highlands, NJ 07732.

The landings of northern quahogs (*Mercenaria mercenaria*) in Great South Bay rose to nearly 700,000 bushels in the mid-1970s, but they fell sharply thereafter and they were negligible by the 1990s and 2000s. In 1975, the recruitment of juvenile quahogs was negligible even though the stocks of adult quahogs were abundant. This suggested that predators had become abundant and were consuming nearly all the juvenile quahogs. This predation must have continued afterwards. Blue crabs may have become abundant during the 1970s and remained abundant. Since the 1980s, starfish (*Asterias forbesi*) have been relatively scarce in Connecticut. Their scarcity coincides with the recent upsurge in the landings of the northern quahogs. The state's northern quahog landings rose to equal about half the landings along the US Atlantic coast in 2004. Another suspected predator of northern quahogs is the rock crab (*Cancer irroratus*).

DIFFERENTIAL TOXIN UPTAKE AND FEEDING STRATEGIES IN *CRASSOSTREA VIRGINICA* AND *MYTILUS EDULIS* EXPOSED TO A TOXIC DIATOM. Luiz Mafra Jr.[1], V. Monica Bricelj[2], and **Michael Quilliam[2].** [1]Dalhousie University, Biology Depatment, Halifax, NS, B3H 4J1, Canada; [2]National Research Council Canada, Institute for Marine Biosciences, Halifax, NS, B3H 3Z1, Canada.

Harvest closures due to domoic acid (DA) contamination are usually applied to all bivalves in an affected area, although toxin levels in oysters rarely attain the regulatory limit of

20 μgDA.g^{-1}. To investigate the species-specific capacity for DA accumulation, oysters and mussels were continuously exposed to *Pseudo-nitzschia multiseries* clones of contrasting cell length during 2-wk trials. DA accumulation was measured by LC-UV in whole animals or separated into digestive glands and other tissues. Clearance rates were determined and allometric relationships developed to predict toxicities over a wide range of body sizes. Weight-specific DA levels were inversely related to shell height in oysters but no relationship was observed in mussels. The contribution of the digestive gland to the total toxin body burden decreased rapidly over time in oysters, especially in smaller animals, but remained constant and at a high level (>80%) in mussels irrespective of size. Oysters accumulated 7–70 times less DA than mussels and the difference in toxicities between the two species was greater when they were fed a larger *P. multiseries* clone. These results are attributed in part to differences in particle processing between the two bivalves and can be applied towards DA management by species in affected areas.

THE HAZARDS OF ADOPTING UNTESTED TECHNOLOGY IN YOUR COMMERCIAL OPERATION. André Mallet[1] and **Claire Carver[2].** [1]Mallet Research Services, [2]ccarver@ns.sympatico.ca.

New methods for cultivating shellfish are being proposed on a regular basis: from floating, to suspended, to off-bottom systems. Claims are made, often without appropriate cost-benefit or environmental impact analyses, about the ability of these systems to improve growth, enhance survival, lower production costs, and improve flesh quality. Site characteristics such as water depth, wind exposure, or the presence of eel grass may have a significant influence on the performance of these shellfish grow-out systems. Examples and economic projections will be provided to illustrate how adopting untested technology may seriously affect the commercial viability of your farm.

USE OF PCR-DGGE TO STUDY THE NATURAL DIET OF MARINE BIVALVES. Aaron P. Maloy[1], Sarah C. Culloty[2], and **John W. Slater[3].** [1]University College Cork, Department of Zoology, Ecology and Plant Science, Cork, Ireland and Centre of Applied Marine Biotechnology (CAMBio), Letterkenny Institute of Technology, Letterkenny, Ireland; [2]University College Cork, Department of Zoology, Ecology and Plant Science, Cork, Ireland; [3]Centre of Applied Marine Biotechnology (CAMBio), Letterkenny Institute of Technology, Letterkenny, Ireland.

Given their ecological and commercial importance, the feeding dynamics of marine bivalves has long been a research focus in shellfish ecology. Most natural diet characterizations are based on physical observations of ingested organisms and/or those removed from the water column during mesocosm experiments. More recently, molecular techniques are being used to gain further insights into the feeding ecology of marine invertebrates. Using a PCR-DGGE (denaturing gradient gel electrophoresis) approach targeting a variable region of the 18S rRNA gene, we are obtaining DNA-based profiles of ingested eukaryotic prey organisms from gut contents of the marine bivalve, *Mytilus edulis*. Profiles obtained are being compared to those of the water column to assess feeding selectivity and individual bands within profiles are being identified through sequencing. PCR-DGGE profiling offers a fast and sensitive way to assess the dietary signature of marine invertebrates across broad temporal and spatial scales. Further refinement and application of this technique will focus on intra and interspecific competition while also exploring trophic level interactions of suspension feeding bivalves.

SO HOW FAST DO OYSTER SPERM SWIM?. Roger Mann[1] and **Mark Luckenbach[2].** [1]Virginia Institute of Marine Science, Gloucester Point, VA 23062; [2]Virginia Institute of Marine Science, Wachapreague, VA 23480.

Nothing is more fundamental to the perpetuation of animal species than the fertilization of an egg by a sperm. Oysters, like the vast majority of sessile marine invertebrates, shed sperm and eggs into the water column where fertilization subsequently occurs. The fate of gametes in this dance of procreation depends on their passive movement at various scales in the high viscosity environment into which they are ejected, the longevity of the ability of the sperm to effect oriented movement within that medium, the rate of movement of the sperm towards an egg target, and the ability of a sperm to effect fertilization. We present data, collected as part of a larger study of fertilization dynamics, on rates of oriented sperm movement, discuss them in terms of the time sequence of spawning and fertilization, and compare them to rates describes for sperm movement of other members of the animal kingdom.

ESTIMATING MORTALITY RATES IN OYSTER POPULATIONS. Roger Mann[1], Melissa Southworth[1], Juliana M. Harding[1], and **James Wesson[2].** [1]Virginia Institute of Marine Science, Gloucester Point, VA 23062; [2]Virginia Marine Resources Commission, P.O. Box 756, Newport News, VA 23607-0756 USA.

The vast majority of published oyster mortality estimates are based on proportions of articulated valves of dead animals (boxes) in a target population. Such estimates are fraught with errors that are generally difficult to estimate or conveniently ignored. These include rates of disarticulation with time, size, local environment and collection method. The acceptance of arguably limited methods for mortality estimation is driven by the lack of data on and/or the inability of researchers to estimate age structure of oyster populations over time, and thus use changes in absolute numbers of oysters present to estimate mortality, preferably by year class, over extended periods in target populations. We present data for a multi-year period from the James River, VA wherein we use a

length at age estimator to recast length demographics as age demographics over multi year periods, and thus estimate year class specific, as well as total mortality over an extended period. We compare these data with mortality estimates calculated using traditional box count methods.

IMPACT OF BROWN RING DISEASE ON THE ENERGY BUDGET OF THE MANILA CLAM, *RUDITAPES PHILIPPINARUM*. **Jonathan Flye Sainte Marie[1], Frederic Jean[1], Stéphane Pouvreau[2], Sebastiaan Kooijman[3],** and **Christine Paillard[1].** [1]LEMAR, IUEM, Place Nicolas copernic, 29280 Plouzané, France; [2]Ifremer Station d'Argenton, IFREMER, Argenton, France; [3]Vrije Universiteit, Amsterdam, The Netherlands.

Brown ring disease (BRD) in the Manila clam is a disease caused by the bacterium *Vibrio tapetis*. This disease induces a brown deposit on the inner shell of infected clams and can be associated with mass weight loss suggesting that the disease affects the energy budget. An experiment was performed in order to asses the effect of the disease clearance and respiration rates and indicated that the clearance rate of severely diseased clams was significantly decreased by both a decrease in filtration capacity and a reduction of the time spent on filtration activity. A starvation experiment allowed to show that in highly infected clams was weigth loss was higher than in uninfected ones indicating that the enery balance is affected independently of the effect on filtration activity. This energtic cost may be assiciated with an increase in maintenance cost due to energy needed for immunity and lesion repair. A model based on Dynamic Energy Budget theory, allowed to quantify the effect of BRD on maintenance costs and indicated that BRD development could be associated with an important increase in the maintenance cost.

***ROSEOVARIUS* OYSTER DISEASE OUTBREAKS IN RHODE ISLAND COASTAL SALT PONDS.** **Kathryn Markey[1], Dina Proestou[1], Jale Korun[2], Dale Leavitt[3],** and **Marta Gomez-Chiarri[1].** [1]University of Rhode Island, Department of Fisheries and Animal Veterinary Science, Kingston, RI 02881, [2]Akdeniz University, Antalya, Turkey; [3]Roger Williams University, Department of Biology and Marine Biology, Bristol, RI 02809.

The Environmental Quality Incentives Program (EQIP), funded by the US Department of Agriculture Natural Resource Conservation Service (USDA/NRCS), provides shellfish farmers in Rhode Island with incentives to improve the environmental quality of their operations. Through this program, data has been collected since 2006 from 10 to 15 participating farms for environmental parameters such as water temperature, dissolved oxygen, and salinity, as well as oyster disease prevalence and intensity. During the summer of 2007, mortalities in oyster seed (4 to 20 mm in shell height) were observed in several upwellers located in local coastal salt ponds. Mortalities ranged from 4 to 100% depending on location, seed source, and seed size. The presence of *Roseovarious crassostreae*, causative agent of *Roseovarius* oyster disease, was confirmed by polymerase chain reaction and slide agglutination tests. Water temperatures at the time of the outbreak ranged from 25 to 32°C, salinity was 28 psu, and dissolved oxygen levels ranged from 2 to 5 mg/L. These observations indicate that *Roseovarius* oyster disease is prevalent in Rhode Island waters, but that severe mortality events are triggered only when oysters less than 20 mm in shell height are exposed to water temperatures above 25°C.

GENETIC AND DEMOGRAPHIC CONNECTIVITY IN NORTH CAROLINA BAY SCALLOP POPULATIONS. **Peter Marko.** Clemson University, Biological Sciences, Clemson, SC, 29631, USA.

For marine species with a planktonic life-history stage, successful management of harvested populations can be enhanced by knowledge of the spatial scale of ecologically significant larval dispersal and supply. Here, I discuss my lab's research on the population genetics of bay scallops in central North Carolina, with an eye towards the role that nearshore currents play in larval transport. Despite having planktotrophic larvae, ecological and physical oceanographic evidence indicates that demographically meaningful larval transport between adjacent sounds or basins in North Carolina is likely infrequent for this species. Analyses of mtDNA sequences and microsatellite genotypes from adult populations support this hypothesis, suggesting that sites separated by relatively small distances (<20 km) are not demographically coupled and are probably best considered as individual ecological units. Inferences about contemporary rates of dispersal from genetic data can be difficult, however, especially in species with complex demographic histories, such as the bay scallop, and the impact of changing effective population size on gene flow and larval transport will also be discussed.

GONADAL CYCLE OF NORTHERN QUAHOGS, *MERCENARIA MERCENARIA* (LINNE, 1758), IN HIGH DENSITY SUBPOPULATIONS IN NARRAGANSETT BAY. **Dora Carolina Marroquin-Mora[1]** and **Michael A. Rice[2].** [1]Centro de Estudios del Mar, Universidad de San Carlos de Guatemala, Ciudad Universitaria Edificio T-14 zona 12, Ciudad de Guatemala, Guatemala 01012; [2]Department of Fisheries, Animal & Veterinary Science, University of Rhode Island, Kingston, RI 02881 USA.

Quahog reproductive potential in areas closed to fishing in Narragansett Bay was studied using two approaches; condition index (CI) and histological gonadal index (GI). Initial sampling of 9 sites for CI was March 25 to Sept. 22, 2005. A subset of 6 of the sites was sampled every three weeks the following year (2006) from

April 15 until Sept. 28 to determine CI and GI. Results show that there is a significant difference between the CI of quahogs from conditional areas and closed areas ($P < 0.001$). There is a significant difference in GI between sites at ($P < 0.10$). The GI in conditional areas was consistently higher than in closed sites. When sites were separated into three categories, the fished sites had lowest indices, the cove sites had intermediate indices, and the Providence River sites always had the lowest indices. Populations of quahogs in sites closed to fishing are not completing the gonadal cycle as expected, and the reproductive capability of quahogs in conditional fishing areas is higher than those in closed areas. Although, not one single characteristic of the environment is solely responsible for the reproductive condition of the quahog subpopulations, density appears to have significant effect.

HOW NUISANCE MACROALGAE AFFECT SHALLOW BURROWING BIVALVES. Islay D. Marsden. School of Biological Sciences, University of Canterbury, Christchurch 8020, New Zealand.

Nuisance macroalgae, *Ulva* spp. and *Gracilaria* sp. occur commonly in shallow estuaries throughout the world, where they have positive and negative effects on shellfish beds. In the Avon-Heathcote Estuary, South Island, New Zealand we have investigated the survival, behaviour and physiology of the native little neck clam *Austrovenus stutchburyi* from an area subjected to regular sea lettuce blooms. Measurements were made on sea lettuce abundance and field experiments used to determine the effects of sea lettuce density on cockle survival and condition. The behavioural and physiological responses of cockles to declining oxygen availability were measured in the laboratory. These studies suggest that low abundances of sea lettuce do not affect the survival or condition of cockles. However, oxygen uptake is reduced in conditions of declining oxygen availability and individuals move upwards to the sediment surface. Here they can be dislodged by the tide and eaten by predators. Macroalgal blooms can therefore have negative effects on cockle populations in estuarine areas.

IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES IN THE EUROPEAN FLAT OYSTER (*OSTREA EDULIS*) IN RESPONSE TO INFECTION BY THE HAPLOSPORIDIAN *BONAMIA OSTREAE* Laura Martín-Gómez[1], Elvira Abollo, and **Antonio Villalba.** Centro de Investigacións Mariñas, Xunta de Galicia, Vilanova de Arousa, 36620, Spain.

Oysters possess an innate immune system whose molecular mechanisms are not well understood. Suppressive subtracted hybridisation (SSH) was used to identify differentially expressed transcripts in oyster haemocytes in response to infection by *Bonamia ostreae*. SSH was performed following an inoculation experiment in oysters: healthy oysters were inoculated with purified *Bonamia ostreae* (infected group) or with filtered seawater (control group). After 80 days, haemolymph from each individual was withdrawn to extract the RNA, which was lately used for the SSH. Two ESTs libraries were obtained after the experiment: one with those transcripts up-regulated during infection and the other with the down-regulated transcripts. ESTs similarities with known genes were performed using BLAST and functional gene classification was done according to KEGG. The subtracted cDNA libraries showed that 34% of the sequences were new ESTs with unknown functions, whereas 13% had already been identified as oyster ESTs. 53% of the clones were identified as known genes, some of them with unreported functions in oysters. Preliminary results obtained in this work show clear difference in expression between infected and control samples. These marks could allow a better understanding of molecular mechanisms involved in mollusc immunity.

OYSTER BREEDING MIXED UP: A NEW SPIN ON OLD SCIENCE. Sean E. Matson[1], Mark D. Camara[2], Will Eichert[3], and **Michael Banks[4].** [1]Department of Animal Sciences, Oregon State University, 2030 SE Marine Science Dr. Newport, OR 97365; [2]Shellfish Genetics Program, USDA Agricultural Research Service, 2030 SE Marine Science Dr. Newport, OR 97365; [3]Coastal Oregon Marine Experiment Station, Oregon State University, 2030 SE Marine Science Dr. Newport, OR 97365; [4]Department of Fish and Wildlife, Coastal Oregon Marine Experiment Station, Oregon State University, 2030 SE Marine Science Dr. Newport, OR 97365.

Pacific oyster breeding is complicated by high variance in reproductive success and high genetic load, which can result in loss of genetic variation and inbreeding depression. Oyster breeding typically utilizes among-family selection with families reared separately to control these negative impacts, but this method presents several disadvantages that may be overcome by a mixed-family selection (MFS) approach, which homogenizes the effects of environmental variation, genetic interactions and density among families, potentially increasing selection intensity and enabling smaller, cheaper, and more informative field trials. Our research focuses on optimizing DNA marker-based pedigree reconstruction for our MFS model of Pacific oyster breeding, and testing its efficacy alongside separate-family selection methods. To increase genotyping efficiency for family identification, we developed software called P-LOCI that identifies the most efficient set of codominant markers for assigning individuals of a mixed sample to their parents. We also conducted an experiment to determine the most efficient stage of development to mix oyster families for selection. We found that among-family variability increases with earlier mixing and the optimum stage to mix depends on the trait. Finally, we conducted field experiments to optimize sampling strategies for mixed-family groups of adults at multiple traits and compare methods side-by-side.

DELAWARE BAY OYSTER RESTORATION PROJECT. **Martha Maxwell-Doyle[1], Jason Hearon[2], Dr. Eric Powell and Kathryn A. Ashton-Alcox[3], Russ Babb[2],** and **Rick Cole[4].** [1]Partnership for the Delaware Estuary, One Riverwalk Plaza, 100 South Poplar Street, Suite 202, Wilmington, DE 19801; [2]NJ Dept. of Environmental Protection, NJDEP Bivalve Field Station at the Haskin Shellfish Research Laboratory, 6959 Miller Ave., Suite A, Port Norris, NJ 08349; [3]Haskin Shellfish Research Laboratory, 6959 Miller Avenue, Port Norris, NJ 08349; [4]Delaware Department of Natural Resources and Environmental Control.

The Delaware Bay Oyster Restoration Project is a cooperative initiative currently underway that is revitalizing Eastern oysters, a signature species of the Delaware Estuary. This work is being carried out by the Delaware Bay Oyster Restoration Task Force: a collaborative group of organizations, institutions and agencies working at the local, state, regional, and federal levels. Together, our goal is the complete revitalization of Delaware Bay oysters and its habitat. The project consists of a reef restoration through an extensive shell planting and transplanting oysters from lower in the Bay, where the salinity is higher, to areas further north in the Bay, where they stand a better chance of surviving. Monitoring component and education and outreach is also a critical part of the initiative. These restoration efforts would not have been possible without the support of ongoing Congressional, State and industry funding support. DCORTF members: Cumberland County Empowerment Zone, Delaware Department of Natural Resources and Environmental Control, Delaware River and Bay Authority, Delaware River Basin Commission, New Jersey Department of Environmental Protection, New Jersey Shellfisheries Council, Partnership for the Delaware Estuary, Rutgers University's Haskin Shellfish Research Laboratory, and U.S. Army Corps of Engineers–Philadelphia District.

A SURVEY FOR POTENTIAL ENDOCRINE DISRUPTION EFFECTS IN BIVALVES IN MARYLAND'S CHESAPEAKE BAY. **Carol B. McCollough[1]** and **Victor S. Kennedy[2].** [1]Maryland Department of Natural Resources, Cooperative Oxford Laboratory, Oxford, MD 21654; [2]Horn Point Laboratory, University of Maryland Center for Environmental Studies, Cambridge, MD 21613.

A variety of natural and anthropogenic compounds in wastewater effluents, including estrogens and estrogen mimics, affect reproduction in diverse aquatic organisms by disrupting endocrine systems. Studies of endocrine disruptors in bivalves have demonstrated effects in several species in Europe and Canada. We investigated the presence and frequency of hermaphrodism, delayed gametogenesis, and unbalanced sex ratios, in Chesapeake Bay epifaunal and infaunal bivalves impacted by and far removed from wastewater treatment plant outfalls. Species examined included eastern oyster *Crassostrea virginica*, hooked mussel *Ischadium recurvum*, softshell clam *Mya arenaria*, stout razor clam *Tagelus plebeius*, and Atlantic clam *Rangia cuneata*. Endocrine disruption was not reflected by the presence of hermaphrodites in adults of any species examined. There was no evidence of delayed gametogenesis; all individuals that had reached the expected size or age of sexual maturity had well developed gonads and identifiable gametes. There were differences in oyster sex ratios between impacted and unimpacted sites, but it is unclear if these reflect endocrine disruption or relatively natural variability. Sex ratios of hooked mussels were not much different from those found in the early 1960s. Sex ratios of the remaining three species demonstrated no consistent patterns that could be associated with potential endocrine disruptors.

A CELLULAR DEFENSE MECHANISM IN THE OOCYTES AND EMBRYOS OF THE MUSSEL, *MYTILUS GALLOPROVINCIALIS*. **Nature A. McGinn[1]** and **Gary N. Cherr[2].** [1]University of California–Davis, Bodega Marine Laboratory, Bodega Bay, CA, 94923, USA; [2]University of California–Davis, Depts. of Environmental Toxicology and Nutrition, Davis, CA, 95616, USA.

Multidrug resistance is one of the few mechanisms active in the very early life history stages of free-spawning marine invertebrates providing effective protection against the chemical challenges of life in the oceanic water column. The multidrug resistance (MDR; also known as multixenobiotic resistance) defense system involves a suite of efflux proteins in the cellular membrane that recognize and remove target substances from cells. MDR activity was measured by comparing the fluorescence of a dye substrate within unfertilized oocytes or early cleavage embryos in the presence or absence of efflux inhibitors specific for the different MDR proteins. Results of MDR functional assays revealed that the oocytes and early embryos of *Mytilus galloprovincialis* have MDR activity levels similar to those of other marine invertebrates. Trends in the data indicate little difference in the contribution of the different MDR proteins to overall MDR activity or in the levels of MDR activity between the two developmental stages. Western blot analysis and immunolabeling with specific antibodies confirmed the expression of several MDR proteins in the mussel oocytes and embryos. Understanding the protective mechanisms of developing mussels may allow us to better predict the survival of economically important species in the face of future environmental challenges.

THE NATIONAL FISH HABITAT ACTION PLAN—A NATIONAL PLAN TO CONSERVE FISH AND SHELLFISH HABITAT. **Katherine A. McGraw.** NOAA Restoration Center.

The National Fish Habitat Action Plan (the Action Plan), is a national effort to conserve the nation's freshwater and coastal/marine fish and shellfish habitats. Modeled after the North American Waterfowl Management Plan, this is the most comprehensive effort ever attempted to treat the causes of fish/shellfish habitat decline, not just the symptoms. It is an investment strategy to leverage federal, state, and privately raised funds directed at fixing

the nation's most pressing aquatic habitat problems. The Action Plan is being implemented by Regional Fish Habitat Partnerships composed of volunteer organizations and requires a science-based approach to habitat conservation and a national assessment of the condition of fish habitats, to be updated every 5 years.

Although thousands of conservation projects have been completed in both fresh water and coastal/marine habitats, they have not kept pace with impacts resulting from population growth, land-use changes, pollution, and climate change. The need has never been greater for increased action and improved coordination of fisheries conservation agencies and groups. This presentation will explain the structure of Action Plan implementation, describe the effort to develop a national "Status of the Nation's Fish/Shellfish Habitats" report, and provide examples of how the Action Plan is currently being implemented.

HABITAT PREFERENCE AND POPULATION STRUCTURE OF WILD EASTERN OYSTER POPULATIONS IN THE LOWER HUDSON RIVER ESTUARY. Tiffany L. Medley[1] and **John R. Waldman[2].** [1]Graduate Center, City University of New York; [2]Queens College, City University of New York.

Though uncommon, isolated patches of wild Eastern Oysters, *Crassostrea virginica*, can be found attached to rock and other hard substrate in the intertidal zone of the East River, Hudson River, western Long Island Sound and Hackensack River of the lower Hudson River Estuary. The environmental factors influencing their survival in the still heavily polluted waters is unknown. Environmental characteristics of the surrounding waters will be compiled and correlated with growth rates. Analysis of mitochondrial DNA and microsatellite markers will determine if the populations are reproductively isolated from one another and/or the general Atlantic Coast population. This study will provide the first assessment of the population structure, abundance, growth, and health of these naturally recruited oysters. Understanding the components of their survival can ensure the success of local oyster restoration efforts and help to reestablish the Eastern Oyster as a keystone species to the estuary.

VARIABILITY AND GENETIC DIFFERENTIATION OF WILD POPULATIONS OF AN INVASIVE SPECIES, THE PACIFIC OYSTER *CRASSOSTREA GIGAS*, ALONG THE ENGLISH CHANNEL—ATLANTIC OCEAN COASTS. Anne-Leila Meistertzheim[1], Nelly Le Goïc[1], Alain Marhic[1], Christian Tartu[1], Pierre Boudry[2], and **Marie-Thérèse Thébault[1].** [1]Laboratoire des Sciences de l'Environnement Marin (LEMAR), UMR-CNRS 6539, Institut Universitaire Européen de la Mer, Université de Bretagne Occidentale, Plouzané, 29280, France; [2]Physiologie et Ecophysiologie des Mollusques Marins, UMR M100, Ifremer, Plouzané, 29280, France.

The Pacific oyster *Crassostrea gigas* is an important commercial species in France. Oysters cultured over extensive areas essentially form one large genetic pool because of important natural and human-mediated gene flow between populations. The wide spreading of this species during the last decade quickly led to the development of "wild" populations mainly on rocky intertidal zones. *C. gigas* now is considered as an invasive species in various part of the world. In fact, more has to be understood about mechanisms of adaptation and plasticity of these species. The purpose of this work was to study the genetic variability in some European populations. Microsatellites, allozymes and DNA polymorphism were used to assess if any genetic neutral and/or selection effects might modify the genetic pool. Discrimination of some populations from the others one using allelic frequencies at 7 allozyme loci and 7 nucleic sequences were measured and discussed. In parallel, some physiological indicators of health and fitness-related traits were assessed. Slightly significant differences were found between populations corresponding to differential physiological performances. In conclusion, these preliminary results suggest that local selection would enable *C. gigas* to successfully populate a broad ecological niche.

A BIOTIC ECOSYSTEM ASSESSMENT: SHELLFISH AS INDICATORS OF ECOSYSTEM HEALTH Gretchen Messick, Shawn McLaughlin, John Jacobs, and **Robert Wood.** Cooperative Oxford Laboratory, NOAA, Oxford, Maryland 21654, USA.

The Cooperative Oxford Lab is conducting a biotic ecosystem assessment in Chesapeake Bay. Multiple biotic indicators must be assayed to determine changes at reference sites. A hierarchical approach to sampling organisms from sub-cellularlevels to populations provides much higher resolution than typical community based approaches. Connecting sub-cellular changes through organism pathology to subsequent population level impacts allows assessment of impacts of specificanthropogenic influences, and thus ecosystem health. Indicators in crabs inthis assessment include population-community composition,shell disease, gillepibionts and parasitology. Initial results found prevalence of shell diseasehigher in Corsica than Rhode or Magothy Rivers and higher in autumn than springor summer. The presence of ciliates significantly varied among season andriver system. Inflammation and gill lesions along with pathogens in tissues including virus, microsporidian, and a gregarine will be presented. Indicators in clams include parasitology, pathology, RNA/DNA ratio's and sediment analysis. Initial results found prevalence of Perkinsus spp. infections in Macoma balthica peaked in fall/winter. Mantle disorder in M. balthica increased in prevalence in July in Corsica and Rhode Rivers. Clams from Corsica River had a higher prevalence of ciliates and otherparasites that the Rhode or Magothy Rivers.

FAST FOOD LOBSTER NATION: THE LONG-TERM CONSEQUENCES OF FEEDING BAIT TO AMERICAN LOBSTERS. **Anita Metzler** and **Michael Tlusty.** New England Aquarium, Research Department, Boston, MA 02110 USA.

The American lobster (*Homarus americanus*) fishery utilizes fish, commonly herring, as bait in lobster traps, with up to three kg of bait used for every kg of lobster landed. Lobsters have been found to rely heavily on bait as a food source, and in the short term, bait has been found to increase weight gain. Previously, we examined long term effects of juvenile lobsters fed 50 or 100% herring, and found that those fed 100% herring had lower survival and higher shell disease incidence. In this study, juvenile lobsters were fed diets containing herring in the amounts of 62, 75, 87, and 100% of the total diet. A standard laboratory diet, commonly used to rear lobsters at the New England Aquarium, was used as a control and to supplement all the diets except the 100% diet. Molt and mortalities were recorded daily. After 200 days, lobsters were analyzed on a regular basis for the occurrence and extent of shell disease. The growth rates, shell disease incidence, and mortality rates in lobsters fed the different bait amounts will be discussed. With the increasing concern surrounding shell disease, the lobsters' diet may provide insight into how lobsters become susceptible to this disease.

SPATIAL POPULATION STRUCTURE IN DELAWARE BAY OYSTERS. **Coren A. Milbury, Ximing Guo, David Bushek,** and **Susan E. Ford.** Rutgers University, Haskin Shellfish Research Lab, Port Norris, NJ 08349.

Eastern oyster (*Crassostrea virginica*) populations along the western mid-Atlantic coastline have been severely impacted by epizootics caused by two protozoan parasites known as MSX (*Haplosporidium nelsoni*) and Dermo (*Perkinsus marinus*). After decades of disease pressure, oyster populations in the Delaware Bay may have undergone a regime shift towards disease resistance, a change that can vary among regions due to vast differences in disease pressure. The objective of this investigation is to determine if the interaction of disease pressure and environmental conditions has resulted in shaping genetically-distinct, spatial population structure throughout the bay. Twenty-one microsatellite markers exhibiting linkage to disease-resistance genes, and three putatively neutral microsatellite markers, were selected to investigate oyster populations from nine locations throughout the Delaware Bay. Pair-wise G_{st}-based analyses revealed significant population differentiation within the bay. While much of the bay is genetically homogenous, the two tributaries, the most northern sampling site, and the most southern sampling site differed significantly from the populations along the main channel of the Delaware Bay. Some possible explanations for the observed differentiation include geographic isolation, environmental conditions, anthropogenic activity, and selection by diseases.

IDENTIFYING BIVALVE LARVAL COHORTS THROUGHOUT THE 2007 SUMMER SPAWNING PERIOD IN WAQUOIT BAY, MA. **Christine M. Mingione[1], Richard York[2],** and **Scott M. Gallager[1].** [1]Woods Hole Oceanographic Institution, Biology Department, Woods Hole, MA 02543 USA; [2]Town of Mashpee Shellfish Department, Mashpee, MA 02649 USA.

Survival and growth of pelagic bivalve larvae have important implications for dispersal and recruitment of commercially-important shellfish species. In Waquoit Bay, a coastal embayment on the south shore of Cape Cod, Massachusetts, chlorophyll levels and phytoplankton counts have been low during the summer spawning months (May-September), which represent an important time for larval populations to feed. In this 2007 field study, we collected weekly samples of larvae from four sites within Waquoit Bay to follow spawns and growth of cohorts from May through October. Size data, grouped together for all species, show relatively small growth for individual cohorts and suggest possible locations for larval source and sink populations. By gathering data on species-specific growth, we hope to determine the survival of individual, commercially-important species. From a bay-wide perspective, this data can provide implications for larval dispersal within the bay and from coastal waters, which can have important consequences for managing these species by broodstock-replacement methods.

***BONAMIA OSTREAE* MODIFIES ACTIVITIES OF *OSTREA EDULIS* HAEMOCYTES.** **B. Morga, I. Arzul, B. Chollet, B. Gagnaire,** and **T. Renault.** French Institut of Research for the Exploitation of the Sea (IFREMER), Laboratory of Genetics and Pathology *(LGP)*, La Tremblade, France.

Bonamia ostreae is an intracellular parasite, infecting haemocytes of flat oyster *Ostrea edulis*. Haemocytes are notably involved in the mechanisms defence of the oyster. In this study, we investigated interactions between parasites and haemocytes by flow cytometry. Analyses were performed after 2 hours of contact *in vitro* between haemocytes and parasites purified from highly infected flat oysters. Flow cytometry analyses consisted in testing haemocyte activities including esterase activities, reactive oxygen species (ROS) production and phagocytosis after contact with live parasites and parasites inactivated by heating at 100°C for 5 minutes. Two amounts of parasites per haemocytes (5 per 1 and 10 per 1) were tested and haemocytes alone were used as controls. Contact experiments were performed three times. Flow cytometry revealed a decrease of esterase activities and an inhibition of ROS production after contact with live parasites, while phagocytosis did not present variation in comparison with haemocytes alone. Inactive parasites induced same modifications of haemocyte activities as live parasites but to a lesser extent.

IDENTIFICATION OF GENES EXPRESSED DURING AN *IN VITRO* INFECTION OF HAEMOCYTES FROM *OSTREA EDULIS* WITH PARASITES *BONAMIA OSTREAE*. **B. Morga, I. Arzul, N. Faury,** and **T. Renault.** French Institut of Research for the Exploitation of the Sea (IFREMER), Laboratory of Genetics and Pathology *(LGP)*, La Tremblade, France.

Bonamiosis due to the parasite *Bonamia ostreae* is a disease affecting the flat oyster *Ostrea edulis*. *B. ostreae* is a protozoan, affiliated to the order of Haplosporidia and to the phylum of Cercozoan. This parasite is mainly intracellular, infecting haemocytes, cells notably involved in the defence mechanisms of the oyster. Suppression subtractive hybridisation (SSH) was performed to study genes expressed during an infection of haemocytes with parasites after two hours of contact. The forward and reverse SSH allowed obtaining 1,104 and 1,344 clones, among which 391 and 480 clones respectively showed a differential expression between both tested conditions (haemocytes alone and haemocytes in contact with parasites). These clones were sequenced. Sequence analysis allowed the identification of genes expressed by haemocytes and parasites during *in vitro* infection including genes potentially involved in oyster defence mechanisms and in parasite survival within haemocyte. We identified oyster genes of interest potentially involved in cytoskeleton (actin, polyubiquitin), respiratory chain (Cytochrome P450, Super oxydedismutase) and immune system (tetraspanin, tissue inhibitor of metalloprotease, Clathrin). These genes have been selected for development of real time PCR in order to follow their expression at different times in the context of experimental *in vitro* infections.

SUSCEPTIBILITY OF CHESAPEAKE BAY BIVALVES TO NON-NATIVE *PERKINSUS* SPECIES; PATHOGEN RISK ASSOCIATED WITH THE INTRODUCTION OF *CRASSOSTREA ARIAKENSIS*. **Jessica A. Moss[1], Christopher F. Dungan[2],** and **Kimberly S. Reece[1].** [1]Virginia Institute of Marine Science, College of William and Mary, Gloucester Point VA 23062, USA; [2]Maryland DNR, Cooperative Oxford Laboratory, 904 S. Morris St., Oxford, MD 21654, USA.

Research is ongoing to examine the potential disease impacts on Chesapeake Bay shellfish populations of the non-native oyster, *Crassostrea ariakensis*, should it be introduced for restoring the commercial harvest of oysters and/or developing a non-native oyster aquaculture industry. During a survey of *Crassostrea* spp. oysters conducted in Asia, the protozoan parasite, *Perkinsus olseni*, was found in *C. ariakensis* and other sympatric oyster species. In addition, *Perkinsus behaiensis*, a newly described oyster pathogen, was found in *C. ariakensis* and *C. honkongensis*. Challenge studies were performed in order to ascertain the pathogenicity of *P. olseni* and *P. behaiensis*, both to their native Asian hosts, as well as to the native Chesapeake Bay eastern oysters and hard clams, *C. virginica* and *Mercenaria mercenaria*. Direct inoculations and a bath challenge experiment were performed, during which naÿve hosts were exposed to cultured or directly-harvested *P. olseni* cells. In order to assess the potential for transmission of *P. beihaiensis*, two separate experiments were performed in which Asian oysters that were naturally exposed to *P. beihaiensis* in native Asian waters were cohabitated with naïve *C.ariakensis*, eastern oysters and clams. Results suggest that all of these bivalves are susceptible to the exotic *Perkinsus* species.

CELLULAR BIOMINERALIZATION IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. **Andrew S. Mount.** Department of Biological Sciences, Clemson University, Clemson, SC 29634 USA.

Granulocytic oyster hemocytes produce calcium carbonate crystals via an intercellular nucleation mechanism. SEM and EDS microanalysis has shown that these cells contain calcium carbonate crystals which increase in abundance upon stimulation of shell formation. It appears that the hemocytes cooperatively assemble crystal aggregates which are subsequently organized into a uniform shell layer. Immunohistochemical TEM has shown that mantle epithelial cells produces shell phosphoproteins which are phosphorylated in the Golgi, packaged in secretory vesicles and subsequently exocytosed across the apical membrane of specialized cells. The secreted phosphoproteins form a component of fibrous organic matrix which contains calcium. We hypothesize that rapid shell growth of the hemocyte deposited crystalline aggregates occurs through provision of calcium enriched phosphoprotein by these mantle epithelium cells.

BAY SCALLOP, *ARGOPECTEN IRRADIANS IRRADIANS*, RESTORATION IN MASSACHUSETTS' WATERS. **Diane C. Murphy[1]** and **William C. Walton[2].** [1]Cape Cod Cooperative Extension, Marine Program, Box 367, Barnstable, MA 02630, USA; SEMAC (SouthEastern Massachusetts Aquaculture Center), Barnstable, MA 02630, USA; [2]Cape Cod Cooperative Extension, Marine Program, Box 367, Barnstable, MA 02630, USA; SEMAC (SouthEastern Massachusetts Aquaculture Center), Barnstable, MA 02630, USA; Woods Hole Sea Grant, 193 Oyster Pond Rd., Woods Hole, MA 02543, USA.

Bay scallops remain somewhat enigmatic in their precipitous decline and explanations commonly list habitat loss, poor water quality, and fishing pressure as probable causes. Causes are rarely independent of one another and it is often the interplay and synergy created by multiple negative factors that contribute to a species decline. Most of the eastern US coastal states have undertaken bay scallop restoration in one form or another and Massachusetts is certainly no exception. With its long history of a scallop fishery, Massachusetts has unfortunately also been carried by the ebb tide of diminished scallop stocks. Various pilot-scale restoration methods have been attempted to help reverse this downward trend and are quite varied in their approaches. Some of

the methods tried have been broadcast release of juvenile scallops by towns, bay scallop spawning sanctuaries, and pediveliger releases by Barnstable County. To complement restoration efforts, work was initiated to develop genetic markers to help evaluate stock enhancement efforts and characterize population dynamics of native populations The most recent pilot-scale method to date is the implementation of underwater fencing to retain scallops for rearing, spawning, and release undertaken by Barnstable County's Cooperative Extension.

METAL CONCENTRATIONS IN TISSUES AND SHELL OF BIVALVES *CRASSOSTREA VIRGINICA* AND *GEUKENSIA DEMISSA* IN NY HUDSON RIVER ESTUARY AND LONG ISLAND SOUND USING SYNCHROTRON RADIATION. **Soren Murray[1]** and **Keith Jones[2].** [1]Kingsborough Community College, Biological Science, Brooklyn, NY, 11235, USA; [2]Brookhaven National Laboratory, Upton, NY, 11973, USA.

Bivalves are shellfish that filter feed by straining suspended food particles in water. Heavy metals and other contaminants found in food and silt in water are absorbed into their shells and tissues. Government and non-government groups have teamed to bring oysters back to the Hudson Estuary and Long Island Sound. Synchrotron radiation because of its detection sensitivity, spatial resolution and multi-element detection was used to determine the concentrations and locations of contaminating elements, in shells indicating multi-year time span, and in soft tissue indicating the compounds deposited in the sediment that may be recycled back into the environment when the bivalve dies. Samples of Eastern oysters *Crassostrea virginica* and ribbed mussels *Geukensia demissa* shell and tissues were taken from NY Hudson Estuary, Long Island Sound, known contaminated and known uncontaminated locations. The gill, adductor muscle, foot and digestive track were dissected and analyzed at the National Synchrotron Light Source using the $\times$ 26a beamline for Ni, Ti, Cr, Zn, Cu, Fe, Mn, Pb, As and Sr at 27 sites. The results show that Ni and Fe tend to be high, Zn was very high at several site and Mn was moderately high. Cu and Pb were surprising low.

SOFT-SHELL CLAM CULTURE IN THE MAGDALEN ISLANDS (SOUTHERN GULF OF ST. LAWRENCE): UPDATE ON THE R&D. **Bruno Myrand[1], Lise Chevarie[2],** and **Réjean Tremblay[2].** [1]MAPAQ - CeMIM - 107-125, chemin du Parc, Cap-aux-Meules, Qc, G4T 1B3; [2]ISMER-UQAR - 310 Allée des Ursulines, Rimouski, Qc, Canada, G5L 3A1.

An extensive R&D program to develop soft-shell clam culture in the Magdalen Islands started in 2000. Over the years, we looked at seed supply, intermediate grow-out and seeding. Spat collection using AstroTurf^{TM} mats has provided the best results for seed supply. These mats could be used as benthic or pelagic collectors. Over the past 6 years, benthic collection provided an average of 1667 clams > 2.5 mm $\pm$ 263 /m^2 with a mean size of 8.4 mm. Pelagic collection provides better results than benthic collection but sorting clams from mussels has not been solved yet. The best results for intermediate grow-out were obtained with sand-filled trays held in suspension in the water column. In the last years, most seeding trials have been done with 15 to 20 mm clams seeded at a density of 500 clams per m^2. After seeding, experimental plots are covered with 4-mm protection nets to limit predation and dispersal. However, these nets must be removed before winter. Heavy losses are observed during the fall-spring period due to high turbulence and ice scouring. Growth rate seems to be limited to about 6-7 mm per year for the 20-mm clams. Consequences for soft-shell clam culture will be discussed.

THE EFFECT OF IMMIGRATION ON DISEASE RESISTANCE IN AN OYSTER POPULATION: A NUMERICAL MODEL STUDY. **Diego A. Narvaez[1], John M. Klinck[1], Eileen E. Hofmann[1], Eric N. Powell[2],** and **Dennis Hedgecock[3].** [1]Old Dominion University, Center for Coastal Physical Oceanography, Norfolk, VA, 23508, USA; [2]Rutgers University/Haskin Shellfish Research Laboratory, Port Norris, USA; [3]University of Southern California, Department of Biological Sciences, Los Angeles, CA, USA.

An individual-based genetics model was used to investigate the effect of addition of individuals by larval oyster transport or transplantation of adult oysters on population disease resistance. Each individual oyster consists of 10 chromosome pairs, with 4 genes per chromosome. Reproduction occurs between a small number of pairs of randomly chosen individuals. An initial population with a random genetic structure was established and a varying number of immigrants with a marker in the gene 1, chromosome pair 2 were added to the population at different intervals. The allele added to the population by the immigrants was either neutral or confered benefit, which was manifest as a longer life span. Simulations are run for 100 generations and the frequency of the new allele determined. Continual addition of immigrants allowed the new allele to become dominant, even if it was neutral. Dominance occurred in several decades for 1,000 immigrants per year. Adding more immigrants reduced the time to dominance. With disease resistance, the new allele was established quicker. The simulation results are similar for larval or adult immigrants. These simulations have implications for the introduction of disease-resistance oysters to populations that are significantly impacted by disease.

GREEN POND SHELLFISH HABITAT ASSESSMENT (FALMOUTH, MA). **Pamela Neubert[1], Paula S. Winchell[1], Stephen B. Aubrey[2],** and **Derek McDonald[3].** [1]ENSR Marine and Coastal Center, Woods Hole, MA 02543; [2]Rogue Wave Field Services, N. Falmouth, MA 02556; [3]Marine Biocontrol Corp., Sandwich, MA 02563-2360.

Anthropogenic impacts from increased summer and year-round Cape Cod population to its coastal habitats has consequently led to ubiquitous degradation. Finding the fine line

between preserving Cape Cod's prized coastal habitats and maintaining economic growth is no simple task. The Town of Falmouth (Town) recognized that healthy marine ecosystems are equally as critical for economic stability as is human utilization of these habitats. To best manage the Town's coastal pond habitat, the Falmouth Coast Ponds Management Committee (CPMC) was initiated. The CPMC was charged with the task of scientifically assessing Falmouth's coastal pond systems to allow the Town to make management decisions including: harbor management plans, shellfish seeding, sewering projects, and eelgrass recovery. ENSR was hired to assist the CPMC to assess Green Pond. ENSR's assessment provided the Town with baseline habitat data that assessed and determined the status of *Mya arenaria* and *Mercenaria mercenaria*, eelgrass habitat, benthic infauna, grain size, and total organic carbon. The data resulting from this survey was incorporated into ArcView GIS 9.2. This allowed ENSR to present the Town with a database of information to improve the Town's understanding of Green Pond dynamics and assist with future coastal habitat management goals.

FORMULATED FEEDS GIVE NEW PERSPECTIVES FOR BLUE MUSSEL HATCHERIES. Nancy Nevejan. INVE Technologies, Hoogveld 93, 9200 Dendermonde, Belgium.

INVE Aquaculture has developed a first series of formulated feeds for the blue mussels, *Mytilus edulis* and *Mytilus galloprovincialis*. Since nutritional requirements change with life stages, the INVE ''mussel line'' includes a broodstock conditioning diet (MyStock) and a growth enhancing diet for spat (MySpat). Mussel broodstock is successfully conditioned when an algae diet of 0.22 g DW algae $day^{-1}kgLW^{-1}$ is supplemented with MyStock at a ratio of 0.2 g kg^{-1}. Normally, mussel broodstock needs 8 times more algae to reach spawning conditions in a period of 6 weeks. The females spawn an average of 3.0 million good quality eggs. The larvae resulting from the MyStock-fed broodstock grow as fast as the larvae resulting from an algae-fed broodstock. Producing sufficient amounts of algae for growing mussel spat at optimal rates is a real challenge. MySpat replaces 2/3 of the algae while supporting a doubling of mussel spat weight per week when supplied at a ratio of 2.8% on life weight. A large scale experiment in a commercial hatchery demonstrated that the number of production cycles in a period of 6 months can almost be doubled from 5 (control) to nine.

RESTORATION OF ENDANGERED MUSSELS IN THE UNITED STATES. Richard Neves[1], Hua Dan[1], Jess Jones[2], and William Henley[1]. [1]Virginia Tech, Department of Fish & Wildlife, Blacksburg, VA 24061 USA; [2]U.S. Fish & Wildlife Service, 106 Cheatham Hall, Virginia Tech, Blacksburg, VA 24061 USA.

The U.S. Bureau of Fisheries established the first freshwater mussel propagation facility at Fairport, IA in 1914, in response to over-harvest of shells for the pearl button industry. Propagation efforts were dormant thereafter until mussel species were listed as endangered in the mid-1970's. Propagation and restoration of the now 70 federally endangered mussel species began 10 years ago, with the successful culture and release of endangered tan riffleshells by the Freshwater Mollusk Conservation Center (FMCC) at Virginia Tech. The FMCC has focused on the 37 protected species of the Tennessee River system and has successfully conducted propagation of 25 of those species. About 100,000 juveniles are released each year. Since 1997, an additional 14 federal and state-operated facilities have become involved, releasing more than 10 million juveniles in U.S. rivers.Diet development for juvenile mussels continues to progress, with a variety of unicellular algae shown to provide adequate nutrition, as well as commercially available micro-algae concentrates used by the marine shellfish industry. The rapid success of culture technology now provides the capability to propagate many mussel species in need of conservation or restoration in state or federal waters.

LONG TERM TRENDS IN SURFCLAM ABUNDANCES ALONG THE ATLANTIC COAST OF NEW JERSEY Jeff Normant[1] and William Burton[2]. [1]New Jersey Department of Environmental Protection, Bureau of Shellfisheries, Nacote Creek Laboratory, Port Republic, New Jersey 08241; [2]Versar, Inc. 9200 Rumsey Road, Columbia, Maryland 21045.

The New Jersey Department of Environmental Protection has been conducting surfclam inventories in New Jersey waters from Manasquan Inlet to Cape May, New Jersey since 1988 out to the three mile limit using a commercial hydraulic surfclam dredge. Nineteen years of surfclam survey records were cataloged and entered into a GIS database comprising catches for 6,060 collections. Number of bushels per 100 m^2 averaged about 1.5 during the first four years of the program (1988 to 1991). From 1992 to 1997 densities increased steadily peaking at just over 3.5 bushels per 100 m^2. From 1998 through 2002 densities dramatically declined to 0.5 bushels 100 m^2 and remained at this low level into 2006. Average surfclam densities were consistently lower 2 to 3 miles offshore relative to 1 to 2 miles offshore, and were generally highest from 0 to 1 mile offshore. Declines in surfclam abundances were apparent in all strata after 1997 but appeared to drop more precipitously in the outer sampling zone. Consistently high densities were observed in near shore water between Absecon and Barnegat inlets over the time series but a major coast-wide decline in surfclam populations was evident in the recent surveys.

BAY SCALLOP CULTURE HISTORY IN VIRGINIA. Michael J. Oesterling and William D. Dupaul. Virginia Sea Grant Program, Virginia Institute of Marine Science, College of William and Mary, Gloucester Point, Virginia 23062 USA.

In the early 1900's, the bay scallop was the source of a small fishery along the seaside of the Eastern Shore of Virginia. Almost 900,000 pounds was taken annually from Virginia waters between 1920 and 1932. The hurricanes of 1993 and simultaneous occurrence

of an eelgrass "wasting disease" contributed to the total collapse of the fishery during the 1930's. Over the next 70+ years, limited numbers of bay scallops were found in Virginia coastal waters. In more recent years, investigations into the possibility of restoration of natural bay scallop stocks has received some attention. Under the direction of Mike Castagna at the Virginia Institute of Marine Science (VIMS), investigations into rearing the bay scallop began in 1968. These investigations demonstrated the potential for bay scallop culture. Unfortunately commercial culture was not initiated as a result of these efforts. Beginning in the late 1980's another attempt, spearheaded by the Virginia Sea Grant Marine Advisory Program at VIMS, revisited the potential for commercial bay scallop culture. This presentation will highlight developmental issues addressed in both research studies, as well as provide a synopsis of other restoration efforts in Virginia waters.

A 130-YEAR LONG TRANSPLANTATION HISTORY OF SARUBOU ARK SHELL *SCAPHARCA KAGOSHIMENSIS* IN JAPAN. Takane Okimoto and **Futoshi Aranishi.** Coastal Lagoon Research Center, Shimane University, Nishikawatsu, Matsue 690-8504, Japan.

The first record of the transplantation of bivalve in Japan was made in 764. Thereafter, transplantation of commercially important bivalves, such as oysters, pearl oysters, scallops, clams, mussels, and ark shells, has been developed for aquaculture all over Japan. One of these aquaculture species, sarubou ark shell *Scapharca kagoshimensis* is a 'red bivalve' distributed at sandy mud bottom in brackish zone of the Honshu Island and southward. Its aquaculture in Japan started by the transplantation within the Seto Inland Sea in 1872 and had been expanded to the Ariake Sea, Nakaumi Sea, Osaka Bay, and Tokyo Bay. It is noteworthy that the aquaculture production of sarubou ark shell dramatically fluctuated in each production area, and thus, its transplantation from high- to low-production areas was indispensable for maintaining the aquaculture resources of sarubou ark shell. Unfortunately, such frequent transplantation resulted not only in the genetic disturbance of local populations of sarubou ark shell but also in the ecological disturbance of its habitats because of unintentional introduction of related species, such as blood ark shell *Anadara granosa* and kuma-sarubou ark shell *S. globosa ursus*, both of which are red bivalves and difficult to be morphologically discriminated from sarubou ark shell.

THE SOFT-SHELL CLAM (*MYA ARENARIA*) IN THE GULF OF ST. LAWRENCE AND THE BAY OF FUNDY: AN OVERVIEW OF RESTORATION, ENHANCEMENT AND CULTURE PROJECTS. Marc Ouellette, Angeline Leblanc, Jean-françois Mallet, and **Thomas Landry.** Fisheries and Oceans Canada, Moncton, NB E1C 9B6 Canada.

The soft-shell clam is an important bivalve species in our aquatic ecosystems. It represents a commercial and recreational resource of considerable socio-economic importance in many coastal regions of eastern Canada. However, reports are indicating that landings are in general decline. Restoration efforts of clam beds, along with changes in the management of this resource, are required if this fishery is to become sustainable. On another front, the shellfish aquaculture industry has grown significantly and has become an important part of the economy in eastern Canada. The bulk of this industry is with the culture of the blue mussel and the American oyster. Research and development of alternate species for diversification of aquaculture activities also increased during the last decade. Clam species such as the soft shell clam, the quahaug (*Mercenaria mercenaria*) and the bar clam (*Spisula solidissima*) have been particularly targeted because of their high market value. However, culture of these species has not attained a level of sustainability due to issues such as slow growth and erratic mortalities often attributed to limiting environmental factors, experimental husbandry techniques and diseases. An evaluation of the prevalence of shellfish diseases in relation to population dynamics and environmental parameters will also be discussed.

POTENTIAL IMPACTS OF OVERLAP OF THE HARMFUL BROWN TIDE ALGA AND LARVAE OF THE NORTHERN QUAHOG, *MERCENARIA MERCENARIA*. Dianna K. Padilla[1], Michael H. Doall[1], Laurie L. Perino[2], and **Anna R. Webb[1].** [1]Stony Brook University, Ecology and Evolution, Stony Brook, NY 11794-5245 USA; [2]Stony Brook University, MSRC, Stony Brook, NY 11794-5000 USA.

Blooms of harmful brown tide alga, *Aureococcus anophagefferens*, have been suggested to pose an important bottleneck for the recovery of populations of the northern quahog, *Mercenaria mercenaria*, in Long Island waters, especially because of impacts on their larvae. We used historical data of water temperature and cell densities of this harmful alga in combination with our data on the temperature dependent timing of clam spawning, the presence of clam larvae in Long Island bays, and the results of laboratory experiments on the impacts of brown tide on clam larval survivorship, growth, time to metamorphosis, and lipid accumulation. With all of these data, we assess the likely annual impact of brown tide on clam populations and the potential for population recovery in Long Island waters.

PRELIMINARY RESULTS OF C-BANDING PATTERN IN THE RED ABALONE *HALIOTIS RUFESCENS*. C. Palma-Rojas[1] and **E. von Brand[2].** [1]Universidad de La Serena, Depto. de Biología, Colina del Pino s/n, La Serena, Chile; [2]Universidad Católica del Norte, Depto. de Biología Marina, Larrondo 1281, Coquimbo, Chile.

Abalone culture is a growing activity in Northern Chile, where the cultured species are the Californian or red abalone *Haliotis rufescens*, and the Pacific or green abalone *Haliotis discus hannai*. Neither of them is native to this country, so the aquaculture systems are landbased and the environmental controls are high.

Some of the growers have reported the appearance of possible hybrids, and to determine whether they are hybrids or not, an alternative method to molecular markers could be the use of C-banding pattern on chromosomes. Both species show a diploid number of 2n = 36 and the present report is the first one so far to detect C-banding pattern in the red abalone *Haliotis rufescens*. The next step will be to determine also the C-bands for *Haliotis discus hannai*, using standardized methods, to be able to complete the comparison between both species. (This work is partially funded by the project FONDEF DO4I-1285 granted to Germãn E. Merino).

IDENTIFYING FAMILIAR RELATIONSHIPS IN COHORTS OF *OSTREA EDULIS* USING MICROSATELLITE LOCI. **Belén G. Pardo[1], Jaime Castro[1], Almudena López[1], Ania Pino-Querido[1], Carmen Bouza[1], José Fuentes[2], Antonio Villalba[2],** and **Paulino Martínez[1].** [1]Departamento de Genética, Facultad de Veterinaria, Universidad de Santiago de Compostela, 27002, Lugo, Spain; [2]Centro de Investigacións Mariñas, Xunta de Galicia, Vilanova de Arousa 36620, Spain.

Handling of *Ostrea edulis* brood-stocks in hatcheries involves several oysters acting as males and others acting as females in the same tank. Thus, individual oysters may hatch larvae derived from spermatozoa released by various oysters, leading to cohorts constituted by half and full-sib families of unknown parents. Identification of familiar relationships is crucial for genetic breeding programmes. In this study a set of four highly polymorphic microsatellite loci were applied to ascertain the parentage of 12 cohorts within a selection programme for resistance to Bonamiosis. Though the parents siring these cohorts were unknown, samples of related individuals, some of them putative full-sibs, from the four possible geographic origins were available. The selected microsatellites exhibited high genetic diversity figures (mean A = 15; He = 0.881) and parentage non-exclusion probabilities (1st parent: 0.0250; 2nd parent: 0.0037), which configure them as a powerful tool for parentage analysis. Different strategies applying software available in the web were followed to obtain the maximum familiar information on these cohorts. Our approach permitted to assign the origin of all parents to the four putative origins. Seven cohorts were constituted by full-sibs (3) and half-sibs (4), while the remaining were more complex involving a minimum of parents between 7 and 11.

BAY SCALLOP CULTURE INNOVATIONS FOR A LARGE-SCALE RESTORATION PROJECT. **R. Michael Patricio, Kim Tetrault,** and **Gregg J. Rivara.** Cornell Cooperative Extension of Suffolk County, Southold, NY, 11971, USA.

The Cornell Cooperative Extension Marine Program is currently in its fourth year of a large-scale bay scallop (*Argopecten irradians*) restoration project where changes to culture techniques have improved production. Conditioning broodstock out of season has employed the use of supplemental lighting to increase gonad condition. An increased variety of algal species are being grown in a continuous algal culture system (SeaCAPS) this year to provide a more nutritional diet to larvae in an attempt to decrease post-set mortality. Post-set culture continues the use of ambient flow through downwellers. Different seawater filtration methods from a drum filter to filter bags have been used with varied results. Reduced effort and decreased mortality have resulted in stocking 2 mm in shell height animals in 750 μm mesh spat bags filled with rigid tubular mesh. On a submerged longline system, scallops >10 mm are grown to adult size. Presently, fourteen 200 meter long Polysteel submerged lines are used for overwintering 500,000 adult scallops to spawn the following spring. To service the longline system, an aluminum pontoon barge uses a lifting davit and hydraulic starwheel hauler. New strategies planned for 2008 will be discussed.

A REVIEW ON THE PRESENT STATUS OF ABALONE POPULATION GENETICS IN MEXICO. **Ricardo Perez-Enriquez.** Centro de Investigaciones Biologicas del Noroeste, S.C. (CIBNOR), La Paz B.C.S., México.

The Mexican abalone fishery has drastically declined over the last years similarly to what has been observed in other *Haliotis* fisheries of the world. Therefore, the study of the recovery potential of the depleted stocks is highly relevant. This potential depends, at least in part, on the dispersal capacity of the species, and it has been generally recognized that this can be indirectly estimated from population genetic analyses. Of the five abalone species distributed along the Mexican Pacific coast, population genetics research has been directed towards the two main fisheries species, the green *H. fulgens* and pink *H. corrugata*, using allozymes, RAPDs and microsatellites as genetic markers. Results have shown some discrepancies, because while some markers suggest genetic differentiation on rather short distances, others indicate that both species maintain single panmictic populations, with an isolation-by-distance pattern for distant island locations. Due to the low abundance of the other abalone species (white *H. sorenseni*, black *H. cracherodii*, and red *H. rufescens*), no genetic information is available in Mexican populations, athough there is for US stocks. Genetic markers are also being developed in Mexico for species identification, parental testing, hybrids and triploids certification, and phylogenetic studies.

EXAMINING BIVALVE CONTROL OVER PHYTOPLANKTON COMPOSITION WITH A SIMPLE MODEL. **Laurie L. Perino[1], Stephan B. Munch[1],** and **Dianna K. Padilla[2].** [1]Stony Brook University, Marine Science Research Center, Stony Brook, NY, 11794-5000, USA; [2]Stony Brook University, Ecology and Evolution, Stony Brook, NY, 11794-5245, USA.

Bivalves, when in high densities, can engineer their environment, including the composition and structure of phytoplankton communities. Knowing the density of bivalves

needed to cause a given change in the environment is an important aspect of conservation and restoration ecology as adult bivalves have the potential to create environmental conditions that are more favorable to larval and juvenile survival. We present a model of how changes in the density of bivalves can alter phytoplankton species composition and density. The model was parameterized for *Mercenaria mercenaria* as the bivalve consumer, and the typical phytoplankton found in an estuarine embayment. The growth environment for the phytoplankton (classified in one of three size classes: 2 μm, 5 μm, 20 μm) was set at 20°C, with light limitation but no nutrient limitation. The pumping rate of clams was taken as the average over a range of clam sizes at 20°C. Simulations were run over a range of clam densities to assess the impact of clams on the composition of the phytoplankton community as well as phytoplankton abundances.

INDENTIFICATION AND EXPRESSION OF REGULATED GENES IN THE HARD CLAM, *MERCENARIA MERCENARIA*, IN RESPONSE TO QUAHOG PARASITE UNKNOWN. **Mickael Perrigault[1], Arnaud Tanguy[2],** and **Bassem Allam[1].** [1]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794-5000, USA; [2]Laboratoire Adaptation et Diversité en Milieu Marin, Station Biologique, Université de Paris 6, Roscoff, France.

The hard clam, *Mercenaria mercenaria* is among the most commercially important bivalves in the United States. This clam species was relatively exempted from pathogens until the 1990's when mass clam mortalities were associated with quahog parasite unknown (QPX). Despite the commercial importance of hard clams, information regarding interactions between hard clams and their parasites is extremely scarce, especially knowledge about hard clam defenses involved against QPX. This study presents results from molecular investigations of hard clam responses to QPX's presence. Suppression subtractive hybridization approach (SSH) and hemocyte cDNA library were used to identify differentially expressed genes related to QPX presence in different tissues of New York clams. From more than 500 sequences, 18 genes involved in defenses, metabolism and cellular signalization were thereafter investigated by quantitative PCR. Results indicate a tissue-specific response of hard clams to the parasite. Several identified genes represent good candidates for the characterization of hard clam response involved during QPX disease as well as for the identification of potential markers related to the resistance of *M. mercenaria* to QPX. In addition, libraries generated during this study will contribute to develop a genetic database on *M. mercenaria*.

CYTOTOXICITY OF THREE QPX (QUAHOG PARASITE UNKNOWN) ISOLATES ON HEMOCYTES FROM DIFFERENT HARD CLAM (*MERCENARIA MERCENARIA*) STOCK. **Mickael Perrigault** and **Bassem Allam.** School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794-5000, USA.

The ability of pathogens to neutralize host defense mechanisms represents a fundamental step in the establishment of a successful infection. Host-pathogen interactions between quahog parasite unknown (QPX) and its hard clam host are poorly understood. Field investigations and laboratory transmission studies revealed some variations in the susceptibility of different hard clam stocks to QPX infection. Similarly, our prior *in vivo* investigations showed that different QPX isolates display various pathogenicity toward clams. This study was designed to investigate the virulence of various QPX isolates toward hemocytes withdrawn from three different clam populations. Our *in vitro* approach evaluates the toxicity of QPX cells and extracellular products toward hemocytes using a neutral red uptake assay. Results demonstrated that QPX produces extracellular virulence factors that are cytotoxic to *M. mercenaria* hemocytes. This cytotoxicity may play an important role in supporting QPX infection and proliferation within the host. Moreover, hemocytes from different clam strains exhibited significant differences in their susceptibility to QPX. Interestingly, these results corroborated our *in vivo* observations with regard to the susceptibility of experimental clam strains. Similarly, the *in vitro* toxicity of different QPX isolates matched well with their *in vivo* pathogenicity.

INVESTIGATIONS OF ANTI-QPX FACTORS IN PLASMA FROM SUSCEPTIBLE AND RESISTANT HARD CLAM STOCKS. **Mickael Perrigault, Chuan Hao Chen, Deenie M. Buggé,** and **Bassem Allam.** School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794-5000, USA.

Quahog parasite unknown (QPX) is a protistan parasite of the hard clam *Mercenaria mercenaria*. Field investigations and laboratory transmission studies revealed some variations in the susceptibility of different clam stocks to QPX infection; hard clams from northern stocks being more resistant to QPX disease than clams from southern stocks. This study presents results from *in vitro* experiments that investigated the effect of clam plasma on QPX growth. Both constitutive (unchallenged clams) and induced (QPX-challenged clams) plasma activities against QPX were investigated in Florida and New York clams using a previously described semi-automated biomass measurement technique. Results demonstrated that QPX growth is altered in presence of plasma from *M. mercenaria*. Inhibition of parasite growth is significant in most tested samples but results also showed some variability among individual clams. Interestingly, plasma from New York clams displayed higher inhibitory activity than the southern strain. Moreover, plasma withdrawn from QPX-challenged

clams exhibited higher anti-QPX activities than unchallenged clams. These results demonstrate that plasma of *M. mercenaria* contain active compounds against QPX. This activity is present constitutively in the plasma and is enhanced after QPX challenge suggesting that clams are able to mount a defense reaction against their parasite.

EFFECTS OF ENVIRONMENTAL PARAMETERS ON DEFENSE FACTORS, QPX DISEASE PROGRESSION AND ASSOCIATED MORTALITIES IN THE HARD CLAM, *MERCENARIA MERCENARIA*. **Mickael Perrigault*[1], Soren F. Dahl*[2], Qianqian Liu[1], Jackie L. Collier[1],** and **Bassem Allam*[1].** [1]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794-5000, USA; [2]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794-5000, USA.

(*These authors contributed equally to this work)

QPX (quahog parasite unknown) is a parasite of the hard clam *Mercenaria mercenaria*. Prior field observations showed that QPX disease outbreaks usually occur during summer months and are characterized by mass mortalities of hard clams. On the other hand, QPX disease was never observed in low salinity embayments in its enzootic range, suggesting some influence of salinity on disease development. Despite these indications, little is known about environmental effects on hard clams and their interaction with QPX. Lab-controlled experiments were performed to investigate the effects of temperature and salinity on hard clam immunity, QPX disease development and resulting mortalities. Naturally- and experimentally-infected clams were maintained at three different temperatures (27°C, 21°C and 13°C) and two salinities (30 ppt and 18 ppt). Mortalities were monitored daily and clams were periodically sampled to assess defense parameters (hemocyte counts, phagocytosis, ROS, anti-QPX activity in plasma) and determine QPX prevalence by quantitative PCR and histopathology. Results demonstrated that both salinity and temperature affect defense parameters and disease progression in *M. mercenaria*. For example, QPX-related mortalities were higher in clams maintained at high salinity as compared to the low salinity treatment. Additional results from these ongoing experiments are still being collected and will be presented.

INNOVATIVE, COST EFFECTIVE APPROACH TO PLANNING, ACQUIRING, PROCESSING, AND PRESENTING MULTIPARAMETER GEOPHYSICAL DATA FOR ALTERNATIVE ENERGY PROJECTS. **Eli J. Perrone, Jonathan D. Alvarez, Charlotte M. Cogswell, John H. Ryther, Jr.,** and **Christopher F. Wright.** CR Environmental, Inc., 639 Boxberry Hill Road, East Falmouth, MA 02536

The simultaneous collection of remote sensing data to characterize benthic habitat is becoming a reality. CR Environmental, Inc. is involved in several alternative energy projects that require the collection of geophysical data from a number of instruments. This talk focuses on the use and knowledge of GIS to effectively plan, acquire, process and present these data. Bathymetry, side scan sonar, sub-bottom profiling, magnetometry, underwater video, and still photography can be combined in GIS to yield a comprehensive map of the seafloor. These substrate maps can be used to plan additional geophysical, chemical or biological sampling of the benthic environment. Examples of data from each instrument will be shown, as well as, how these data layers can be integrated using GIS to create innovative imagery for planning.

MAPPING QTL CONTROLLING GROWTH AND BODY SIZE IN THE PACIFIC OYSTER. **Guy M. L. Perry[1], Marie-Luise Voigt[2],** and **Dennis Hedgecock[1].** [1]University of Southern California, Department of Biological Sciences, Los Angeles, CA 90089-0371, USA; [2]Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Dept. of Cytogenetics, Gatersleben, D-06466, Germany.

The Pacific oyster (*Crassostrea gigas*) exhibits classical growth heterosis in crosses of inbred lines. To determine number and action of QTL controlling growth heterosis, we typed 52 microsatellite markers (482 cM, 11 Linkage Groups) in tagged F_2 oysters (93 males, 92 females) weighed monthly through their second summer. Growth was sex-dependent and logistic. As source lines were partially inbred, we used both classical F_2 and four-way genotype coding for QTL mapping, with highly concordant results. We detected largely non-overlapping sets of QTL for the exponential and asymptotic growth phases. Permutation thresholds for QTL likelihood were affected by genotype-dependent mortality at earlier life stages. Three negative dominant QTL were detected for size and growth during the exponential phase, two on LG 1b and one on LG V. Five QTL were detected altogether for growth during the asymptotic phase: two QTL on LG III, one negative dominant and the other dominant; a negative dominant QTL on LG V; and a pair of antagonistic QTL on LG IX, one underdominant, one additive. Given growth heterosis, QTL showing negative dominance were unexpected. Although epistasis was not detected, weak correlation of growth with marker heterozygosity and significant differences between hybrid genotypes suggested F_2 breakdown.

A TALE OF TWO COASTS: POPULATION GENETICS OF THE PACIFIC LION-PAW SCALLOP. **Jessica L Petersen[1], Ana Maria Ibarra[2],** and **Bernie May[1].** [1]University of California, Department of Animal Science, Davis, CA 95616, USA; [2]Centro de Investigaciones Biologicas del Noroeste S.C., Aquaculture Genetics, La Paz B.C.S., México.

Natural populations of the Pacific lion-paw scallop *(Nodipecten subnodosus)* are found in waters on both the Pacific and Gulf of California coasts of the Baja California Peninsula, Mexico. 390 samples from seven aggregations were collected from the Lagoon

Ojo de Liebre on the Pacific coast, and 135 samples were obtained from Bahia de Los Angeles, Ligui, and Bahia de La Paz, which span the distribution of the scallops along the eastern coast of the peninsula. Microsatellite genotyping of these individuals reveals significant population differentiation when comparing samples from Ojo de Liebre to those sites on the eastern coast. However, no significant population structure exists within the three Gulf coast populations, or within the Lagoon Ojo de Liebre. In addition, despite the smaller sample size, private alleles are twice as prevalent in the Gulf populations as in Ojo de Liebre. These data and further results will be discussed in respect to future monitoring and conservation of the species as well as in regard to the implications of potential translocation and introgression resulting from aquaculture.

CASCADING TROPHIC EFFECTS ON A SEASONAL FISHERY: DECIMATION OF BAY SCALLOP, *ARGOPECTEN IRRADIANS*, POPULATIONS IN NORTH CAROLINA. **Charles H. Peterson, Stephen R. Fegley,** and **David Gaskill.** Univ. of North Carolina Institute of Marine Sciences, Morehead City, NC 28557.

Over the past three decades the abundances of many species of rays, skates, and small sharks (mesopredators) have increased along the US east coast as the numbers of their predators (great sharks) have declined dramatically from overfishing. A 20-fold increase in the abundance of one mesopredator, the cownose ray, has led to enhanced predation of bay scallops in North Carolina waters so severe that the century-old NC fishery collapsed in 2004. It has yet to re-open. Bay scallops have disappeared from locations where they were abundant historically. Where scallops survive cownose ray predation, their field densities are too low (<1–2 individuals m^{-2}) generally to produce fishable densities of new recruits. Scallop recovery may also be threatened by loss of seagrass habitat. Bay scallops are the primary prey of migrating cownose rays in NC. If scallops are not available, hungry rays consume secondary prey species such as hard clams (*Mercenaria mercenaria*), eastern oysters (*Crassostrea virginica*), and soft-shell clams (*Mya arenaria*). As some of these prey are infaunal and occur in seagrass beds increased foraging by rays would lead to broad, persistent community alterations via ray destruction of seagrass habitat.

EVALUATION OF AN ADJUSTABLE LONG LINE SYSTEM TO INCREASE OYSTER SURVIVAL IN DERMO ENDEMIC AREAS AND REFRIGERATED SHELF-LIFE AFTER HARVEST. **Jerome La Peyre[1], Sandra Casas[1], Yanli Li[1],** and **John Supan[2].** [1]Louisiana State University Agricultural Center, Department of Veterinary Science, Baton Rouge, LA 70803, USA; [2]Louisiana State University, Office of Sea Grant Development, Baton Rouge, LA 70803, USA.

The advantages of increased growth rate and decreased fouling of oysters cultured off-bottom using adjustable longline systems (ALS) have been described. Controlling the time oysters in ALS are held out of the water may also increase their survival when grown in areas endemic for *Perkinsus marinus* (*Pm*) and increase their refrigerated shelf-life after harvest. To test these hypotheses, four month-old oysters were divided into four groups and cultured in ALS for two years, beginning in September 2005. The first and second group were exposed to air daily and weekly, respectively. The third group was exposed to air daily from September 2005 to June 2006 and then left in the water to mimic seed hardening. The fourth group was left in the water as a control. Oyster growth and mortality rates, condition index and *Pm* body burden were then determined every three months while refrigerated shelf-life and *V. vulnificus* (*Vv*) load were determined in summer and early fall. Summer mortalities were delayed, *Pm* infection intensities tended to be lower and condition indices were significantly higher in group 1 and 3 compared to group 2 and 4. No consistent differences were found in *Vv* loads or refrigerated shelf-lives between the groups.

EFFECTS OF FRESHWATER DIVERSIONS: AN EXPERIMENTAL DETERMINATION OF THE EFFECTS OF FRESHETS ON THE OYSTER PARASITE, *PERKINSUS MARINUS*. **Megan La Peyre[1], Bryan Gossman[2],** and **Jerome F. La Peyre[3].** [1]U.S. Geological Survey, Louisiana Fish and Wildlife Cooperative Research Unit, Louisiana State University Agricultural Center, School of Renewable Natural Resources, Baton Rouge, LA 70803, USA; [2]Louisiana State University Agricultural Center, School of Renewable Natural Resources, Baton Rouge, LA 70803, USA; [3]Louisiana State University Agricultural Center, Department of Veterinary Science, Baton Rouge, LA 70803, USA.

In coastal Louisiana, the development of large–scale freshwater diversion projects has led to significant controversy over the effects of these flows on oyster resources; changes in freshwater flow may impact oyster production through effects on salinity, which affects oyster health both directly and indirectly, through its effects on disease dynamics. Using a series of controlled laboratory experiments in combination with a field study, we examined the effects of single and consecutive pulsed freshwater events (freshet) on oyster dermo infection intensities and oyster condition. Low salinity freshets (1 ppt) consistently resulted in lowered dermo infection intensities regardless of length, timing or repetitiveness of the freshet in laboratory studies. Similarly, in the field, dermo infection intensities were lower at sites experiencing lower spring–time salinities. Oyster condition was either unaffected or increased in oysters exposed to freshet in the laboratory; in contrast, oyster condition decreased and mortality increased in the field as salinity means decreased. This difference may be due to the fact that oyster plasma osmolality at our lowest salinity field site decreased to a greater extent than in lab experiments. These data suggest that the timing and length of freshwater diversion events are key to optimizing the health of oyster populations.

OYSTER RECRUITMENT AND GROWTH ON AN ARTIFICIAL REEF STRUCTURE IN GRAND ISLE, LA **Mason Piehler[1], Megan La Peyre[2], Bryan Gossman[1], Bryan Piazza[1],** and **Jerome La Peyre[3].** [1]School of Renewable Natural Resources, LSU Agricultural Center, Baton Rouge, LA; [2]USGS Louisiana Fish and Wildlife Cooperative Research Unit, School of Renewable Natural Resources, LSU Agricultural Center, Baton Rouge, LA; [3]Department of Veterinary Science, Louisiana State University, Agricultural Center, Baton Rouge, LA.

A potential method to build strong reef structures and enhance recruitment and growth of oysters was tested between June 2006 and May 2007. Eight electrified rebar reefs were constructed at the Louisiana Sea Grant oyster hatchery. The reefs were assigned low, medium, high or control (no) levels of electrical current; accretion of calcium carbonate precipitate and spat recruitment and size were monitored June through November 2006. Significant differences were found by current for accretion with bars receiving the highest electrical current accreting more calcium carbonate as compared to the lower current and control bars. Most accretion occurred during the first three weeks after deployment. Spat numbers and sizes differed significantly by current with the control bars having significantly greater numbers and larger spats than any of the bars receiving electrical current when sampled every 3 and 6 weeks but not at 22 weeks. From November 2006 through May 2007, oyster growth of reef-cemented oysters was monitored. No significant difference between treatments and controls for oyster growth was found. While the use of electrified reef structures provides a potential approach to develop cheap strong structures, the evidence does not support the hypothesis that oyster recruitment or growth are enhanced on these structures.

YOU MIGHT BECOME WHAT YOU EAT: FUNCTIONAL ALGAL GENES WITHIN A MOLLUSCAN GENOME. **Sidney K. Pierce, Julie A. Schwartz,** and **Nicholas E. Curtis.** Univ. of South Florida, Department of Biology, Tampa, FL 33556 USA.

The sacoglossan sea slug, *Elysia chlorotica* (Gould) feeds on the chromophytic algae, *Vaucheria litorea* (C. Agardh) and sequesters chloroplasts in specialized cells lining the digestive diverticula. These chloroplasts actively photosynthesize within the slug for as long as nine months and many chloroplast proteins are synthesized while the plastid resides in the slug cell. Previously we have demonstrated the presence of at least three nuclear-encoded, algal genes for chloroplast proteins in the mRNA and DNA of adult slugs and in the DNA in pre-hatched, un-fed veliger larvae. Thus, genes for chloroplast proteins have been transferred from the algal nucleus into the slug's genome. To identify additional transferred genes we have sequenced about 25% of the *E. chlorotica* transcriptome. So far, BLAST analysis of approximately 8000 contig sequences has identified at least 40 additional transferred, nuclear-encoded algal gene candidates. Generally, there are few *Vaucheria* or other heterokont algal sequences in the database for comparison, so we are preparing the *Vaucheria* transcriptome for sequencing which will allow for direct comparison of the slug and algal sequences. However, these preliminary results suggest that around 200 genes may have been transferred from the alga to the slug. (supported by NSF-IBN 0315221)

TEMPORAL EXPRESSION OF GENETIC LOAD IN TWO FAMILIES OF THE PACIFIC OYSTER, *CRASSOSTREA GIGAS*. **Louis Plough, Jason Curole, Sydney Glassman,** and **Dennis Hedgecock.** University of Southern California, Biological Sciences, Los Angeles, CA, 90089, USA.

Discovery of a large number of highly deleterious recessive mutations (genetic load) in the Pacific oyster explains distorted segregation ratios, seen widely in bivalves, and supports the dominance theory of heterosis and inbreeding depression. Linkage map positions and, especially, temporal expression patterns of these mutations are not well characterized. We crossed pairs of inbred lines derived from Dabob Bay, WA and mated sibling F_1 hybrids to produce two F_2 families, in which we analyzed segregation of microsatellite DNA markers. Families were sampled daily from 4 hours post fertilization through metamorphosis. We surveyed post-metamorphic samples, first, to determine which markers had previously been affected by selection against linked recessive mutations. Distorted markers were then assayed in larval samples to determine when selection against linked mutations had first distorted the segregation ratio. In one family, 28 of 48 markers in adult samples were significantly distorted; of the 26 markers amplified from larval samples, one was expressed before 24 hours; four were expressed in veligers (day 10–11); 6, in pediveligers (day 16–18); and 12, during or after metamorphosis. Some markers were linked to two mutations with different expression patterns. QTL mapping methods are providing better resolution of the number, position, and effect of deleterious mutations.

OPTIMAL ALGAL DIETS FOR BAY SCALLOPS, *ARGOPECTEN IRRADIANS*. **Kari Pohl** and **Karin Tammi.** Roger Williams University.

The bay scallop (*Argopecten irradians*) is a well known filter feeder whose diet consists of a variety of phytoplankton. By improving algal diets, shellfish hatcheries will increase survival and production. It has been hypothesized that a mixed diet of high lipid algal strains will promote larval growth and survival. During the summer of 2007, research was executed under an EPSCoR fellowship to determine the optimum microalgae for the bay scallop larvae. Using three microalgae strains, *Isochrysis galbana* sp. T-iso, *Chaetoceros muelleri*, and *Tetraselmis* sp. Ply 429, four diet combinations were set up to measure larval survival, growth rate, and lipid content of bay scallop larvae (from 60 u to 10 days after post set). The diet combinations were as follows: a control with T-Iso, a binary diet of T-Iso and *C. muelleri*, a binary diet of *C. muelleri* and T. Ply 429, and a multidiet of all three strains. The

results concluded that the diet which produced the best growth rate and survival to be the binary diet of *C.muelleri* and T-iso for veliger larvae and T-iso and T. Ply 429 for juveniles.

UNEXPECTED SEX RATIOS IN *CRASSOSTREA VIRGINICA* POPULATIONS IN TEXAS BAYS. **Jennifer Beseres Pollack[1], Sammy Ray[2],** and **Paul Montagna[1].** [1]Harte Research Institute for Gulf of Mexico Studies, Texas A&M University-Corpus Christi, Corpus Christi, TX, 78412-5869, USA;[2]Texas A&M University-Galveston, Galveston, TX, 77553-1675, USA.

Eastern oysters *Crassostrea virginica* are generally known as protandrous hermaphrodites—most individuals first mature as males and have the ability to later change to females. Reversals to the opposite sex may be modified by environmental factors such as temperature, salinity or food availability. Reversals are known to occur during the winter months when oyster gonads are quiescent. Under normal environmental conditions, the proportion of females within a population increases with an increase in the mean size of individuals. Following a summer with higher than average rainfall, we began collecting oysters monthly in September 2007 from reefs throughout the Mission-Aransas Estuary. At each reef, we have been measuring oyster biomass, gonadal tissues for sex determination, and water quality parameters (e.g. nutrients, chlorophyll, and detritus). As of mid-January 2008, gonads were fully developed in all months except November and December 2007; undifferentiated cells prevented accurate sex determination in these two months. Although *C. virginica* have the capacity to undergo sex reversals, our preliminary results indicate that the predicted sex ratios based on differences in oyster size do not always occur. We are conducting further research to examine potential influences on the unusual sex ratios.

VIRTUAL POPULATION ANALYSIS OF GREAT SOUTH BAY HARD CLAM (*MERCENARIA MERCENARIA*) POPULATIONS. **Olga Polyakov[1], Eric N. Powell[2], John N. Kraeuter[2], John M. Klinck[1], Eileen E. Hofmann[1], V. Monica Bricelj[3],** and **Stuart C. Buckner[4].** [1]Center for Coastal Physical Oceanography, Old Dominion University, Norfolk, VA 23529; [2]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ 08349; [3]Institute for Marine Biosciences, National Research Council, Halifax, Nova Scotia, Canada B3H 3Z1; [4]Town of Islip, Environmental Control, Islip, NY 11751.

The Town of Islip, NY conducts annual surveys in Great South Bay to assess hard clam (*Mercenaria mercenaria*) abundance and distribution. A Virtual Population Analysis (VPA) model was applied to this hard clam data set with the objectives of analyzing changes in the stock structure from 1977 to 2004 and estimating yearly mortality rates. A particular cohort was followed for 5 years to calculate population mortality rate. Age classes 1 through 3 were clearly under-represented and the source of this under-representation does not appear to be related to the sampling method. Age classes 4 and 5 were assumed to provide a correct estimate of the animals in the population in those size ranges; the decline in hard clams between the fourth and fifth age class was used to calculate the mortality rate. The mortality rate clustered into two primary groups. From the 1980s to the early 1990s, hard clam abundances remained at 0.4–0.5 ind m^{-2} and the population mortality rate was –0.4 yr^{-1}. From the mid-1990s to present, Great South Bay hard clams have been characterized by lower population densities and by an apparent decline in 7–8 cm clams that is not observed in larger clams.

MULTIPLE STABLE POINTS IN OYSTER POPULATIONS. **Eric N. Powell[1], John M. Klinck[2], Kathryn A Ashton-Alcox[1],** and **John N. Kraeuter[1].** [1]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ 08349 USA; [2]Center for Coastal Physical Oceanography, Old Dominion University, Norfolk, VA 23529.

A 54-year time series for the oyster population of Delaware Bay was analyzed to identify biological reference points and rebuilding goals. The time series is characterized by two regime shifts delineating alternate stable states. Multiple stable states are described by a complex array of reference points. A carrying capacity exists for each stable state. Each carrying capacity has associated with it a point at which surplus production reaches a local maximum. These represent rebuilding goals for each stable state. Between them is an intermediate low in surplus production. If this minimum is negative, a point-of-no-return exists below which the population has little chance of recovery to the higher stable state. The differential in surplus production between the lower maximum and the minimum expresses the difficulty of rebuilding to the higher stable state. The depth of the minimum expresses the sensitivity of the population to collapse from high abundance. The abundances defining the minimum and maxima are relatively stable over a range of uncertainties in recruitment and mortality. The surplus production values associated with them are much more uncertain. Thus, different models are needed for management decisions, one for short-term catch forecasts; the other for establishing long-term abundance goals.

OYSTER REEF RESTORATION IN MOBILE BAY, ALABAMA. **Sean P. Powers** and **Robert L. Shipp.** Department of Marine Sciences, University of South Alabama, Mobile, AL 36688.

Restoration of oyster reefs in Mobile Bay and adjacent waters has become a priority for both state and federal agencies. In Mobile Bay, oyster reefs represent the primary subtidal biogenic habitat for fish and invertebrates as well as an exploitable fishery. Although some areas of Mobile Bay (*e.g.*, Cedar Point) still support extensive oyster reefs, overall coverage of oyster reefs in Mobile Bay has likely decreased over the last century. Several challenges, which are also common to other Gulf Atlantic estuaries, must be addressed to implement a bay-wide restoration program. Chief among these challenges are low larval supply in the

southeastern portion of Mobile Bay, episodic low dissolved oxygen events, lack of suitable settlement substrate and high oyster mortality from oyster drills. The relative importance of these problems changes along bio-physical gradients across Mobile Bay. As part of a comprehensive research and restoration program, we have conducted several targeted research projects to address these and other restoration challenges and tested hypotheses through construction of replicate experimental reefs. Here, we present a spatially explicit synthesis of these results to facilitate future restoration efforts in Mobile Bay.

SNP DISCOVERY WITHIN A MATRIX METALLOPROTEINASE GENE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. Dina A. Proestou, Nathan Rubien and **Marta Gómez-Chiarri.** Department of Fisheries, Animal, and Veterinary Science, University of Rhode Island, Kingston RI 02881.

The purpose of our research is to isolate Single Nucleotide Polymorphisms (SNPs) within an oyster metalloproteinasegene (Cv1MMP). MMPs are recognized for their ability to degrade the extracellular matrix, repair wounded tissue, and participate in immune responses. The Cv1MMP open reading frame is composed of 1590 nucleotides (530 amino acids), and the sequence contains conserved domains characteristic of MMPs. Cv1MMP DNA sequences from five strains of *Crassostrea virginica* with varying levels of resistance to oyster pathogen are being evaluated in this project to determine if strain-specific variation has functional consequences with respect to disease resistance and performance. cDNA from at least five individuals from three of the five strains has been amplified using gene specific primers and five SNPs have been discovered within the first 600 bp of the Cv1MMP sequence. In addition, genomic DNA is being analyzed from all five strains for intron-exon structure.To date, two introns have been identified within the Cv1MMP prodomain; intron1 spans 90 bp while intron 2 spans 661 bp. We also plan to compare the prevalence of SNPs between coding and non-coding sequences. This information can be used to development molecular markers for use in marker-assisted selection breeding projects in oysters.

RETENTION OF HUMAN ENTERIC VIRUSES BY OYSTER (*CRASSOSTREA VIRGINICA*) HEMOCYTES. Keleigh Provost and **Gulnihal Ozbay.** Delaware State University.

The goal of this study is to determine why human enteric viruses such as hepatitis A (HAV) and norovirus (NV) readily persist within bivalves. Shellfish bioaccumulate water-borne pathogens and concentrate virus particles suspended in the water column. Unlike fecal bacteria, gastrointestinal viruses can not be efficiently removed by depuration (placing live shellfish in clean water for a few days). Our current hypothesis is that these viruses persist within phagocytic hemocytes, cells that have both digestive and immunological functions. The presence of HAV within hemocytes after oyster exposure to HAV-contaminated water has been demonstrated by RT-PCR. Hemocytes removed from oysters test positive for up to 20 days following a single overnight exposure to HAV-contaminated water. Currently three separate approaches are being followed to evaluate the persistence of viruses within shellfish. 1) Adoptive transfer of HAV-contaminated hemocytes from HAV-exposed oysters to naÿve, unexposed oysters will be evaluated. 2) Silica is being evaluated as a functional blocker of phagocytosis and hemocyte function. Preliminary data on the survivability of oysters injected with silica indicates that it can be used a function blocker of the phagocytic activity. 3) Fluorescence-activated cell sorting will be employed to determine which hemocyte subgroup or groups(s) take up these enteric viruses.

THE ROLE OF TRANSMISSION AND INFECTION IN ESTABLISHING REFUGIA FROM TWO PROTOZOAN OYSTER DISEASES IN DELAWARE BAY. Jeffrey R. Pydeski[1] and **David Bushek[2].** [1]West Virginia University, Division of Forestry and Natural Resources, Morgantown, WV 26506-6125 USA; [2]Rutgers, Haskin Shellfish Research Laboratory, Port Norris, NJ, 08349 USA.

Eastern oyster (*Crassostrea virginica*) populations in Delaware Bay have been a plagued by protozoan organisms *Perkinsus marinus* and *Haplosporidium nelsoni*, which cause Dermo and MSX disease, respectively. The combination of temperature, salinity, and disease prevalence determines the health and structure of molluscan populations in the Delaware Bay. Disease refugia exist in the upper bay. However, it is unknown whether these refugia exist as a result of physical factors that limit parasite dispersal, or if environmental conditions inhibit infectivity. This study compared infection levels with pathogen presence in refugia to determine if limited dispersal (transmission) or limited infectivity is responsible for creating the refugia. MSX prevalence was low (<20%) during the study period at all sites, therefore it was not possible to determine factors limiting transmission and infection by *H. nelsoni*. Dermo infections were prevalent at lower bay, high salinity sites, but absent or rare from putative refugia. Dermo infection compared with *P. marinus* prevalence indicated that sufficient parasite dispersal occurred in the refugia. Because these oysters are highly susceptible to dermo disease, this observation indicates that environmental conditions inhibit infectivity, thereby creating the refugia. This work was supported by an NSF REU supplement to award #0622642.

***VIBRIO PARAHAEMOLYTICUS* IN ALASKA: RESULTS THREE YEARS AFTER THE PRINCE WILLIAM SOUND OUTBREAK. Raymond RaLonde.** University of Alaska Fairbanks, Alaska Sea Grant Marine Advisory Program, Anchorage, Alaska, 99501, USA.

In 2004, Alaska experienced its first encounter of *Vibrio parahaemolyticus* with confirmed illnesses making the outbreak the third largest case outbreak in United States history. An immediate

response and further research in cooperation with the Food and Drug Administration Gulf Coast Seafood Laboratory and the Alaska Department of Environmental Conservation revealed unusual and disturbing features of the outbreak and development of a prevention plan. Temperature monitoring, changing aquaculture practices, and attention to time/temperature during shipment appear to control the problem. After three years of applying a prevention plan, this presentation will describe the results of the outbreak, immediate response efforts, follow-up research and monitoring results, current and future research plans, and a description of the current prevention program administered by the Alaska Department of Environmental Conservation.

THE ALASKA SHELLFISH FARMING FINANCIAL PLANNING PROGRAM. **Raymond RaLonde.** University of Alaska Fairbanks, Alaska Sea Grant Marine Advisory Program, Anchorage, Alaska, 99501, USA.

The Alaska shellfish aquaculture industry is undergoing profound changes as production increases are expected. To prepare farmers for industry development, the Alaska Sea Grant Marine Advisory Program through funding from the Cooperative Research, Education, and Extension Service (CSREES) Western Center for Risk Management Education began a financial planning program for Alaskan shellfish farmers. The program includes business management training sessions provided by business professionals, development of shellfish farming financial models, customized pro forma and record keeping software, development of a website, and continuing education. To date, one training section has been completed, an oyster production model has been develop, and draft pro forma software being tested. A website is under development, and additional activities are underway. This presentation will provide a glimpse of the program accomplishments and goals for the future.

DEVELOPMENT OF EXPERIMENTAL PROCEDURES FOR DETERMINING THE ROLE OF MARINE AGGREGATES IN THE TRANSMISSION OF *PERKINSUS MARINUS* IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*) **Gina Ralph[1], J. Evan Ward[1], Sarah M. Winnicki[2], Wade Carden[2], Bassem Allam[2],** and **Bridget Holohan[1].** [1]Department of Marine Sciences, University of Connecticut, Groton, CT 06340; [2]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794.

Aggregates are ubiquitous in the marine environment and may serve as both vectors and reservoirs of marine pathogens. Our study focused on *Perkinsus marinus*, a protozoan parasite of the eastern oyster that has caused epizootic mortalities along the eastern coast of the United States. We found that *P. marinus* cells can be incorporated into aggregates made in the laboratory. Incorporation percentages varied from approximately 25 to 75%, with higher particle concentration generally resulting in higher incorporation efficiencies. Feeding bioassays were used to evaluate the function of marine aggregates in the transmission of *P. marinus*. Initial experiments focused on the procedural aspects of the bioassays, as few previous studies have attempted to use aggregates to infect suspension-feeding bivalves with a disease. Using a standard diagnostic technique, the fluid thiogloycollate medium method, we found that oysters exposed to aggregated *P. marinus* had higher infection intensities than those exposed to freely suspended *P. marinus*. Our results suggest that aggregates may be a vector of *P. marinus*.

PATTERNS OF GENE EXPRESSION DURING SALINITY ACCLIMATION IN THE BLUE MUSSEL, *MYTILUS EDULIS*. **Paul Rawson** and **Eugene Katsman.** School of Marine Sciences, University of Maine, Orono, ME 04469, USA.

Blue mussels (*Mytilus* spp.) tolerate a wide range of salinities. Upon a reduction in salinity, the rate of respiration in mussels is initially depressed while the rate of nitrogen excretion increases. Under prolonged exposure mussels eventually acclimate and physiological rates return to normal within hours to days depending upon the severity of the stress. During acclimation mussels achieve osmotic equilibrium by adjusting intracellular concentrations of amino acid and other small organic osmolytes. This cellular response occurs within hours to days after the onset of stress even though the overall acclimation response may take several days to weeks. We are interested in how the patterns of gene expression change in blue mussels (*M. edulis*) during acclimation to a hypoosmotic challenge. We exposed larval and juvenile mussels to reduced salinity and through subtractive hybridization identified >100 gene transcripts whose expression level appears to be altered in response to decreased salinity. Using quantitative PCR we have estimated the magnitude of the change in gene expression for a subset of these transcripts in relation to physiological acclimation during prolonged hypoosmotic challenge. The results of our work will help to elucidate the genetic pathways by which mussels adjust to osmotic challenge.

CROSS-BREEDING AND FIELD TRIALS OF DISEASE-RESISTANT EASTERN OYSTERS. **Paul Rawson[1], Ximing Guo[2],** and **Scott Lindell[3].** [1]University of Maine, School of Marine Sciences, Orono, ME 04469, USA; [2]Haskin Shellfish Research Laboratory, Rutgers University, Port Norris, NJ 08349, USA; [3]Program in Aquaculture, Marine Biological Laboratory, Woods Hole, MA 02543 USA.

Disease is one of the most serious impediments to the increased production of cultured eastern oysters, *Crassostrea virginica*. Oyster culture in southern New England is often impacted by MSX and Dermo while *Roseovarius* oyster disease (ROD) has a bigger impact in northern New England. However, the intensity

and geographic distribution of all three diseases continue to increase so that ROD, MSX and Dermo are of concern to the entire New England region. Although MSX and Dermo resistant stocks are available they do not fare well when challenged by ROD, and visa versa. Using common garden field-trials we ask whether enhanced resistance to MSX, Dermo, and ROD can be realized in a single stock through interline crossing between currently available genetically improved stocks. In addition, we are examining whether oysters selected from local natural environments in southern New England that have survived heavy, annual disease pressure will survive well, grow better and yield more than currently available lines. Seed oysters were deployed in June, 2007 and interim results indicate interline crosses performed well under a variety of disease pressures. These results are encouraging for the production of a stock that performs well when challenged by all three diseases.

CURRENT STATUS OF DERMO DISEASE AND OYSTER HARVEST IN WEST BAY, GALVESTON, TEXAS. Sammy M. Ray. Texas A&M University-Galveston, Marine Biology Department, Galveston, TX, 77554, USA.

The coastal areas of Texas received above normal rainfall during 2006 and 2007. Thereby, reducing the salinity in West Bay, the high salinity arm of the Galveston Bay System. This condition has resulted in reduced Dermo disease intensity in oysters and increased oyster harvest. West Bay water salinity usually varies from the high 20's to the low 30's ppt. In 2007 the salinity generally ranged 20 ± 2 ppt. Although the incidence of Dermo infections remained high, the intensity of (weighted incidence) was below usual levels. Preliminary results of studies regarding Dermo infections of oyster spat show that infection initiation is "proximity" dependant. Speculation is advanced regarding the observation that inter-tidal oyster populations appear to survive Dermo disease better than sub-tidal populations.

TEXAS A&M UNIVERSITY FOUNDATION PROJECTS 9 AND 23, AND THE EMERGENCE OF SHELLFISH PATHOLOGY. Sammy M. Ray[1] and **Thomas M. Soniat[2].** [1]Texas A&M University Galveston, Department of Marine Biology, Galveston, TX 77553 USA; [2]Nicholls State University, Department of Biology, Thibodaux, LA 70310 USA.

The rapid expansion of the oil industry into oyster-growing areas of Louisiana just prior to World War II led to inevitable conflicts. In 1946–1947 leaseholders in Louisiana filed claims against mineral companies based on abnormally high mortalities of oysters on their leases. A consortium of oil companies contracted with the fledgling Texas A&M University Foundation to undertake an impartial scientific study of the cause and extent of oyster mortality in Louisiana and Texas. Project 9 was born. At the height of the investigation, approximately 90 people were employed. Studies were conducted on the effects of crude oil, bleedwater, natural gas, drilling mud and seismographic surveys on oysters. None of these pollutants or activities explained the widespread mortalities observed. Instead, investigators realized that the mortalities observed were caused by a previously unknown pathogen, described by Mackin, Owen and Collier in 1950 as *Dermocystidium marinum* (now called *Perkinsus marinus*). Project 9 and its continuation, Project 23, engaged many of the world's top shellfish biologists, trained a new generation of scientists, launched the Department of Oceanography at Texas A&M University, encouraged expansion of marine laboratories along the Gulf Coast, and stimulated the emergence of the new science of shellfish pathology.

EFFECTS OF CURRENT VELOCITY, TURBULENCE, TYPE OF SUBSTRATUM AND CLAM SIZE ON DISPERSAL OF *MYA ARENARIA*: LESSONS FOR CLAM CULTURE. Iften Redjah[1], Réjean Tremblay[1], Bruno Myrand[2], Frédéric Olivier[3], Fabrice Pernet[4], Urs Neumeier[1], and **Lise Chevarie[1].** [1]ISMER-UQAR – 310 Allée des Ursulines, Rimouski, Qc, Canada, G5L 3A1; [2]MAPAQ - CeMIM – 107-125, chemin du Parc, Cap-aux-Meules, Qc, G4T 1B3; [3]MNHN – 17, Avenue George V, BP 70134, 35801 Dinard, France; [4]IRZC – 232B, Ave de l'Église, Shippagan, NB, Canada, E8S 1J2.

Mya arenaria lives into soft substrates in the tidal zone and burial depth is correlated to clam size. Thus, small clams are buried near the surface and prone to passive dispersal. The purpose of this study was to measure the effects of currents, substratum and clam size on dispersal in a flume. Laminar currents with increasing velocities (0 to 60 cm/sec) were applied upon three substrates (medium- and large-grain sand and mud) in which were clams from one of three size classes (10, 15 and 20 mm). Secondly, the effects of turbulent currents on the erosion of medium-grain sand and clams from the three size-classes were examined. Turbulent energy was created with a home-made device acting on the laminar currents. Nearly 95% of buried clams (all substrates and size-classes together) resisted to erosion from laminar currents up to 60 cm/sec but only 10% to turbulent currents of 10.1 J m^{-3}. Fall is probably a critical period for the dispersal of small seeded clams. Indeed, the protective nets placed on the newly seeded plots must be removed in fall. From that time, the small clams are no longer protected against dispersal through the erosion caused by turbulence.

PREDATION PREFERENCE OF THE COMMON SEA STAR ON A DOMINANT EPIFAUNA, *CREPIDULA FORNICATA*, ASSOCIATED WITH OYSTER CULTURE. Matthew Reichert and **Matthew Sclafani.** Cornell University Cooperative Extension Marine Program, Centerport, NY, 11721, United States.

The American Oyster, *Crassostrea virginica*, is among the top three commercial shell fisheries in New York State and has also been recognized for the important role it plays in ecosystem function. Predation is an important factor that is believed to regulate oyster abundance in northeastern marine ecosystems. One

of the primary predators on oyster that has been identified in the field is the sea star *Asterias forbesi*. Oyster beds are typically observed to have an abundance of epigrowth, especially by the North Atlantic Slipper Snail (*Crepidula fornicata*). In this study we tested the hypothesis that the slipper snail, as epifauna on the oyster, actually acts as an alternate prey item for the sea star predator. Our laboratory experiments demonstrated that sea star predation on slipper snails was significantly greater than predation on juvenile to mid-sized oysters. This distinct predatory preference for slipper snail indicates that the presence and high abundance of slipper snails in their native northeastern waters may positively affect oyster beds by offering an alternate and preferable prey item for predatory sea stars.

QUANTITATIVE STOCK ASSESSMENT OF OYSTER BIOMASS. **Bellamy Reynolds, Keleigh Provost,** and **Gulnihal Ozbay.** Delaware State University, Department of Agriculture and Natural Resources, Dover, DE 19901-2277, USA.

Every year in the Delaware Bay, Delaware Department of Natural Resources and Environmental Conservation (DNREC) conducts a survey of the Eastern oyster (*Crassostrea virginica*) population to set a new quota for the next fishing season. In an effort to make the process quantitative in relationship to the actual biomass of oysters, and not simply the biomass of the oysters that are brought up in the dredge each year, a dredge calibration was done in conjunction with a slightly different process of sorting the samples taken. For the dredge calibration process, dredge samples along with GPS coordinates were taken. Afterwards, on parallel tracks, divers were sent down to collect everything in given quadrats and samples were brought back up to the surface. These samples were then sorted and are used to calibrate the dredge efficiency for each site. This calibration is used in conjunction with the numbers from the DNREC stock assessment dredge samples that were worked up in a similar way to find a total biomass of oysters on each bed as well as a total biomass of oysters in the Delaware side of the bay. Data collected in 2007 is being processed, and the results will be discussed.

PROS AND CONS OF ON-BOTTOM OYSTER CULTURE VS RACK-AND-BAG. **Robert B. Rheault.** Moonstone Oysters, 1121 Mooresfield Road, Wakefield, RI 02879 USA.

There are significant differences between growing oysters in bottom culture vs. rack-and-bag systems. Each method requires different handling, suffers different mortality rates and poses unique challenges. We will discuss the two systems, the pros and cons of each, the differences observed in labor and operating costs. Even in the same waters, the two methods will produce very different products in terms of the oysters themselves. On-bottom oysters grow slower, but they have a thicker shell that is less brittle and there are fewer problems with shells chipping in transit or shattering while shucking. Depending on how hard the bottom is, bottom-cultured oysters often will become partially buried so they have less fouling and the shell is cleaner and more appealing visually. The overall the shell quality is further improved because bottom cultured oysters are far less susceptible to attack by *Cliona* (boring sponge) and *Polydora* (mud blisters). Oysters spread on the bottom also have better condition index and a firmer, larger meat because they have better access to food than do bag-grown oysters which often suffer from competition and food-limitation when bags become fouled.

ENVIRONMENTAL INFLUENCES ON RECRUITMENT OF NORTHERN SHRIMP, *PANDALUS BOREALIS*. **Anne Richards[1], Maureen Taylor[1],** and **Jay O'Reilly[2].** [1]Northeast Fisheries Science Center, Woods Hole, MA 02540 USA; [2]Northeast Fisheries Science Center, Narragansett, RI 02881 USA.

Ocean temperature has long been thought to affect the population dynamics of Northern shrimp (*Pandalus borealis*) in the Gulf of Maine, where the population is at its southern distributional limit in the Atlantic Ocean. We developed times series of data relevant to shrimp biology (spawning stock biomass and recruitment indices, timing of the annual hatch) from fishery-independent and fishery-dependent sources, and also created time series of environmental variables (temperature, salinity, mixed layer depth, wind direction and strength, river flow, chlorophyll concentration and spatial distribution, NAO index) from existing *in situ* hydrographic and remotely sensed data collections. These data sets were used to test hypotheses concerning environmental effects on Northern shrimp recruitment, especially the role of temperature in early life survival.

HEMOLYTIC STRAINS OF *SHEWANELLA*, *PHOTOBACTERIUM* AND *LISTONELLA* IN DELAWARE BAY OYSTERS AND SEAWATER. **Gary P. Richards[1], Edward J. Crane III[2],** and **David Bushek[3].** [1]United States Department of Agriculture, Agricultural Research Service, Delaware State University, James W.W. Baker Center, Dover, DE 19901; [2]Pomona College, Department of Chemistry, Claremont, CA 91711-6338; [3]Haskin Shellfish Research Laboratory, Rutgers University, 6959 Miller Ave., Port Norris, NJ 08349-3167.

During a 3-year survey of bacterial levels in 138 oyster (*Crassostrea virginica*) and 138 seawater samples from the Delaware Bay, 170 isolates from 1421 colonies picked, were identified as presumptive *Shewanella putrefaciens* at levels exceeding 2×10^4/g and 2×10^3/ml, respectively. Colonies were characteristically small (<3 mm diameter) and usually orange to pink on tryptic soy agar. Their identification was hampered by the generally non-fermentative nature of these isolates toward nine sugars used for biochemical identifications. Twenty-two presumptive *S. putrefaciens* were further identified by sequencing of their 16S rRNA genes as: *Shewanella algae*, *Shewanella baltica*, *Photobacterium damselae* subspecies *damselae*, and *Listonella anguillarum*. Additionally, these strains

produced beta-hemolysis on blood agar plates at 37°C; therefore, we believe this is the first study to identify sequence confirmed, hemolytic strains of *Shewanella*, *Photobacterium* and *Listonella* in the Delaware Bay. Both *S. algae* and *P. damselae* are opportunistic human pathogens involved in skin infections, abscesses, septicemia and death, while *L. anguillarum* is an important fish pathogen. Since *Photobacterium* is a genus in the *Vibrionaceae* family and *Shewanella* and *Listonella* were recommended for inclusion in the family, they, like the vibrios, may emerge as more significant pathogens as seawater temperatures continue to rise.

ANTIOXIDANT RESPONSES OF OYSTERS TO HYPOXIC CONDITIONS. **Amy H. Ringwood[1], Charles Keppler[2], Amanda Brunson[1],** and **Tina Changela[1].** [1]University of North Carolina-Charlotte, Department of Biology, Charlotte, NC 28223 USA; [2]Marine Resources Research Institute, Charleston, SC 29412, USA.

Hypoxic conditions in estuarine and coastal habitats continue to increase in both frequency and extent. During hypoxia, reducing equivalents accumulate that contribute to the generation of reactive oxygen species (superoxide, peroxide, and hydroxyl radicals) and cellular damage. Therefore, maintaining sufficient antioxidant levels is critical to hypoxia tolerance. Moreover, if antioxidant capacities are depleted, organisms are likely to be more susceptible to other stressors (e.g., disease, chemical pollutants, algal toxins). Therefore the purpose of these studies was to determine the effects of hypoxic conditions on glutathione (GSH, the most abundant antioxidant in all eukaryotic cells) levels of oysters, *Crassostrea virginica*. Glutathione levels were significantly reduced during laboratory exposure studies in which oysters were exposed to hypoxic conditions. Similarly, field studies were conducted in which dataloggers were deployed *in situ* at uncontaminated sites, and oysters were then collected and analyzed for GSH levels. Oysters from hypoxic environments had lower GSH levels than those from well-oxygenated sites. These results support the hypothesis that antioxidant responses are likely targets of hypoxia stress. Reduced antioxidant capacities, regardless of the cause, should be regarded as a major risk factor that would make organisms especially susceptible to further perturbations.

BAY SCALLOP GENETIC DIVERSITY AND POPULATION STRUCTURE IN MASSACHUSETTS. **Steven Roberts.** University of Washington, School of Aquatic and Fishery Sciences, Seattle, WA, 98105, USA.

Bay scallops are a species of significant conservation concern as populations have experienced dramatic declines. Numerous approaches have been implemented in attempts to preserve and restore populations. Without basic population information it is sometimes difficult for parties to assess potential or realized benefits. The principal objective of this study was to determine bay scallop genetic diversity and population structure in Massachusetts. Simple sequence repeat markers were used to characterize bay scallops from Wellfleet, Chatham, West Falmouth, Yarmouth, Oak Bluffs, and Menemsha. Four loci (G340, M26, N391, and S336) were selected for characterization. The number of alleles per locus ranged from 3 to 14. Overall, limited genetic differences were observed among the 6 populations examined. One of the interesting findings was that Chatham scallops were distinct from other scallops. The Chatham site has limited water exchange and thus the distinction is likely related to limited natural recruitment from other areas. Genetic similarity among other populations could be attributed to natural recruitment and/or enhancement practices. This information will be valuable for resource managers in making decisions related to enhancement and harvesting activities. This research was supported by the United States Department of Agriculture (grant #2003-35206-12834) and the County of Barnstable Massachusetts.

CHARACTERIZING DISEASE RESISTANCE IN NATIVE OYSTERS THAT HAVE EXPERIENCED DISEASE PRESSURE. **Steven Roberts[1], Roxanna Smolowitz[2],** and **Rick Karney[3].** [1]University of Washington, School of Aquatic and Fishery Sciences, Seatte, WA, 98105, USA; [2]New England Aquarium, Boston, MA, USA; [3]Martha's Vineyard Shellfish Group, MA, USA.

Oyster populations along the east coast have been devastated by diseases such as Dermo, caused by the parasite *Perkinsus marinus*. The objective of this research was to characterize disease tolerance in local, naturally selected for oysters in relation to factors such as *P. marinus* infection, growth and genetics. In order to carry out this objective, oysters that have experienced disease pressure and oysters that have not, were grown-out in a disease prone location. Oysters were continually monitored and sampled to assess survival, growth, *P. marinus* prevalence, and hemocyte gene expression patterns. Increased survival was consistently observed in oysters that have experienced disease pressure. Average abundance of the parasite in infected oysters was lower in that same group. Gene expression patterns differed among the two oyster groups suggesting gene expression levels could be used as a marker for improved performance. In addition, this study demonstrates seed originating from local, wild oysters could contribute to the development of disease resistance in cultured oysters. This research was supported in part by the Cooperative State Research Education, and Extension Service, US Department of Agriculture, under Agreement No. 2003-38500-13505.

CHARACTERIZATION OF SERINE PROTEASE GENE EXPRESSION IN QPX. **Steven Roberts[1], Roxanna Smolowitz[2],** and **Jacquelin Defaveri[3].** [1]University of Washington, School of Aquatic and Fishery Sciences, Seatte, WA, 98105, USA; [2]New England Aquarium, Boston, MA, USA; [3]Marine Biological Laboratory, Woods Hole, MA, USA.

Quahog Parasite Unknown (QPX) is a protist, genetically identified as belonging to the family Thraustochydriidae in the phylum Labyrinthulomycota (slime mold). It proliferates by endosporulation

and has been identified as a significant cause of hard clam mortality in the northeast United States. QPX causes significant disease and mortality in both cultured and wild clam populations in the region. In order to better understand what genes are present in the extracellular proteins of QPX mucus and are associated with QPX virulence; we have started to characterize select genes that are expressed in QPX using quantitative RT-PCR analysis. One gene we have focused on, a serine protease, is differentially expressed across strains of QPX and under different temperatures. In addition, levels of expression significantly increase when QPX is cultured in the presence of hard clam tissue. These data suggest serine protease activity is an important virulence mechanism in QPX and provides insight into potential targets for identifying hard clam broodstock with improved disease tolerance. This research is supported in part by the Northeastern Regional Aquaculture Center.

OFFSHORE CLAM ASSESSMENTS IN EASTERN CANADA. **Dale Roddick.** Bedford Institute of Oceanography, Dept. Fisheries and Oceans, Dartmouth, Nova Scotia, B2Y 4A2, Canada.

The offshore clam fishery in eastern Canada is still developing. It started with a fishery for the Arctic surf clam (*Mactromeris polynyma*) in 1986, and is currently looking at expanding to other species. The Department of Fisheries and Oceans and the Industry partners conduct surveys of the stocks under Joint Project Agreements. For the species not currently being fished, the objective of the surveys is to obtain as much information on the stock as possible so that recommendations on allowable catches can be made. The surveys provide data on biomass, growth rates, longevity, natural mortality, recent recruitment trends, age and size of maturity, and data on the selectivity and efficiency of the survey gear. With this data, a model for setting the allowable catch can be chosen and applied. As the fishery progresses, commercial fishing data such as CPUE can be incorporated into the assessment process. Since most of the species involved are long-lived and slow growing, the surveys rotate through the banks, so surveys of an individual bank occur every 4 to 5 years.

OYSTER HARVEST AND PROCESSING EFFICIENCY. **Dave Roebuck[1]** and **Robert Rheault[2].** [1]Salt Pond Oyster Company, Narragansett, RI 02882 USA; [2]Moonstone Oysters, 1121 Mooresfield Road, Wakefield, RI 02879 USA.

Production and processing efficiency using hand picking will be compared with a hydraulically controlled washer tumbler. Construction of the hydraulic tumbler set up will be detailed and the operating cost will be compared with hand picking.

IDENTIFYING WILD LARVAL AND NEWLY SETTLED RED ABALONE IN NORTHERN CALIFORNIA **Laura Rogers-Bennett[1], Toyomitsu Horii[2],** and **Masami Hamaguchi[3].** [1]California Department of Fish and Game, Bodega Marine Lab, 2099 Westside Rd., Bodega Bay, CA 94923, USA; [2]National Research Institute of Fisheries Science

6-31-1 Nagai, Yokosuka, Kanagawa, 238-0316 Japan; [3]Fishery Research Agancy, Research Institute of Seto Inland Sea, Tidal Zone Environment Section, Maruishi 2-17-5, Hatsukaichi, Hiroshima 739-0452 Japan.

Abalone resources are in decline around the Pacific emphasizing the need to better understand early life history stages during the critical recruitment period. Here we report on the progress we have made examining early life history stages of abalone in northern California. We have developed genetic species identification methods using PCR for all four species of abalone, *Haliotis rufescens*, *H. cracherodii*, *H. walallenisis* and *H. kamtschatkana*, found in the region. We used PCR-RFLPs with two restriction enzymes Fok I and Xba I and confirmed with DNA-barcoding analysis. Field surveys for planktonic larvae were conducted using integrated plankton tows. Over 300 planktonic abalone larvae were found in the plankton samples. According to the species identification results using PCR-RFLPs and DNA barcoding, the larvae were red abalone. Field surveys were conducted to find newly settled larvae. We found 10 newly settled larvae ranging in size from 350 to 652 um in shell length and 10 juvenile abalone 1-5mm. According to our PCR-RFLP, results these newly settled larvae and juveniles were red abalone. These tools can now be used to assess abalone during the critical period, early in the life history, to aid in fishery management and restoration.

TISSUE PATTERNS OF A MATRIX METALLOPROTEINASE IN THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. **Scott Salger[1], Dina Proestou[1], Caitlin Vaughn[1], Antonio Remacha-Trivino[1], Christopher Dungan[2],** and **Marta Gomez-Chiarri[1].** [1]Department of Fisheries, Animal and Veterinary Sciences, University of Rhode Island, 20A Woodward Hall, Kingston, RI 02881; [2]Maryland Department of Natural Resources, 904 S. Morris St., Oxford, MD 21654.

Matrix metalloproteinases (MMPs) are zinc-dependent proteases that break down the extracellular matrix (ECM). MMPs have roles in many normal physiological processes including tissue remodeling during development, cell migration, and innate immune responses. Immunofluorescent analysis of *Cv1*-MMP, a MMP of the eastern oyster, *Crassostrea virginica*, was performed on tissues of larvae, juveniles, and adults. Labeling of *Cv1*-MMP was restricted to the apical border of epithelial cells lining the lumen of the stomach and coelomocytes in larvae; the apical border of mantle epithelium and migrating hemocytes in juveniles; and sections of the lumen digestive tissue, and the outer lobe of the mantle in adults oysters. Labeling was also seen on hemocytes migrating through connective tissues and in and out of the

intestinal lumen in adult oysters after feeding. *Cv1*-MMP labeling in the mantle increased after shell damage. *Cv1*-MMP labeling was also detected in some hemocytes containing *Perkinsus marinus* merozoites. Oysters infected with *Roseovarius crassostreae*, as shown by the presence of bacterial cells in mantle and conchiolin, exhibited a continuous layer of *Cv1*-MMP labeling on the surface of the mantle. These results indicate that *Cv1*-MMP may have key roles in development, digestion, shell formation, and immune defenses in oysters.

TEMPORAL VARIATION IN MEAT YIELD OF SEA SCALLOPS IN THE GEORGES BANK FISHERY. Christopher L. Sarro and **Kevin D.E. Stokesbury.** University of Massachusetts Dartmouth, School for Marine Science and Technology, Fairhaven, MA 02719, USA.

Georges Bank supports the largest sea scallop (*Placopecten magellanicus*) fishery in the world with 26,765 metric tons (US$385.95 million) landed in 2006. Sea scallop fisheries managers use one shell height to meat weight relationship (meat yield) for Georges Bank and another for the mid-Atlantic. However, reports from commercial fishermen and preliminary data indicate meat yield varies seasonally, annually, and spatially. Since 1998, as part of a cooperative research program, 31 commercial scallop vessels have provided 14,302 live scallops for dissection, from the last tow of their trip. From these dissections we examined the pattern and intensity of temporal variation in sea scallops across Georges Bank. These data indicate substantial temporal variation in meat yield. For example mean meat weight varied by 28% between June and October for 100-105 mm scallops (101.6 mm rings on dredges). These temporal variations in meat yield have the potential to affect the timing and harvest limits of the limited area access fisheries, where boats are allowed into selected areas to harvest set poundage of scallops, on Georges Bank. Estimates show a 29% difference in total biomass between June and October.

GROWTH AND SURVIVAL OF TRIPLOID HARD CLAMS *MERCENARIA MERCENARIA* IN FLORIDA WATERS. John Scarpa[1], Leslie N. Sturmer[2], Susan E. Laramore[1], Eman Elwazzan[3], Shirley M. Baker[4], and **Charles M. Adams[5].** [1]Harbor Branch Oceanographic Institute at Florida Atlantic University, Center for Aquaculture and Habitat Restoration, Ft. Pierce, FL 34946 USA; [2]University of Florida, Cooperative Extension Service, Cedar Key, FL 32625 USA; [3]Florida Institute of Technology, Department of Biology, Melbourne, FL 32901 USA; [4]University of Florida, Department of Fisheries and Aquatic Sciences, Gainesville, FL 32653 USA; [5]University of Florida, Department of Food and Resource Economics, Gainesville, FL 32653 USA.

The project assessed the value of triploid hard clams, *Mercenaria mercenaria*, for aquaculture in Florida as clam farmers in southern Florida report below average survivals during the prolonged hot summers. Triploidy was induced in the hard clam, *Mercenaria mercenaria*, by suppressing polar body I (PBI) or polar body II (PBII) formation in fertilized eggs with cytochalasin B. Two three-week controlled laboratory experiments with juvenile triploid clams (~85 and 12 mg) were performed to examine growth (weight gain). Triploids grew significantly less by the end of both experiments (Exp I: PBI-250%, PBII-269%, Diploid-341%; Exp II: PBII-422%, Diploid-549%). At the end of field culture, differences were found between triploids and diploids and between sites. At Cedar Key, triploids were similar in length (46 mm) and weight (30 g), but had a higher condition index (5.3 vs 4.8) and lower survival (69 vs 80%) compared to diploids. At Charlotte Harbor, triploids were similar in length (48-50mm) and condition index (4.6), but lower in weight (34 vs 44 g) and survival (43 vs 49%) compared to diploids. The additional cost associated with triploid production in the hatchery was calculated to be minimal ($0.14-0.27/1000 seed, depending on survival). This research was supported by USDA-ARS and FL Sea Grant.

HARD CLAM (*MERCENARIA MERCENARIA, M. CAMPECHIENSIS*) HYBRIDS FOR FLORIDA AQUACULTURE: HATCHERY CULTURE. John Scarpa[1], Leslie Sturmer[2], William Arnold[3], Stephen Geiger[3], and **Shirley Baker[4].** [1]Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, FL 34946 USA; [2]University of Florida, Cooperative Extension Service, Cedar Key, FL 32625 USA; [3]Florida Fish & Wildlife Conservation Commission, Florida Fish & Wildlife Research Institute, St. Petersburg, FL 33701 USA; [4]University of Florida, Department of Fisheries & Aquatic Sciences, Gainesville, FL 32653 USA.

Hard clam aquaculture in Florida has expanded primarily through increased acreage rather than increased productivity. Over the years, clam production in Florida has seen various mortality events resulting from hurricanes, low salinities, and high water temperatures. The local southern hard clam (*Mercenaria campechiensis*) may offer improved production characteristics and hybridizes readily with *Mercenaria mercenaria*. Therefore, an examination of production characteristics of the parental species and their reciprocal crosses under commercial conditions has been undertaken. Cultured *M. mercenaria notata* and wild *M. campechiensis* were used as broodstock. Spawning was induced by thermal shock and single parent crosses performed. The resulting larvae from each group within a spawn (n = 5 spawns performed) were cultured separately in 400-L vessels utilizing standard hatchery practices of daily water change and batch feeding of microalgae (*Isochrysis* sp.). Larvae were transferred to downwelling systems for metamorphosis after 7 days culture. Differences were sometimes noted in fertilization between hybrid crosses. DNA amounts, as measured by flow-cytometry using DAPI stain, differed slightly (six fluorescent units) between the parental species, but hybrids exhibited values of the maternal parent. Therefore, protein gel electrophoresis of known markers will be conducted on parental tissue samples and on progeny to ensure hybrid identity.

EVALUATION OF THE SUNRAY VENUS CLAM *MACROCALLISTA NIMBOSA* FOR AQUACULTURE IN FLORIDA. **John Scarpa[1], Leslie N. Sturmer[2], Jose Nuez[3],** and **R. Leroy Creswell[4].** [1]Harbor Branch Oceanographic Institute at Florida Atlantic University, Fort Pierce, FL 34946 USA; [2]University of Florida, Cooperative Extension Service, Cedar Key, FL 32625 USA; [3]University of Florida, The Whitney Laboratory for Marine Bioscience, St. Augustine, FL 32080 USA; [4]University of Florida, Cooperative Extension Service, Fort Pierce, FL 34945 USA.

The sunray venus clam is being evaluated as a potential new aquaculture species to diversify the hard clam culture industry in Florida. Wild broodstock were collected, conditioned, spawned and larvae reared through setting: pediveligers (~220 μm) appeared at 7 days at 26–28°C and 28–30 ppt. Land-based culture of juveniles occurred in downwellers with a 46–63% return. A feed density trial was initiated with juveniles to determine maximum cell density for growth. Triplicate 4-L beakers each containing 24 clams (42 ± 3 mg) were fed 0, 50, 100, or 200 K cells/mL of *Isochrysis* sp. twice/day over a four week period. Growth (absolute and % weight change) did not increase above the 100K cells/mL treatment. Approximately 118,000 sunray venus nursery clam seed (9.3–18.5 mm shell length) were field-planted in soft bags or hard cages. After four months, survival ranged from 32–94% with 0.12–0.25 mm/day shell length growth. Sunray venus clams are being further cultured in soft bags, soft bags with internal frames, cages, and bottom plants at densities of 20–70/ft^2; a portion of which will be used for market perception tests. This research was supported by Florida Sea Grant (Project R/LR-A-44).

MICROSATELLITE DIFFERENTIATION OF *PANULIRUS ARGUS* POPULATIONS. **Samantha Schmitt** and **Mike Tringali.** Florida Fish and Wildlife Conservation Commision, Genetics, Saint Petersburg, FL, 33701, USA.

In this preliminary analysis, genomic DNA was isolated from *Panulirus argus* samples collected throughout the Gulf of Mexico and western Atlantic coasts.PCR amplifications were conducted with twelve microsatellite DNA loci to genotype. Genetic diversity within each sample was assessed and unbiased estimates of heterozygosity were computed for each locus and averaged over all. Genotypes were evaluated in conformance to Hardy-Weinberg equilibrium (HWE) genotypic proportions by using the permutation test implemented in GENETIX (version 4.02). Mean values of gene diversity, allelic richness, and heterozygosity were similar across samples. Null hypothesis of HWE was not rejected at any locus with the exception of one locus; deviated significantly from HWE samples from St. Croix and Bahamas. In exact tests for allele frequency heterogeneity significant differences were observed between 11 of the 36 tested sample pairs (over all loci). Little overlap was observed among members of samples from the Bahamas, St. Croix, St. Kitts, and Tennessee Reef Light FL. Results suggest that spiny lobsters are highly interconnected in gene flow along coastal US. Differences in allele frequencies, trends in fixation indices, spatial separation of genotypes among some of the tested sample locations provides preliminary evidence for regional population connectivity or perhaps localized self-recruitment.

POLYMORPHIC GENETIC MARKERS FOR THE HARD CLAM *MERCENARIA MERCENARIA*. **Gail P. Scott[1], Sharon J. Furiness[1], Mark D. Camara[2], Ryan B. Carnegie[1],** and **Kimberly S. Reece[1].** [1]Virginia Institute of Marine Science, P.O. Box 1346, Gloucester Point, Virginia 23062; [2]USDA Agricultural Research Service, Hatfield Marine Science Center, 2030 SE Marine Science Drive, Newport, Oregon 97365.

The hard clam, or northern quahog (*Mercenaria mercenaria* L.), is one of the most valuable aquaculture products grown in the United States with an economic value that increased 1200 percent between 1995 and 2005. Common breeding practices are based on phenotypic selection using broodstock strains of uncertain lineage. This process can rapidly decrease genetic variability in hatchery stocks and is likely to have an effect on natural populations adjacent to aquaculture grow out areas. Studies in other bivalves demonstrate that loss of genetic variability leads to detrimental effects on performance traits such as disease susceptibility, growth rate and survival. Genetic variability is measured using polymorphic molecular markers such as those we are developing for the hard clam. We are isolating and characterizing microsatellite loci and single nucleotide polymorphic sites (SNPs). We have assessed null alleles, observed and expected heterozygosities, linkage disequilibrium and departures from Hardy-Weinberg equilibrium (HWE) for a suite of these markers. As is common in bivalves, many microsatellite loci exhibit significant deviations from HWE, probably due to null alleles. Nonetheless, these markers provide a valuable tool for genetic investigations including marker informed selective breeding, parentage analyses, population genetic studies, and genetic diversity monitoring.

SHORELINE STABILIZATION AND FISHERIES BENEFITS OF OYSTER REEF RESTORATION IN COASTAL ALABAMA. **Steven B. Scyphers[1,2], Sean P. Powers[1], Kenneth L. Heck Jr.[1,2],** and **Carly R. Steeves[2].** [1]University of South Alabama, Marine Sciences, Mobile, Alabama 36688, USA; [2]Dauphin Island Sea Lab, Dauphin Island, Alabama 36528, USA.

Shorelines at the interface of marine and terrestrial biomes are one of the most degraded and threatened habitats in the coastal zone because of their sensitivity to sea level rise, storms, and increased utilization by man. Previous efforts to restore shorelines have largely involved introducing unnatural structures to dampen wave energy. Recently, restoration efforts have shifted towards biogenic, or "living reefs". Beyond shoreline stabilization, living reefs may provide additional ecosystem services such as habitat for resident species of shellfish and finfish, providing feeding resources for transient fishes, and improved water quality via the filter-feeding bivalves. Currently, a large-scale bioengineering restoration project is being undertaken by the University of South

Alabama and the Dauphin Island Sea Lab. This "living breakwater" project involves construction of four networks of reefs (each with three 5 × 50 m reefs) in close proximity to eroding shorelines in coastal Alabama. We hypothesized that over time the presence of eastern oyster (*Crassostrea virginica*) reefs could stabilize and possibly facilitate the expansion of shoreline marsh grass as well as provide habitat for additional fishes. Our preliminary results support our hypothesis that created oyster reefs will be utilized by transient fishes and provide substrate for oyster reef recruitment.

RECENT RESEARCH ON ABALONE (*HALIOTIS* SPP.) METAMORPHOSIS INDUCTION AND POSTLARVAL CULTURE. Ricardo Searcy-Bernal. Instituto de Investigaciones Oceanológicas, Universidad Autónoma de Baja California, P.O. Box 453, Ensenada, B.C., Mexico.

In the cultivation of abalone (*Haliotis spp.*), metamorphosis induction and postlarval culture are critical stages. Recent research to improve the successful induction of metamorphosis has focused on natural and chemical inducers, how these are provided in culture systems and on the effects of larval quality. Inducers commonly tested include benthic diatoms, macroalgae, con-specific mucus and gamma-aminobutyric acid (GABA). Regarding postlarval culture, research has emphasized nutritional, ecological and pathological issues. Feeds tested for postlarvae include diatom strains, macroalgal spores or plantules and formulated diets. The digestive system development of postlarvae including the role of gut microflora is also beginning to be understood. Ecological factors studied include boundary layer conditions, light intensity and water flow, among others. On the other hand, several bacteria have been associated with mass postlarval mortalities. Genetic factors that might influence these culture stages have also been considered. In this paper some of these recent investigations and their importance for abalone culture are discussed.

LARVAL RELEASES AS A METHOD OF BAY SCALLOP RESTORATION IN BOGUE SOUND NORTH CAROLINA. Mark Sherman[1], Dana Schmidt[2], and **Ami E. Wilbur[1].** [1]UNCW, Department of Biology and Marine Biology, Wilmington, NC 28409 USA; [2]128 Goose Creek Loop Rd., Newport, NC 28570.

The recent decline in bay scallop (*Argopecten irradians*) abundance in North Carolina has prompted interest in the investigation of methods for restoration. This fall we initiated a project aimed at evaluating the success of larval releases as a method of bay scallop stock propagation. Broodstock scallops were collected from the wild in Bogue Sound. Six separate spawns of 10-20 scallops resulted in over 2.5 million 10-15 day old larvae that were released into two sites in western Bogue Sound. Each release took place amidst a healthy seagrass bed at low tide. Six collectors were placed surrounding the release sites, and remained deployed for 1 month following each release. Scallops captured on the collectors and those to be sampled (diver surveys) in spring 2008 will be subjected to genetic analysis (mtDNA and microsatellites) to quantify the proportion of the post release population that can be attributed to the larval releases. Genetic analysis is ongoing and the preliminary results from the spat caught on the collectors will be presented.

THE SCALLOP SPAT ROLLERCOASTER—MULROY BAY, IRELAND 1980-2005. John W. Slater[1], Iarlaith Connellan[2], Mark Norman[3], and **Gavin Burnell[4].** [1]Centre of Applied Marine Biotechnology (CAMBio), Letterkenny Institute of Technology, Letterkenny, County Donegal, Ireland; [2]Cartron Point Shellfish Ltd., New Quay, County Clare, Ireland; [3]Taighde Mhara Teo., Carna, County Galway, Ireland; [4]Department of Zoology, Ecology and Plant Science, University College Cork, Cork, Ireland.

Despite significant research efforts since the 1980's, cultivation of the king scallop *Pecten maximus* has not developed in Europe. In those countries where fishery landings have expanded, such increases have resulted only from further exploitation of already overfished natural resources. Farm production and the development of stock enhancement programmes are severely constrained by the availability of a reliable source of scallop spat. In 1979, a local aquaculture co-operative, the North Water Co-operative Soc. Ltd. inadvertently collected over five million scallop spat on 12 mm diameter polypropylene rope in the North Water of Mulroy Bay, Ireland; by far the greatest number obtained at the time in European waters. As a result, research trials commenced to support the development of this site as a scallop spat collection centre. This presentation provides a review of some of the data covering a twenty-five year period, focusing particularly on the last ten years during which spat collection has been spectacularly inconsistent and asks the question: What are the requirements for a good spatfall year?

THE INTERACTION OF TEMPERATURE AND HARD CLAM (*MERCENARIA MERCENARIA*) STRAIN ON THE OCCURRENCE OF QPX DISEASE IN THE LABORATORY AND IN THE FIELD. Roxanna Smolowitz[1], Jackie Defaveri[2], William Walton[3], Diane Murphy[3], and **Dale Leavitt[4].** [1]New England Aquarium, Central Wharf, Boston, MA 02110; [2]Marine Biological Laboratory, Woods Hole, MA 02543; [3]Barnstable County Cooperative Extension, Barnstable, MA 02630; [4]Roger Williams University, Bristol, RI 02809.

Disease caused by Quahog Parasite Unknown (QPX) continues to devastate hard clam aquaculture in Massachusetts. Laboratory studies investigated the effect of temperature on QPX infection of clams. Two clam strains (Florida and Massachusetts) were either injected with QPX at the dorsal ligament or were exposed via the water column to QPX that was either cultured in media or in sea water with macerated clam tissue. Results showed only Florida clams developed significant disease and only QPX cultured in

seawater with clam tissue caused disease to occur. Furthermore, infections occurred only in clams held at either 16°C or 18°C, but not at 22°C. In the field, three strains of clams (Massachusetts, Florida and New Jersey) were deployed in two locations in Barnstable Harbor, MA and evaluated for occurrence of QPX disease 3 × /year for greater than 2 years. QPX caused mortality was significantly higher in the Florida strain than in either Massachusetts or New Jersey strains. There was a trend showing slightly higher QPX disease and mortality in Massachusetts vs. NewJersey clams.

THE EL-NIÑO SOUTHERN OSCILLATION AND THE NORTH ATLANTIC OSCILLATION DIFFERENTIALLY MODULATE *PERKINSUS MARINUS* AND *HAPLOSPORIDIUM NELSONI* IN EASTERN OYSTER POPULATIONS. **Thomas M. Soniat[1], Eileen E. Hofmann[2], John M. Klinck[2],** and **Eric N. Powell[3].** [1]Nicholls State University, Department of Biology, Thibodaux, LA 70310 USA; [2]Old Dominion University, Center for Coastal Physical Oceanography, Norfolk, VA 23529 USA; [3]Rutgers, The State University of New Jersey, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349 USA.

The Eastern oyster is affected by two protozoan parasites, *Perkinsus marinus* (Dermo) and *Haplosporidium nelsoni* (MSX). Both diseases are largely controlled by water temperature and salinity and thus are potentially sensitive to climate variations. A 10-year time series of temperature and salinity and *P. marinus* infection intensity from Louisiana and a 52-year time series of air temperature and freshwater inflow and oyster mortality from Delaware Bay were analyzed to determine patterns in disease and disease-induced mortality in oyster populations that resulted from ENSO and NAO climate variations. Wavelet analysis was used to determine the dominant modes of variability and the time variability of the modes. For the Louisiana site, salinity and Dermo disease infection intensity are correlated at a periodicity of 4 years, which corresponds to ENSO; the high-salinity La Niña phase of ENSO favors parasite proliferation. For Delaware Bay, the primary correlation was between temperature and oyster mortality, with a periodicity of 8 years, which corresponds to the NAO; warmer temperatures during the positive phase of the NAO favor the parasites causing increased oyster mortality.

MULTI-YEAR RECRUITMENT PATTERNS OF OYSTERS (*CRASSOSTREA VIRGINICA*) ON CONSTRUCTED REEFS IN CHESAPEAKE BAY. **Melissa Southworth[1], Roger Mann[1], Juliana Harding[1],** and **James Wesson[2].** [1]Virginia Institute of Marine Science, Fisheries Department, Gloucester Point, VA, 23062, USA; [2]Virginia Marine Resources Commission, Fisheries Division, Newport News, VA, 23607, USA.

Constructed, three dimensional substrate (typically shell) reefs have been employed as a major tool in oyster (*Crassostrea virginica*) restoration in the Chesapeake Bay since 1993. We present a critical evaluation of the performance of more than 20 of these reefs through 2007 with focus on the time sequence and intensity of recruitment post construction. On eight of these reefs, recruitment patterns were highest in the first year post construction, but the intensity of the recruitment signal declined in subsequent years. There was no direct relationship observed between the addition of culchless cultured broodstock (<75 mm shell height) oysters to the reefs or in the immediate vicinity (<100 m) of the reef and observed recruitment of oysters on the reef within the same year. In general, observed recruitment patterns on constructed reefs are driven by single localized recruitment events that are related to favorable environmental conditions.

MONITORING THE PROGRESSION OF EPIZOOTIC SHELL DISEASE IN AMERICAN LOBSTERS (*HOMARUS AMERICANUS*) USING A QUANTITATIVE SEVERITY INDEX. **Bradley G. Stevens.** School of Marine Science and Technology, University of Massachusetts–Dartmouth, North Dartmouth, MA 02747 USA.

The incidence of epizootic lobster shell disease (LSD) has increased dramatically in New England since 1997. Biologists record LSD in the field using a 4-level visual severity index (VSI). No long term studies have yet been conducted on disease progression or its effects on survival and reproduction. We began a study in November 2007, with 60 lobsters having LSD in various stages, from absent (0) to severe (3). Lobsters were examined monthly using a regional disease index (RDI), by averaging across three major body regions. Lobsters were digitally photographed from both sides, and affected areas of the exoskeleton were measured using image analysis. A quantitative disease index (QDI) was calculated as the ratio of total diseased area to estimated total surface area of each lobster. Monthly differences in mean severity for all lobsters were not detectable, but differences in monthly QDI for individual lobsters depended on both the stage of the disease (i.e. initial severity) and water temperature. LSD can accelerate the molt cycle, causing loss of fertilized eggs, and death due to complications of molting. Most lobsters that molted successfully were free of disease symptoms, but some had residual lesions or reacquired them within 1-2 months.

AN OVERVIEW OF BIVALVE GENETICS. **Sheila Stiles, Joseph Choromanski,** and **Dorothy Jeffress.** U.S. Department of Commerce, National Oceanic & Atmospheric Administration, National Marine Fisheries Service, Northeast Fisheries Science Center, Milford Laboratory, 212 Rogers Ave., Milford, CT 06460 USA.

Deficiencies in previous technology may have inhibited the profitable culture of bivalve molluscs, such as oysters, clams and scallops. Application of new and innovative technology in genetics,

however, could advance the culture of commercial species. Such applications would include: (1) genetic selection and breeding for improving growth and survival; (2) genetic analyses with innovative molecular techniques for evaluation of diversity and population structure; and (3) identification, monitoring and tracking of populations and stocks in natural ecosystems for enhancement and restoration. As a goal toward increasing production of cultured bivalves, genetically-based variability in survival and growth can be investigated to develop strategies for identifying and characterizing genetic differences in production traits. Such genetic methodology encompasses a combination of breeding, genomics and field evaluations. Genetic methods can be used to develop improved stocks of bivalves, possibly incorporating polyploidy or other chromosomal manipulation, as well as, to assess genetic variation in cultured stocks and wild populations. To complement breeding, molecular approaches can be employed to analyze DNA, RNA and protein variation within and among groups of various populations and selected lines for phenotypic and genotypic frequencies. An overview with examples of genetic approaches used with bivalves will be presented.

MARITIME ADAPTATION AND NUTRITION IN CALIFORNIA. Victoria Stosel. California State University, Los Angeles, CA.

California possesses an abundance of natural resources. However, securing adequate nutrition presented challenges to aboriginal populations living within the state. The population on San Nicolas Island, California relied primarily upon maritime resources. An examination of twenty archaeological sites indicates a heavy dependence upon varieties of shellfish. The Coastonoan Ohlone population also lived in California, adjacent to the San Francisco Bay, and utilized maritime resources. While shellfish is an excellent source of protein it provides only small quantities of vitamins, folic acid and vitamin C in particular. These populations suffered from a variety of pathologies, cribra orbitalia enamel hypoplasia and spina bifida occulta, that left skeletal markers, many related to malnutrition. Stable isotope analysis and traditional archaeological techniques provide insight into paleodiets but provide little insight into how nutrition impacted aboriginal populations. Although the characterization of paleodiets is challenging to reconstruct, the relationship between malnutrition and skeletal pathology may provide an additional means of dietary reconstruction.

ARE WE FINDING THE NEEDLE IN THE HAYSTACK? VALIDATION AND RE-EXAMINATION OF PCR ASSAYS FOR OYSTER DISEASES. Nancy A. Stokes, Ryan B. Carnegie, Rita K. Crockett, and **Eugene M. Burreson.**

Virginia Institute of Marine Science, Environmental and Aquatic Animal Health, Gloucester Point, VA, 23062 USA.

Until recently protozoan infections in oysters could only be detected by Ray's fluid thioglycollate medium (RFTM) for *Perkinsus* spp. or by histological examination of tissue sections for other groups. The first PCR assays for oyster diseases were published in 1995, targeting various regions of the ribosomal gene complex of *P. marinus*, *Haplosporidium nelsoni* and *H. costale*. Development of DNA-based diagnostic tools opened new areas for research and allowed for species discrimination not possible morphologically. There are now multiple PCR assays available for the major disease agents affecting oysters and PCR diagnosis has become routine. These assays have been shown to be more sensitive and specific than traditional methods; however, the parameters of PCR efficacy are seldom rigorously tested nor are the limitations of its usefulness considered. Every PCR assay that is to be used for disease diagnosis should be validated by comparison against other detection methods for that parasite, preferably using samples with various infection levels and from multiple locations. Additionally an assay's effectiveness needs to be re-examined when new geographic isolates are found and closely related species are discovered. Such considerations will be examined for PCR assays for *H. nelsoni*, *P. marinus*, and *Bonamia* spp.

GENETIC DIVERSITY AMONG CULTURED GEODUCK (*PANOPEA ABRUPTA*) AND IMPLICATIONS FOR WILD CONSPECIFICS. Kristina M. Straus[1], Brent Vadopalas[1], Jonathan P. Davis[2], and **Carolyn Friedman[1].** [1]University of Washington School of Aquatic and Fishery Sciences Seattle WA 98115 USA; [2]Baywater Inc., 15425 Smoland Lane, Bainbridge Island, WA 98110, USA.

Before advancing an aquaculture program for native species, it is important to consider genetic risks to wild populations. If hatchery and wild geoducks are genetically differentiated, the potential exists for aquaculture to negatively impact wild populations by reducing their genetic diversity and adaptive potential. Genetic differences between wild and cultured geoducks may arise if broodstock are collected distantly, if selective pressures differ between the hatchery and the wild, or if genetic drift occurs in the hatchery due to low effective numbers of breeders (N_b). In a retrospective study, we used microsatellites to compare allele frequencies, observed heterozygosity, and N_b estimates among five year classes (1999–2003) of farmed geoducks and a wild population. In a complementary study of contemporary hatchery production, broodstock and samples of their progeny will be genotyped to assign seed clams to parents, determine relative reproductive success and estimate N_b. If cultured and wild geoducks are genetically differentiated, reproduction between these groups could jeopardize wild populations by decreasing their adaptive potential and should be avoided.

ESTABLISHING A TRAJECTORY OF TEMPORAL CHANGE IN NATURAL VERSUS CONSTRUCTED INTERTIDAL OYSTER REEFS IN THE NORTHERN GULF OF MEXICO. **Alix G. Stricklin[1], Mark S. Peterson[1], John D. Lopez[1], Christopher A. May[2], Christina Watters[3]**, and **Mark S. Woodrey[4].** [1]The University of Southern Mississippi, Department of Coastal Sciences, Ocean Springs, MS; [2]Grand Bay National Estuarine Research Reserve (GB-NERR), Moss Point, MS; [3]Environmental Cooperative Science Center, Tallahassee, FL; [4]Mississippi State University, Coastal Research and Extension Center, Biloxi, MS and GB-NERR, Moss Point, MS.

Oyster reefs enhance the sustainability of estuarine ecosystems in the northern Gulf of Mexico in several ways: (1) they increase habitat structure and complexity, (2) subsequently attracting diverse faunal assemblages, and (3) stabilize marsh edge by sediment deposition. We evaluated temporal changes in faunal assemblage and physical characteristics of constructed and natural reefs in three subsystems of GB-NERR. Each constructed reef was comprised of randomly interspersed plastic sampling trays filled with *Crassostrea virginica* cultch and paired with a natural oyster reef within the same subsystem. Faunal diversity and density and spat, seedling and adult oyster density was quantified for all reefs. Additionally, changes in adjacent marsh edge position relative to the reef were monitored. Stable isotopes were used to evaluate faunal interactions and reef-supported food-web dynamics. Spat and seedling density and taxa richness were significantly higher in constructed reefs versus natural reefs, regardless of subsystem. Adult oysters were more abundant in one subsystem compared to others, but did not differ between constructed and natural reefs within any subsystem. Further, though adult oyster density was initially greater in natural reefs in this subsystem, constructed reefs eventually surpassed natural reefs over time. Marsh edge showed seasonal changes in relative position to reefs.

WHAT'S IN THE CLAM BAG? A PICTORIAL GUIDE TO MARINE ORGANISMS FOUND IN, ON, AND AROUND A CLAM CULTURE BAG. **Leslie N. Sturmer[1], Jonathan S. Fajans[2], Shirley Baker[3],** and **Kevin Hulen[4].** [1]University of Florida, Cooperative Extension Service, Cedar Key, FL, 32625, USA; [2]Florida Institute of Oceanography, Keys Marine Laboratory, Long Key, FL, 33001, USA; [3]University of Florida, Department of Fisheries and Aquatic Sciences, Gainesville, FL, 32653, USA; [4]University of Florida, Department of Biological Sciences, Gainesville, FL, 32611, USA.

Hard clam, *Mercenaria mercenaria*, aquaculture supports many small businesses in Florida with over 100 million clams produced annually. Farms are located on submerged land leases in inshore coastal waters. In siting a lease, the area undergoes a resource survey and must be devoid of seagrasses and other marine life. Once in production, a clam farm may have 1000 culture bags planted per acre. When clams are harvested, there are many more "critters" that inhabit the bag than just the crop. The clam bag creates a favorable environment and provides habitat and protection for a myriad of plants and animals. A pictorial guide has been developed to assist clam farmers in identifying over 150 of these organisms. The guide is divided into easily recognizable, but not taxonomic, categories. Biographical sketch pages describe the organism as well as characteristics that make it a friend, foe, or neighbor to clam farming. Information is provided on the organism's effects on the crop and what a farmer might do to lessen those effects. *What's in the Clam Bag?* is accessible at <http://shellfish.ifas.ufl.edu and is available as a CD-ROM. This educational tool highlights the diversity and abundance of marine organisms stimulated through clam farming activities.

INVERTEBRATE FOULING COMMUNITY COMPOSITION AND SUCCESSION ASSOCIATED WITH PACIFIC OYSTER *CRASSOSTREA GIGAS* DEEP-WATER SUSPENDED TRAY CULTURE. **Soleil E. Switzer[1], Penelope A. Barnes[2],** and **Robert Scott Mckinley[1].** [1]Centre for Aquaculture and Environmental Research, University of British Columbia, Vancouver, British Columbia, V6T 1Z4, Canada; [2]Centre for Shellfish Research, Malaspina University-College, Nanaimo, British Columbia, V9R 5S5, Canada.

Deep-water oyster culture supports diverse invertebrate communities which colonize both the farm equipment and the cultivated oysters themselves. The composition of invertebrate fouling communities is dependant primarily on local recruitment, hydrodynamics and habitat conditions. Fouling invertebrates, potentially, can adversely effect the growth and health of the oysters through competition and predation. Also, the market value of the oysters may be negatively influenced by the external appearance of the oyster. To minimize the negative impact of invertebrate fouling, some farmers have altered farming practices by changing the composition of the trays and/or revising the cleaning schedule of the trays and oysters. I conducted a comparative study, over the course of one year at a deep-water Pacific oyster farm located off the east coast of Vancouver Island in southern British Columbia, Canada, to determine if cleaning schedule and tray composition influence the composition of the invertebrate fouling community found on the culture trays and oysters. The potential significance of these fouling communities is becoming increasingly apparent in BC with the expansion of bivalve aquaculture and with an increased awareness of the potential problems associated with invasive fouling species.

THE REINTRODUCTION AND SUBSEQUENT STATUS OF BAY SCALLOPS IN THE MARYLAND COASTAL BAYS—A 10-YEAR RETROSPECTIVE. **Mitchell L. Tarnowski** and **Mark L. Homer.** Maryland Department of Natural Resources, Shellfish Program, Annapolis, Maryland 21401, USA.

In 1997/1998, the MDNR Shellfish Program introduced 1.2 million bay scallops to southern Chincoteague Bay. Seed scallops were planted in large (0.06 ha–0.09 ha) predator exclosures. Survivorship to first spawning during the subsequent spring was

80% to 85%. The scallops spawned twice in their first reproductive year and approximately 10 % survived to spawn a third time in their second spring. Subsequent colonization occurred rapidly, and by 2002 scallops were found throughout the Maryland coastal bays system. Even while this population was expanding its range, densities in Chincoteague Bay, which were patchy and never high (peaking at 1 scallop/3 m^2), gradually declined. By 2005, the density in the lower bay where scallops previously were most abundant had dropped to 1 scallop/72 m^2, and scallops were not observed anywhere in Chincoteague Bay in 2006 and 2007. The populations in the other bays are tenuous. Some possible reasons for the decline and disappearance of scallops in Chincoteague Bay include poor flushing, brown tide outbreaks, and an elevated temperature anomaly in 2005 with an associated large-scale eelgrass die-off which reduced habitat and refuge from predation.

AN ASSESSMENT OF HABITAT VALUE OF CONSTRUCTED INTERTIDAL OYSTER REEFS AND OYSTER AQUACULTURE SYSTEMS IN DELAWARE BAY, USA. **Jaclyn Taylor** and **David Bushek.** Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349, USA.

The lower Delaware Bay, USA includes an extensive high-energy intertidal zone that consistently receives high oyster (*Crassostrea virginica*) settlement. Presumably, high predation, disease, ice and freezing limit the formation and persistence of intertidal oyster reefs. If protected, however, disease-resistant oysters survive and grow well, supporting oyster aquaculture. Rack and bag culture systems increase structural diversity of habitat and the cultured oysters provide ecological services as they filter water and remineralize nutrients. Thus, rack and bag culture systems may be artificial analogs of oyster reefs. This study compared motile fauna habitat utilization of rack and bag culture systems, constructed oyster reefs and the surrounding sand flats. Motile macrofauna were sampled around six aquaculture racks, six shell-bag reefs and six plots on the adjacent sand flats using minnow traps, crab pots and eel traps. Species richness for aquaculture racks (25 species) and shell-bag reefs (22 species) were comparable and significantly greater than on the sand flats. Seven species were unique to aquaculture racks. Species abundance was five times greater around aquaculture racks and three times greater around shell-bag reefs compared to sand flats. Intertidal oyster reefs and aquaculture structures increased habitat complexity and attracted similar assemblages of motile macrofauna.

BAY SCALLOP RESTORATION EFFORTS IN NEW YORK. **Stephen T. Tettelbach**[1] and **Christopher F. Smith**[2]. [1]Dept. of Biology, C.W. Post Campus of Long Island University, Brookville, NY 11548 USA; [2]Marine Program, Cornell Cooperative Extension of Suffolk County, Riverhead, NY 11971 USA.

Bay scallop (*Argopecten irradians irradians*) populations and fisheries in eastern Long Island, New York were virtually eliminated by a series of brown tides (*Aureococcus anophagefferens*) in the 1980's. Genetic analyses confirmed that planted broodstock contributed to increased recruitment in the Peconic Bays during 1988–1990, but these successes were thwarted by a severe brown tide in 1995—which again decimated New York populations. Our subsequent restoration work has focused on improving overwintering survival and design of spawner sanctuaries. Our current restoration strategy relies on moderate density deployments in lantern nets (35 scallops/tier) and high density plantings directly to the bottom (100+ scallops/m^2), to ensure a high probability of fertilization success. In Fall 2007, our *in situ* dive surveys documented increases in juvenile scallop recruitment of 8-80X at most sites in Orient Harbor, the location of our large scale spawner sanctuary, compared to levels in 2005–2006. By contrast, juvenile scallop abundances in other nearby embayments which lacked a significant spawning stock were equal to or lower than those seen in the past 2 years. For 2007, our group stocked >600,000 40+ mm scallops into our lantern net systems and another ~240,000 scallops of comparable size were free-planted in a total of four different embayments.

THE IMPORTANCE OF FALL RECRUITMENT IN NEW YORK BAY SCALLOP POPULATIONS: VARIABILITY IN SIZE OF ANNUAL GROWTH RINGS AND TOTAL SHELL SIZE. **Stephen T. Tettelbach** and **Dennis Bonal.** Dept. of Biology, C.W. Post Campus of Long Island University, Brookville, NY 11548 USA.

We have made opportunistic, annual collections of adult bay scallops, *Argopecten irradians irradians*, from waters of eastern Long Island, New York during the commercial harvest season (October–March) since 1989, at a total of 12 different sites, to examine variability in size of the annual growth ring and total shell size. Of the >4,000 scallops examined, ~23% exhibited "small" annual growth rings, i.e. ≤20 mm from the hinge; these individuals are likely the result of "late" season spawns (after Sept. 15). Sample prevalence of scallops with small rings ranged from 0–100% depending on the site and year of collection. Statistically significant differences in mean ring size, prevalence of scallops with small rings, and total shell size were detected at given sites during different years and between different sites during the same year. Potential reasons for these patterns as well as the critical importance of small ringed individuals in bay scallop populations are discussed. Data are also presented on sample prevalence of visually ripe individuals (i.e. with orange ovary), interannual variability in scallop adductor muscle weights, and infestation rates of parasitic female pea crabs, *Tumidotheres* (*Pinnotheres*) *maculatus*.

DIRECT OBSERVATION OF BAY SCALLOP, *ARGOPECTEN IRRADIANS IRRADIANS*, SPAWNING IN LONG ISLAND, NEW YORK WATERS. **Stephen T. Tettelbach** and **Andrew Weinstock.** Dept. of Biology, C.W. Post Campus of Long Island University, Brookville, NY 11548 USA.

We opportunistically observed and photographed a mass spawning of northern bay scallops, *Argopecten irradians irradians*, while diving in Northwest Harbor, East Hampton, New York on 7

June 2005. Spawning occurred in late afternoon on an ebbing tide, 1 d after a new moon, and coincided with a sharp spike in water temperature (3.82°C in 6 hrs; 4.96°C in 12 hrs) and increased wave action (due to sustained winds of 22–31 km hr^{-1}) which caused scallops to gently rock in place. Both eggs and sperm were seen being shed into the water; gamete release occurred at 10–30 sec intervals. Spawning synchrony in the population (the percentage of scallops spawning at any given time) was estimated at ~3–12%. Analyses of temporal changes in gonad mass, water temperature and wind speed over a 7 month period suggest that, when individuals are fully ripe and temperature is above some threshold level, the occurrence of a sharp spike in water temperature coupled with wind events that promote increased wave action and physical disturbance may prompt mass spawning in bay scallop populations. There was no evidence to suggest that spawning coincided with a phytoplankton bloom.

LOST SCALLOP SPAT SURVEY IN THE BAY OF GASPE, QUEBEC. **Benoit Thomas[1], Michel Giguère[2],** and **Éric Tamigneaux[3].** [1]MAPAQ, DIT-CAMGR, Grande-Rivière, Québec, G0C 1V0, Canada; [2]MPO-IML, Mont-Joli, Québec, G5F 3Z4, Canada; [3]ÉPAQ-Halieutec, Grande-Riviére, Québec, GOC 1V0, Canada.

A past survey of Sea scallop (*Placopecten magellanicus*) spat collectors in the Gaspésie and the Magdalene Islands shows that 70–90% of spat is lost before the usual recuperation time. Following the 2004–2006 project, a second survey was planed in 2007 on a series of collectors immersed in the bay of Gaspe at the end of August 2006 at a depth of about 7 m. Collectors were sampled by scuba diving every two weeks from June to August, and once a month from September to November. Divers retrieved each collector individually from the main line into a bag constructed of 500 μm mesh Nitex. Recuperated collectors were washed and sorted in the following days to determine the progression of spat loss, its growth and the evolution of marine biofouling. A slight decrease of abundance of Sea scallop spat was observed in the early part of the season until the end of July. The quantity then stays about the same for the rest of the survey (~1200 Sea scallop spat/bag). Sea scallop spat obtained were double the size of Island scallop spat at the end of the survey in early November (13,6 vs. 6,6 mm).

MICROSATELLITE ANALYSIS OF *PERKINSUS MARINUS* GENOTYPES FROM FLORIDA AND NEW JERSEY INDICATES LIMITED PARASITE MIGRATION BETWEEN POPULATIONS. **Peter Thompson[1], Benjamin Rosenthal[2],** and **Matthew P. Hare[3].** [1]University of Maryland College Park, BEES Program, College Park, MD, 20742, USA; [2]USDA, Agricultural Research Service, Beltsville, MD, 20705, USA; [3]Cornell University, Department of Natural Resources, Ithaca, NY, 14853, USA.

Anecdotal evidence suggests that *Perkinsus marinus* has the ability to spread quickly over large distances. Such high migration would reduce the extent of genotypic variation among geographically proximate populations. In order to examine genetic differentiation among localities, we characterized multilocus *P. marinus* genotypes from infected oyster tissue collected from six sites spanning the east and west coasts of Florida and one location in New Jersey. Each multilocus genotype was defined by five single nucleotide polymorphisms and seven microsatellite loci. Although the occurrence of related genotypes among disparate locations apparently confirmed the long distance dispersal capacity of *P. marinus*, local parasite populations maintained distinct allele frequencies over time. Thus, although migration appears to contribute diversity to local populations, migration does not occur frequently enough to erase differences among parasite populations endemic to particular localities. High frequencies of specific local genotypes suggest that certain parasites may propagate as clones. No locality, however, comprised solely one clone, indicating that population dynamics are not exclusively epidemic. Moreover, a lack of pairwise linkage disequilibrium suggests that recombination occurs within *P. marinus* populations. Taken together, genetic analysis of *Perkinsus marinus* shows a high degree of endemism with limited migration between geographically proximate populations of oysters.

INTERANNUAL VARIABILITY IN SCALLOP LARVAL DISPERSAL AND SETTLEMENT ON GEORGES BANK: A MODELING EXPERIMENT **Rucheng C. Tian, Changsheng Chen, Kevin Stokesbury, Brian Rothschild, Geoffrey Cowles, Qichun Xu, Song Hu, Brad Harris,** and **Michael Marino.** Department of Fisheries Oceanography, School for Marine Science and Technology, University of Massachusetts Dartmouth, New Bedford, MA 02744, USA.

The interannual variability of the dispersal and settlement of the sea scallop larvae spawned on Georges Bank (GB) was studied through a Lagrangian simulation experiment using an individual based population dynamics model and FVCOM (Finite-Volume Coastal Ocean Model). The scallop model consists of four pelagic life stages (egg, trochophore, veliger and pediveliger) and three benthic life stages (juvenile, young adult and adult). The results showed that the total number of settled larvae varied up to 5-fold on an interannual basis over GB. Larval settlement and distribution followed the current patterns: being retained on GB by the tidal-mixing-front recirculation in some years or advected southward to the Middle Atlantic Bight (MAB) by the along-shelf current in other years. Exchanges of larvae between GB and the GSC were produced in the simulation, with 83% of larvae settled in the GSC being spawned on GB, while 46% of larvae settled on GB being spawned in the GSC on average from 1995 to 2005. Significant differences between larval settlement and adult scallop distribution indicate that postlarval survivorship is one of the major factors influencing scallop distribution and population dynamics in the region.

PRIVATE INSURANCE FOR SHELLFISH MORTALITIES DUE TO DISEASES, ACCIDENTS, OR DELAY CAUSED BY HARVEST CLOSURES. **Christopher Trainer** and **Seth Shapiro.** Frank Crystal and Company, Aquaculture Practice, Seattle,WA 98101.

Unexpected mortality losses can mean the difference between profit and loss, and sometimes mean the difference between survival and demise for a grower's business. Also, cash flow interruptions resulting from harvest restrictions can make it difficult for growers to cover expenses, and force them to discharge valued employees, forego maintenance, bypass business opportunities, etc. These actions can have negative long-term implications for the business. Frank Crystal & Company, recognizing the need for a widely-available private insurance program for shellfish growers, has developed a new program, Commercial Shellfish Protector, underwritten by Royal SunAlliance. This program, launched January 1, 2008, can be written to cover any species of mollusc grown in the United States, including: Oysters, Clams, Geoducks, Mussels, and Scallops. In the event of a covered loss involving mortality, the Commercial Shellfish Protector will indemnify the insured grower in respect of the declared value of the insured stock at the time the mortality manifests itself. ''Functional mortality'' covers, on a *per diem* basis, the grower's ongoing expenses during a government-imposed harvest restriction.

TEMPERATURE DEPENDENT VIBRIOSIS OF THE EUROPEAN ABALONE, *HALIOTIS TUBERCULATA*. **Marie-Agnès Travers[1], Olivier Basuyaux[2], Jean-Louis Nicolas[3], Carolyn Friedman[4], Sylvain Huchette[5], Marcel Koken[1],** and **Christine Paillard[1].** [1]Institut Universitaire Européen de la Mer, Université de Bretagne Occidentale, LEMAR, Plouzané, 29280, France; [2]SMEL, ZAC de Blainville, Blainville sur mer, 50560, France; [3]IFREMER Brest, LPI, Plouzané, 29280, France; [4]School of Aquatic and Fishery Sciences, University of Washington, 355020, Seattle, WA 98195 USA; [5]France Haliotis, Plouguerneau, 29880, France.

Vibrio harveyi strains, isolated from moribund abalone, were found responsible for episodic mass mortalities of *Haliotis tuberculata* (1998–2007, France). Mortalities were recorded at the end of summer, when temperatures reached 19°C and abalone were sexualy mature. In order to facilitate management of this recently emerged disease, mechanisms of this interaction were investigated. Abalone at various reproductive stages were challenged by bacterial immersion at 19°C. Mature abalone were more susceptible (80% of mortalities within 12 days) than those which had spawned two months before (40%) or immature abalone (0%). Experimental infections conducted at different temperatures using mature abalone revealed an absence of mortality below 17°C, yet over 80% died at 18° or 19°C after 4 days. These results support field observations and emphasize the importance of temperature and host reproductive status on susceptibility to *V. harveyi*. To further understand its pathogenic potential, abalone were exposed to several strains of *V. harveyi*. Interestingly, only the strain isolated from moribund European abalone was pathogenic. Thus, recent epidemic losses of European abalone appear to be caused by the emergence of rare pathogenic *V. harveyi* in conjunction with host reproductive stress and elevated temperatures.

ASSESSMENT OF POPULATION STRUCTURE IN *CRASSOSTREA VIRGINICA* THROUGHOUT THE SPECIES RANGE USING SINGLE NUCLEOTIDE POLYMORPHISMS. **Robin L. Varney** and **Patrick M. Gaffney.** University of Delaware, College of Marine and Earth Studies, Lewes, DE, 19958 USA.

The eastern oyster, *Crassostrea virginica*, is distributed along the east coast of North America from Atlantic Canada to the Yucatan Peninsula. As larval dispersal of this species allows for considerable gene flow, the extent of subdivision of the species into genetically distinct subpopulations remains unclear. Previous work on mitochondrial and nuclear DNA markers has suggested population structure in the Gulf and Atlantic regions, but has included analysis of limited geographic coverage. Single nucleotide polymorphisms (SNPs) are widespread variations in genomic sequences that provide valuable population genetic markers. We have developed a set of 10 nuclear SNP markers to examine the genetic diversity of *C. virginica* throughout the species range and provide multiple markers for genetic linkage mapping. Oysters collected from 35 sampling locations from Canada to Mexico have been analyzed for population structure among and within geographic regions. Significant genetic differentiation among and within geographic regions was observed for each locus. Our results are consistent with the Gulf-Atlantic split previously observed with other markers; in addition, clinal patterns in allelic frequencies in Atlantic populations are suggested for some loci.

ENERGY AND NUTRIENT UTILIZATION OF JUVENILE GREEN ABALONE *HALIOTIS FULGENS* DURING STARVATION. **Maria Teresa Viana[1], Louis R. D'Abramo[2], Marco Antonio Gonzalez[1], Julieta Vanesa Garcia-Suarez[3], Armando Shimada[4],** and **Carlos Vasquez-Pelaez[5].** [1]Instituto de Investigaciones Oceanologicas, Universidad Autonoma De Baja California, 453, 22860, Ensenada, B. C. Mexico; [2]Mississippi State University, Department of Wildlife and Fisheries, Mississippi State, MS 39762 USA; [3]Facultad de Ciencias Marinas, Universidad Autonoma de Baja California, Ensenada, B.C. Mexico; [4]Laboratorio de Rimiologia y Metabolismo Nutricional, Facultad de Estudios Superiores Cuautitlan, Universidad Nacional Autonoma de Mexico, Juriquilla, Qro, Mexico; [5]Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autonoma de Mexico, Mexico, DF, Mexico.

Juvenile green abalone *Haliotis fulgens* were held within a flow-through system, fed a formulated, conditioning diet during a 15-day acclimation period, and then starved for 27 days. Crude

protein loss was 68.1% of total dry weight loss during starvation. During the first 7 days of the starvation period, plasma levels of carbohydrates dramatically decreased, (34 μm/mL to 10 μm/ml), then leveled at 15 μm/mL. Protein decreased from 3.33 to 2.6 mg per ml of plasma. Taurine was the principal free amino acid, comprising approximately 60–70%. For the essential amino acids, the gross levels of histidine, arginine, and valine decreased significantly and the proportional composition of each correspondingly decreased. For the non-essential amino acids, levels of alanine, proline, tyrosine, glutamic acid, and serine had decreased significantly by day 27 or earlier and sometimes proportional decreases correspondingly occurred. Based upon net changes in the amino acid levels of the muscle (mg amino acid/abalone), non-essential amino acids (–41.8) were utilized more than essential amino acids (–8.9) as sources of energy. The amount of energy used for basal metabolism during starvation was estimated to be 2.8 cal g org^{-1} day^{-1}.

THE EFFECTS OF BRINE, LIME AND ACETIC ACID ANTIFOULING TREATMENTS AND TRANSPORT CONDITIONS ON THE SHORT AND LONG TERM PERFORMANCES OF MUSSEL SEED (*MYTILUS* SPP.) **Andrew Vickerson[1], Cyr Couturier[2],** and **Cynthia Mckenzie[3].** [1]Memorial University of Newfoundland, Aquaculture, St. John's, Newfoundland, A1C 5R3, Canada; [2]Marine Institute of Memorial University of Newfoundland, School of Fisheries, St. John's, Newfoundland, A1C 5R3, Canada; [3]Northwest Atlantic Fisheries Centre, Department of Fisheries and Oceans, St. John's, Newfoundland, A1C 5X1, Canada.

Transferring mussel seed from collection sites to grow-out sites can subject seed to unique and multiplicative stressors (e.g. long transport times, treatments for mitigating the spread of invasive species) that could compromise their health and subsequent performance. Batches of mussel seed (30–40 mm length) were stored on ice or at ambient air temperature (4°C, 100% humidity) and subjected to the following antifouling treatments, either before (30-s seawater rinse or no rinse), or after a 24-h simulated storage/transport period: 300 ppt brine, 4% lime, or 4% acetic acid (30-s. dip). Short term health of seed was assessed via the Neutral Red Assay and attachment via byssal threads 24-hrs post treatment. Seed stored at ambient air temperature and treated with lime or brine had Neutral Red Retention (NRR) times that were significantly lower than the control (ANOVA, $p < 0.05$), indicating greater levels of stress. Seed treated with acetic acid and not rinsed had NRR times and attachment post-24-hrs that were significantly lower than the control. The findings show that the stress level of mussel seed treated with brine or lime can best be mitigated by storing seed on ice during transport and seed treated with acetic acid should be rinsed post-treatment.

TRIPLOID INDUCTION METHOD DEVELOPED FOR HATCHERY SCALE FOR NORTHERN CHILEAN SCALLOP *ARGOPECTEN PURPURATUS*. **E. von Brand[1], C. Palma-Rojas[2], G. E. Merino[3], E. Uribe[3], E. Dupré[1]** and **K. Lohrmann[1].** [1]Depto. de Biología Marina, Universidad Católica del Norte, Larrondo 1281 Coquimbo, Chile; [2]Universidad de La Serena, Depto. de Biología, Colina del Pino s/n La Serena–Chile; [3]Depto. de Acuicultura, Universidad Católica del Norte, Larrondo 1281 Coquimbo, Chile.

Chile is the third biggest scallop producer worldwide, and around 70% comes from aquaculture, mainly from Northern Chile. Searching for new products, an obvious choice is triploidy. Trials on experimental level were promising using cytochalasin—B and 6—DMAP, but hatchery scale trials using cytochalasin—B produced mass mortalities. 6-DMAP instead, showed a similar efficiency on triploid induction, but has lower toxicity level and is water soluble making it easier to apply. To increase the amount of embryos treated with 6-DMAP, following actions were taken: 1) analysis of early stages of cell divisions determining through "*timing*" the best moment to start treatment to block polar body 2; 2) evaluate the highest density of zygotes kept during treatment time without significant mortality at D larvae; 3) improve treatment condition to maintain zygotes in suspension during a given period of time. The method developed considered mass spawning, checking self fertilization percentages, if lower than 10%, spermatocytes were added in an amount of about 10:1. At the moment when zygotes showed 50% expulsion of polar body 1, treatment started using a density of 10,000 to 15,000 zygotes in the treatment tank previously saturated with oxygen. During the treatment air in small bubbles was added. After completing the treatment time, the content was poured into a larvae rearing tank with water recirculation, stopping 6-DMAP action by dilution. The development of triploid scallops was funded by FONDEF (Chile) D98I1044 and D02 I 1095.

THE NORTHWEST ATLANTIC DEEP-SEA RED CRAB (*CHACEON QUINQUEDENS*) POPULATION BEFORE AND AFTER THE ONSET OF HARVESTING. **Richard A. Wahle[1], Charlene E. Bergeron[1], Antonie Chute[2], Larry Jacobson[2],** and **Yong Chen[3].** [1]Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME 04575; [2]Northeast Fisheries Science Center, National Marine Fisheries Service, Woods Hole, MA; [3]University of Maine, School of Marine Sciences, Orono, ME.

We compare the population structure of deep-sea red crab, *Chaceon quinquedens*, in a nearly unexploited state to its condition three decades later after more than a decade of sustained harvesting. Our study is based on a camera and net trawl survey conducted in 1974 which we repeated during 2003–2005 on the southern New England shelf break. While the overall biomass of red crabs was estimated to be higher than in 1974, the abundance of large males, which are targeted by the fishery, was considerably lower. In

particular, the biomass of large males (≥114 mm carapace width), considered in 1974 to be marketable, declined by 42%. Declines were most evident at depths and regions most accessible to the southern New England-based fishing fleet. We observed no declines in the biomass of female and smaller male crabs not targeted by the fishery. Indeed, juvenile abundance appears to be considerably higher than in 1974. It is possible that adverse effects on reproduction due to reduction in numbers of large males may occur as a result of fishing, but fishery impacts and productivity are difficult to assess because key biological information is lacking.

FIELD TEST OF CULTURE METHODS TO REDUCE LOSSES OF FARMED NORTHERN QUAHOGS (*MERCENARIA MERCENARIA*) TO QPX (QUAHOG PARASITE UNKNOWN). **William C. Walton[1], Diane Murphy[2],** and **Roxanna Smolowitz[3].** [1]Cape Cod Cooperative Extension & Woods Hole Sea Grant, Barnstable, MA 02642, USA; [2]Cape Cod Cooperative Extension, P.O. Box 367, Barnstable, MA 02642, USA; [3]Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543, USA.

Shellfish farmers confronted with disease are often not in the position to let acreage lay fallow, switch crops, etc. This is the case for northern quahog (*Mercenaria mercenaria*) farmers in Barnstable Harbor, MA (USA) where QPX is prevalent. Are there other culture methods these farmers can use to reduce losses to QPX? We conducted a fully randomized 3 factor field test of culture methods/decisions anecdotally believed to be effective in reducing losses: seed from an in-state (MA) hatchery vs. an out-of-state (NJ) hatchery; removing dead and dying clams from plots or not tending; and planting at 3 different densities (25, 75 & 150 quahogs*ft^{-2}). Seed were planted in the summer of 2004 in replicate1 m^{-2} plots spaced 2 m apart at a site in Barnstable Harbor where QPX had previously been documented. Survival, growth, and QPX prevalence were monitored in fall 2004, 2005 & 2006. By 2005, losses to QPX were significant. Though percent survival decreased with increasing density, NJ-bred clams survived better than MA-bred clams at 75*ft^{-2}. QPX prevalence, though, was significantly less in MA-bred clams than NJ-bred clams, and increased significantly with increasing planting density.

'QUAHOG TRIAGE': IDENTIFYING AND RESPONDING TO AN OUTBREAK OF QPX (QUAHOG PARASITE UNKNOWN). **William C. Walton[1], Diane Murphy[2],** and **Roxanna Smolowitz[3].** [1]Cape Cod Cooperative Extension & Woods Hole Sea Grant, Barnstable, MA 02642, USA; [2]Cape Cod Cooperative Extension, P.O. Box 367, Barnstable, MA 02642, USA; [3]Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543, USA.

In November 2005, three quahog (*Mercenaria mercenaria*) farmers in Wellfleet, MA (USA) contacted local extension agents, reporting very high quahog mortalities. The animals were identified as being infected with Quahog Parasite Unknown (QPX), the first documentation of the disease in Wellfleet Harbor. Mortalities were highly correlated with runways planted with 'seed' provided by a single supplier. The disease was a cause of major concern in Wellfleet, which led the state in aquaculture production of quahogs and supported a major public fishery. Working with extension agents, a local pathologist and the Massachusetts Division of Marine Fisheries, the community held a public meeting at which the affected growers volunteered to remove the animals surviving in the infected runs in an effort to halt the spread of the disease. Over the course of the winter, other growers assisted with the removal and disposal of over 1 million quahogs. In a harbor-wide survey in the summer of 2005, QPX was observed in only very low prevalence at the original sites and not found in neighboring areas. Over the last two years, additional mortalities have not been reported. Monitoring continues but quick action by the affected growers appears to have prevented spread of the disease.

A LOW-COST TOOL TO QUANTITATIVELY ASSESS SHELLFISH HABITAT. **William C. Walton[1]** and **Diane Murphy[2].** [1]Cape Cod Cooperative Extension & Woods Hole Sea Grant, Barnstable, MA 02642, USA; [2]Cape Cod Cooperative Extension, P.O. Box 367, Barnstable, MA 02642, USA.

Site selection is believed to be key to the success of shellfish restoration, propagation and private culture. In contrast to field surveys, computer models, satellite imagery, etc., we present here an alternative low-cost quantitative method, based on field deployment of juvenile shellfish that allows direct statistical comparisons of sites. Juvenile shellfish are deployed at a known, standard size for ~60 days (typically July 1st to September 1st) in replicate fashion, allowing a comparison of relative growth and survival among sites. Though we have conducted these assessments in a wide variety of locations in Massachusetts (MA, USA) from 2003 to 2007, here we present two case studies, involving shellfish farming and tidal flow restoration. First, we compare oyster, *Crassostrea virginica*, and quahog, *Mercenaria mercenaria*, growth and survival at 4 Massachusetts aquaculture sites (Wellfleet Harbor, Pleasant Bay, Brewster Flats, and Barnstable Harbor) over a 5 year period, noting trends and differences, including significant differences between oysters and quahogs. Second, we present our results on the capacity for East Harbor/Pilgrim Lake (Truro, MA, USA) to support quahogs and oysters given the restoration of tidal flow to that water body. Other applications of this method, as well as limitations, will be addressed.

DETECTION OF NATURALLY OCCURRING HYBRIDS AMONG *CRASSOSTREA* SPECIES ALONG CHINA'S COAST. **Xiaoxue Wang[1], Haiyan Wang[1], Lumin Qian[2], Guofan Zhang[3], Xiao Liu[3],** and **Ximing Guo[1].** [1]Rutgers University, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, NJ 08349, USA; [2] Third Institute of Oceanography, State Oceanic Administration, Xiamen, China; [3] Institute of Oceanology, Chinese Academy of Sciences, Qingdao, Shandong, China.

China is home to at least five *Crassostrea* species, *C. angulata*, *C. ariakensis, C. gigas*, *C. hongkongensis*, and *C. sikamea*, all sympatric with at least one sister species. Laboratory studies have shown that hybridization among most of the five species is possible. To determine if hybridization occurs naturally, we collected and analyzed 1238 oysters from three estuaries co-inhabited by *Crassostrea* species: Weifang in the north with *C. ariakensis* and *C. gigas*, Nantong in the middle with *C. ariakensis* and *C. sikamea*, and Xiamen in the south with *C. ariakensis, C. angulata, C. hongkongensis* and *C. sikamea*. Species and hybrids were identified using diagnostic markers from several genes including the mitochondrial cytochrome oxidase I (COI) and internal transcribed spacers between the major rRNA genes. Contamination was identified with COI as having two maternal species identities, and with a microsatellite marker UcdCg-172 as showing more than two alleles. Only one hybrid is detected at Xiamen, among all 1238 oysters, and the hybrid is between *C. ariakensis* (female) and *C. sikamea* (male). The low occurrence of natural hybrids indicates that there are strict barriers to interspecifc hybridization that may have played an important role in the speciation of the five *Crassostrea* species.

VARIATION IN THE HEAT SHOCK COGNATE PROTEIN (HSC70) GENE OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA* GMELIN. **Xiaoxue Wang** and **Ximing Guo.** Rutgers University, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, NJ 08349, USA.

The heat shock cognate protein (HSC70) is a molecular chaperone with essential functions in protein maintenance. It binds to polypeptides to facilitate proper folding. It is constitutively expressed in all cells and highly conservative cross species. We obtained the full-length cDNA sequence of the HSC70 gene of the eastern oyster and resequenced it in 18 individuals from three populations (MA, NJ and AL). Sequence analysis revealed 86 single-nucleotide polymorphisms (SNPs) in the 1980 bp coding regions. Only one of the 86 SNPs is non-synonymous, suggesting that the Hsc70 gene is under strong purifying selection. The non-synonymous change is at amino acid position 644 and involves a nucleotide change of GáA, and amino acid change from Alaá Thr. Tm-shift assays were designed to genotype this and other SNPs in oysters from different populations. The "A" allele at the non-synonymous SNP was abundant (27–48%) in the Gulf of Mexico (TX and FL), but rare (0–5%) in Atlantic populations (NJ and MA). Four synonymous SNPs showed no differentiation between the Atlantic and Gulf populations. Our results suggest that the differentiation at the non-synonymous SNP is likely caused by selection. The "A" allele may have a selective advantage in the Gulf environment.

DEVELOPMENT AND CHARACTERIZATION OF 42 MICROSATELLITE LOCI FOR THE SURFCLAM, *SPISULA SOLIDISSIMA*. **Yan Wang[1], Aimin Wang[2],** and **Ximing Guo[1].** [1]Rutgers University, Haskin Shellfish Research Laboratory, Port Norris, NJ 08349, USA; [2]Hainan University, Ocean College, Haikou, Hainan 570228, China.

The surfclam, *Spisula solidissima*, is an important fishery species with a wide distribution along the Atlantic coast of North America. Studies on the population structure of the surfclam have been limited by a lack of genetic markers. In this study, we developed and characterized 42 microsatellite markers for the surfclam. A genomic library was constructed and enriched with $(CA)_{12}$, $(GA)_{12}$, $(ACA)_8$, $(AGA)_8$, $(GACA)_6$ and $(GATA)_6$ oligo-nucleotides. We sequenced 199 clones and found 128 microsatellite sequences with di- (28.1%), tri- (7.8%), tetra- (22.7%), penta- (6.3%), hexa- (1.6%), octa-nucleotide (4.7%) and compound (35.2%) repeats. Fifty-seven primer pairs were designed and characterized in 32 clams from a wild population. Amplification was successful with 42 primer pairs, all of which were polymorphic with allele numbers ranging from 2 to 14 per locus. The expected and observed heterozygosity ranged from 0.1942 to 0.9122 and from 0.125 to 0.875, respectively. Six loci showed significant ($p < 0.05$ after Bonferroni correction) deviation from Hardy–Weinberg equilibrium. Four of the six loci and five additional loci might contain null alleles as suggested by MICEO-CHECKER. Most of the microsatellite markers developed here should be useful for population genetics studies in this species.

MAPPING DISEASE-RESISTANCE GENES IN THE EASTERN OYSTER (*CRASSOSTREA VIRGINICA*). **Yongping Wang** and **Ximing Guo.** Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349, USA.

The eastern oyster, *Crassostrea virginica* Gmelin, faces two major diseases: MSX (caused by *Haplosporidium nelsoni*) and Dermo (caused by *Perkinsus marinus*). While the two diseases are highly infectious, there is considerable evidence that some oysters are genetically resistant. The identification of disease-resistance genes is important to our understanding of disease resistance and the development of disease-resistant oysters. The objective is to identify and map disease-resistance genes in the eastern oyster through family-based association studies. A backcross family was produced and deployed for field exposure to diseases. Oysters were sampled before and after a mortality episode that was primarily

caused by Dermo. The before and after mortality samples (100 each) were genotyped at 158 microsatellite and 43 single-nucleotide polymorphism loci. Linkage analysis resulted in a sex-average map that contained 150 markers in 10 linkage groups in accordance to the haploid number. The map had a total length of 837 cM with an average marker interval of 5.6 cM. Markers showing significant post-mortality shifts in genotype frequency formed clusters on the genetic map, indicative of linkage to disease-resistance genes. Eight clusters of affected markers were identified, suggesting that at least eight loci/genes are involved in Dermo-resistance in the eastern oyster.

TRIPLOID HARD CLAMS (*MERCENARIA MERCENARIA*) FOR FLORIDA AQUACULTURE: EFFECT OF TEMPERATURE ON OXYGEN UPTAKE RATES. **Kerry Weber[1], Shirley Baker[1], Debra Murie[1], John Scarpa[2],** and **Leslie Sturmer[3].** [1]University of Florida, Department of Fisheries and Aquatic Sciences, Gainesville, Florida, 32653, USA; [2]Harbor Branch Oceanographic Institution at Florida Atlantic University, Fort Pierce, Florida 34946; [3]University of Florida, Cooperative Extension Service, Cedar Key, Florida 32625.

Hard clam, *Mercenaria mercenaria*, production in Florida experiences high mortalities during summer months due to physiological stresses, such as low salinities and high water temperatures. Triploid clams may offer improved stress resistance and production over diploids. The current study characterized and compared the metabolic efficiency of diploid and triploid clams at typical water temperatures in Florida. Oxygen uptake rates were determined at 20, 25, 27, 30, and 32°C for clams of similar sizes (54.61 and 51.2 mm average shell length for diploids and triploids, respectively). Attempted acclimation to 35°C resulted in 100% mortality. Oxygen uptake rate varied significantly as a function of temperature ($P < 0.000$). Oxygen uptake rate increased with temperature from 481 μg g^{-1} hr^{-1} at 20°C to 1479 μg g^{-1} hr^{-1} at 27°C and did not change significantly above 27°C. These results suggest that 27°C is a temperature threshold, beyond which there may be an onset of partial anaerobic metabolism. Oxygen uptake rates of triploid and diploid clams were not statistically different ($P = 0.694$). Therefore, triploid clams may not offer any significant physiological advantage over diploids for Florida culturists.

BAY SCALLOP HABITAT SUITABILITY MODELS: PREDICTIONS OVER SPACE AND TIME. **Eric J. Weissberger[1]** and **Marnita M. Chintala[2].** [1]U.S. Environmental Protection Agency, Atlantic Ecology Division, Narragansett, RI 02882 USA; [2]U.S. Environmental Protection Agency, Atlantic Ecology Division, Narragansett, RI 02882.

A survey of Lagoon Pond, Martha's Vineyard, MA, USA was conducted in September 2005 to determine the combination of habitat factors most highly correlated with bay scallop (*Argopecten irradians*) abundance. A stratified random sampling design was used. Within each stratum, divers surveyed two adjacent 25 m transects for scallops, sediment type and amount of vegetative cover. Bottom temperature, dissolved oxygen, and salinity were also measured. Multiple linear regression was used to relate habitat variables to scallop abundance, with separate models being created for juvenile and adult scallops. The models were tested using data from scallop-habitat surveys conducted in Nantucket Harbor and Lagoon Pond in September 2006. The adult model predicted abundance in Lagoon Pond moderately well, but failed to predict abundance in Nantucket Harbor. The juvenile model did not predict abundance in either Lagoon Pond or Nantucket Harbor. These results suggest that adult scallops may occupy different habitats in Lagoon Pond and Nantucket Harbor, and that a factor other than habitat may be controlling the abundance of juveniles. The Nantucket scallop population is not managed as aggressively as the Lagoon Pond population, and this may also explain the poor predictive ability of the Lagoon Pond model for the Nantucket population.

SEA URCHIN EGGS AND EMBRYOS: THEN AND NOW. **Gary M. Wessel.** [1]Brown University, Department of Molecular and Cellular Biology, Providence RI 02912 USA.

Over 160 years ago, Karl Ernst von Baer and Alphonse Derbes published papers that changed biology. In 1846, von Baer sought an animal whose embryos could be observed under normal developmental conditions and found that sea urchins were an excellent option. This is the first published study of sea urchin embryos. A year later, Derbes described in exquisite detail the process of fertilization, development, and metamorphosis in sea urchins. These two studies changed future research opportunities for the myriad of investigators looking for animal models with which to study developmental events. The list of subsequent researchers of sea urchins is a Who's Who of biological scientists at the turn of the 20th century. Today this animal remains an essential representative for scientific study. This animal is essential for our understanding of gene regulatory mechanisms, of fertilization processes, and of many developmental events. With the recent sequencing of the genomes of several sea urchin species, this animal is poised to lead research in many areas of the future as well. This talk will begin by summarizing the historical context of investigations in sea urchin development, and then highlight current studies in the mechanisms of fertilization and stem cell processes in development.

SOFTSHELL CLAM CULTURE: BROODSTOCK CARE THROUGH SEED PRODUCTION. **Scott Weston, Mark Fregeau,** and **Joseph K. Buttner.** Salem State College, Northeastern Massachusetts Aquaculture Center, Salem, MA 01970 USA.

Spawning of broodstock softshell clams (*Mya arenaria*) and culture of resultant young have been pursued successfully by personnel at the Cat Cove Marine Laboratory and Northeastern Massachusetts Aquaculture Center for nearly a decade. Since 2000, nearly 14 million clams have been produced and distributed to nearly two dozen coastal communities in Massachusetts. In 2007, 3.8 million seed (>2 mm Shell Length, SL) were produced. In early

January, broodstock clams are relocated into the Laboratory and maintained on a mixture of *Tetraselmis*, *Isochrysis* and *Nannochloropsis* for approximately two months. In late February/early March, broodstock are typically spawned. Larvae are collected, transferred to conical rearing tanks and fed predominantly *Isochrysis*. As larvae metamorphose into benthic organisms they are collected and transferred to downwellers. Post-metamorphic clams are maintained in the Laboratory until ~2 mm SL. When clams reach 2 mm SL, they are transferred to a FLUPSY located in Smith Pool. By June/July significant numbers of clams reach the minimum size (10–15 mm SL) desired for stocking. Clam survival and growth in the Laboratory and FLUPSY is good, though variation among years has been observed.

NRAC AQUACULTURE PROGRAMS. **Fred Wheaton.** NRAC, 2113 Animal Science Building, University of Maryland, College Park, Maryland 20742-2317, USA.

The Northeastern Regional Aquaculture Center (NRAC) moved to the University of Maryland in 2005. The Center was reorganized after the move with a new Board of Directors, Technical Advisory Committee, and Industry Advisory Committee. The general organization of NRAC will be described, and the methodology NRAC uses to develop projects through both Requests for Applications (RFA) and Project Teams will be outlined to assist potential applicants in understanding how to apply for funding. The unique requirements for NRAC proposals will be discussed to assist potential investigators interested in applying for funding. Current research and extension projects that have been funded or are in the process of being funded will be described.

A MOLECULAR PHYLOGENY OF THE GENUS *BONAMIA* BASED ON INTERNAL TRANSCRIBED SPACER REGION SEQUENCES. **Delonna White[1], Nancy Stokes[1], Kristina Hill[1], Marina Kroeck[2], P. Mike Hine[3], Nejla Aloui-Bejaoui[4], Ryan Carnegie[1], Kimberly Reece[1],** and **Eugene Burreson[1].** [1]Virginia Institute of Marine Science, EAAH, Gloucester Pt., VA, 23062; [2]Inst. de Biolog. Mar. y Pesq., San Antonio Oeste, Argentina; [3]17450, FOURAS, France; [4]Institut National Agronomique de Tunisie, Unite de Biologie,Tunis, Tunisia.

Oyster parasites of the genus *Bonamia* have been described from Europe (*Bonamia ostreae*), Australia (*B. roughleyi*), New Zealand (*B. exitiosa*), and North America (*B. perspora*). In addition, various congeneric parasites have been observed in the following oysters on five continents: *Ostrea angasi*—NSW, Australia; *O. puelchana*—San Antonio Bay, Argentina; *O. chilensis*—Chiloe Island, Chile, *Crassostrea ariakensis*—North Carolina, USA; *O. edulis*—Spain; and *O. stentina*—Tunisia. This study used the nucleotide sequences of the internal transcribed spacer (ITS) regions and the 5.8S rRNA gene to examine the taxonomic relationships among these recently discovered, congeneric parasites. Collectively, the described *Bonamia* parasites and the congeneric *Bonamia* parasites were sequenced using haplosporidian- and *Bonamia*-specific ITS region primers. Sequences were aligned using ClustalW in MacVector and phylogenetically analyzed in PAUP. Parsimony analyses suggest that a single *Bonamia* species may occur in New Zealand, Australia, Argentina, and North Carolina, USA. The *Bonamia* sp. infecting oysters from these areas most resembles *B. exitiosa*. Results also suggest that a separate species of *Bonamia* exists in Chile.

HEMOCYTE RESPONSES IN BIVALVE MOLLUSCS EXPOSED TO HARMFUL OR TOXIC ALGAE: OVERVIEW AND PRELIMINARY SYNTHESIS. **Gary H. Wikfors[1], Hélène Hégaret[2], Eve Galimany[3], Inke Sunila[4], Philippe Soudant[2],** and **Sandra E. Shumway[5].** [1]NOAA Fisheries Service, Milford, CT 06460 USA; [2]LEMAR, IUEM, Brest, France; [3]IRTA, St. Carles de la Rápita 43540, Spain; [4]State of Connecticut, Department of Agriculture, Bureau of Aquaculture, Milford, CT 06460 USA; [5]University of Connecticut, Department of Marine Sciences, Groton, CT 06340 USA.

Among the bivalve responses to Harmful Algal Bloom species (HABs) described are those of hemocytes, the cells primarily responsible for protective, innate-immune defense, among other functions. Diverse results from studies of several bivalve species exposed experimentally to a number of HABs led to an initial characterization of these trophic interactions as "species-specific." Is it possible, though, to identify unifying themes in results obtained to date? Theoretically, two fundamental effects of toxic or noxious particles upon bivalve hemocyte immune functions can be hypothesized: activation of protective responses, or inhibition of physiological function. Examples of each can be identified. The dinoflagellate *Prorocentrum minimum* activates a protective immune response in blue mussels, *Mytilus edulis*, and Manila clams, *Ruditapes philippinarum*, wherein massive diapedesis of hemocytes into the alimentary canal hastens elimination in feces—an example of "post-ingestive selection." In contrast, *in vitro* and *in vivo* responses of oyster, *Crassostrea virginica*, and blue mussel hemocytes to the PSP-producing dinoflagellate *Alexandrium fundyense* suggest suppression of some hemocyte functions, but a general detoxification response. Activation vs. suppression of immune functions by HAB species may be a consequence of both the mechanism of HAB effect and the most-successful response of a bivalve species over evolutionary time.

REGIONAL GENETIC POPULATION STRUCTURE OF BAY SCALLOPS. **Ami E. Wilbur[1], Elizabeth Hemond[1], Theresa M. Bert[2], Seifu Seyoum[3],** and **William Arnold[2].** [1]UNCW, Department of Biology and Marine Biology, Wilmington, NC, 28409 USA; [2]Florida FWC Fish and Wildlife Research Institute, St. Petersburg, Florida 33701, USA; [3]Georgia Institute of Technology, Atlanta, Georgia 30332, USA.

Geographic variation in the bay scallop, *Argopecten irradians* has been reported for a wide range of morphological and physiological traits. This variation has led to the recognition of at least 3 extant subspecies, but genetic analysis indicates that significant differences may exist within these recognized taxa. We have evaluated the

genetic variation among populations of bay scallops from using mtDNA sequencing and the analysis of 9 microsatellite loci. Preliminary results reveal significant differentiation was not only detected among regions (New England, mid-South Atlantic, and Gulf of Mexico) but also within regions, suggesting a greater degree of population subdivision than was previously suspected. The mtDNA analysis confirms previous findings that showed substantial differentiation between Florida and North Carolina scallops, with additional differentiation among north and south Atlantic populations. Microsatellite analysis indicates that New York, North Carolina and Florida populations differ significantly and that finer scale population structure may be present within regions.

PRELIMINARY INVESTIGATIONS INTO THE OCCURRENCE OF A NOVEL PARASITE (*BONAMIA* SP.) ASSOCIATED WITH THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. Ami E. Wilbur[1], Julie D. Gauthier[2], Troy D. Alphin[3], and **Martin H. Posey[1].** [1]UNCW, Department of Biology and Marine Biology, Wilmington, NC 28409 USA; [2]Loyola University, Department of Biological Sciences, 6363 St. Charles Avenue, New Orleans, LA 70118 USA; [3]UNCW, Center for Marine Science, Wilmington, NC 28409 USA.

Recent grow-out trials involving triploid *Crassostrea ariakensis* revealed the presence of a novel oyster parasite in southeastern North Carolina. Heavy mortalities of *C. ariakensis* (<15 mm) oysters from experimental deployments in Bogue and Masonboro Sounds were attributed to a parasite belonging to the genus *Bonamia* (based on histological examination). Initial evidence from environmental screening using molecular assays suggested that the co-occurring oyster, *Ostreola equestris*, could be the natural reservoir for this parasite (CAP-*Bonamia* sp.), but more recent screening found a high proportion of small *C. virginica* from Bogue Sound also test positive. To extend our knowledge of the geographic extent and potential impact of this oyster-parasite relationship, we evaluated prevalence, intensity (quantitative real-time PCR assay) and assessed the condition (soft tissue/ shell volume) of three size classes of *C. virginica* (<30 mm, 30–50 mm, >50 mm) from three estuaries (White Oak, New Rivers, Hewletts Creek) in southeastern North Carolina. Sampling was conducted in December 2006 and in July 2007. Oysters from all three estuaries were found to be positive, although the number of positives differed both geographically and seasonally. No significant difference in condition (between qPCR positive and negative oysters) was observed.

ARE GIS TOOLS AVAILABLE ON THE WORLD-WIDE WEB ACCURATE AND USEFUL FOR ENVIRONMENTAL ASSESSMENTS: A CAPE COD AND NANTUCKET (MA) PERSPECTIVE?. Paula S. Winchell and **Pamela Neubert.** ENSR Marine and Coastal Center, Woods Hole, MA 02543, USA.

Web-based Geographic Information Systems (GIS) have become a commonly used tool among agencies, industry, and scientists to provide project planning and execution information. The Massachusetts Office of Geographic and Environmental Information (MassGIS) website http://www.mass.gov/mgis/massgis.htm allows internet users the opportunity to view data layers such as current and historic eelgrass mapping and shellfish suitability areas. ENSR Marine and Coastal Center has performed several eelgrass and shellfish assessments throughout Cape Cod and Nantucket Island and utilizes GIS web-tools for project development. We ask the question, is GIS web-data accurate and reliable when compared to ground-truth surveys? Because management decisions and permitting of projects often rely upon web-based GIS data layers, ENSR compared the expected results (obtained through the MassGIS database) to our observed field results. Results suggest that MassGIS datalayers for eelgrass and shellfish habitat on Cape Cod and Nantucket are accurate when compared to ground-truth surveys, and substantiate the importance of utilizing GIS data layers for coastal land-use and restoration project development.

ESTABLISHMENT OF *PERKINSUS MARINUS* INFECTION IN *CRASSOSTREA VIRGINICA*: INSIGHTS INTO THE PORTAL OF ENTRY AND THE POTENTIAL ROLE OF MARINE AGGREGATES. Sarah M. Winnicki[1], Wade Carden[1], Bridget Holohan[2], Gina Ralph[2], Evan Ward[2], and **Bassem Allam[1].** [1]School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY 11794, USA; [2]Department of Marine Sciences, University of Connecticut, Groton, CT 06340, USA.

Recent findings made by our group showed that the pallial organs of the Eastern oyster (*Crassostrea virginica*) are an important site of initial infection by the protistan parasite, *Perkinsus marinus*. The present study had two objectives: (1) to further characterize *P. marinus* initial infection in pallial organs, and (2) to investigate the role of marine aggregates in the infection process. The latter objective is relevant since the handling of seston by pallial organs varies based on particle size. Naive oysters were exposed to freely suspended or aggregated *P. marinus* cells. Following incubation, oysters were dissected and parasite loads were separately determined for visceral mass, gills, mantle, and the principal pseudofeces discharge area of the mantle (PDA). *P. marinus* counts were measured using quantitative Ray's fluid thioglycollate medium combined with PCR confirmation. Infection of exposed oysters was observed in both the freely suspended and the aggregate treatments, however, infection was more pronounced in the aggregate treatments. Among all biopsies, PDA displayed the highest parasite loads. These data suggest that *P. marinus* can be acquired in oysters through the pseudofeces discharge area and that parasite uptake is enhanced if presented in association with aggregates.

STATUS OF BAY SCALLOPS (*ARGOPECTEN IRRADIANS*) IN TEXAS (USA). **Kim Withers** and **Matt Hubner.** Texas A&M University-Corpus Christi, Center for Coastal Studies, Corpus Christi, TX 78412, USA.

Currently, bay scallops are not widely distributed in Texas waters and their abundance is highly variable. This is the reason that, despite appearing in commercial fisheries statistics in 1985–86, a bay scallop fishery has never been established. Archeological records indicate that bay scallops were abundant over much of the central Texas coast prior to formation of the barrier island-bay-lagoon system 4,500 years ago, when salinities were likely essentially marine and relatively stable. Today, bay scallops exhibit "boom-bust" cycles of abundance in the bay systems between Aransas Bay and upper Laguna Madre, with large population increases occurring at 10–15 year intervals since the 1950s. Abundance in lower Laguna Madre is low, but more consistent. Few scallops have ever been found on the upper Texas coast. Following a boom year in 2004, we initiated larval recruitment studies in the upper Laguna Madre in 2005–2006. No larval scallops were collected and very few adults were found during summer 2006. There is evidence that salinity is the primary driver in bay scallop population dynamics, particularly in the upper Laguna Madre.

EFFECTS OF INTERACTIONS BETWEEN STONE CRABS (MENIPPE MERCENARIA) AND BLUE CRABS (*CALLINECTES SAPIDUS*) ON THEIR PREDATION AND SIZE SELECTION OF HARD CLAMS (*MERCENARIA MERCENARIA*). **Melisa C. Wong[1]** and **Charles H. Peterson[2].** [1]Department of Fisheries and Oceans, Ecosystem Research Division, Bedford Institute of Oceanography, Dartmouth, NS, B2Y 4A2, Canada; [2]University of North Carolina - Chapel Hill, Institute of Marine Sciences, Morehead City, NC 28557 USA.

A potential northward distribution shift of stone crabs caused by warming sea water may increase interactions with blue crabs and have implications for hard clams. We examined this system to determine: (i) if multiple predators had non-independent effects on prey, (ii) predator selection of different sized prey, and (iii) underlying behavioural mechanisms. Using laboratory experiments, five predator treatments (blue crab alone, stone crab alone, blue + blue, stone + stone, blue + stone) were offered different sized clams (10–60 mm shell length) simultaneously. In tanks with conspecific predators, proportional mortality of small clams was lower than predicted values generated from single predator treatments. This non-independent effect of multiple predators on prey was not observed with interspecific pairs of predators. Because blue crabs strongly selected small clams while stone crabs consumed all sizes, weaker competition for prey between interspecific than conspecific pairs of predators occurred. Also, high encounter rates between conspecific pairs of predators led to reduced time spent foraging in these treatments. Our study suggests that large clams with a current size refuge from blue crab predation may become susceptible to stone crabs. If small clams become limiting, competition between blue crabs may increase. Claw damage may also result if blue crabs switch to readily available large clams.

GENETIC STRUCTURE OF *CRASSOSTREA ARIAKENSIS* IN ASIA AND GENETIC COMPARISONS WITH INTRODUCED STOCKS IN THE U.S. AS DETERMINED BY MICROSATELLITE POLYMORPHISMS. **Jie Xiao, Jan F. Cordes,** and **Kimberly S. Reece.** Virginia Institute of Marine Science, The College of William and Mary, Gloucester Point, VA 23062 USA.

Though hatchery stocks of *Crassostrea ariakensis* have been used for various laboratory and field trials assessing performance and comparative studies among species, the population genetic structure in its native region, and the genetic variability within and among wild and hatchery populations, has not been comprehensively examined. Genetic structure among natural populations of *C. ariakensis* in Asia was assessed, and genetic variability among wild populations was compared to that in stocks introduced into the US, using eight microsatellite markers. Genetic heterogeneity with significant global Φ_{ST}(0.0183) was observed among the natural populations. Genetic structure was characterized by a significant linear correlation between Cavalli-Sforza & Edwards's genetic distance and geographic distances. No obvious geographic barrier was discovered along this region and no significant temporary environmental variation is known to have potentially impacted this structure. A slight decline of allelic diversity from south to north was observed and several possible reasons will be discussed. All five hatchery populations show reduction in genetic variability with only allelic diversity reduction in young stocks, while declines in both allelic diversity and heterozygosity was observed in older hatchery stocks indicating the potential for serious bottlenecks occur over several generations with US hatchery stocks of *C. ariakensis*.

CV-LYSOZYME 3, FURTHER EVIDENCE OF ADAPTIVE EVOLUTION OF I-TYPE LYSOZYMES FOR NUTRITION IN THE EASTERN OYSTER. **Qinggang Xue[1], Naoki Itoh[2], Kevin Schey[3], Yanli Li[1], Richard Cooper[1],** and **Jerome La Peyre[1].** [1]Department of Veterinary Science, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, USA; [2]Department of Veterinary Science, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, U.S.A.; Aquacultural Biology Laboratory, Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi 981-8555, Japan; [3]Department of Cell and Molecular Pharmacology, Medical University of South Carolina, Charleston, SC 29425, USA.

The major biological role ascribed to lysozymes is host defense. Adaptive evolution of c-type lysozymes for nutrition in certain animals is however well accepted. Recently, we proposed that a

similar adaptive evolution of i-type lysozymes for nutrition occurred in the eastern oyster based on differences between two lysozymes (i.e., cv-lysozyme-1 and 2) molecular, enzymatic and antibacterial characteristics. Cv-lysozyme-1, a 17,861.0 Da protein, was originally purified from plasma and cv-lysozyme-2, a 12,984.6 Da protein was purified from digestive glands. A third lysozyme, cv-lysozyme-3, has now been purified from oyster shell liquor. Mass spectrometry determination of molecular mass and amino acid sequence indicated the protein is made up of 168 amino acids and has a molecular mass of 17,782.3 Da. Cv-lysozyme-3 cDNA cloning and sequencing revealed a 564 bp open reading frame encoding a 187-residue polypeptide which included a 18-residue signal peptide. The expected C-terminal amino acid lysine was absent in the purified protein. While cv-lysozyme-3 molecular mass and site of gene expression were comparable to cv-lysozyme-1, its lower isoelectric point, protease cutting sites, antibacterial activity and optimal ionic strength for muramidase activity resembled cv-lysozyme-2s'. Cv-lysozyme-3 may therefore represent an intermediate form in the adaptive evolution of oyster lysozyme for nutrition.

EFFECTS OF BLOCKING AGENTS ON MANGANESE AND CADMIUM ACCUMULATIONS IN GILL OF THE EASTERN OYSTER, *CRASSOSTREA VIRGINICA*. **Mona Yates, Yamel Perdomo, Margaret A. Carroll,** and **Edward J. Catapane.** Medgar Evers College, Biology, Brooklyn, NY, 11225, USA.

Manganese is needed in small amounts for physiological functions. High amounts are toxic, causing Manganism. Metal workers are targets for Manganism. Cadmium has no known functions in humans but damages organs, including bone, kidney, liver and lung. Routes of exposure include cigarette smoke and ingestion of contaminated food. Cadmium pollution is widespread in aquatic environments. Marine animals accumulate it. P-aminosalicylic acid (PAS) is being used to alleviate Manganism, but its mechanism is unknown. *Crassostrea virginica* possesses a dopaminergic innervation of gill. Our previous work showed manganese disrupts this innervation. We studied effects of PAS and EDTA on manganese and cadmium accumulations in gill using Atomic Absorption spectrometry. Gills were exposed to 0.5 mM manganese or cadmium for 10 hours, then treated with PAS or EDTA for three days. PAS treated gill, but not EDTA treated, had lower accumulations of manganese compared to controls. PAS did not reduce cadmium accumulations. High concentrations of EDTA reduced cadmium accumulations. This study shows the mechanism of PAS for alleviating symptoms of Manganism may be partly due to reducing tissue manganese. Cadmium accumulations cause toxic effects in animals and it is valuable to find effective agents that remove cadmium from tissues and blood.

A NEW SERINE PROTEASE INHIBITOR IN THE EASTERN OYSTER REVEALS THE EXISTENCE OF A NOVEL FAMILY OF PROTEASE INHIBITOR WITH MULTIPLE MEMBERS IN BIVALVE MOLLUSCS. **Qing-gang Xue[1], Naoki Itoh[2], Kevin Schey[3], Yanli Li[1], Richard Cooper[1],** and **Jerome La Peyre[1].** [1]Department of Veterinary Science, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, USA; [2]Department of Veterinary Science, Louisiana State University Agricultural Center, Baton Rouge, LA 70803, U.S.A.; Aquacultural Biology Laboratory, Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi 981-8555, Japan; [3]Department of Cell and Molecular Pharmacology, Medical University of South Carolina, Charleston, SC 29425, USA.

Protease inhibitors (PI) are ubiquitous in organisms and regulate proteases involved in numerous physiological processes. While there is abunbant information on PI and their target enzymes in vertebrates little is known about PI and their functions in bivalves. The first PI to be purified and characterized from a bivalve was cvSI-1. CvSI-1 strongly inhibited the serine proteases subtilisin and perkinsin in a slow-tight binding mode and had no homology to any known proteins. A second PI, named cvSI-2, has now been purified from plasma and inhibited serine proteases in a similar kinetic mode as cvSI-1. CvSI-2 cloned cDNA encoded a 85-residue polypeptide leading to a mature polypeptide of 67 amino acids with a molecular mass of 7,203.0 Da. cvSI-2 sequence showed 38% identity and 54% similarity with cvSI-1. BLAST search in GenBank databases revealed the presence of multiple ESTs encoding nine polypeptides in eastern oysters and several polypeptides in Pacific oysters, Mediterranean mussels, and Zebra mussels that were similar in sequence to cvSI-1 and cvSI-2. While cvSI-1 inhibit the growth of the protozoan parasite *Perkinsus marinus*, the antimicrobial activities of cvSI-2 and other potential host defense effector polypeptides of this newly discovered PI family remain to be determined.

USING A TOWED OPTICAL HABITAT MAPPING SYSTEM TO MONITOR THE INVASIVE TUNICATE SPECIES *DIDEMNUM* SP. ALONG GEORGES BANK. **Amber York[1], Scott Gallager[1], Richard Taylor[2], Norman Vine[2],** and **Steve Lerner[1].** [1]Woods Hole Oceanographic Institution, Woods Hole, MA 02543 USA [2]Advanced Habitat Imaging Consortium.

The invasive tunicate *Didemnum* sp. is a colonial ascidian mats of which have been found to overgrow gravel, pebble, cobble, and boulder substrates as well as sessile organisms including mussels, sponges, bryozoa, hydrozoa, and other ascidians. *Didemnum* growth has been found on dead *Placopecten magellanicus* (sea scallop) shells. While the impacts of *Didemnum* growth on Georges Bank are currently unclear, efforts are underway to document its spread, predators, effects on biodiversity, possible shellfish mortality, and responses to repeated substrate disturbance. Optical image surveys conducted with HabCam (habitat camera mapping system) average

about 100 nautical miles a day of continuous bottom imagery and have to date revealed three areas of *Didemnum* growth on Georges Bank: the Northern Edge, Nantucket Shoals and Eastern Great South Channel, the latter two being previously unknown before this study. The population along the Northern Edge spans from outside to inside of an area closed to groundfish and scallop fishing thereby providing a site to study the differences in *Didemnum* growth under disturbed and undisturbed conditions. The association between percent cover of *Didemnum*, bottom substrate type, and oceanographic features, including benthic shear stress will assist modeling efforts to predict areas at risk to *Didemnum* spread.

PROGRESS TOWARDS UNDERSTANDING THE OVER-WINTER MORTALITY OF JUVENILE *MERCENARIA MERCENARIA*. Chester B. Zarnoch. Baruch College, City University of New York, Department of Natural Science, New York, NY 10010, US.

Northern quahog (= hard clam), *Mercenaria mercenaria*, aquaculturists in the northeast US and Canada often experience significant mortalities (>50%) in their juvenile crops during the winter period. This mortality has been referred to as "winter-kill" but few efforts have been made to determine underlying physiological and ecological mechanisms. In order to better understand winter mortality, field experiments have been conducted in New York since 2001. Results indicate that there is significant year-to-year variation in the magnitude of the mortality. The severity of the winter as well as the amount of food that is available to the clams as they become active during early spring influences the mortality. A mild winter, such as 2001–2002, resulted in survival >98%. In 2002–2003 (a severe winter) mortalities as high as 1% day^{-1} was observed during early spring. Mortality occurred as water temperature increased from 5°C to 12°C and when food levels were low (Chl-a < 3.0 $\mu g\, l^{-1}$). Carbohydrate reserves decreased ~50% during this period suggesting the use of reserves to support increased metabolic activity. Conversely, during the severe winter of 2004–2005 food levels were high in the early spring and mortality was low. Current research efforts are focused on mitigating "winter-spring" mortality.

MAPPING QUANTITATIVE TRAIT LOCI CONFERRING DERMO RESISTANCE IN THE EASTERN OYSTER *CRASSOSTREA VIRGINICA*. Liusuo Zhang, Ximing Guo, David Bushek, and **Susan E. Ford.** Rutgers university, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, 6959 Miller Avenue, Port Norris, NJ 08349, USA.

Dermo, caused by the parasite *Perkinsus marinus*, is a serious disease of the eastern oyster. The identification and mapping of Dermo-resistance genes are important to our understanding of this disease and possible genetic improvement of oysters through marker-assisted selection. The objective of this study is to map quantitative trait loci (QTLs) related to Dermo resistance through laboratory-based challenges and composite interval mapping. Three hundred oysters from a F2 family were challenged with *P. marinus* in the laboratory, and resistance was measured by infection intensity, days survived after the challenge and a resistance-index incorporating both. Ninety-four individuals with varying infection intensity and days survived were genotyped at 80 microsatellite and 38 single-nucleotide polymorphism markers. Linkage analysis produced a genetic map with 100 markers, a total length of 526 cM and an average marker interval of 5.9 cM. Composite interval mapping identified five putative Dermo-resistance QTLs on four chromosomes, with two being supported by more than one measurement. Significant differences in genotype frequency between the deceased and survived oysters were observed at 28 loci, and seven were mapped to or near the QTLs. Three of the QTLs identified in this study are supported by data from other families.

A DUAL FRAME ESTIMATOR OF BLUE CRAB HARVEST. Randal S. ZuWallack and **Kristian S. Omland.** Macro International Inc., 126 College Street, Burlington, Vermont 05401.

Since 2005, the New Jersey Department of Environmental Protection and Macro International conducted surveys in New Jersey with recreational crabbers to estimate the blue crab harvest and catch. The estimation model combines the estimated number of trips as collected in telephone interviews with biological data and trip harvest collected during on-site intercept interviews. The estimated number of trips and the average trip harvest are combined to estimate the total blue crab harvest. This dual-frame, dual-mode estimation is modeled after the Marine Recreational Fisheries Statistics Survey program. In the 2006 Review of Recreational Fisheries Survey Methods, the National Research Council criticized several assumptions to this model, some of which apply to the recreational crabbing application. For instance, despite interviewing at the conclusion of the crabbing trip, interviewers must rely on crabbers to accurately report the amount of unseen harvest. In this presentation, we discuss the estimation procedures for measuring recreational blue crab harvest and discuss some criticisms of the model with a focus on their relevance to the blue crab application.