Results of a Study of Bivalve Larval Abundance in Greenwich Bay, Rhode Island, 1993

Michael A. Rice and Joseph Goncalo
Department of Fisheries, Animal, and Veterinary Science
University of Rhode Island
Kingston, RI 02881

Abstract Greenwich Bay, in Narragansett Bay, Rhode Island, is known to be an area that has supported recreational and commercial fisheries of the northern quahog, Mercenaria mercenaria. Sustained annual catches of approximately 1 million pounds of mostly smaller-sized "littlenecks" in the bay suggest annual recruitment, but few studies of early life history stages have been undertaken in this area since 1952. Weekly water samples (100 L each) were taken on an incoming tide from 0.3 and 1.6-m depths at seven locations in Greenwich Bay. Samples were taken using a 30 L/minute, 12-volt electric bilge pump, and water was passed through a 60-µm mesh plankton net. Larvae were fixed in the field with 10 percent buffered formalin in filtered seawater and transferred to a 25 percent ethanol/seawater mixture for storage. Larvae in 1.0 mL subsamples of the preserved samples were identified and counted. Larvae from several vertebrate and invertebrate taxa were identified. Identifiable bivalve larvae were distinguished as to developmental stage: D-hinge veliger, umbonate veliger, and pediveliger. Maximum bivalve abundance occurred June 14 at all sites, with a bay-wide average of 7,800 larvae/100L. A secondary peak of abundance occurred August 3, with 580 larvae/100L. The D-hinge veligers were much greater in number than umbonate veligers, which in turn were greater in number than pediveligers. This suggests predation loss or export of the developing larval stages. Larvae were not uniformly distributed throughout Greenwich Bay. Maximum bivalve larval abundances were found in the open bay sites, rather than in coves and inlets. This is a surprising result, because presumed "spawner stocks" reside in the coves. Further studies are needed to identify the most probable sources of larvae leading to quahog recruitment in Greenwich Bay.

Introduction

Greenwich Bay is known to be one of the most productive areas for the quahog (Mercenaria mercenaria) fishery. A number of studies have focused on adult quahog populations in the bay (Stringer, 1955; Stickney and Stringer, 1957; and Rice et al., 1989), and have shown that the natural adult population densities are among the highest reported. According to Rhode Island Department of Environmental Management figures, annual harvests are approximately 450 metric tons (1 million pounds) from the 1,300-hectare (ha) (3,200-acre) bay (Lazar et al., this volume). These sustained harvests of mostly 48-millimeter (mm) to 55-mm valve-length "littlenecks" from the bay suggest that there is annual recruitment into the actively fished areas.

Although there is a considerable amount of information available about populations of adult quahogs in Greenwich Bay, few studies have focused on the early life history stages. Landers (1954) studied the abundance of bivalve larvae in Greenwich Bay between 1950 and 1952. He reported that maximum bivalve larval abundance—assumed to be quahogs—was during the month of June, when water temperatures exceeded 20°C. The sampling protocol of Landers (1954) did not allow for a description of the spatial distribution of the larvae in the bay.

The highest quahog population densities in Greenwich Bay are near the mouth of Greenwich Cove, and at the Mary's Creek area near the mouth of Apponaug Cove (Stickney and Stringer, 1957; Lazar et al., this volume). These dense populations are in areas closed to fishing, and consist mainly of large adults. These large adult quahogs are poten-
tially quite fecund (Peterson, 1986), and are assumed to be the parental stocks for Greenwich Bay quahog recruitment (Ganz, 1991). The aim of this study is to describe the spatial and temporal patterns of bivalve larvae in Greenwich Bay, with special attention to areas where adult quahogs are abundant.

Materials and Methods

Zooplankton samples were collected from seven stations in Greenwich Bay on a weekly basis from June 7 to August 3, 1993 (Figure 1). Water sampling and temperature measurements were carried out on an incoming tide, one to two hours prior to high tide. Water samples (100 liter (L)/sample) were collected at 0.3-meter (m) and 1.6-m depths using a 12-volt battery-powered bilge pump with a nominal rating of 500 gallons/hour (approximately 30 L/minute). Water samples were filtered using a 60-micron (µm) mesh plankton net. Materials retained by the net were fixed in the field using 10 percent buffered formalin in seawater. Samples were then transferred to a 25 percent ethanol/seawater mixture for storage prior to examination. Duplicate 1.0-milliliter (mL) subsamples of the preserved plankton were observed and counted using a stereoscopic microscope and a Sedgewick-Rafter counting chamber, and the data presented are the mean of the duplicate counts. The holoplankton and meroplankton in each of the samples were classified to the lowest identifiable taxon, using available references (e.g., Gosner, 1971; Conn, 1991). Rapid identification of bivalve larvae in subsamples was aided by the use of cross-polarizing light filters on a stereoscopic microscope. The developmental stages of bivalve molluscan larvae were
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<tr>
<th>Date</th>
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<th>14</th>
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<th>74</th>
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<td>22.3 ± 1.6</td>
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<td>24.4 ± 0.8</td>
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<td>26.0</td>
<td>25.0</td>
<td>24.0</td>
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<td>25.3 ± 0.9</td>
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Table 1. Average temperatures (C) by site and sample date in 1993.

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Table 1. Average temperatures (C) by site and sample date in 1993.

Counts and classified as to developmental stage: D-hinge veliger, umbonate veliger, and pediveliger (Loosanoff et al., 1966; Chanley and Andrews, 1971).

**Results**

Temperature and salinity measurements were taken at the sample-collection sites and depths on all sample-collection days. Table 1 shows the average temperature measurements at all sites. On any given day, temperatures did not vary from site to site by more than 2°C.

Planktonic adults and larvae from several phyla of marine invertebrate taxa were found in the plankton net samples from all areas sampled in Greenwich Bay. Table 2 shows some of the groups of organisms found in the net samples.

Particular attention was paid to quantifying the various larval stages that are particular to bivalve mollusks, namely the D-hinge veligers, the umbonate veligers, and the pediveligers. Figures 2a and 2b show D-hinge and fully developed umbonate larvae, respectively. Pediveligers were relatively large in size, usually greater than 270 μm in length, and have a prominent "foot." Total bivalve abundance was highest during the June 14 sampling day (Figure 3). These samples yielded a total of 119,000 larvae in 14 samples (seven sites and two samples per site). This works out to an average larval density of 8,500 larvae/sample, or 85 larvae/L. A secondary peak of bivalve larval abundance was noted during the end of the sampling period on August 3.

The distribution of bivalve larvae was not uniform by depth or by developmental stage. Figures 4 and 5 show the average number of larvae per sample at 0.3-m and 1.6-m collection depths. On all days sampled, the average number of D-hinge larvae greatly outnumbered the umbonate veligers, which in turn outnumbered the pediveligers. Peak abundance of umbonate veligers occurred on June 28, two weeks after the peak in D-hinge veligers. A first peak in pediveliger abundance occurred on June 28, but this was a relatively small number of larvae, amounting to about 15 larvae/100-L sample in the samples collected at 0.3 m, and 32 larvae per sample in those collected at 1.6 m. A greater peak in umbonate veliger and pediveliger abundance occurred on August 3. Abundances of pediveligers appear to be higher in samples from the greater depth.

The distribution of bivalve larvae was not uniform by sample location in Greenwich Bay. Figure 6 shows a running cumulative total of bivalve larvae at each site. On the initial sampling date, June 7, all sites were almost completely free of
that peak bivalve abundances were highest in mid-June of 1951 and 1952 in Greenwich Bay.

The high average number of D-hinge larvae in Greenwich Bay can be used to estimate total larvae. The area of Greenwich Bay is 1,299 ha (data courtesy of Peter August, Rhode Island Geographical Information System, University of Rhode Island), and the average depth is 4.0 m (NOAA Bathymetry Chart Number 13221) for a total volume of $5.2 \times 10^4$ m$^3$. Based on this, there would have been about $4.4 \times 10^{13}$ bivalve larvae in Greenwich Bay on June 16. This considerable number of larvae leads us to conclude that the unavailability of larvae or lack of spawning stock are most likely not the limiting factors in quahog recruitment into Greenwich Bay.

The difference between numbers of D-hinge larvae and the further-developed larval forms can give an indication of the degree of larval mortality in Greenwich Bay. The average number of umbonate and pediveliger larvae in the water column on Julian date 179 (June 28) would be about 4.3 larvae/L (Figures 4 and 5). If we were to assume that umbonate veligers and pediveligers present on June 28 represented the same cohort that were D-hinge larvae on June 14, then there would have been a 95.0 percent natural mortality loss to the larvae. This finding is not out of line with previous studies. Carriker (1961) found that only about 2 percent of M. mercenaria larvae settle and metamorphose to become juvenile clams in Little Egg Harbor, New Jersey.

The larvae of M. mercenaria, like most bivalves, must spend time in the water column to develop. Typically, bivalve larvae exhibit positively phototoxic (light-seeking) behavior as D-hinge larvae and umbonate veligers, and switch to negatively phototoxic (dark-seeking) behavior once they become pediveligers and are capable of settlement and metamorphosis (Pechenik, 1985, 1990). This behavioral phenomenon may explain the relatively higher numbers of pediveligers found in the 1.6-m samples in comparison to the 0.3-m samples (Figures 4 and 5).

The distribution of bivalve larvae was not uniform throughout the seven sample stations (Figure 6), with most larvae present in the open bay, rather than in the coves. This is a surprising result, in that three studies have indicated that major assemblages of adult

<table>
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<td>Brachistaria larvae (class Asteroidea)</td>
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<td>barnacles</td>
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<td>bivalves</td>
</tr>
<tr>
<td>Gastropod veliger larvae</td>
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<tr>
<td>(various species)</td>
<td>crabs</td>
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<tr>
<td>Megalopa larvae (class Decapoda)</td>
<td>crabs</td>
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<td>Nauplius larvae (class Copepoda)</td>
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<td>Trochophora larvae (phyla Annelida and Mollusca)</td>
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<td>Umbonate veliger larvae (class Bivalvia)</td>
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<tr>
<td>Zoae larvae (order Decapoda)</td>
<td>crabs</td>
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Table 2. Listing of groups of zooplankton present in at least one sample from the sites throughout the study period.

bivalve larvae. A week later, the peak abundance of larvae occurred, but the larvae were confined to samples from sites 132, 116, 75, and 52. These four sites were in the open area of Greenwich Bay, but the three sites in, or near, coves were relatively free of bivalve larvae. As the summer progressed, there was a trend of increasing larval abundance in the coves, but they never reached the abundances of larvae seen in the open bay.

Discussion

Peak abundances of D-hinge veliger larvae were on June 16, as water temperature reached about 20°C (Table 1, Figures 3 and 4). This result correlates closely with results from earlier studies that suggest that M. mercenaria commence spawning as water temperature reaches 20°C (Loosanoff, 1937). Our results also match those of Landers (1954), who showed
Figure 2. (a) Two D-hinge veligers (arrows) from station 132, taken on June 14, 1993, from a depth of 1.6 m. (b) A drawing of a fully developed pediveliger larva, showing prominent umbo and developed "foot." Drawn from Galtsoff (1964).
Figure 3. Cumulative total of bivalve larvae in all samples taken on the indicated sampling date. Julian date refers to the sequential date of the year (January 1 is day 1, and December 31 is day 365). The frequency is total larvae in a 1,400-L volume.

Figure 4. Cumulative total of bivalve larvae at all sites from a depth of 0.3 m, and sorted by developmental stage. The numbers of D-hinge larvae in June 14 and June 28 samples exceeded graph scale, so total numbers are indicated in parentheses. Frequency refers to total numbers in a 700-L volume.
Figure 5. Cumulative total of bivalve larvae at all sites from a depth of 1.6 m, and sorted by developmental stage. The numbers of D-hinge larvae in the June 14 sample exceeded graph scale, so total number is indicated in parentheses. Frequency refers to total numbers in a 700-L volume.

Figure 6. Running cumulative larval totals, by time and site. Two 100-L samples were taken from each site on sampling days (0.3-m and 1.6-m depths). The frequencies reported are the total number of larvae collected at each site, up to the date indicated.
quahogs occur near the mouth of Greenwich Cove and the Mary's Creek area near Apponaug Cove (Stickney and Stringer, 1957; Rice et al., 1989; Lazar et al., this volume). Samples from stations 6 and 14 remained relatively free of bivalve larvae throughout the summer, despite their location, which is in close proximity to these dense adult assemblages. We collected all of our samples on an incoming tide, usually two hours prior to high tide, so a tidal "washout" explanation is unlikely. Likewise, the summer of 1993 was relatively dry, making the "freshwater washout" explanation unlikely. Alternative explanations, such as mortality of larvae due to some unknown pollutant, or filtration of the larvae from the water column by the dense adult assemblages, have not been ruled out. Kurkowski (1981) reported that adult quahogs can filter their own larvae out of suspension in the laboratory, but this phenomenon has not been clearly demonstrated by field studies.

Care must be taken with the interpretation of the bivalve larval identification. We—as did Landers (1954)—assumed that the majority of the bivalve larvae sampled and enumerated were larvae of the northern quahog, *M. mercenaria*. This is based on the fact that, in terms of biomass, quahogs are dominant in Greenwich Bay. But in spite of the existence of materials to aid in the identification of various species of bivalves from their larva (e.g., Chanley and Andrews, 1971), the visual discrimination of species—especially in early stage larvae—remains problematic. The bivalve larvae found in Greenwich Bay could conceivably be one of a number of species other than quahogs. These possibilities include oysters (*Crassostrea virginica*), scallops (*Argopecten irradians*), soft-shell clams (*Mya arenaria*), false quahogs (*Pitar morrhuanus*), mussels (*Mytilus edulis*), gem clams (*Gemma gemma*), or nut clams (*Nucula annulata*), among others.

A number of new approaches are being attempted to differentiate larval species. Use of computer-imaging software to accurately measure length and shell-height ratios from microscopic images may make the use of published identification aids more useful. Recently, fluorescent antibodies have been developed that are specific for detecting scallop (*Placopecten magellanicus*) larvae (Demers et al., 1993), and this approach may be useful for identifying quahog larvae (Feller, 1986). Scanning electron microscopy of larval hinge structures has been shown to be useful for identifying individual species, but the key drawback is that it is too cumbersome for routine identification of large numbers of larvae (Lutz et al., 1982; Tremblay et al., 1987). It is probable that techniques for discriminating genetic markers, either through DNA or expressed proteins, will allow species-specific identification of bivalve larvae (see Twombly and Goldsmith, this volume).

In summary, the key period of bivalve spawning in Greenwich Bay is during mid-June, as the water temperature reaches 20°C. There is no shortage of bivalve larvae in the water during spawning events, so it is unlikely that lack of broodstock hinders quahog recruitment into Greenwich Bay. And finally, distributions of bivalve larvae in Greenwich Bay are not uniform. There is an apparent lack of bivalve larvae in coves with high numbers of large adult quahogs that are the presumed broodstock. The explanation for this discrepancy remains unclear.

Acknowledgement

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References


**Questions and Answers**

**Q:** (Robert Rheault, Ocean State Aquaculture Association (OSAA))

Your data, along with Najih Lazar's, seem to show an inverse relationship between adult abundance and larval abundance. A number of studies that I have read suggest that adults may be filtering the larvae out of the water. Can you comment on this?

**A:** (Michael Rice) Yes, that's a possibility. Another possibility might be crowding effects that somehow reduce the fecundity of the animals. Another possibility might be that larvae are killed by certain pollutants in coastal runoff, but the adults are not. There could be a number of explanations.

**Q:** (Joseph DeAlteris, URI department of fisheries, animal and veterinary science (FAVS)) It seems that you are working in the water column here, and there are a great many studies that have focused on adult populations. I think that a missing part of the puzzle is just how many larvae are actually settling and metamorphosing. There is one researcher at Brown—Steve Gaines—who has used formalin-filled settlement traps to look at crustacean settlement. Has anyone done this with quahogs, to answer the question about how many are actually reaching the bottom?

**A:** (Rice) Yes, there is a researcher at the University of Connecticut at Avery Point—Robert Whittatch—who has used settlement traps to look at settlement of a number of invertebrates, including *Mercenaria*.

**Q:** (DeAlteris) Don't you believe that this type of information is of interest, particularly since there is good evidence that adult quahog abundance is strongly influenced by post-settlement survival? So the question might be: How many settle and how many of those survive?

**A:** (Rice) You are absolutely right. This is an area of research that deserves much more attention.
than it has received. But I caution that these types of studies are difficult—not intractable, just difficult. From the data presented, we can see that there is probably a great deal of mortality in the larval stages. I would not be surprised at all if similar high mortalities are found among fresh post-set animals. We need the data.

Q: (Wayne Durfee, professor emeritus, URI) I was surprised by the data showing less larvae in the coves. Is there a possibility that freshwater runoff killed larvae or outgoing tides swept the larvae into the open bay?

A: (Rice) The freshwater runoff killing the larvae is unlikely. There were no major rainfall events around the data collection periods, and our salinity measurements in the coves were only one or two parts per thousand less than the open bay. The tidal flushing hypothesis may be a possibility. During the next Sea Grant funding cycle, there is a group proposing a major study of the hydrodynamic flow patterns in Greenwich Bay. Their data may be useful for answering this question. But I was particularly struck by the time-series data. Larvae seemed to be consistently lower in numbers in the coves from week to week.

Q: (John Williams, Warwick Cove Marina) Did you take any temperature measurements?

A: (Rice) Yes we did, and our data showed what is already well-known from the literature. Once the water temperature reached about 20°C, the spawning commenced.

Q: (Williams) Was there any temperature disparity between the coves and the open bay?

A: (Rice) Not very much.

A: (Joseph Goncalo) On any given day, the temperatures in the coves did not vary by more than 1°C from the open bay sites. Also, sampling was always done on an incoming tide, so the likelihood of larvae being swept out from the coves is not high.

Q: (Kim Tetrault, FAVS) Dr. Rice, you did a study of quahog recruitment in Greenwich Bay in 1988, right?

A: (Rice) No, it was a study of adult populations and juveniles greater than 5-mm valve length.

Q: (Neal Perry, Rhode Island Divers Association and OSAA) Getting back to Bob Rheault’s question. We have an idea how many quahogs are in the coves, and an idea of how much water might be pumped by individuals. Would it be feasible to calculate the amount of water filtered during a tide cycle?

A: (Rice) Yes, we have enough data to make those types of feasibility calculations. I suspect that water filtered by the quahogs will be in the same ballpark as the amount of physical water exchange during a tidal cycle. This is true of the quahog population in the Providence River.

Comment: (Jeffrey Kassner, Town of Brookhaven, N.Y.) I think one of the key factors to remember is that there is a redistribution of quahogs when they are small post-set animals. Storms kick up the top layers of the sediment, and there is good evidence for secondary settlement. Larval abundances may not account for secondary redistribution. The other point I want to make is that larval abundances should be coupled with hydrodynamic models to make predictions as to sources and settlement areas.

A: (Rice) I agree.

Q: (Rod Pierce, shellfish aquaculture student) Do you have time-series data on the larvae?

A: (Rice) No, this is the first time we did this.

Q: (Pierce) So it is likely that the heavy set of littlenecks and top necks is from earlier years?

A: (Rice) Yes. It is very likely that recruitment has been occurring annually in Greenwich Bay since before shellfishermen started shellfishing. If recruitment were not relatively constant, the million-pound-per-year harvests would not be sustainable for as long as they have been. There is evidence for very sporadic quahog recruitment into other areas. (Editor’s note: See paper by Steve Malinowski in the Proceedings of the Second Rhode Island Shellfish Industry Conference.) What makes Greenwich Bay such a great area for recruitment is a real mystery.

Q: (Pierce) Would you hazard a guess as to the cause of the lack of larvae in the coves?

A: (Rice) No, these are just observations. I don’t want to commit to any particular explanation without more data.

Saran Twombly and Marian R. Goldsmith  
Department of Zoology  
University of Rhode Island  
Kingston, RI 02881-0816

Abstract: Harvests of the northern quahog, *Mercenaria mercenaria*, the most valuable commercial fishery in Narragansett Bay, have declined during the 1990s. The future of this fishery depends critically on development of an effective management strategy. Investigations of the quahog’s population genetic structure—and particularly, identification of brood stocks and assessment of the impact of overfishing—play a critical role in the formulation of such policy. Many aspects of the biology of *M. mercenaria* increase the likelihood that established molecular genetic techniques can provide population-specific markers—markers that can be used to identify the origin of new recruits and to quantify loss of genetic variation due to overfishing. We outline the genetic techniques available and briefly describe our plans to use two of these techniques—allozyme electrophoresis and randomly amplified polymorphic DNA (RAPDs)—to investigate the population genetic structure of *M. mercenaria*. Our ultimate goal is to develop a suite of molecular tools that can be used for effective management of a variety of commercially important species in Narragansett Bay.

Introduction

Many problems in fisheries science center on the genetics of natural populations and on the ability to discriminate among individuals or populations over spatial and temporal scales (Wirgin and Waldman, 1994). Individual growth, survival, and reproductive output depend directly on levels of genetic diversity or heterozygosity, which also determine a population’s resilience to environmental change. The degree of genetic differentiation among populations of a species—due to isolation or to selection—indicates the rate at which individuals adapt to local environmental conditions, the amount of inbreeding present (and thus loss of vigor due to inbreeding depression, e.g., Neal, 1935; Mukai, 1964) and the dynamics of recruitment. For example, a species whose recruitment depends on input from only one or a few subpopulations may be more vulnerable than one in which many populations contribute to overall dynamics. An important consequence of genetic differentiation among populations is that individuals or populations can be identified, providing the possibility of identifying brood stocks, and of answering a number of important management questions.

The increasing importance of effective management practices for species of commercial importance has resulted in the widespread use of genetic techniques to understand and to manage exploited species (see Wirgin and Waldman, 1994). These techniques rely on markers that use gene products such as proteins (enzyme electrophoresis) or nuclear and mitochondrial DNA molecules directly (DNA sequencing, restriction fragment length polymorphisms, randomly amplified polymorphic DNA). Although these techniques are routinely used to investigate population dynamics (see Harrison, 1989; Wirgin and Waldman, 1994), they have not as yet been applied to commercially important species in Narragansett Bay.

*Mercenaria mercenaria* provides the most important commercial fishery in Rhode Island, based on biomass landed, catch value, and the number of fishermen supported (Rice and Grossman-Garber, 1993). Considerable data on abundances, growth rates, and fishing pressures exist for sub-
populations of *M. mercenaria* throughout the Bay (e.g., Campbell, 1959 a,b,c; Canario and Kovach, 1965 a,b; Sall et al., 1967; Sisson, 1977; Rice et al., 1989; Pratt et al., 1992). However, questions concerning patterns of recruitment and the identification of subpopulations contributing new recruits are as yet unanswered (Rice, 1993), despite their importance to the maintenance of harvestable populations.

Our goal is to use molecular genetic techniques to address important basic and applied questions for *M. mercenaria*. In this paper, we first outline questions or issues that lend themselves to genetic analysis. This is followed by a brief review of aspects of the biology of *M. mercenaria* that enhance the potential for producing genetic differences among populations and for identifying specific populations (thereby allowing for the identification of brood stocks or particularly vulnerable populations). Finally, we describe the genetic techniques that can be used to address these questions. Preliminary investigations indicate that two of these techniques will work well with *M. mercenaria* in Narragansett Bay.

**Population Structure: Genetics and Practical Applications**

*M. mercenaria* occupies diverse habitats in Narragansett Bay, which divide this species into many subpopulations. Pressing management issues depend directly on this spatial population structure. From the perspective of the entire Bay population, individual subpopulations form the basis for the quahog fishery, and may freely mix (and therefore be genetically uniform), or may effectively be isolated from one another and genetically distinct. The degree of differentiation among subpopulations tells us a great deal about the extent of larval dispersal and exchange, and whether a few or all subpopulations contribute new recruits to areas open for fishing. In addition, each subpopulation may be genetically diverse (heterozygous) or genetically uniform (homozygous). This information is important, as heterozygotes are more vigorous, grow faster (e.g., Zouros et al., 1988; Gaffney et al., 1990; Pogson and Zouros, 1994), survive better, and are more fecund than homozygotes (e.g., Zouros et al., 1980; Koehn and Gaffney, 1984; Koehn et al., 1988). Moreover, genetically diverse populations may be more resistant to environmental changes or disturbance (such as fishing) than are genetically uniform populations (Philipp et al., 1993).

Answers to these issues can form the basis for assessing a number of management questions that gain added importance as evidence of declining populations in Narragansett Bay accumulates (Rice and Grossman-Garber, 1993; contributions to this symposium). Should specific subpopulations (major "brood stocks") be protected from fishing, or their habitats targeted for environmental restoration? Should currently profitable subpopulations continue to be fished heavily? Some studies suggest that overfishing reduces levels of genetic variation (see Smith et al., 1991), and that existing levels of diversity indicate whether a population shows signs of overfishing, can sustain further fishing, or can recover if fishing is suspended. How much additional fishing can be supported by currently exploited subpopulations? How rapidly will harvested subpopulations recover from heavy fishing or overfishing? An understanding of the genetic structure of *M. mercenaria* can also identify individuals (genotypes) that will be best suited for aquaculture programs (Dillon, 1992).

Each of these questions targets the poorly understood aspects of the biology of *M. mercenaria* in Narragansett Bay, and each relies on the ability to identify genotypes and to discriminate genetically between subpopulations of the same species, or between individuals from the same population.

**Potential for Genetic Variation in Mercenaria mercenaria**

Why is *M. mercenaria* a good subject for these questions and for the application of molecular genetic techniques? Aside from its commercial importance in Narragansett Bay, many aspects of its biology increase the likelihood that subpopulations are differentiated to some extent, and that genetic techniques will identify specific genotypes or subpopulations. The habitats occupied by *Mercenaria mercenaria* in Narragansett Bay cover a spectrum of natural environmental conditions (temperature, salinity, turbidity, sediment characteristics),
population sizes, fishing or natural predation pressures, and pollution levels. These habitats represent divergent selection pressures that may encourage genetic differentiation among subpopulations. For example, sediment or bottom characteristics, the kind and abundance of natural predators, and levels of toxins or pollutants all allow for differential growth and survival rates (reviewed in Rice and Pechenik, 1992). Population density has a large effect on survival of new recruits (Bricelj, 1993; Malinowski, 1993), so that habitats of differing population sizes (or population age or size structure) will have different inputs of new recruits each year. In addition to this spatial variation, major recruitment events in *M. mercenaria* may be sporadic (Malinowski, 1993), adding an important temporal component to long-term population dynamics.

The physics of water movement in the Bay may further encourage isolation among subpopulations. Despite studies showing that larvae can be dispersed by wind or currents throughout estuaries like Narragansett Bay (e.g., Wood and Hargis, 1971; Andrews, 1983), a recent study on the barnacle *Semibalanus balanoides* (Gaines and Bertness, 1992; Bertness and Gaines, 1993) shows genetic differences between subpopulations from Mt. Hope Bay and Little Compton, within Narragansett Bay. The authors claim that flushing rates in Mt. Hope Bay are low enough in some years (years with low rainfall and low freshwater runoff) to effectively isolate its barnacle subpopulation from subpopulations in lower portions of the Bay. These low flushing rates, together with the overall current flow in the Bay (through the East Passage and out of the Bay through the West Passage) may further prevent free larval exchange, and may encourage isolation among subpopulations.

When habitat variation, population size and structure, current patterns, and dispersal abilities are taken together, the resulting potential for genetic divergence among subpopulations of *M. mercenaria* provides a strong rationale for being able to use genetic markers to identify specific populations and to answer the kinds of questions posed here.

**Genetic Techniques**

**Enzyme Electrophoresis**: Molecular genetic techniques used in population studies differ in their ease of application, cost, and in the level of genetic resolution produced. Enzyme electrophoresis was the first method used to detect genetic variation in natural populations (Hubby and Lewontin, 1966; Lewontin and Hubby, 1966; Harris, 1969), and studies using this method have revealed large amounts of genetic variation in diverse natural populations (e.g., Clegg and Alard, 1972; Richmond, 1972; Powell, 1975; Levin, 1978; Lewontin, 1978; Nevo, 1978). This technique is based on the idea that one gene codes for one protein (enzymes are most commonly used), and a slight change in a gene (a mutation) will therefore code for a slightly different form of the same enzyme (called an allozyme) that often has a slightly different electrical charge. Differences between two or more allozymes are detectable as proteins that migrate different distances when subjected to an electrical field. The result is a series of bands on a gel matrix (Figure 1), with differing banding patterns representing individuals having different genetic makeups. A wide range of enzymes are detectable by their biochemical reactions and can be analyzed in natural populations. Quantification (or scoring) of the resulting gels allows identification of genotypes in a subpopulation, measurements of the amount of genetic variation present in a single subpopulation, and quantification of differences between subpopulations or populations of the same species.

Although we now know that a single protein is not encoded by a single gene, and that other assumptions underlying the technique are questionable (see discussion in Hartl and Clark, pp. 23–24), allozyme electrophoresis continues to be a relatively cheap, fast, and a powerful way to characterize the genetic structure of many populations, and has been widely used for marine bivalves (reviewed by Hibbsh and Koehn, 1985; Koehn and Hibbish, 1987; Zouros and Foltz, 1987; Zouros et al., 1988; see also Dillon, 1991). For example, Koehn and colleagues used allozyme electrophoresis to document genetic variation in *Mytilus edulis* over a small spatial scale.
Electrophoresis Setup

Typical Gel Pattern for dimeric enzyme

<table>
<thead>
<tr>
<th>Genotype</th>
<th>F/F</th>
<th>F/S</th>
<th>F/S</th>
<th>S/S</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Type of Dimer</strong></td>
<td>fast + fast</td>
<td>fast + slow</td>
<td>slow + slow</td>
<td></td>
</tr>
</tbody>
</table>

Figure 1.
in Long Island Sound (Koehn et al., 1980). The basis for this variation was post-settlement selection for one allele (or genetic form) of leucine aminopeptidase (Lap-94), which is present in highest frequencies in high-salinity environments. Genotypes carrying this allele suffer higher mortality as salinity declines toward inner Long Island Sound.

Although there is still considerable controversy over whether the different enzymes detected by this method are themselves responsible for population attributes of ecological or practical importance (e.g., Pogson and Zouros, 1994; Mitton and Grant, 1984), enzymes clearly are extremely useful markers for distinguishing genetically different populations.

DNA Analysis: More recently, a variety of techniques have been developed that analyze DNA molecules directly, rather than analyzing the expressed products of genes. These are loosely classified as "fingerprinting techniques," because they can yield results that are unique to a single individual. Techniques based on DNA analysis are better able to detect variation in natural populations than allozyme electrophoresis, because they scan the DNA directly, examining both coding and non-coding portions of the genome—the latter of which are known to be more variable (e.g., Kreitman, 1983; Li et al., 1985; Aquadro et al., 1986). The ultimate level of DNA analysis is DNA sequencing, which identifies the order of the four possible bases (A, T, G, or C) along an entire molecule. DNA sequencing has proven extremely valuable in answering many evolutionary questions (see Hartl and Clark, 1989, for a review), but is time-consuming, technically demanding, and costly. Most population-level questions are adequately answered with somewhat lower levels of genetic resolution.

More commonly used techniques for population studies identify fragments of DNA produced by digestion with restriction enzymes that recognize and cut the DNA at specific sequences, generating restriction fragment length polymorphisms, or RFLPs. These will have different lengths when the base sequences at target sites differ, or if insertions or deletions have occurred between them. This approach is most easily used with mitochondrial DNA molecules, which are smaller in size (by several orders of magnitude) than nuclear DNA, and which evolve faster in most organisms (e.g., Avise, 1986; Brown, 1985). Analysis of mitochondrial DNA variation promises considerable advantages over allozyme electrophoresis for studying geographic structure of populations or subpopulations (Harrison 1989), but is primarily maternally inherited, and so leaves out an important component of genetic analysis—namely the participation of the paternal genome. Detailed sequence information about mitochondrial DNA molecules is also required to use this technique to its best advantage.

A second DNA technique that has gained significant popularity in recent years identifies fragments of nuclear DNA of varying length known as randomly amplified polymorphic DNA, or RAPDs, which are generated using specific, short, arbitrary DNA primers in the polymerase chain reaction (PCR). The primers are used to scan the entire DNA molecule and bind to all complementary target sequences, coding or non-coding. When two primers bind in opposite orientation within a critical distance of each other, the intervening DNA is copied by an added DNA polymerase, and the resulting fragments can be detected by electrophoresis, similar to allozymes. Because the arbitrary primers for the PCR reaction are relatively short (around 10 base pairs), mutations in the target DNA of the individual will result in a different number or size of fragments identified, due to alterations in priming sites, or, as with RFLPs, changes in the intervening DNA, yielding individual-specific patterns on gels (Figure 2). Although there are some problems in interpreting RAPD bands—which may correspond to different sequences of similar lengths, this technique is especially attractive for ecological and population studies (e.g., Chapko et al., 1992; Hadrys et al., 1992), due to the relative ease of setting it up with any organism, using commercially available sets of primers, without knowing any specific characteristics of the organism's DNA; the relative speed and simplicity of performing the assay on many samples at one time; and because of the high degree of variation observed using different primers.
DNA has 3 target sites in region

Mutation eliminates 1 target site

Primer identifies 2 internal fragments

Primer identifies 1 internal fragment

fragment A

fragment B

fragment C

PCR and Electrophoresis

Figure 2.
Proposed Study

We plan to survey individuals from subpopulations distributed throughout Narragansett Bay, using two of the molecular techniques described here: allozyme electrophoresis and RAPDs. The first phase of our study will quantify the level of genetic differentiation among spatially discrete subpopulations, and will analyze the temporal stability of these subpopulations over a two-year period. These data will then be used (Phase II) to address the basic and applied questions raised above.

Allozyme electrophoresis has been used extensively to quantify genetic variation in marine mollusks, and published protocols (Dillon, 1991, 1992) greatly facilitate application of this method to *M. mercenaria*. Dillon reports results for 14 different enzyme systems, using starch gel electrophoresis. In a preliminary study of *M. mercenaria*, using a different protocol (cellulose acetate electrophoresis, Hebert and Beaton, 1989), we identified at least six polymorphic enzymes (phosphogluconeisomerase, *PgI*; phosphoglucone mutase, *PgM*; malate dehydrogenase, *MdH*; mannose-6-phosphate isomerase, *Mpi*; glutamate oxaloacetate transaminase, *Got*; and arginine phosphokinase, *Apk*) for two subpopulations (Wickford Harbor and Patience Island). We will assay individuals from specified subpopulations of commercial importance, such as Providence River, Mt. Hope Bay, and Greenwich Bay, for these and other polymorphic marker enzymes to measure allele and genotype frequencies over space and time. These data will quantify genetic differentiation among and within subpopulations, and may also provide the means to identify specific subpopulations by revealing localized, rare alleles (Slatkin, 1981, 1985) or distinctive localized allele frequencies.

To obtain a finer resolution of genetic differentiation in *M. mercenaria*, we plan initially to use anonymous nuclear DNA markers identified by the RAPD technique. This will entail screening single random oligonucleotides as primers for PCR, and analyzing the products of these reactions on standard agarose gels to look for ones that generate reproducible, distinctive patterns on sample DNAs. In preliminary studies, we have found that a published protocol for extracting DNA from mollusks (Winnepannickx, Backeljau, and DeWachter, 1993) gives high yields of *M. mercenaria* DNA. We primed this DNA with four of the several hundred primers available; three yielded amplification products, while the fourth did not. Amplification of DNA extracted from two subpopulations (Pine Hill and Patience Island) showed considerable variation among individuals within each subpopulation, as well as between subpopulations, with both common and unique bands.

Future Prospects

Our preliminary investigations show abundant genetic variation in *M. mercenaria* in Narragansett Bay. A large number of enzymes and DNA primers remain to be tested to find subpopulation-specific markers. Enzyme electrophoresis is relatively easily accomplished and inexpensive, but provides a cruder level of genetic analysis than RAPDs. Analysis of nuclear DNA is more expensive and technically demanding, but provides a level of genetic resolution necessary to identify specific individuals. By using both techniques, we will maximize our ability to identify specific subpopulations (and thus “brood stocks”), to quantify levels of genetic variation (on spatial and temporal scales) throughout the Bay and, eventually, to test many of the questions raised earlier in this paper. Our long-term goal is to develop molecular tools that can be used to address basic and management questions for a variety of commercially important species in Narragansett Bay.

References


Campbell, R. 1959b. Quahog investigations: Potowomut River. Rhode Island Division of Fish and Game Leaflet No. 2.

Campbell, R. 1959c. Quahog investigations: Kickamuit River. Rhode Island Division of Fish and Game Leaflet No. 3.


Questions and Answers

**Q:** (Kim Tetrault, URI department of fisheries, animal, and veterinary science) From my experience, if you spawn one female and get 400,000 larvae, and treat the animals alike in terms of food, water conditions, etc., the animals will grow at vastly different rates. How do you handle genetic variability among individuals?

**A:** (Saran Twombly) The process of finding population-specific markers is more tedious than you might think. You may screen a large number of primers before you find one that is specific for populations. Many primers pick up individual variability, but the trick is to find one that “fingerprint” a population. With isozymes, the problem is even more difficult. Allozyme electrophoresis yields allele frequencies. For example, the Greenwich Bay population might be characterized by a high frequency of a specific allele or gene product, whereas quahogs from the West Passage may have a lower frequency of the same allele.

**Q:** (Walter Blogoslawski, National Marine Fisheries Service, Milford, Conn.) There is a genetic strain used by most quahog culturists called Mercenaria mercenaria notata. It carries chestnut-colored shell markings, and is used by aquaculturists as an identifying mark for their stock. What kind of differences do you find in a “notata” strain? Or what kind of variation would you expect to find once you have selected for one trait, such as this color morph trait?

**A:** (Twombly) The color morph is only one trait. My guess is that you can probably find a great deal of variation in other traits. Along another line, such rare color morphs or “color markers” are valuable in population studies to quantify the amount of gene flow or mixing among discrete subpopulations. In *M. mercenaria*, this color morph could be used, if placed in a specific location or subpopulation, to quantify larval dispersal from specific areas of the Bay.

(Discussion on this topic followed—Dr. Blogoslawski said that the “notata” strain is cultured in Connecticut, and someone from Rhode Island interjected that there are Rhode Island populations of “notata.” These strains give us a known genetic and morphological marker to use in our studies.)

Habitat Enhancement as a Means to Increase the Abundance of the Northern Quahog, *Mercenaria mercenaria*

Jeffrey Kassner
Town of Brookhaven
Division of Environmental Protection
3233 Route 112
Medford, New York 11763

Abstract ■ The northern quahog (*Mercenaria mercenaria*) has historically been a commercially important shellfish species harvested from the coastal waters of the East Coast of the United States. Because of the quahog’s economic importance, there has been a longstanding interest in undertaking projects to augment the natural population abundance of this species. Population-based augmentation projects seek to increase the harvestable quahog population by adding more individuals to a habitat, while habitat enhancement—based projects seek to increase the harvestable population by increasing the “suitability” of benthic habitats to support a higher abundance of quahogs. A review of available information suggests that modifying the substrate by the addition of shell may be an effective habitat enhancement project. Habitat enhancement, however, is more than just manipulating habitat, and must occur in the context of comprehensive planning.

Introduction

Projects to augment the naturally occurring abundance of quahogs in a population are generally popular undertakings because they are seen as an active solution to the “problem” of a low abundance of harvestable shellfish. Shellfish harvesters generally support projects to augment existing quahog populations because they offer the potential of sustained and possibly increased harvests, and, at the same time, provide an attractive alternative to many other management options, such as harvest restrictions. Population augmentation projects typically enjoy the political support needed for funding and regulatory approvals, because they are seen as protecting the viability of the shellfish industry, and because they benefit an important local constituency.

There is a fairly large and diverse number of population augmentation projects that offer at least some theoretical potential to increase the abundance of quahogs on the public beds. Determining which particular project to implement is not, however, an easy task for several reasons: decisions often need to be made without adequate information; there is often an extreme sense of urgency; the alternative projects vary with respect to cost and length of time required to achieve results; logistics may eliminate several potentially viable candidate projects; and some projects may be more acceptable to shellfish harvesters and/or regulatory authorities than others.

The decision first to implement population augmentation, and then the choice of which particular project to implement, is extremely critical. Most important, because the amount of money available for quahog management is generally fixed, the spending of certain funds to implement a population augmentation project often means that alternative management options and other augmentation projects may not be implemented. Additionally, if augmenting quahog populations becomes the cornerstone of a quahog resource management program, it may create a false sense of security, such that the implementation of other measures—which may, in reality, be more effective—is precluded. Thus, making the “wrong” choice can have negative consequences beyond simply not increasing abundance.

Augmentation projects to increase the size of harvestable shellfish populations in general, and
quahog populations in particular, can be divided into two basic strategies: population-based and habitat enhancement-based. The population-based augmentation strategy seeks to increase a harvestable quahog population by adding more individuals to a habitat. The habitat enhancement-based augmentation strategy seeks to manipulate ("improve") habitats so that they will be capable of supporting a higher abundance of quahogs. Habitat enhancement-based projects thus seek to take advantage of a quahog population's existing biotic potential that is "lost," while population-based projects seek to supplement the biotic potential of a quahog population.

Population-based projects, which include the planting of undersized (seed) quahogs, spawner transplants, and relays, have been extensively studied, and have been undertaken in a number of locations, often with considerable success (COSMA, 1985). Habitat enhancement-based projects, even though offering a number of advantages, have received comparatively little attention, and the results of only a few habitat enhancement projects have been reported. This paper will provide a general overview of quahog habitat enhancement as a means to augment quahog populations. It will also review the planting of shell as one example of a potentially effective large-scale habitat enhancement project, and will offer a protocol for undertaking habitat enhancement.

Quahog Habitat Requirements

In order to undertake projects to enhance habitat and thereby increase the abundance of quahogs, the habitat requirements of the quahog must first be identified. Useful information can be obtained from two sources—the distribution of quahog abundance with respect to environmental conditions and the environmental biology of the quahog. By knowing what factors are associated with high quahog abundance, and then what factors are absent from a particular habitat, a habitat enhancement project can be designed.

Although the quahog is widely distributed, the abundance of quahogs varies considerably from one habitat (eelgrass beds, mud bottoms, relict oyster reefs) to another. Thus, within the quahog’s geographic range, the different habitats have a different "suitability" with respect to quahogs, and this suitability determines the abundance of quahogs. The objective of habitat enhancement is, therefore, to manipulate habitat characteristics so as to increase the habitat’s quahog suitability, and thereby transform a habitat with low suitability and low quahog abundance into one with high suitability and high quahog abundance.

While many factors influence the size of a quahog population, the distribution of the abundance of quahogs is closely related to the distribution of substrate type. Wells (1956) observed in Chincoteague Bay, Md., the highest density of adult quahogs in sand and sand/shell bottom. In Christmas Bay, Texas, the highest abundance of quahogs was in sediment containing shell fragments (Craig and Bright, 1986). In Great South Bay, N.Y., quahogs were distributed throughout the bay, but areas of muddy sediments and of sandy sediments lacking shell had lower abundances of quahogs relative to areas of sandy sediment containing shell (Kassner et al., 1991). In Delaware Bay, quahogs were most common in and near oyster bars, and oystermen considered old, noncultivated oyster beds as productive sites for the harvest of quahogs (Maurer and Watling, 1973). Similar patterns have been reported by Pratt (1953), Walker and Tenore (1984), Saila et al. (1967), and Carriker (1961).

Numerous studies have been undertaken on the environmental biology of the quahog, and many are relevant to the enhancement of quahog habitats. The following observations are particularly noteworthy:

1. Newly set quahogs seek out hard surfaces covered with a thin layer of material into which they burrow and then anchor (Carriker, 1961).

2. In laboratory experiments, quahogs set at higher densities in sand substrates than in mud substrates and appeared to be gregarious (Keck et al., 1974).

3. In flume experiments, quahog settlement appears to be passive, that is, determined by flow conditions and not by larval choice (Batcheler et al., 1992).

4. Shells and gravel offer the quahog refuges from predation (Sponagule and Lawton, 1990).
5. Quahog growth and survival is reduced in the presence of organisms causing bioturbation (Murphy, 1983).

6. Quahog settlement appears to be reduced by the presence of adults and other filter feeders (Maurer, 1983).

**Shell Planting as a Habitat Enhancement Option**

Based on the distribution of quahog abundance and the environmental biology of quahogs, substrate modification—through the addition of shells to low-quahog-abundance sediments lacking shell—would appear to be an effective approach to habitat enhancement. Several anecdotal reports provide support for this approach. In Long Island Sound, for example, shell (culch), distributed on the bottom to provide substrate for oysters to set upon, was also associated with increased quahog abundance (Volk, 1986). In the Broadkill River, Del., quahogs were found in an area that had been recently covered with surf clam shells to create oyster habitat (Maurer and Watling, 1973).

There have been three reported pilot-scale projects that added ("planted") shell to bottom sediments in order to increase quahog abundance. In North Carolina, in the early 1970s, Parker (1975) planted scallop shells at a density of 0.81 cubic meters (m³) of shell/m² of bottom, and found that the average initial recruitment was 10 times greater in the planted shell than in an unshelled control. In 1989 in the Great South Bay, N.Y., 100 m³ of surf clam shells were planted in two 0.4-hectare (ha) plots located in muddy, low-quahog-abundance areas that lacked shells (Kassner et al., 1991). The planting, however, did not result in increased quahog abundance, because the shell sank into the bottom and the project's scale was deemed to be too small to give meaningful results (Kassner, unpublished). In 1990, 120 tons of clam shell were planted in Barnegat Bay, N.J., in six plots, each measuring 20 m by 70 m (Cronin, 1990). Three of the plots were covered with "heavy" shell, and three were covered with "light" shell, while three unshelled plots served as controls. Three years later, the shelled plots had slightly more than five times more recruits than the unshelled control (Clyde MacKenzie, National Marine Fisheries Service, Sandy Hook, N.J., personal communication).

**A Recommended Protocol for Habitat Enhancement**

Based on the pilot projects and what is known about quahog biology, shell planting as a habitat enhancement project appears to offer considerable utility as a quahog management tool. However, successful habitat enhancement requires more than just manipulating habitat to improve its suitability for quahogs, as the project must also be acceptable to shellfish harvesters and other groups that may be directly or indirectly affected, as well as to fishery managers and environmental regulators. Because even the most technically sound habitat enhancement proposal is likely to be blocked by any opposition that develops, bringing these groups into the decision-making process is critical, and obtaining their support and concurrence is essential.

Therefore, the successful implementation of a habitat enhancement project for the quahog or any other shellfish species requires a comprehensive planning process that integrates biology and ecology, management goals, design constraints, and user- and interest-group concerns. The following sequence of steps is presented as one possible comprehensive planning protocol:

**Step 1.** A preliminary assessment of existing conditions is undertaken to determine if habitat suitability is limiting the size of the quahog population. If habitat manipulation appears to be viable, then the planning process for a habitat enhancement project can continue. If habitat enhancement does not appear to be viable, then consideration can be given to population-based enhancement strategies.

**Step 2.** Having identified a specific habitat enhancement project, it is necessary to develop the project's goals, objectives, and scope, in order to provide a basis by which the project can be evaluated. It is also beneficial to establish what level of increase in quahog abundance can reasonably be anticipated from the habitat enhancement project, so as to minimize the dangers of unrealistic and unfulfilled expectations. Concurrently, all involved and interested groups are brought into the
planning process, and alternative and potential funding sources contacted.

Step 3. The design of the project is finalized, making sure that locational, budgetary, logistical, engineering, and maintenance considerations have been taken into account. The regulatory approvals and funding commitment are obtained. Consultation with interested groups and involved parties is continued.

Step 4. Once regulatory approvals and funding are secured, and assuming any opposition to the project has been addressed, the implementation of the project is initiated. Considerable oversight must be provided during implementation to ensure that what is actually undertaken matches the project’s design.

Step 5. Following implementation, the project is monitored to provide information to determine the project’s contribution to the quahog population. Engineering and logistical aspects are evaluated, and consideration given to any input from the shellfish industry. Based on this information, together with a cost-benefit analysis, a decision is made to expand the scale of the project, modify its design, or abandon it entirely.

Discussion

The planting of shell to improve the suitability of quahog habitat appears to have considerable potential as a means to increase the abundance of quahogs. How shell planting brings about an increase in quahog abundance is not readily apparent, and there are several possible mechanisms. In the final analysis, however, the reason why it, or any other enhancement project, is successful is not as important as the fact that it is successful.

For the quahog, shell planting to enhance habitat suitability offers a number of benefits as a management tool. Shell planting should be self-sustaining and long-term, so that future recurring expenditures will be minimized. It can be used to replace or restore habitat that has been degraded, and it can be used as a mitigation measure to compensate for the closure of high-abundance shellfish beds when they do not meet water quality standards.

There are several other positive aspects of using shell to enhance quahog habitats that are worth noting. In some areas, the disposal of shell by shellfish processors is a problem, and using shell to create quahog habitat provides a beneficial use of what would otherwise be a solid waste. Shell is a natural component of sediments, so that the addition of shell would not be expected to have any significant adverse environmental impacts, and shell should not pose a significant obstacle to the harvest of quahogs. Finally, it should be possible to undertake shell planting on a large enough scale to make a meaningful contribution to the quahog harvest.

Habitat enhancement is used for other species of shellfish. Shell planting is a traditional and well-accepted oyster management practice. Habitat enhancement by substrate modification has also been used on the Pacific coast of the United States to enhance the abundance of another clam species, the Manila clam (Thompson and Cooke, 1991). Between 1974 and 1988, nine Washington-state beaches, with a total area of 6 ha, were covered with gravel to depths ranging from 13 to 60 centimeters. Beach graveling was found to increase Manila clam on the order of two to 10 times over ungraveled beaches. According to Toba et al. (1993), most of the productive clam beds are already being cultivated, and any significant increase in clam production will come from the enhancement of less-productive beds.

Given its potential, it is not obvious why the habitat enhancement—based strategy has not received as much interest as the population-based strategy. One possibility is that population-based augmentation directly and visibly adds more shellfish, and is more immediate and tangible than habitat enhancement, which is not as obvious, and more long-term and indirect. A second possibility is that population abundance is perceived as being more limited by the supply of individuals to a habitat than by habitat conditions, making population-based augmentation more philosophically compatible. In the particular case of seed clam planting, this population-based strategy is the beneficiary of the promise of mariculture technology and an extensive mariculture research effort. Finally, it may simply be because habitat enhancement is a nontraditional quahog management activity, and there is an underlying resistance to change.
In conclusion, one cautionary note is in order. Projects that augment the natural quahog population are generally seen as a panacea to the problem of low shellfish abundance, but the basic assumptions have not been adequately evaluated. In particular, population augmentation is premised on the basic, but largely untested, belief that the environment is capable of sustaining a higher level of quahog abundance. However, if the maximum abundance of quahogs is determined by prevailing environmental conditions, it may well be that augmentation projects will only be successful when environmental conditions naturally favor a high quahog abundance and not when natural quahog production fails. Thus, population enhancement may not work when it is most needed.

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References


Questions and Answers

Comment: (Joseph DeAlteris, URI department of fisheries, animal, and veterinary science) We seem to be putting a lot of faith in habitat enhancement without stepping back to analyze underlying causes. There is evidence of greater recruitment in coarser sediment environments. But, coarser sediment environments are usually associated with higher-energy hydrodynamic conditions. Perhaps there is greater recruitment because the higher-energy hydrographic conditions somehow clean things out or bring more food. An example may be some artificially created oyster reefs in Chesapeake Bay. The oyster industry has created numerous artificial reefs in low-energy hydrographic areas by placing about 5,000 bushels of oyster shells/acre, but in most cases there has been relatively little spatfall of natural oysters. These artificial reefs are generally used for placement of seed oysters from elsewhere for final grow-out.

A: (Jeffrey Kassner) You are absolutely right; however, I wish to point out that we really need to get away from such methods as seed clam planting and relays, which don’t work very well. The oyster industry along Long Island Sound has been planting cultch for 150 years, and it does seem to work. What we need to do is refine our ideas about where we put the enhancement projects. It is clear that placing shell on any bottom type and expecting increases in quahog recruitment is rather foolish. I think that time should be spent working on the details, but I think it is an option that we should not overlook.

Q: (name not stated) What are you going to do differently in next year’s shellfish project?

A: (Kassner) I don’t think that shell planting in a very muddy-bottom area is the best way. We’re going to look for firm-bottom areas and we are not going to plant shell only, but a mixture of sand and shell. It is not entirely clear what the role of the shell is. At least in the case of relict oyster reefs, we often find them topographically elevated from the rest of the bottom. Shell in those areas is usually covered by 1 or 2 centimeters of sediment. Perhaps we are looking to “roughen” up the bottom, thereby creating improved hydrodynamic conditions in the near-bottom water.

Q: (name not stated) How do you expect the quahogs to be harvested from the shelled areas?

A: (Kassner) I have found shellfishermen to be incredibly creative when it comes to harvesting shellfish. If we are careful not to plant the shell too thickly, I don’t think that the industry will have any problem getting the shellfish out.

Q: (Gerald Carvalho, shellfisherman) Have you done anything with just “cultivated bottom”?

A: (Kassner) I have not. One of Joe DeAlteris’ students reported at the last Rhode Island conference (1992) such a study. To my knowledge, projects of this type have not worked very well.

Q: (Gregg Rivara, Cornell Cooperative Extension, N.Y.) Where do you think the larvae go if the shell weren’t there? Wash out to the ocean?

A: (Kassner) They probably just die.

Q: (Rivara) Yes, but what if the larvae originate in one area and are destined for settlement in the usual place, but they are intercepted by the new shell. Something of larval stealing?

A: (Kassner) I haven’t thought of it that way, but with the great numbers of larvae available it is most likely that they are in such great excess that the “larval stealing” scenario would be pretty unlikely. I don’t envision larval supply being a limiting factor. The converse of this is if you increase the geographic extent of the spawning population, you further increase the larval supply.
Trends in U.S. Clam Production and Marketing

Priscilla M. Brooks
Department of Resource Economics
University of Rhode Island
Kingston, RI 02881

Abstract Total landings of clams in the United States have risen dramatically since the 1950s, largely due to the increased production of ocean quahogs (Arctica islandica) and surf clams (Spisula solidissima). Landings of the higher-valued northern quahogs (Mercenaria mercenaria) and soft-shell clams (Mya arenaria) have decreased significantly in the last decade, due to many factors, including habitat degradation and overfishing. Meanwhile, aquaculture of clams—mainly M. mercenaria—in the United States has increased steadily. This paper provides a broad overview of trends in clam production and marketing in the United States, along with insight into consumer perceptions of clam products. Results of two recent surveys examining consumer perceptions of seafood safety and aquaculture suggest that (1) consumers in the Northeast perceive some risk in consuming clams; and (2) they perceive aquacultured clams to be better, safer, or more protected from pollution than wild-harvested clams. The adoption of a more consumer-oriented approach to shellfish marketing that focuses on product quality, packaging, and consumer education will be essential for competing in the domestic and global marketplace.

Introduction

Total U.S. clam landings have increased dramatically since the 1950s. Much of this is due to large increases in the production of surf clams (Spisula solidissima) and ocean quahogs (Arctica islandica), which typically are used for processed clam products. Meanwhile, the higher-valued species—soft-shell or steamer clams (Mya arenaria), and northern quahogs (Mercenaria mercenaria), often known as hard clams or hard-shell clams (terms used interchangeably in this paper)—have seen substantial decreases in landings over the last decade, due to a variety of factors, including disease, overfishing, and habitat degradation. Clam aquaculture, particularly that of quahogs, has experienced some success with a resultant steady increase in production during the past decade.

Increased consumer concerns about seafood safety highlight a need for innovative marketing of clam products and consumer education. This paper provides a brief overview of trends in U.S. clam production, with a focus on the Northeast. Consumer perceptions of seafood safety and aquaculture are discussed, along with results of two recent consumer surveys, and implications for the marketing of clam products.

U.S. Clam Production

Total U.S. clam landings have experienced an erratic, but overall, increase in production over the last 35 years (Figure 1). Much of this increase is due to expanded production of ocean quahogs in response to stringent regulations imposed on the surf clam industry in the late 1970s.

While ocean quahogs and surf clams account for the bulk of clam landings in the United States, soft-shell clams and hard-shell clams are the higher-valued, premium products. Hard-shell and soft-shell clams accounted for an average of 15 percent of the total U.S. landings since 1980. However, these high-value species made up an average of 57 percent of the total value (Figure 2).

Maryland, Massachusetts, and Maine are the leading suppliers of soft-shell clams (steamers). Steamer clam production has declined steadily from a 13.5-million-pound (meat weight) peak in 1980 to a low of 6 million pounds in 2000. The primary reason for the decline was a smaller harvest of ocean quahogs, the preferred clam for steamers, which is typically caught during the winter months when new growth is slow.

1Present address: Conservation Law Foundation, 62 Summer St., Boston, MA 02110.
1969 to a low of 3.9 million pounds in 1992 (USDC, various years). Steamer production rebounded slightly in 1993 to 4.5 million pounds.

**U.S. Hard Clam Production**

Landings of hard clams have historically been concentrated in the Northeast, mainly in New York, Rhode Island, and Massachusetts. However, due to aquaculture, hard clams are now produced all along the East Coast, from Maine to Florida. Since 1980, hard clams have accounted for an average of 10 percent of the total clam landings, but 42 percent of the total value (USDC, various years). In fact, hard-shell clams are the most highly valued species of clams produced in the United States. Since 1980, hard clam landings have exhibited dramatic increases and decreases in annual production. For example, landings in 1981 increased 36 percent, to 18 million pounds, their highest level in almost three decades (USDC, various years).

After peaking again in 1985, hard clam landings fell sharply to a low of 9.2 million pounds in 1989. Landings have since slowly increased to 15.6 million pounds, at a value of $59.1 million in 1993 (USDC, various years).

Rhode Island landings of hard clams are down significantly from the high levels exhibited in the early 1980s (Figure 3). The year 1983 saw a peak in production of hard clams in Rhode Island, with landings of 4.3 million pounds at a total dockside value of $10.3 million (National Marine Fisheries Service, Fisheries Statistics Division, personal communication; A. Valliere, personal communication). Landings have since declined to a low of 1.7 million pounds, at a dockside value of $8.2 million. This represents a 59 percent decrease in landings since 1983, with only a 20 percent decline in value.

New York wholesale prices for fresh littlenecks—the highest-value size class of hard clam—have exhibited a general downward trend during the
1990s (Figure 4). Monthly average prices during the 1985 to 1993 period ranged from a high of 29 cents/clam in December of 1990 to a low of 14 cents/clam in November of 1992 (Urmie Barry, 1985-1993) (per-clam prices were calculated by dividing wholesale prices per bushel by a typical count of 480 littlenecks per bushel).

**U.S. Clam Aquaculture**

U.S. aquaculture of clams has seen a steady and large increase in the past decade. Production since 1983 has increased over 150 percent, with a 13 percent increase in 1992 alone (USDC, 1994b). Supply of farm-raised clams is expected to increase, particularly as some large-scale operations come on-line. In an article in *Seafood Leader* magazine (1993), Atlantic Little Neck Clam Farms of South Carolina indicated a production target of 100 million clams by the year 1995-1996, equal to about one-fifth of current U.S. production. While this production goal may be optimistic, it does underscore the potential of aquaculture to significantly increase supplies of clams in the United States.

Production of farm-raised hard clams in the Northeast was estimated to be about 216,000 bushels at a farm-gate value of $15.6 million (Bush and Anderson, 1993). Connecticut accounts for the bulk of production, with about 57 percent, followed by Massachusetts with 21 percent, New Jersey with 12 percent, and New York with 9 percent. Other states active in hard-shell clam aquaculture include Maine and Delaware. Much of the Connecticut production comes from natural sets of clams that inhabit oyster-bed leases. Hard clam aquaculturists surveyed for the *Northeast Aquaculture Situation and Outlook Report* (Bush and Anderson, 1993) received prices ranging from 14 cents to 25 cents in 1992.
Issues in Shellfish Marketing

Shellfish producers in the United States are faced with several challenging issues regarding the marketing of their products, particularly in the area of seafood quality and safety, consumer education, and product packaging. Increased consumer concern for seafood safety, fueled by an intense barrage of media reports assailing the safety of seafood—particularly bivalve mollusks—have had a negative impact on shellfish markets (Brooks, 1993). Studies indicating consumer preference for aquacultured products suggest that aquaculturists may have a marketing advantage over the wild-harvesters. Quality and safety assurance, consumer education, and innovative product packaging will be essential tools for shellfish producers to maintain a competitive edge in the domestic and global marketplace.

Seafood Safety and Consumer Perceptions

Shellfish, particularly filter-feeding mollusks such as clams, mussels, and oysters, have long been associated with the transmission of such health problems as paralytic shellfish poisoning caused by red tide, and hepatitis due to pollution of shellfish beds. In the last few years, there has been a succession of media reports that have questioned the safety of seafood, fueling public pressure for increased seafood inspection in the United States (see Brooks (1993) for a detailed discussion of consumer perceptions of seafood safety and the impact of media reports on the demand for shellfish). However, during the period 1978–1988, seafood—both shellfish and finfish—only accounted for approximately 3.6 percent of all reported cases of food-borne illness (Committee on the Evaluation of the Safety of Fishery Products, 1991).
Figure 4. Average monthly wholesale prices for fresh little necks in New York from 1985 to 1993.

Figure 5. U.S. aquaculture production of clams in landings and harvest value for the period 1983–1992.
mately 2.3 percent of food-borne illness cases were attributed to shellfish, while 1.2 percent were attributed to finfish. Beef, on the other hand, was responsible for 4 percent of the total number of food-borne illness in the period 1978–1988, followed by turkey with 3.7 percent, pork with 2.7 percent, and chicken with 2.6 percent. If one considers shellfish and finfish separately, the percentage of cases of food-borne illnesses attributed to shellfish and finfish is lower than any other animal meat category.

Despite the relatively low incidence of illness, consumers are nonetheless concerned about the safety of seafood, particularly that of shellfish. Studies by Brooks (1993) and Wessells et al. (1994) underscore the pervasiveness of these concerns among consumers in the Northeast. For example, in a shellfish consumption survey of 1,529 consumers in the Northeast, 52 percent said that they were very doubtful or somewhat doubtful that shellfish contained nothing harmful to one’s health (Wessells et al., 1994). Only 5 percent of the respondents were completely confident, and 44 percent were somewhat confident that shellfish contained nothing harmful to one’s health. When asked whether all shellfish currently in the marketplace were harvested from government-certified waters, about 35 percent did not know, 22 percent strongly disagreed, and 23 percent somewhat disagreed. Surprisingly, less than 10 percent of the respondents strongly or somewhat agreed that all shellfish in the marketplace were from government-certified waters.

In another survey of 400 consumers in the Northeast, Brooks (1993) asked consumers to rate their chances of getting ill from eating the following foods: cod, clams, bluefish, mussels, lobster, salmon, chicken, and beef. Consumers were asked to rate their chances on a scale of zero to 100, where zero indicated no chance at all and 100 was a certain chance. It is important to note that the relative perceived risk of eating mussels compared to other foods is the key issue here, rather than the absolute level of risk, since the zero-to-100 scale is not appropriate for eliciting realistic risk estimates.

Results from the risk rating are particularly revealing regarding consumer perceptions of risk from eating bivalve mollusks relative to the risk perceived from eating some other foods. Figure 6 illustrates the mean risk ratings of the total sample for all eight foods. Clams and mussels scored higher risk ratings than the other foods, with aver-
age risk ratings of 26.9 and 23.7, respectively. Furthermore, mussels and clams were rated as having a significantly greater health risk (at the 99 percent significance level, based on a two-tailed t-test) than all other seafood. Mussels and clams also scored a higher risk rating than chicken or beef, with finfish (cod, bluefish, and salmon) scoring the lowest perceived risk ratings.

The Brooks (1993) and Wessells et al. (1994) studies underscore the need to educate consumers about the safety of shellfish products and the associated inspection and water quality monitoring programs now in place. Consumers would also benefit from information on safe handling and preparation of shellfish products. Strict quality and safety standards must be maintained if the shellfish industry is to bolster consumer confidence in its products. The net result will be better-informed purchase decisions, as well as a likely increase in the demand for shellfish products.

**Consumer Preference for Wild Versus Aquacultured Shellfish**

Results from the Brooks (1993) and Wessells et al. (1994) surveys strongly suggest that consumers in the Northeast perceive aquacultured shellfish to be better or safer than wild-caught shellfish. When consumers were asked what they thought was a better mussel, one that was farm-raised or one that was wild, about 42 percent said that they thought farm-raised mussels would be better, while only 5.4 percent preferred wild, 2 percent were indifferent, and 50 percent said that they didn’t know (Brooks 1993). Many of the respondents preferring cultivated mussels claimed that cultivated mussels were grown under controlled conditions and in cleaner waters.

Similar results were obtained in the Wessells et al. (1994) survey, in which consumers were asked if farm-raised shellfish were safer than wild-harvested shellfish. Nearly 45 percent of the respondents strongly or somewhat agreed that farm-raised shellfish were safer than wild-harvested, 33 percent did not know, 15 percent were neutral, and less than 5 percent strongly or somewhat disagreed. Nearly 70 percent of the respondents strongly or somewhat agreed that water pollution was more likely to create a problem for wild shellfish than farm-raised shellfish.

Clearly, these results suggest that consumers perceive aquacultured products to be somehow better, safer, or more protected from pollution than wild-harvested product. To the extent that this is true, aquaculturists may be able to use these product attributes to their advantage in promoting cultivated shellfish. Conversely, these results indicate that consumers lack confidence in the safety of wild-harvested shellfish. Again, these results point to a need to educate the consumer about the safety and handling of bivalve shellfish.

**Packaging**

Hard-shell clams have long been marketed to the consumer without any packaging, brand naming, or information, except that which may be supplied by the retail clerk. In fact, most hard clams are moved through the wholesale market in a commodity-like fashion, in onion bags, often with labels that have nothing to do with the actual shellfish product. With aquaculture production increasing, and a clear need for consumer education about the safety of shellfish products, packaging and point-of-purchase materials will become a key avenue for distinguishing one's product and for educating consumers. Packaging can provide consumers with essential safety, handling, and preparation information, along with a brand name that can build repeat sales.

To the extent that consumers prefer aquacultured or wild-harvested clams, or clams from a particular geographical region, shellfish marketers can use packaging and point-of-purchase materials to convey these product attributes. Shellfish marketing clearly needs to move out of the bulk processing commodity approach, to a more consumer-oriented packaging and information approach.

**Conclusion**

While total U.S. clam production has increased dramatically since the 1950s, production of high-valued hard-shell and soft-shell clams has, more recently, decreased. Rhode Island hard clam producers have experienced a dramatic decline in hard clam production since the mid-1980s. In addition,
New York wholesale prices for fresh littlenecks have been on a downward trend. Consumer seafood safety concerns exacerbate this already-difficult situation.

Continued increases in aquaculture production will ease the shortages in wild production, while at the same time bringing new competition to producers of wild clam product. This is particularly significant, as recent research suggests that consumers in the Northeast perceive aquacultured clams to be better, safer, or more protected from pollution than wild-harvested product. All of the above factors indicate a very clear need for increased consumer education about the safety of clam products. Packaging and point-of-purchase materials can be very effective in educating consumers about the positive attributes of a product, while brand naming can build consumer loyalty and stimulate repeat purchases. The adoption of a more consumer-oriented approach to shellfish marketing, as opposed to the traditional one of commodity sales, will be essential for competing in the domestic and global marketplace of the 21st century.

References


Questions and Answers

Q: (Arthur Ganz, Rhode Island Department of Environmental Management, Division of Fish, Wildlife, and Estuarine Resources) Do you think that labels stating the exact location of harvest from Narragansett Bay would be useful? Could someone who works on the water know where each and every quahog in his catch came from?

A: (Priscilla Brooks) I don’t think that it is so much a particular area in the Bay, but if they are from Rhode Island, New York, Florida, and so forth.

Comment: (Ganz) But that level of identification is a requirement already.

A: (Brooks) It is required on the onion bag, not at the consumer level...fish markets or restaurants.

Comment: (Neal Perry, Rhode Island Shellfish Divers Association and Ocean State Aquaculture Association) For most aquacultured shellfish, you know exactly where they come from. Moonstone oysters, Cotuit oyster, Blue Points, and others are well labeled. It goes to good marketing.

Comment: (Gerald Carvalho, shellfisherman) Marketing is of prime importance. In this state, the quahog industry submitted a bill to the legislature to identify all shellfish, whether fresh or previously frozen, and its state and country of origin. The bill failed. During the debates, some of the representatives argued, “Who cares where it comes from?” Well, the consumer cares, and the people care. The strongest lobby against us was the supermarkets. They just did not want to reveal their sources.
A. (Brooks) The irony is that the supermarkets have the most to gain by having informed customers.

Comment. (Ed Agin, Rhode Island Shellfishermen's Association) The Narragansett Bay quahog is the best-tasting, and is renowned all over the world. When someone buys a Rhode Island quahog, they assume that it is from Narragansett Bay. All too often, this is just not so. If one goes into the back of many shellfish dealers, whatever clams are around—whether they are from Florida or wherever, are comingled with Rhode Island clams and shipped out. This is not right. This practice can severely hurt the reputation of our product.

A. (Brooks) Don't the tagging requirements take care of that?

Comment. (Agin) Only as far as the wholesalers, after that you don't know what you have.

Comment. (Kenneth Smith, Rhode Island Department of Health) That's a pretty strong statement you are making there.

Comment. (Agin) It's pretty strong because it's true.

Comment. (Smith) Can you prove that?

Comment. (Agin) Yes, I can.

Comment. (Smith) Let's talk afterwards.

Comment. (Agin) This has been a problem since there have been sales of Narragansett Bay quahogs. When we pointed this out to Kenneth Kovach of the Department of Health, his reply was that he knew, but there was nothing that could be done about it.

Comment. (Smith) That is a wrong statement.

Comment. (Agin) It's true.

Comment. (Smith) John Mullen and I are the Department of Health representatives here.

Comment. (Agin) You did not make the statement. Kenny Kovach did.

Comment. (Smith) There is a big difference between a Florida clam and a Rhode Island clam. There must be something very wrong if people can't see the difference.