

Woods Hole Sea Grant: 2002-2004 Projects

Developmental Effects of Contaminants on Salinity Preference and Seawater Survival for Atlantic Salmon: Integrating Physiology and Behavior

Stephen D. McCormick, Darren T. Lerner, and Emily Monosson, University of Massachusetts, Amherst

Over the last 20 years populations of Atlantic salmon (*Salmo salar*) in northern New England have decreased ten-fold, resulting in their recent listing as an endangered species in Maine. Although the reason for the decline is unknown, contaminants are a leading candidate. The parr–smolt transformation is a critical and highly sensitive life history stage of Atlantic salmon that coincides with downstream migration and seawater entry. Nonylphenol (NP) and PCBs are common contaminants found in the effluent from sewage treatment plants, industrial sites, and storage facilities. In addition to possible impacts on wild Atlantic salmon, contaminants are also an important issue for the salmon aquaculture industry. This project will investigate the possible effects of low-level contamination, particularly the effects of known endocrine disruptors on key developmental stages in salmon, such as the parr–smolt transformation. Specifically, investigators will determine the capacity of contaminants to act as endocrine disruptors of the parr–smolt transformation by adversely affecting salinity preference and tolerance of smolts following exposure at different developmental stages; determine how contaminant exposure affects smolt capacity to cope with stressful events (swimming fatigue, dam passage, capture or handling); and investigate the mechanisms by which contaminant exposure affects seawater survival. The results of this study should be broadly applicable to other aquatic vertebrates and may indicate a need for improvement and modification to sewage treatment plants, commercial waste protocols, pesticide applications, and remediation efforts. (R/B-165)

Larval Spread and Population Mixing Between Onshore and Offshore Lobster Populations

Stephen R. Palumbi, Stanford University and C. Sarah Cohen and Colleen M. Cavanaugh, Harvard University

The American lobster (*Homarus americanus*) produces more fisheries income than any other species in the Mid-Atlantic and New England states. In recent years, record landings have been reported. Overall, 80 percent of the landings are caught inshore, within three miles of the coast. As fishing effort has increased, an offshore fishery has developed in both nearshore federal waters and in distant deepwater areas. The fishery is considered 'growth overfished,' meaning that a high percentage of lobsters are taken just after reaching minimum legal size, leaving few animals to reproduce. So how can the fishery sustain record landings year after year? One possibility, say lobster researchers, is the presence of 'refuge populations' in deeper offshore waters that may produce eggs and larvae that replenish inshore populations. If such populations exist, it remains unclear how significantly local populations of lobsters are replenished by the import of larvae. To better understand lobster larval population mixing and adult migration, investigators will conduct a series of genetic analyses for different life-history stages of lobsters south of Cape Cod, Massachusetts, in both inshore and offshore populations. Working with lobster fishers and managers, the researchers will collect lobster larvae across inshore areas starting in New Bedford, Massachusetts. New Bedford Harbor, closed to lobster fishing since 1979 due to contaminated sediments associated with the EPA Superfund site, is a known lobster marine reserve. The large and reproductive source populations there produce 'larval clouds' from which larvae can be genetically marked and their dispersion mapped. Findings may help determine the usefulness of lobster reserves as a management tool. Researchers will investigate whether stage I larvae are well mixed in inshore areas or if there is genetic patchiness. Evidence of patchiness would indicate that local management of the population may be called for. The same question will be investigated for stage IV larvae. At this stage, genetic patchiness would indicate that the larval supply is not constant on a regional scale and that lobster recruits do not come from a single larval pool as assumed in most fisheries models. Lastly, investigators will determine whether adult lobsters sampled from inshore versus offshore areas differ in gene frequencies. While sample size limitations preclude a definitive answer to this question, genetic differences, if apparent, could be used to predict the degree of onshore–offshore larval mixing by using maximum likelihood mixed-stock techniques. (R/O-34)

Tidal Exchange Among Soft-shell Clam Populations Using Natural Tags

Lauren S. Mullineaux and Simon R. Thorrold, Woods Hole Oceanographic Institution

Though most adult coastal benthic invertebrates, such as clams, are sedentary, they are mobile during a planktonic larval phase. Adult clams harvested in one area may not have originated in that area. Researchers, shellfishers and fishery managers could benefit from knowledge of the source of the larvae, how they disperse from one habitat to another, and how this dispersal affects regional recruitment. Most models of population dynamics assume that recruitment into the population is related directly to the reproductive capacity of the local population. In species with dispersive larvae, this can lead to substantial errors in modeling population growth and stability over generations. A more useful approach—using site-specific geochemical signatures (natural tags)—has proven effective in other migratory species, including birds, fish, butterflies, and some marine invertebrates. This project builds on a Sea Grant laboratory-based study (Mullineaux and Hart, R/O-32) and will adapt techniques developed for fish otoliths and apply them to study the larval dispersal of soft-shell clam (*Mya arenaria*) populations in the coastal regions of Massachusetts. Soft-shell clams are locally common, economically important, cover a wide geographic range, and tolerate a broad range of environmental conditions. Investigators will conduct field studies to: characterize geographic variation in the geochemistry of *Mya arenaria* shell material (shells will be measured from six locations to determine the unique combination of elemental composition and environmental conditions of each habitat); characterize interannual variation in the geochemistry of the shell material (elemental composition of post-larval shell material in newly-recruited individuals will be measured in two separate years at each site to determine if temporal variation in shell elemental composition is significant); and measure the geochemistry of the initial larval shell in newly recruited individuals for comparison to location-specific elemental signatures (to distinguish between recruits from local sources versus remote sources). (R/O-35)

Resolving Population Structure with Molecular Genetics to Enhance Management of the Highly Exploited Squid Fishery

Roger T. Hanlon and Kendra M. Buresch, Marine Biological Laboratory, and Jon K.T. Brodziak and Steve Cadrin, National Marine Fisheries Service Northeast Fisheries Science Center

The long-finned squid, *Loligo pealeii*, is a commercially valuable and heavily exploited resource in the northeast U.S. Boats fish squids in

inshore summer grounds along Cape Cod, Long Island, and Rhode Island, and, increasingly, in offshore winter grounds. According to the National Marine Fisheries Service (NMFS), current Loligo catch levels have exceeded maximum sustainable yield. Investigators in this project will build upon previous Sea Grant-supported work on the Loligo mating system and preliminary work on genetic diversity to determine if the population structure is a single genetic stock or if Loligo represents more than one distinct population throughout its fished range (Nova Scotia to North Carolina). These data will be useful in assessing the current stock management plan, which assumes a single unit stock for the entire fishery. Employing molecular genetic techniques—DNA fingerprinting using microsatellites as genetic markers—a research team of fisheries biologists, fishermen, and molecular biologists will determine the Loligo stock structure within the fished population along the Atlantic coast. Researchers will compare samples from nine inshore spawning sites to determine geographic population structure along the Atlantic coast. They will also compare population samples from three offshore locations to determine if genetic differentiation exists among the offshore sites. Finally, they will compare inshore population samples with offshore population samples to determine if inshore and offshore squid represent more than one single unit stock. If the genetic data indicate evidence of multiple populations, then the current squid exploitation model must be altered to ensure genetic variation within Loligo populations. If the evidence does not show multiple stocks, then impacts of the growing offshore fishery should be addressed. (R/B-166)

The following project is part of a National Strategic Investments (NSI) competition in Marine Environmental Biotechnology, funded through the National Sea Grant College Program.

Estrogen- and Aryl hydrocarbon-receptor Mediated Reproductive Effects and Adaptations in the Marine Environment

Gloria V. Callard, Boston University

By comparing killifish (*Fundulus heteroclitus*) populations from polluted New Bedford Harbor (NBH), Massachusetts with a nearby, unpolluted estuarine environment (Scorton Creek (SC) in Sandwich, Massachusetts), this study seeks to understand the ongoing, long-term effects of pollutants on reproduction and development in marine fish. Using sensitive, tissue-specific, mechanism-based markers of endocrine disrupting chemical action and effect, together with standard methods of reproductive endocrinology, this study will extend the researcher's findings in laboratory fish (zebrafish, goldfish) to wild fish populations. Killifish are non-migratory, estuarine fish that are considered to be reliable indicators of environmental quality. The NBH killifish population is an extremely valuable resource for understanding long-term, multi-generational effects of pollutants on a wild fish population in a natural environment. The history of pollution in NBH indicates that the killifish population there has survived exposure to high levels of PCBs, metals, and other contaminants for over 50 years, or 15–20 generations: unequivocal evidence that they survive, reproduce, develop—even thrive—in that environment. For all that is known about the NBH killifish population, relatively little is known about endocrine disruption and reproductive adaptation in killifish at NBH or at other polluted sites. This study will attempt to gather direct scientific evidence for a mechanism-based cause-and-effect relationship between pollutants and endocrine disruption in nature, and to begin to understand how a population might adapt and evolve mechanisms for sustaining reproduction under conditions of human induced adversity. Using a molecular endocrinological approach, this study seeks to increase the degree of certainty in formulating sound regulatory and policy decisions relating to endocrine disruption in a natural marine environment and can serve as a model for additional studies of aquatic and terrestrial species. (R/P-68)

The following project is part of a National Strategic Investments (NSI) competition in Aquatic Nuisance Species, funded through the National Sea Grant College Program.

Aquatic Nuisance Species: Assessments of Economic Impacts and Evaluations of Rational Management Alternatives

Porter Hoagland III, Hauke L. Kite-Powell, and Di Jin, Woods Hole Oceanographic Institution

Although thousands of non-native aquatic nuisance species (ANS) are known to exist in U.S. aquatic systems, the U.S. Congress has estimated the economic “disruption” to communities from the introduction and spread of just one—the zebra mussel, *Dreissena polymorpha*—at \$5 billion. To date, only a few analysts have attempted to publish estimates of the economic impacts of ANS introductions into freshwater and marine ecosystems and these estimates may differ by as much as two orders of magnitude. As such, it has been difficult for policymakers, natural resource managers, industry officials, scientists, and the public to make well-reasoned decisions about how to mitigate ANS introductions. This project seeks to develop an economic framework for making rational decisions about the introduction and spread of non-indigenous ANS on regional and national scales in the U.S. Investigators will focus their assessments of the economic impacts of such introductions on sport, commercial, and tribal fisheries; the recreation and tourism industries; the shipping and navigation industries; and municipal and industrial water uses. Investigators will develop estimates of output and employment impacts and changes in value-added, measured in both dollars and jobs. These estimates can be used to improve our understanding of the scale and distribution of economic effects across a wide range of activities in the economy. Investigators will document methods for data collection and analysis, model building, data table updating, and relevant documentation for the future application of the model for assessing policy responses to ANS events. (R/M-48)

The following project is part of the Sea Grant Industry Fellowship Program, funded through the National Sea Grant College Program.

A Scanning Electron Microscopy Study of Epidemic Shell Disease of the American Lobster, *Homarus americanus*

Roxanna Smolowitz, Marine Biological Laboratory, and Andrea Hsu, Boston University Marine Program

In recent years, shell disease in lobsters (*Homarus americanus*) has been found in high levels from eastern Long Island Sound to Buzzards Bay, Massachusetts, and most recently in Cape Cod Bay, Massachusetts. As the region's most lucrative fishery, the health of

the lobster population is of great concern. While it is widely believed that shell disease etiology is bacterial, no studies thus far have presented results. Preliminary scanning electron microscopy (SEM) imaging of diseased lobsters from Vineyard Sound, Massachusetts, presented viable proof that shell disease etiology is bacterial, with specific bacterial mechanisms involved to initiate lesion formation. This study pairs a pathologist and aquatic veterinarian with a graduate student to use SEM to examine lesions of epizootic and impoundment lobsters from sites along the New England coast to verify preliminary findings and examine the migration and transmission qualities of the causative shell disease bacteria. To do this, normal lobster and lobsters with impoundment or epizootic shell disease will be acquired with the help of industrial partners and taken to the laboratory for analyses. While previous studies of lobster shell disease have focused primarily on impounded lobsters, this project will focus on epidemic shell disease in wild lobsters to understand the causes and implications and to learn more about the biology of the animal and the economics of the fishery. (R/B-167)

Last updated: June 24, 2014

Copyright ©2007 Woods Hole Oceanographic Institution, All Rights Reserved.

Mail: Woods Hole Oceanographic Institution, 266 Woods Hole Road, Woods Hole, MA 02543, USA.

E-Contact: info@whoi.edu; press relations: media@whoi.edu, tel. (508) 457-2000

Problems or questions about the site, please contact webdev@whoi.edu